wwPDB EM Validation Summary Report ⓘ

Nov 5, 2024 – 04:23 PM EST

PDB ID	:	8TO7
EMDB ID	:	EMD-41438
Title	:	Cryo-EM structure of HERH-b*01 Fab in complex with HIV-1 Env trimer BG505.DS SOSIP
Authors	:	Roark, R.S.; Hoyt, F.; Hansen, B.; Fischer, E.; Shapiro, L.S.; Kwong, P.D.
Deposited on	:	2023-08-03
Resolution	:	3.39 Å(reported)

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

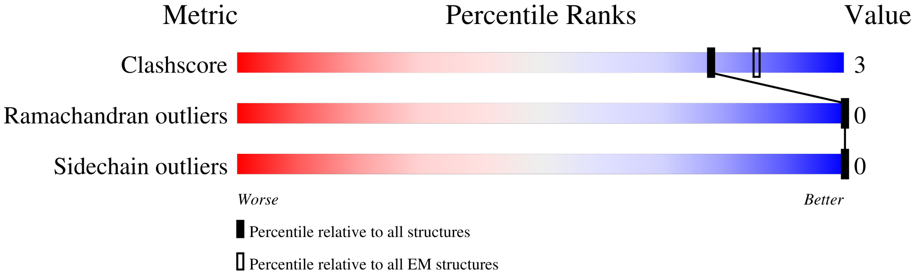
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance ⓘ

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

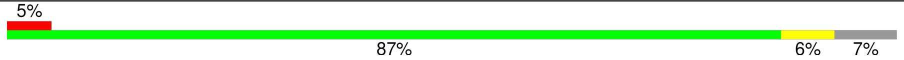
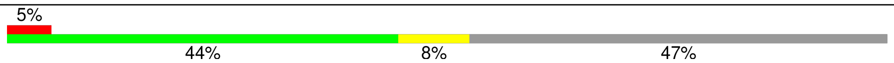
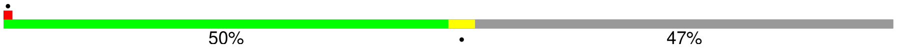
The reported resolution of this entry is 3.39 Å.

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.



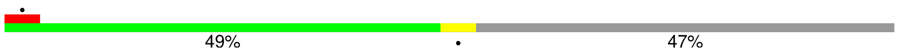
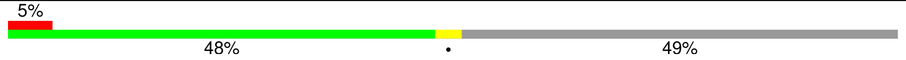
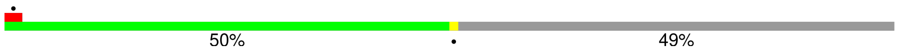
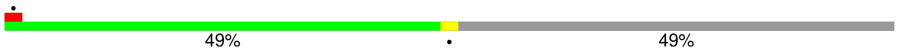
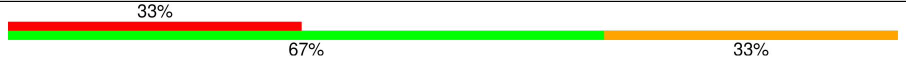
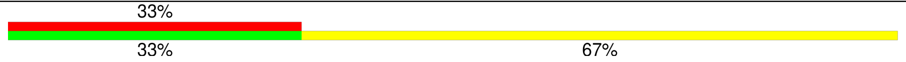
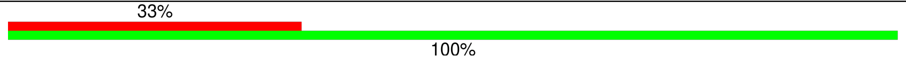
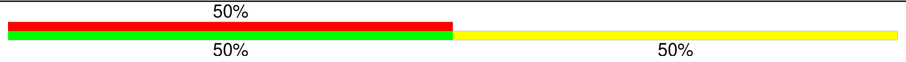
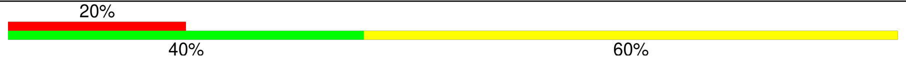
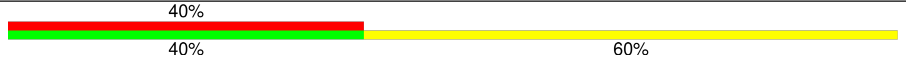
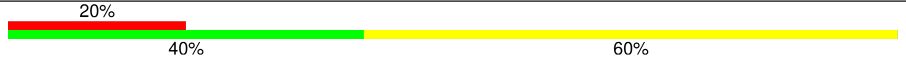
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	D	481	
1	E	481	
1	F	481	
2	A	153	
2	B	153	
2	C	153	
3	G	238	
3	H	238	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	I	238	
4	J	219	
4	K	219	
4	L	219	
5	M	3	
5	Q	3	
5	R	3	
5	V	3	
5	W	3	
5	a	3	
6	N	2	
6	O	2	
6	S	2	
6	T	2	
6	X	2	
6	Y	2	
7	P	5	
7	U	5	
7	Z	5	

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 20361 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 Surface protein gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	E	446	3509	2200	622	657	30	0	0
1	D	446	3509	2200	622	657	30	0	0
1	F	446	3509	2200	622	657	30	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	201	CYS	ILE	conflict	UNP Q2N0S5
E	332	ASN	THR	conflict	UNP Q2N0S5
E	433	CYS	ALA	conflict	UNP Q2N0S5
E	501	CYS	ALA	conflict	UNP Q2N0S5
E	509	ARG	GLU	conflict	UNP Q2N0S5
E	510	ARG	LYS	conflict	UNP Q2N0S5
E	512	ARG	-	expression tag	UNP Q2N0S5
E	513	ARG	-	expression tag	UNP Q2N0S5
D	201	CYS	ILE	conflict	UNP Q2N0S5
D	332	ASN	THR	conflict	UNP Q2N0S5
D	433	CYS	ALA	conflict	UNP Q2N0S5
D	501	CYS	ALA	conflict	UNP Q2N0S5
D	509	ARG	GLU	conflict	UNP Q2N0S5
D	510	ARG	LYS	conflict	UNP Q2N0S5
D	512	ARG	-	expression tag	UNP Q2N0S5
D	513	ARG	-	expression tag	UNP Q2N0S5
F	201	CYS	ILE	conflict	UNP Q2N0S5
F	332	ASN	THR	conflict	UNP Q2N0S5
F	433	CYS	ALA	conflict	UNP Q2N0S5
F	501	CYS	ALA	conflict	UNP Q2N0S5
F	509	ARG	GLU	conflict	UNP Q2N0S5
F	510	ARG	LYS	conflict	UNP Q2N0S5
F	512	ARG	-	expression tag	UNP Q2N0S5
F	513	ARG	-	expression tag	UNP Q2N0S5

- Molecule 2 is a protein called Transmembrane protein gp41.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	B	131	Total C N O S 1032 655 177 194 6	0	0
2	A	131	Total C N O S 1032 655 177 194 6	0	0
2	C	131	Total C N O S 1032 655 177 194 6	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	559	PRO	ILE	conflict	UNP Q2N0S5
B	605	CYS	THR	conflict	UNP Q2N0S5
A	559	PRO	ILE	conflict	UNP Q2N0S5
A	605	CYS	THR	conflict	UNP Q2N0S5
C	559	PRO	ILE	conflict	UNP Q2N0S5
C	605	CYS	THR	conflict	UNP Q2N0S5

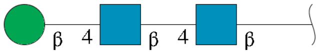
- Molecule 3 is a protein called HERH-b*01 heavy chain.

Mol	Chain	Residues	Atoms	AltConf	Trace
3	H	125	Total C N O S 974 618 161 193 2	0	0
3	G	125	Total C N O S 974 618 161 193 2	0	0
3	I	125	Total C N O S 974 618 161 193 2	0	0

- Molecule 4 is a protein called HERH-b*01 light chain.

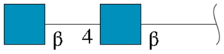
Mol	Chain	Residues	Atoms	AltConf	Trace
4	L	112	Total C N O S 867 543 156 166 2	0	0
4	J	112	Total C N O S 867 543 156 166 2	0	0
4	K	112	Total C N O S 867 543 156 166 2	0	0

- 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.



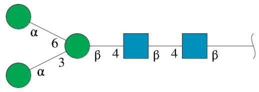
Mol	Chain	Residues	Atoms	AltConf	Trace
5	M	3	Total C N O 39 22 2 15	0	0
5	Q	3	Total C N O 39 22 2 15	0	0
5	R	3	Total C N O 39 22 2 15	0	0
5	V	3	Total C N O 39 22 2 15	0	0
5	W	3	Total C N O 39 22 2 15	0	0
5	a	3	Total C N O 39 22 2 15	0	0

- Molecule 6 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



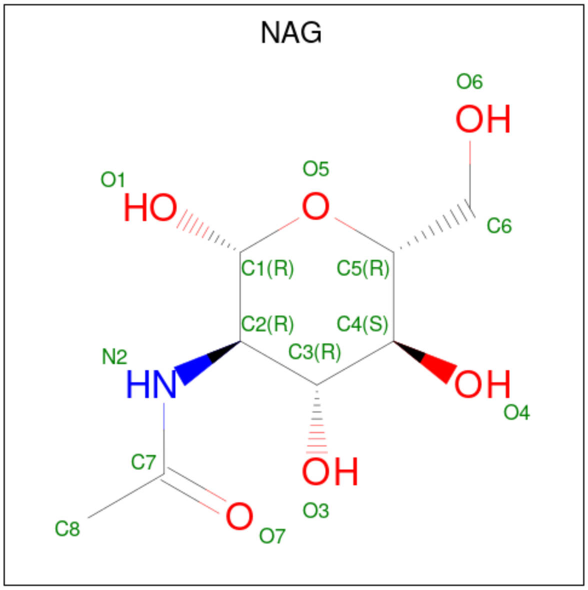
Mol	Chain	Residues	Atoms	AltConf	Trace
6	N	2	Total C N O 28 16 2 10	0	0
6	O	2	Total C N O 28 16 2 10	0	0
6	S	2	Total C N O 28 16 2 10	0	0
6	T	2	Total C N O 28 16 2 10	0	0
6	X	2	Total C N O 28 16 2 10	0	0
6	Y	2	Total C N O 28 16 2 10	0	0

- Molecule 7 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
7	P	5	Total C N O 61 34 2 25	0	0
7	U	5	Total C N O 61 34 2 25	0	0
7	Z	5	Total C N O 61 34 2 25	0	0

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

Continued on next page...

Continued from previous page...

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

Continued on next page...

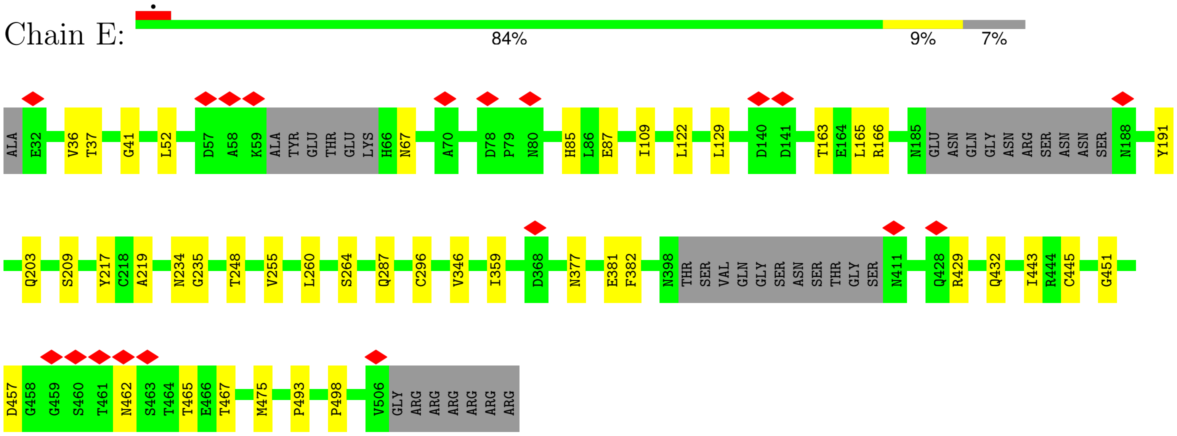
Continued from previous page...

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

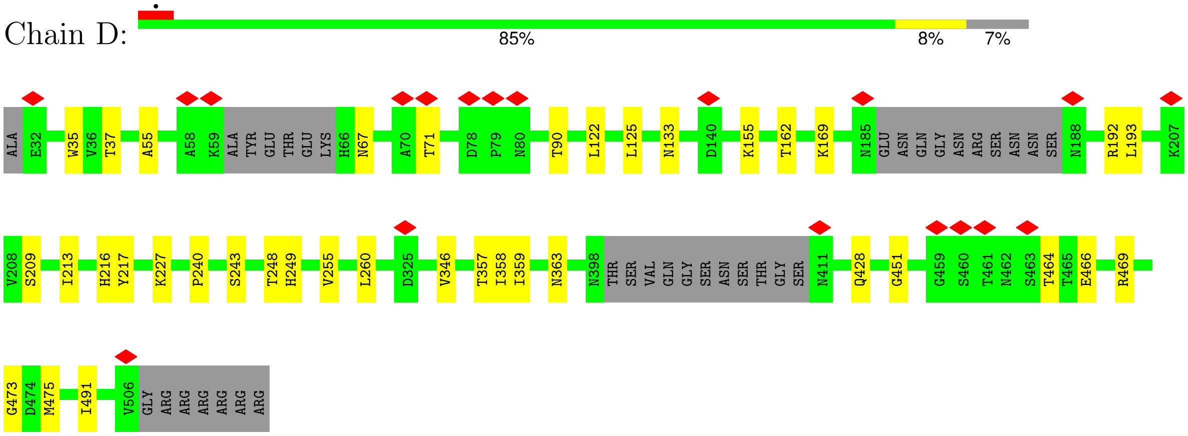
3 Residue-property plots ⓘ

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.

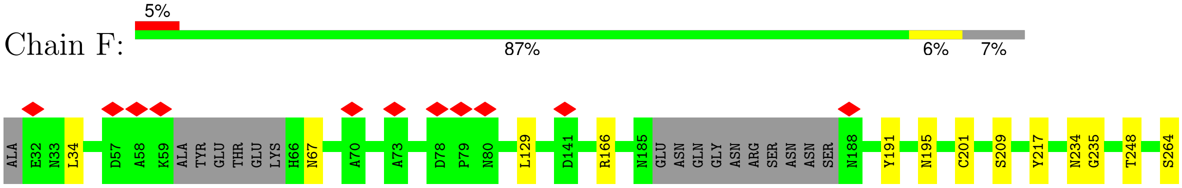
- Molecule 1: Surface protein gp120

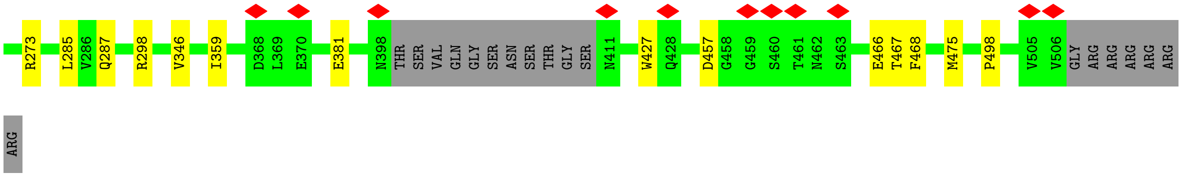


- Molecule 1: Surface protein gp120



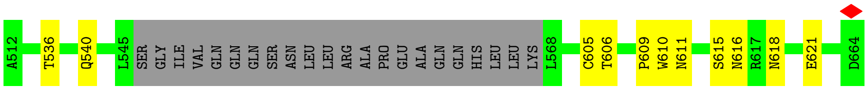
- Molecule 1: Surface protein gp120





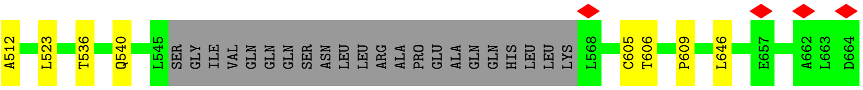
- Molecule 2: Transmembrane protein gp41

Chain B:



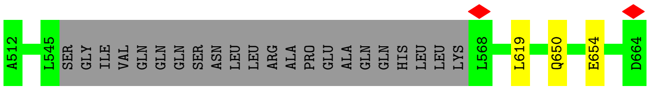
- Molecule 2: Transmembrane protein gp41

Chain A:



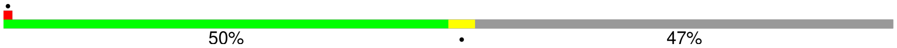
- Molecule 2: Transmembrane protein gp41

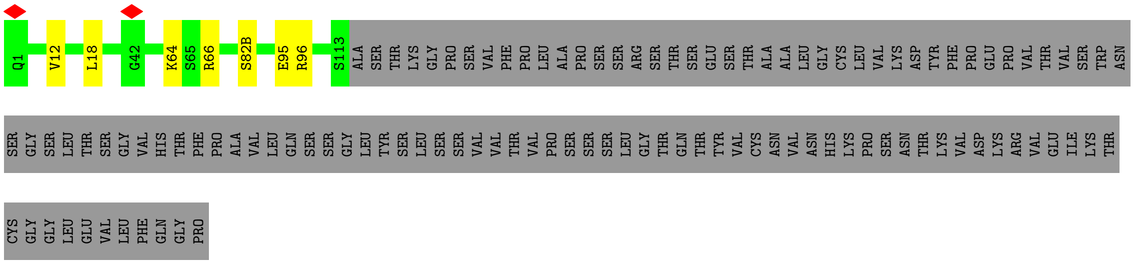
Chain C:



- Molecule 3: HERH-b*01 heavy chain

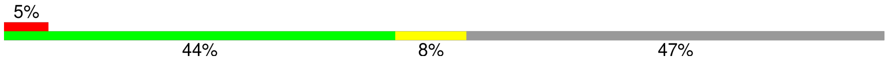
Chain H:

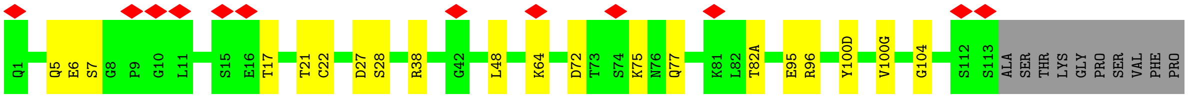


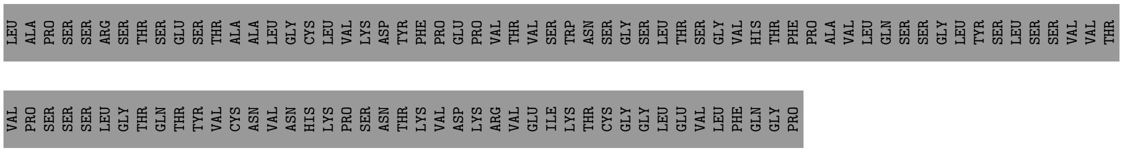


- Molecule 3: HERH-b*01 heavy chain

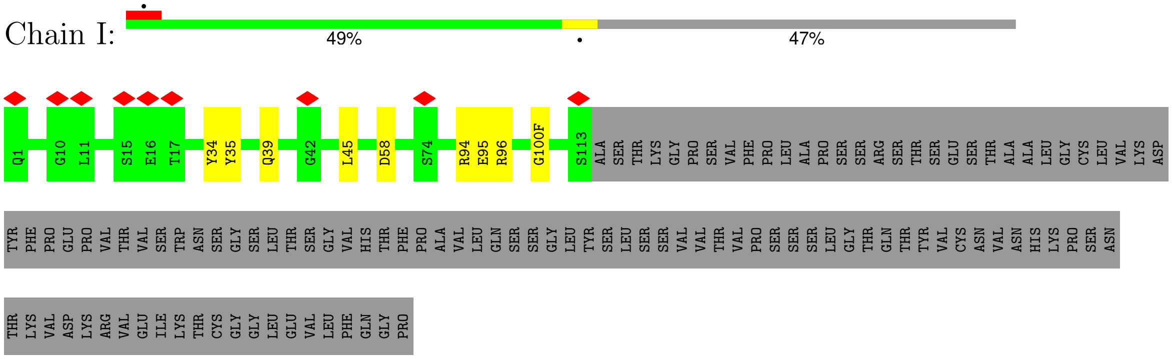
Chain G:



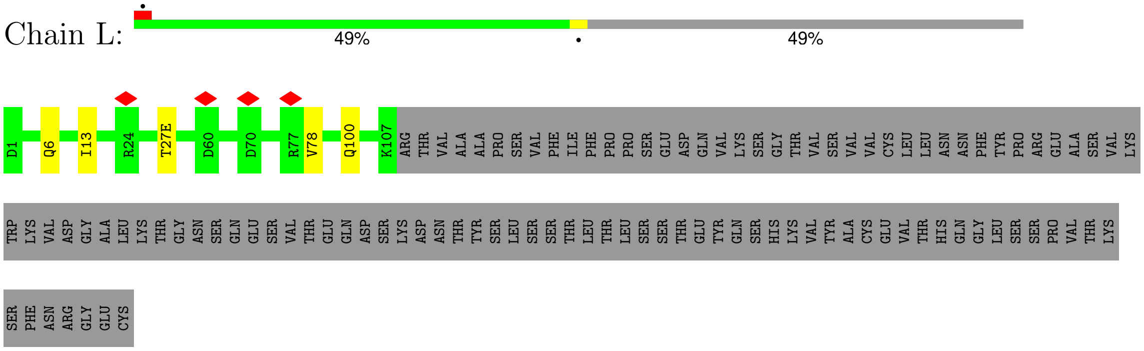




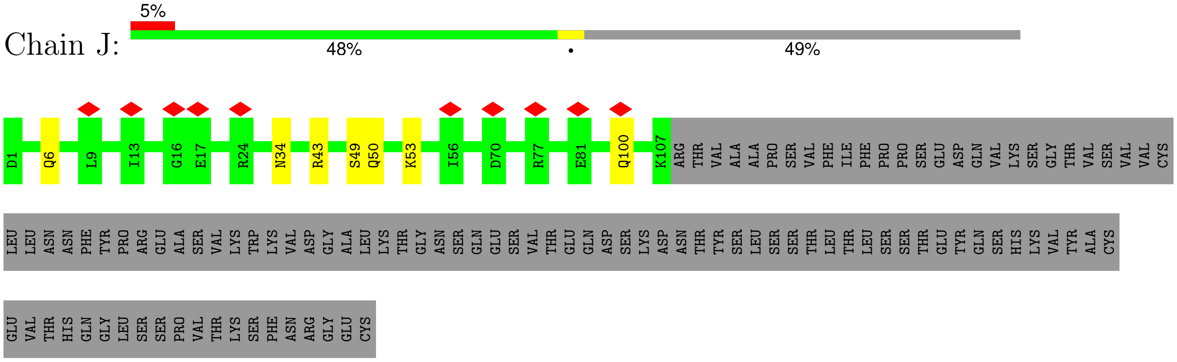
- Molecule 3: HERH-b*01 heavy chain



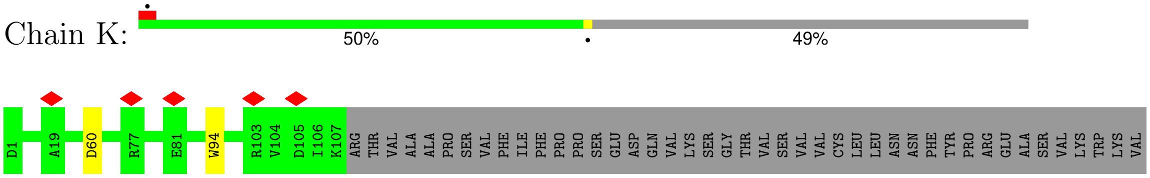
- Molecule 4: HERH-b*01 light chain

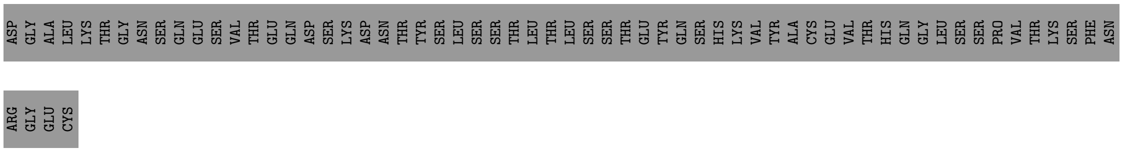


- Molecule 4: HERH-b*01 light chain



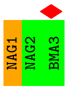
- Molecule 4: HERH-b*01 light chain





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

Chain M:

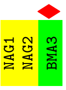


- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Q:

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

Chain R:

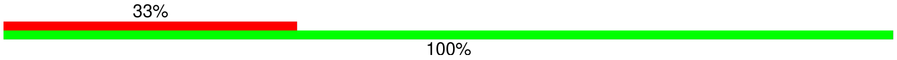


- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain V:

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

Chain W:



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

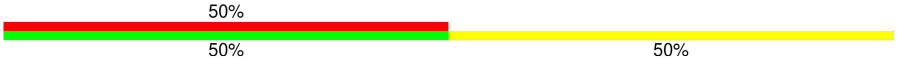
Chain a:

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

Chain N:

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

Chain O:



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

Chain S:

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

Chain T:

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

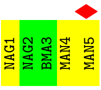
Chain X:

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

Chain Y:

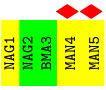
- Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:



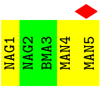
- Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain U:



- Molecule 7: 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 Z:



4 Experimental information

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	562633	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\AA^2)$	58	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.114	Depositor
Minimum map value	-0.045	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.027	Depositor
Map size (Å)	322.56, 322.56, 322.56	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.42, 0.42, 0.42	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, MAN, 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	D	0.31	0/3581	0.64	0/4861
1	E	0.31	0/3581	0.63	0/4861
1	F	0.30	0/3581	0.64	0/4861
2	A	0.31	0/1050	0.63	0/1425
2	B	0.35	0/1050	0.62	0/1425
2	C	0.32	0/1050	0.61	0/1425
3	G	0.34	0/998	0.70	0/1356
3	H	0.32	0/998	0.70	0/1356
3	I	0.33	0/998	0.71	0/1356
4	J	0.33	0/886	0.66	0/1201
4	K	0.27	0/886	0.67	0/1201
4	L	0.29	0/886	0.65	0/1201
All	All	0.31	0/19545	0.65	0/26529

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3509	0	3440	24	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	3509	0	3440	29	0
1	F	3509	0	3440	17	0
2	A	1032	0	1014	7	0
2	B	1032	0	1014	10	0
2	C	1032	0	1014	2	0
3	G	974	0	935	13	0
3	H	974	0	935	4	0
3	I	974	0	935	6	0
4	J	867	0	858	4	0
4	K	867	0	858	2	0
4	L	867	0	858	3	0
5	M	39	0	34	1	0
5	Q	39	0	34	0	0
5	R	39	0	34	0	0
5	V	39	0	34	0	0
5	W	39	0	34	0	0
5	a	39	0	34	0	0
6	N	28	0	25	0	0
6	O	28	0	25	0	0
6	S	28	0	25	0	0
6	T	28	0	25	0	0
6	X	28	0	25	0	0
6	Y	28	0	25	0	0
7	P	61	0	52	0	0
7	U	61	0	52	0	0
7	Z	61	0	52	0	0
8	A	28	0	26	0	0
8	B	28	0	26	2	0
8	C	28	0	26	0	0
8	D	182	0	169	0	0
8	E	182	0	169	0	0
8	F	182	0	169	0	0
All	All	20361	0	19836	108	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 3.

The worst 5 of 108 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)
2:B:615:SER:O	2:B:616:ASN:CG	2.13	0.87

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:615:SER:O	2:B:616:ASN:OD1	1.99	0.80
1:E:296:CYS:HB2	1:E:445:CYS:HB3	1.71	0.72
1:F:359:ILE:HG22	1:F:466:GLU:HB3	1.73	0.70
1:F:195:ASN:ND2	1:F:201:CYS:SG	2.66	0.68

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	D	438/481 (91%)	418 (95%)	20 (5%)	0	100	100
1	E	438/481 (91%)	418 (95%)	20 (5%)	0	100	100
1	F	438/481 (91%)	419 (96%)	19 (4%)	0	100	100
2	A	127/153 (83%)	122 (96%)	5 (4%)	0	100	100
2	B	127/153 (83%)	119 (94%)	8 (6%)	0	100	100
2	C	127/153 (83%)	122 (96%)	5 (4%)	0	100	100
3	G	123/238 (52%)	117 (95%)	6 (5%)	0	100	100
3	H	123/238 (52%)	116 (94%)	7 (6%)	0	100	100
3	I	123/238 (52%)	120 (98%)	3 (2%)	0	100	100
4	J	110/219 (50%)	99 (90%)	11 (10%)	0	100	100
4	K	110/219 (50%)	108 (98%)	2 (2%)	0	100	100
4	L	110/219 (50%)	103 (94%)	7 (6%)	0	100	100
All	All	2394/3273 (73%)	2281 (95%)	113 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	D	400/429 (93%)	400 (100%)	0	100	100
1	E	400/429 (93%)	400 (100%)	0	100	100
1	F	400/429 (93%)	400 (100%)	0	100	100
2	A	110/129 (85%)	110 (100%)	0	100	100
2	B	110/129 (85%)	110 (100%)	0	100	100
2	C	110/129 (85%)	110 (100%)	0	100	100
3	G	107/206 (52%)	107 (100%)	0	100	100
3	H	107/206 (52%)	107 (100%)	0	100	100
3	I	107/206 (52%)	107 (100%)	0	100	100
4	J	96/193 (50%)	96 (100%)	0	100	100
4	K	96/193 (50%)	96 (100%)	0	100	100
4	L	96/193 (50%)	96 (100%)	0	100	100
All	All	2139/2871 (74%)	2139 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	462	ASN
4	L	100	GLN
4	J	34	ASN
2	C	607	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

45 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	NAG	M	1	5,1	14,14,15	0.25	0	17,19,21	0.70	1 (5%)
5	NAG	M	2	5	14,14,15	0.59	0	17,19,21	0.52	0
5	BMA	M	3	5	11,11,12	0.68	0	15,15,17	0.77	0
6	NAG	N	1	1,6	14,14,15	0.38	0	17,19,21	0.51	0
6	NAG	N	2	6	14,14,15	0.47	0	17,19,21	1.00	1 (5%)
6	NAG	O	1	1,6	14,14,15	0.41	0	17,19,21	1.02	1 (5%)
6	NAG	O	2	6	14,14,15	0.38	0	17,19,21	0.50	0
7	NAG	P	1	1,7	14,14,15	0.43	0	17,19,21	1.07	2 (11%)
7	NAG	P	2	7	14,14,15	0.40	0	17,19,21	0.56	0
7	BMA	P	3	7	11,11,12	0.70	0	15,15,17	0.72	0
7	MAN	P	4	7	11,11,12	0.76	0	15,15,17	0.88	1 (6%)
7	MAN	P	5	7	11,11,12	0.81	0	15,15,17	0.86	1 (6%)
5	NAG	Q	1	5,2	14,14,15	0.24	0	17,19,21	0.40	0
5	NAG	Q	2	5	14,14,15	0.34	0	17,19,21	1.01	1 (5%)
5	BMA	Q	3	5	11,11,12	0.84	1 (9%)	15,15,17	0.82	1 (6%)
5	NAG	R	1	5,1	14,14,15	0.28	0	17,19,21	0.67	1 (5%)
5	NAG	R	2	5	14,14,15	0.50	0	17,19,21	1.14	1 (5%)
5	BMA	R	3	5	11,11,12	0.70	0	15,15,17	0.72	0
6	NAG	S	1	1,6	14,14,15	0.24	0	17,19,21	0.46	0
6	NAG	S	2	6	14,14,15	0.39	0	17,19,21	0.95	1 (5%)
6	NAG	T	1	1,6	14,14,15	0.32	0	17,19,21	0.96	1 (5%)
6	NAG	T	2	6	14,14,15	0.32	0	17,19,21	0.46	0
7	NAG	U	1	1,7	14,14,15	0.39	0	17,19,21	0.99	1 (5%)
7	NAG	U	2	7	14,14,15	0.19	0	17,19,21	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
7	BMA	U	3	7	11,11,12	0.65	0	15,15,17	0.79	0
7	MAN	U	4	7	11,11,12	0.74	0	15,15,17	1.04	2 (13%)
7	MAN	U	5	7	11,11,12	0.75	0	15,15,17	0.96	2 (13%)
5	NAG	V	1	5,2	14,14,15	0.22	0	17,19,21	0.42	0
5	NAG	V	2	5	14,14,15	0.31	0	17,19,21	1.00	1 (5%)
5	BMA	V	3	5	11,11,12	0.70	0	15,15,17	0.83	1 (6%)
5	NAG	W	1	5,1	14,14,15	0.32	0	17,19,21	0.57	0
5	NAG	W	2	5	14,14,15	0.43	0	17,19,21	0.47	0
5	BMA	W	3	5	11,11,12	0.67	0	15,15,17	0.73	0
6	NAG	X	1	1,6	14,14,15	0.25	0	17,19,21	0.45	0
6	NAG	X	2	6	14,14,15	0.39	0	17,19,21	0.95	1 (5%)
6	NAG	Y	1	1,6	14,14,15	0.29	0	17,19,21	0.97	1 (5%)
6	NAG	Y	2	6	14,14,15	0.31	0	17,19,21	0.45	0
7	NAG	Z	1	1,7	14,14,15	0.39	0	17,19,21	1.02	1 (5%)
7	NAG	Z	2	7	14,14,15	0.24	0	17,19,21	0.53	0
7	BMA	Z	3	7	11,11,12	0.70	0	15,15,17	0.75	0
7	MAN	Z	4	7	11,11,12	0.79	0	15,15,17	1.00	2 (13%)
7	MAN	Z	5	7	11,11,12	0.74	0	15,15,17	0.99	2 (13%)
5	NAG	a	1	5,2	14,14,15	0.24	0	17,19,21	0.42	0
5	NAG	a	2	5	14,14,15	0.35	0	17,19,21	1.00	1 (5%)
5	BMA	a	3	5	11,11,12	0.94	1 (9%)	15,15,17	0.84	1 (6%)

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
5	NAG	M	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	M	2	5	-	4/6/23/26	0/1/1/1
5	BMA	M	3	5	-	1/2/19/22	0/1/1/1
6	NAG	N	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	N	2	6	-	2/6/23/26	0/1/1/1
6	NAG	O	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	O	2	6	-	0/6/23/26	0/1/1/1
7	NAG	P	1	1,7	-	4/6/23/26	0/1/1/1
7	NAG	P	2	7	-	0/6/23/26	0/1/1/1
7	BMA	P	3	7	-	2/2/19/22	0/1/1/1
7	MAN	P	4	7	-	0/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MAN	P	5	7	-	1/2/19/22	0/1/1/1
5	NAG	Q	1	5,2	-	0/6/23/26	0/1/1/1
5	NAG	Q	2	5	-	2/6/23/26	0/1/1/1
5	BMA	Q	3	5	-	0/2/19/22	0/1/1/1
5	NAG	R	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	R	2	5	-	2/6/23/26	0/1/1/1
5	BMA	R	3	5	-	0/2/19/22	0/1/1/1
6	NAG	S	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	S	2	6	-	2/6/23/26	0/1/1/1
6	NAG	T	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	T	2	6	-	2/6/23/26	0/1/1/1
7	NAG	U	1	1,7	-	4/6/23/26	0/1/1/1
7	NAG	U	2	7	-	0/6/23/26	0/1/1/1
7	BMA	U	3	7	-	0/2/19/22	0/1/1/1
7	MAN	U	4	7	-	0/2/19/22	0/1/1/1
7	MAN	U	5	7	-	1/2/19/22	0/1/1/1
5	NAG	V	1	5,2	-	2/6/23/26	0/1/1/1
5	NAG	V	2	5	-	2/6/23/26	0/1/1/1
5	BMA	V	3	5	-	0/2/19/22	0/1/1/1
5	NAG	W	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	W	2	5	-	1/6/23/26	0/1/1/1
5	BMA	W	3	5	-	0/2/19/22	0/1/1/1
6	NAG	X	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	X	2	6	-	2/6/23/26	0/1/1/1
6	NAG	Y	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	Y	2	6	-	2/6/23/26	0/1/1/1
7	NAG	Z	1	1,7	-	4/6/23/26	0/1/1/1
7	NAG	Z	2	7	-	1/6/23/26	0/1/1/1
7	BMA	Z	3	7	-	2/2/19/22	0/1/1/1
7	MAN	Z	4	7	-	0/2/19/22	0/1/1/1
7	MAN	Z	5	7	-	1/2/19/22	0/1/1/1
5	NAG	a	1	5,2	-	2/6/23/26	0/1/1/1
5	NAG	a	2	5	-	2/6/23/26	0/1/1/1
5	BMA	a	3	5	-	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	a	3	BMA	C1-C2	2.34	1.57	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	Q	3	BMA	C1-C2	2.03	1.57	1.52

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	R	2	NAG	C2-N2-C7	3.25	127.26	122.90
6	Y	1	NAG	C2-N2-C7	3.08	127.02	122.90
7	P	1	NAG	C2-N2-C7	3.07	127.01	122.90
5	Q	2	NAG	C2-N2-C7	3.07	127.01	122.90
5	V	2	NAG	C2-N2-C7	3.06	127.00	122.90

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	P	1	NAG	C4-C5-C6-O6
7	Z	1	NAG	C4-C5-C6-O6
7	U	1	NAG	C4-C5-C6-O6
5	a	1	NAG	O5-C5-C6-O6
5	a	1	NAG	C4-C5-C6-O6

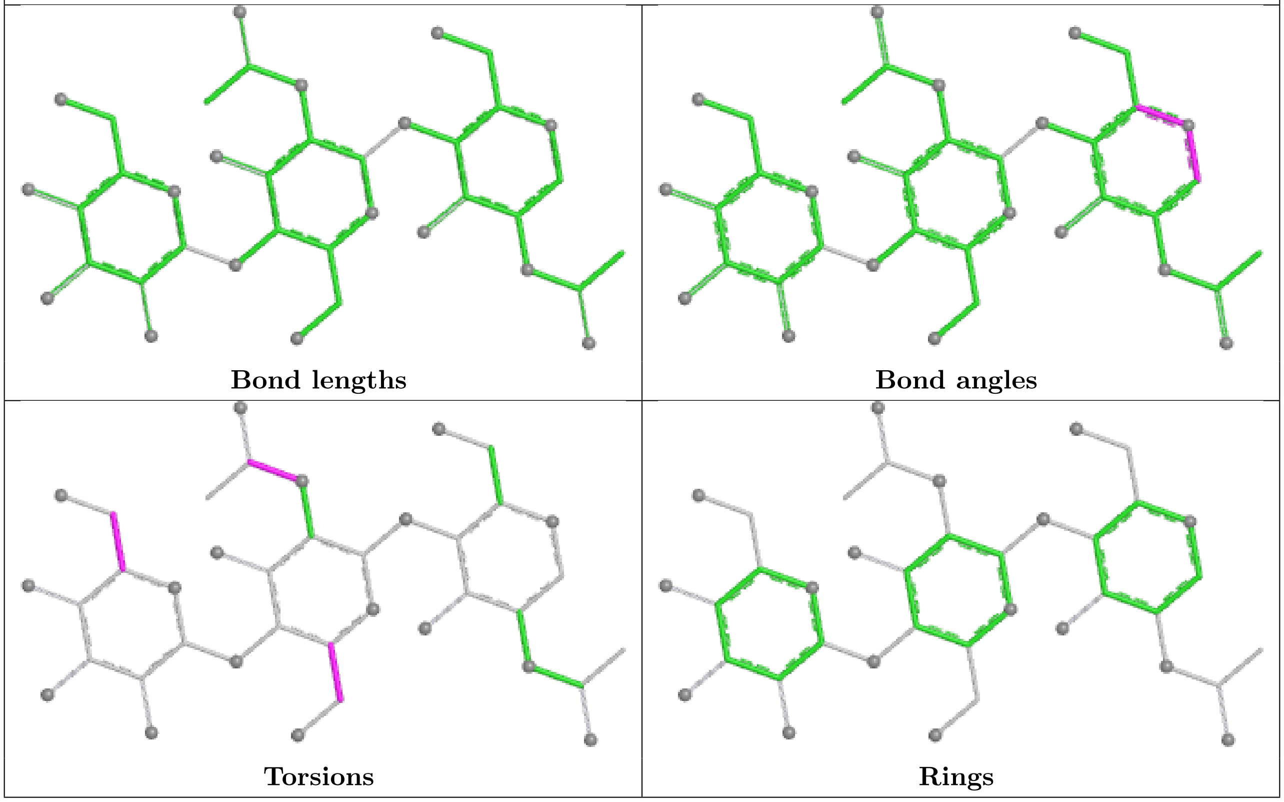
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	M	1	NAG	1	0

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

Oligosaccharide Chain M



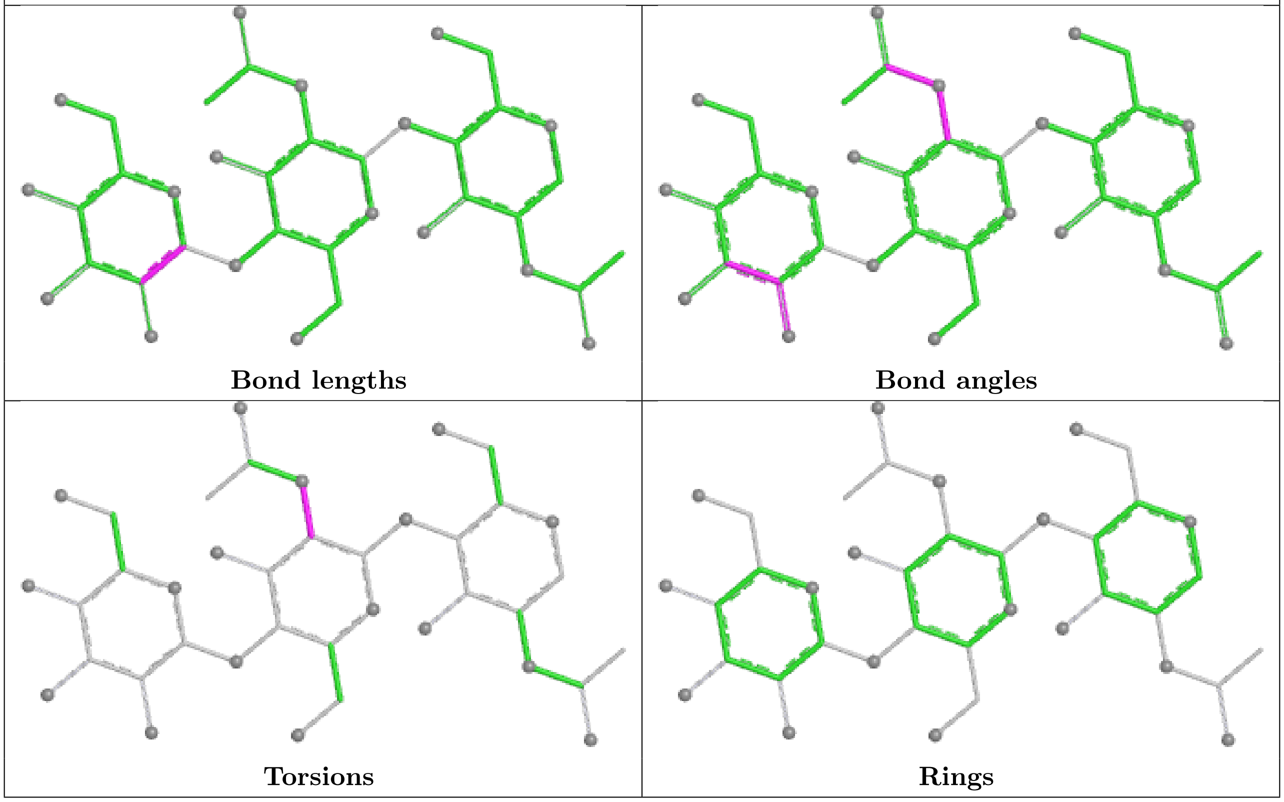
Bond lengths

Bond angles

Torsions

Rings

Oligosaccharide Chain Q



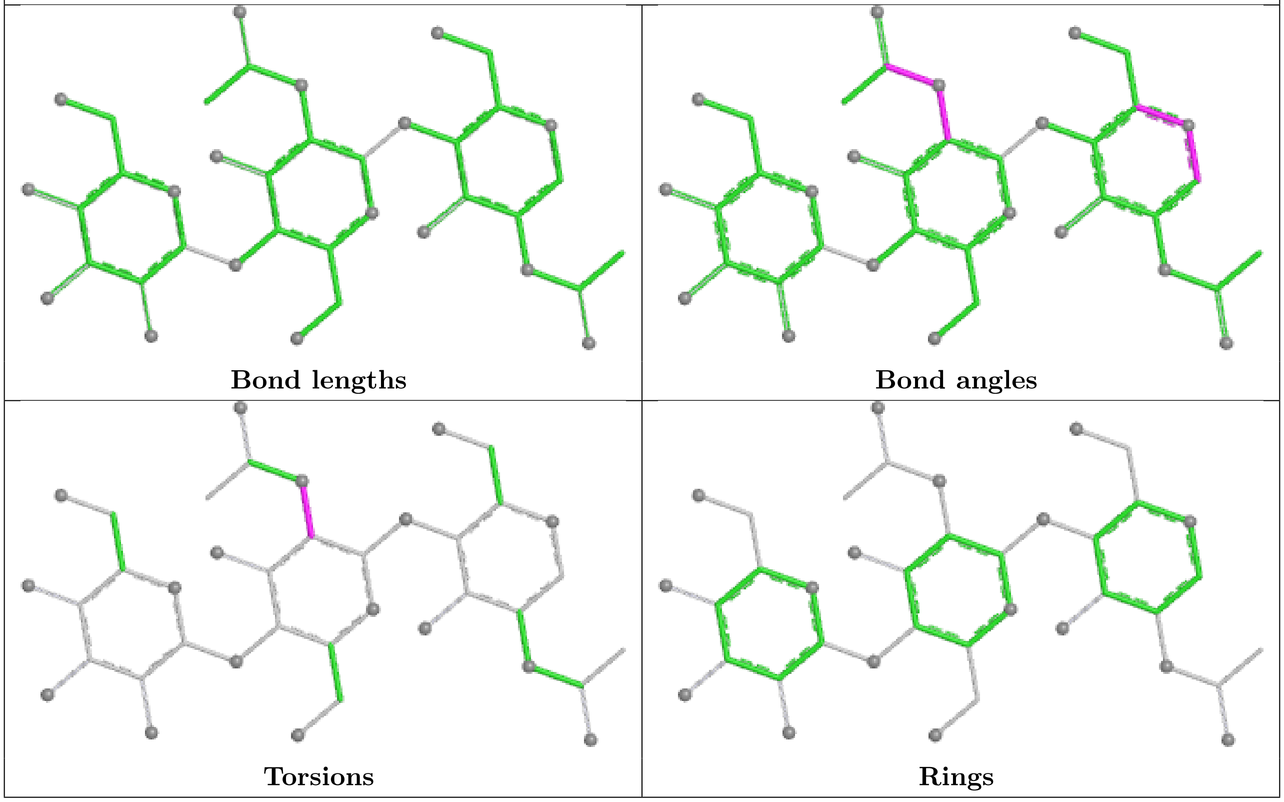
Bond lengths

Bond angles

Torsions

Rings

Oligosaccharide Chain R



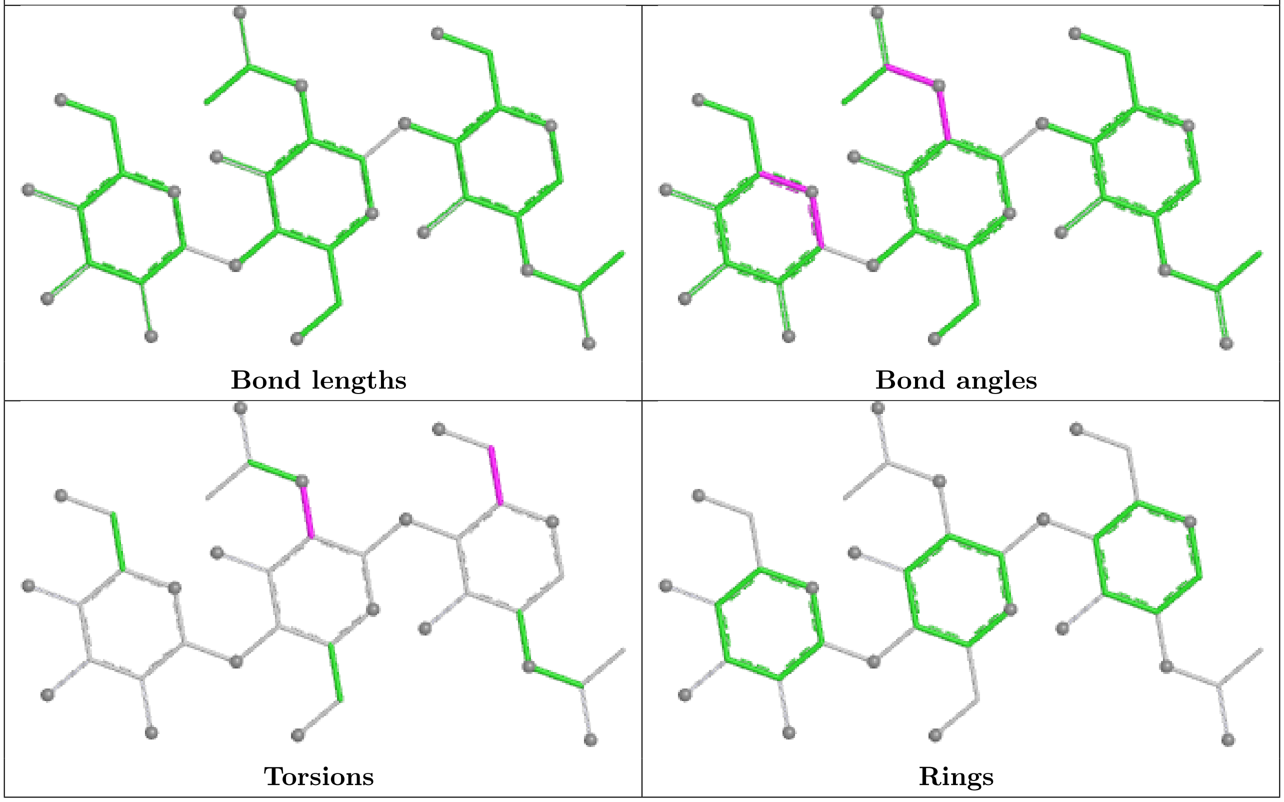
Bond lengths

Bond angles

Torsions

Rings

Oligosaccharide Chain V



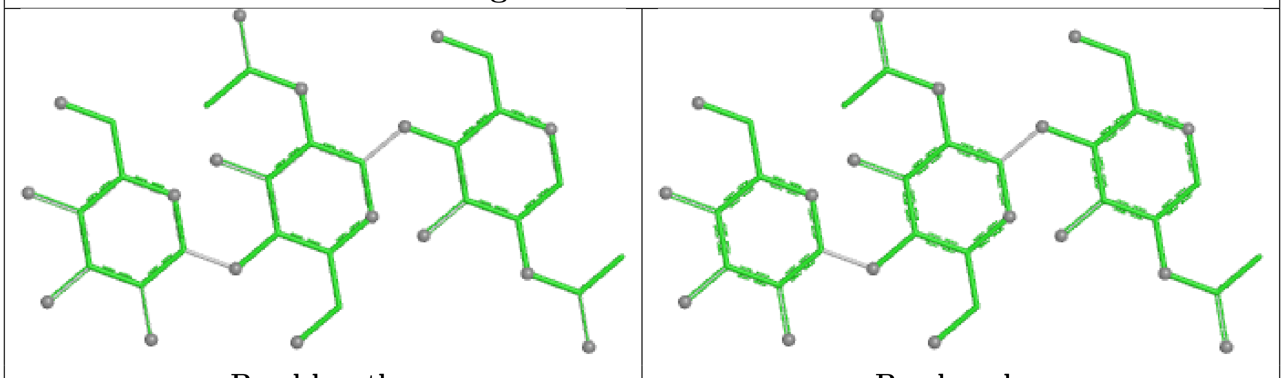
Bond lengths

Bond angles

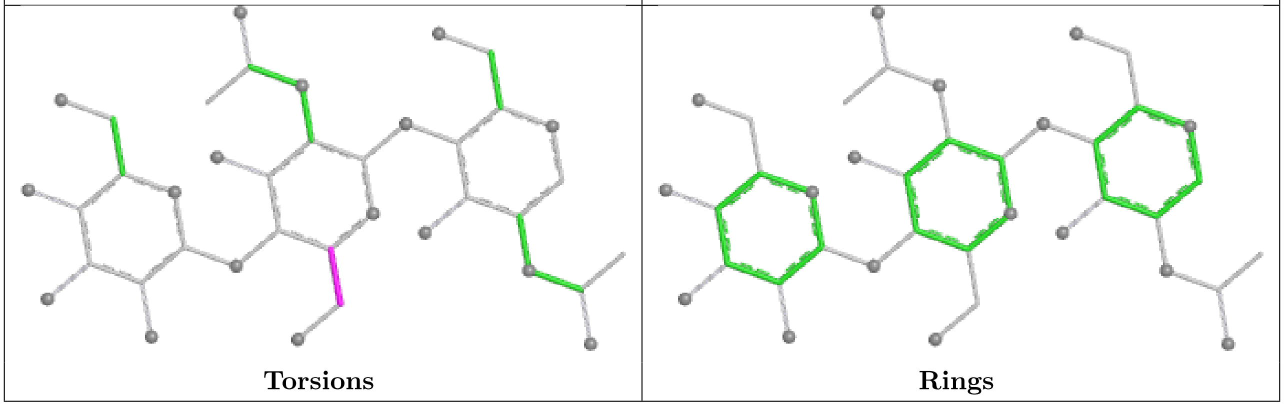
Torsions

Rings

Oligosaccharide Chain W

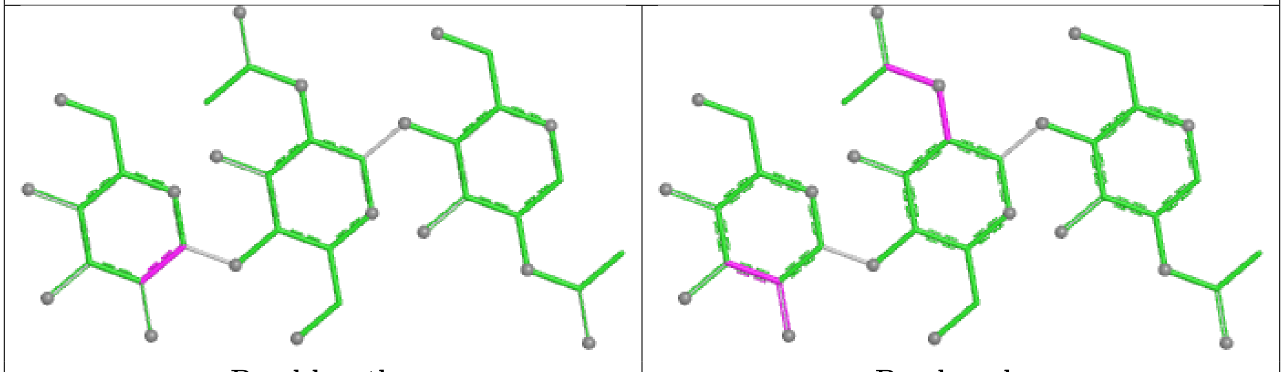


Bond lengths Bond angles

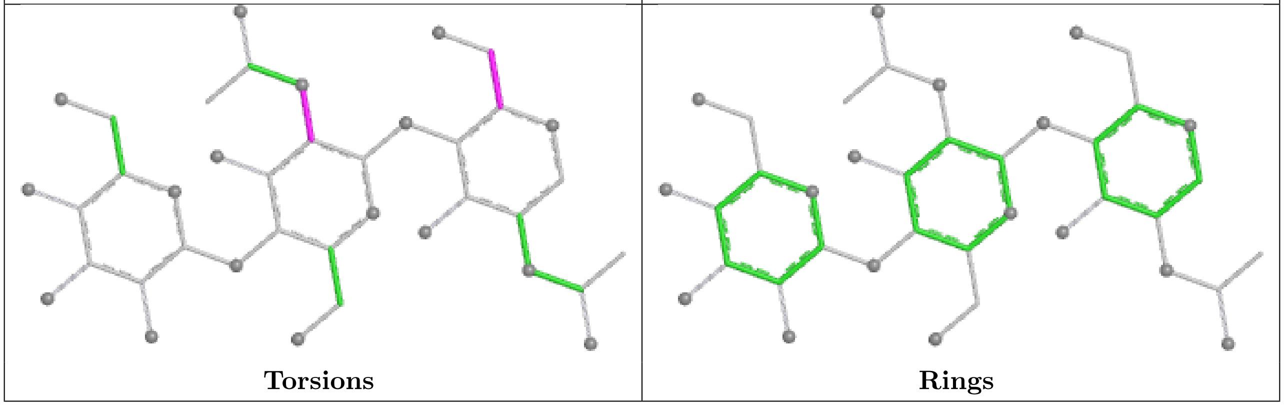


Torsions Rings

Oligosaccharide Chain a

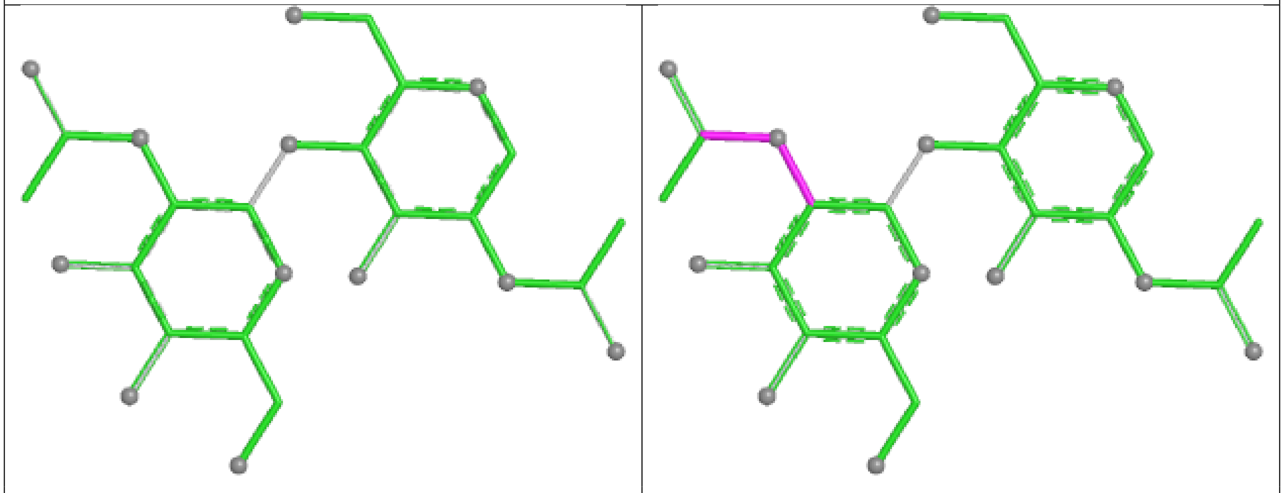


Bond lengths Bond angles



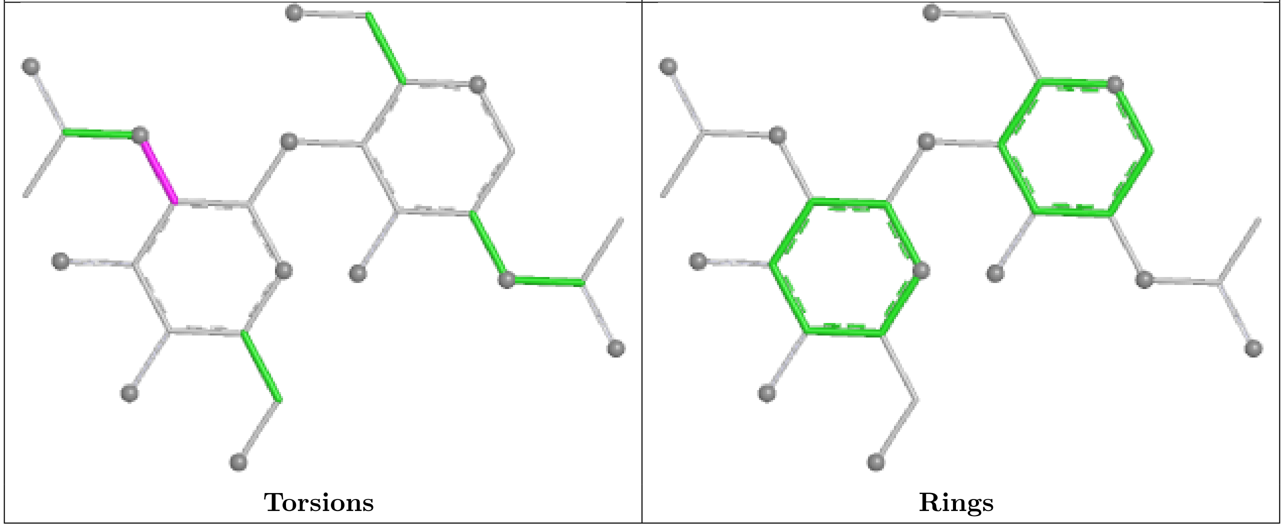
Torsions Rings

Oligosaccharide Chain N



Bond lengths

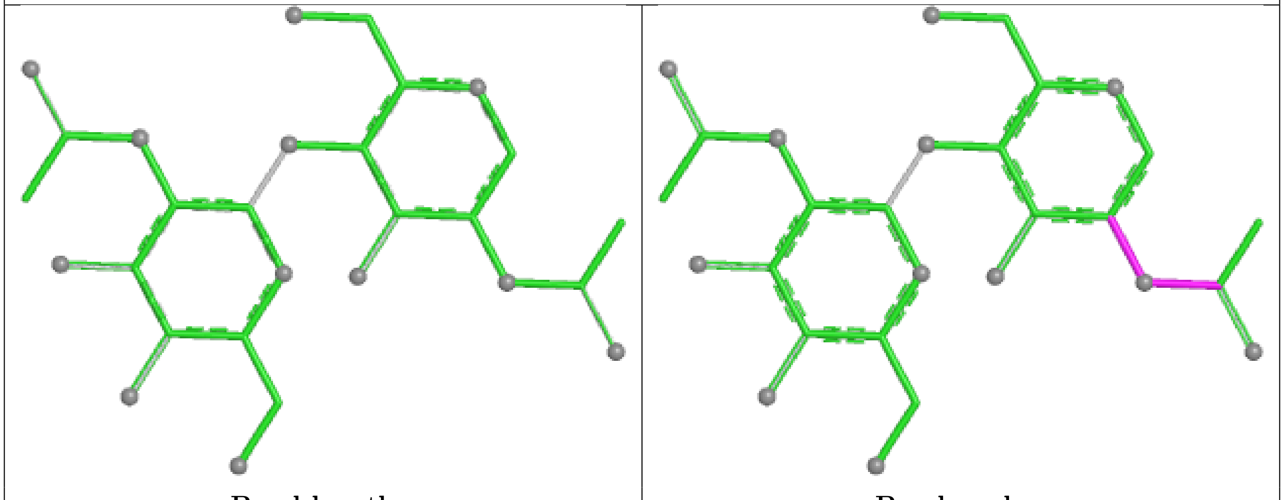
Bond angles



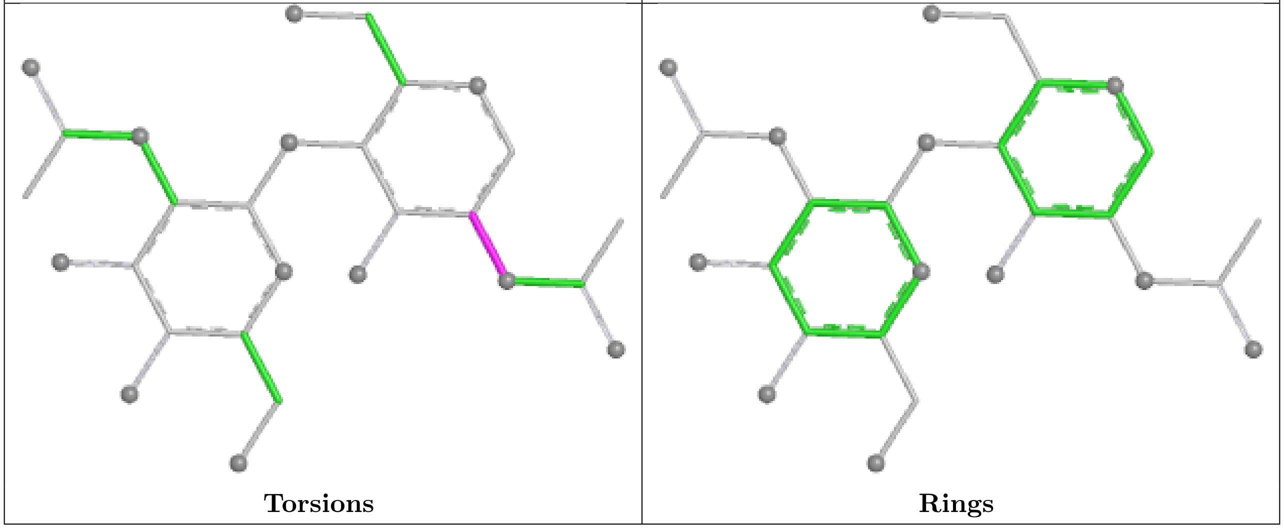
Torsions

Rings

Oligosaccharide Chain O

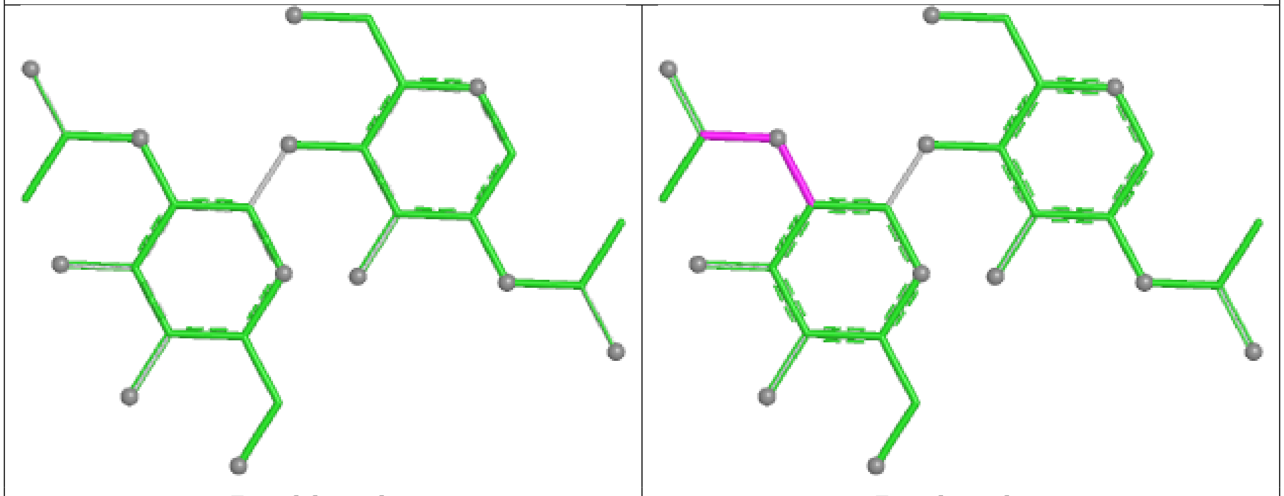


Bond lengths **Bond angles**



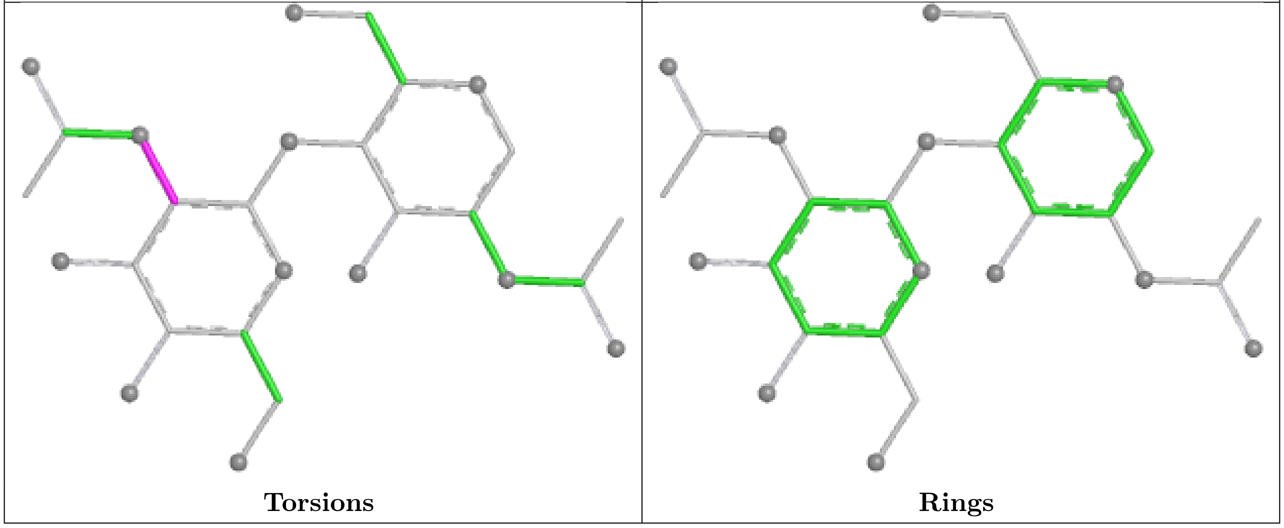
Torsions **Rings**

Oligosaccharide Chain S



Bond lengths

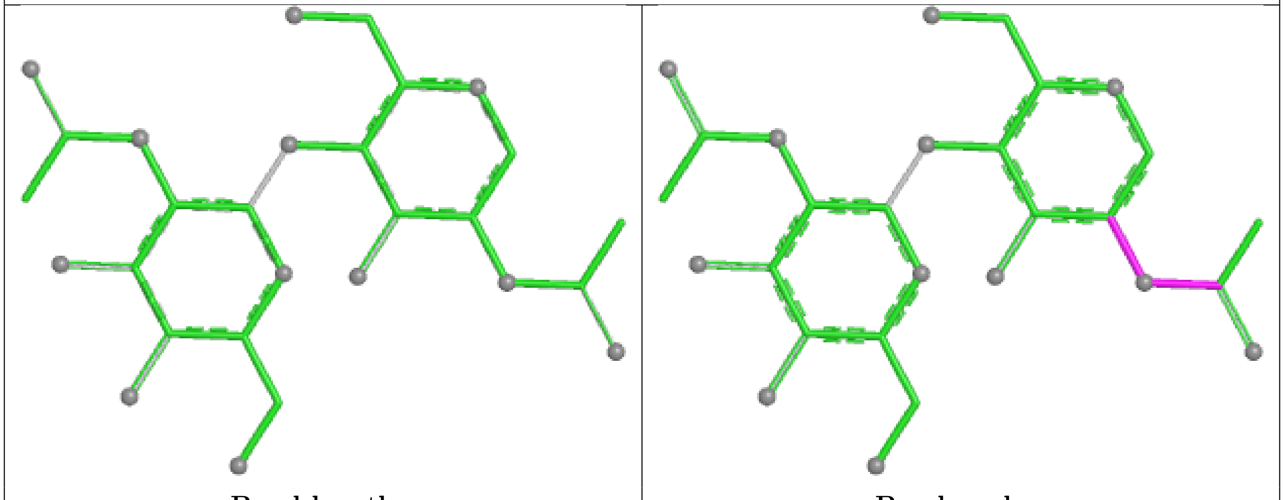
Bond angles



Torsions

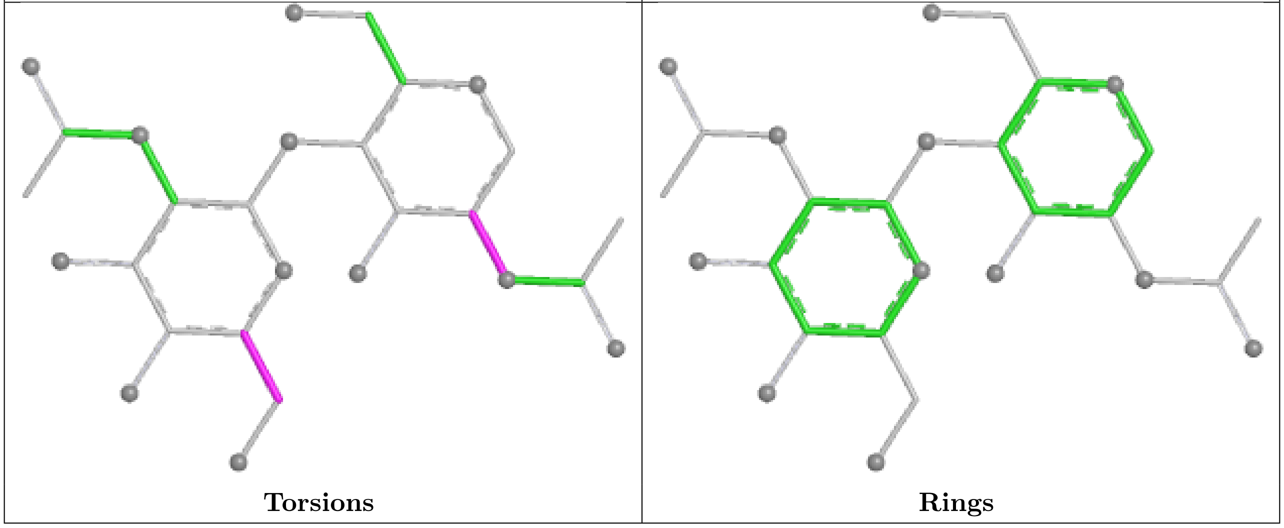
Rings

Oligosaccharide Chain T



Bond lengths

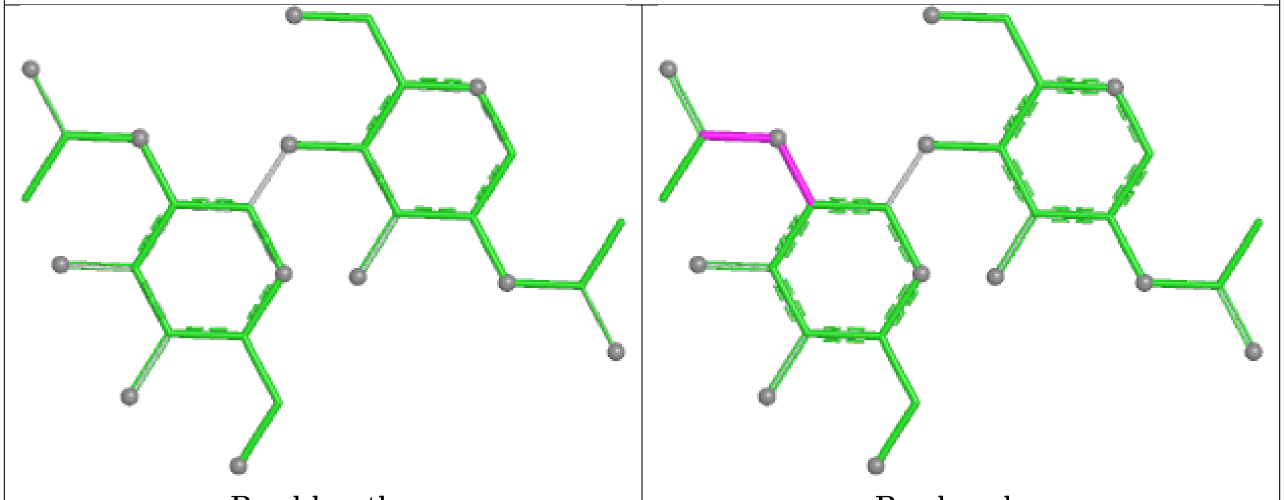
Bond angles



Torsions

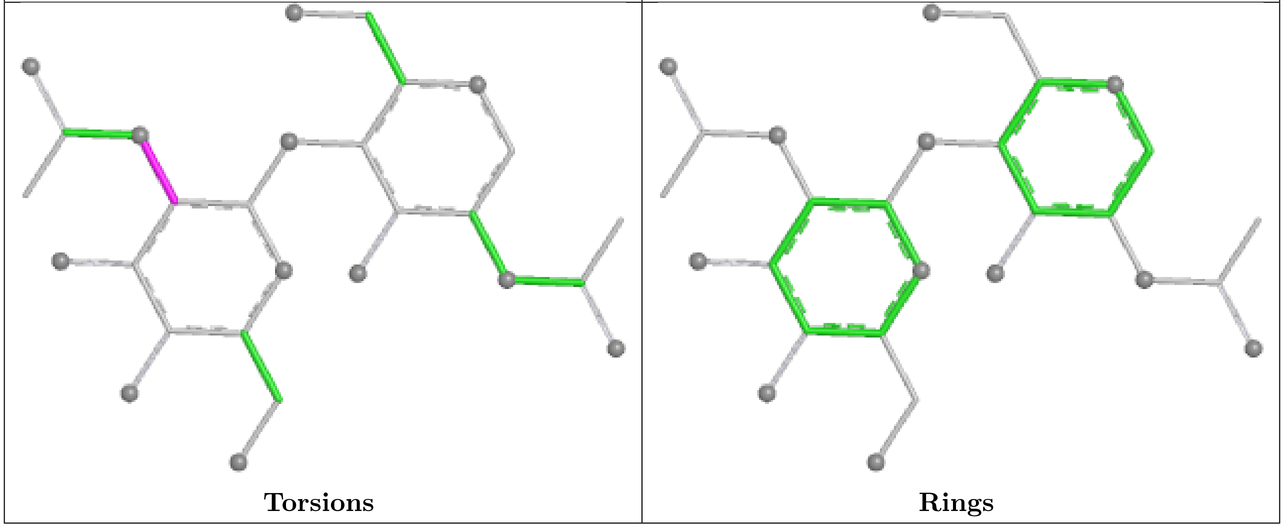
Rings

Oligosaccharide Chain X



Bond lengths

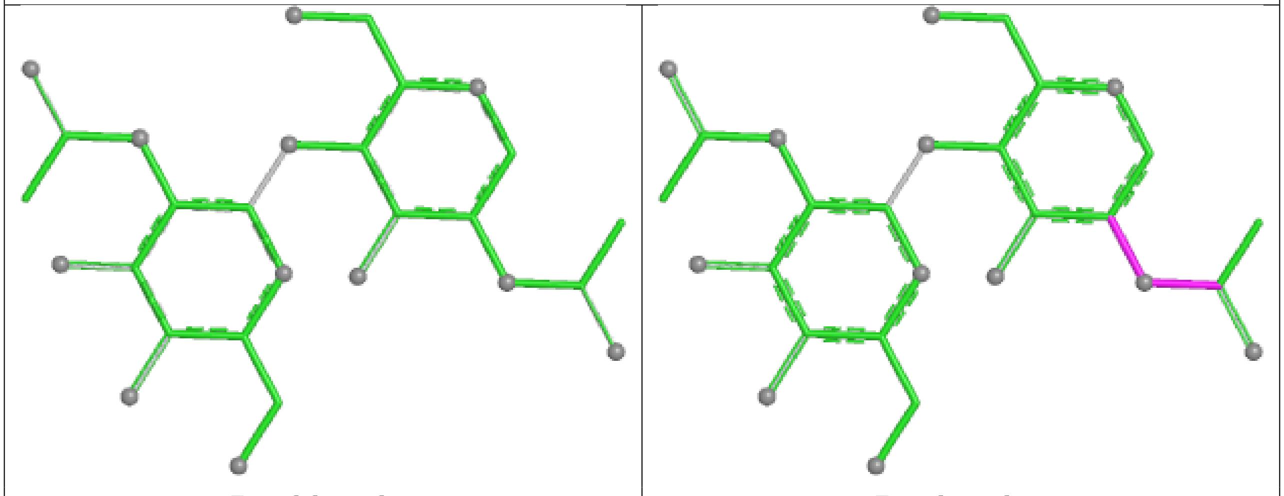
Bond angles



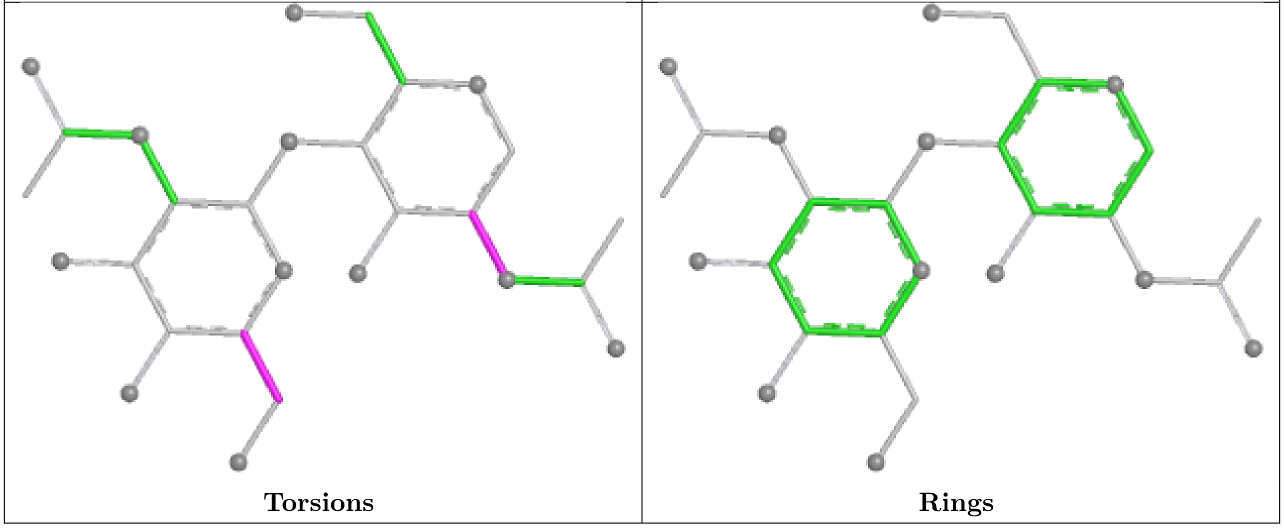
Torsions

Rings

Oligosaccharide Chain Y

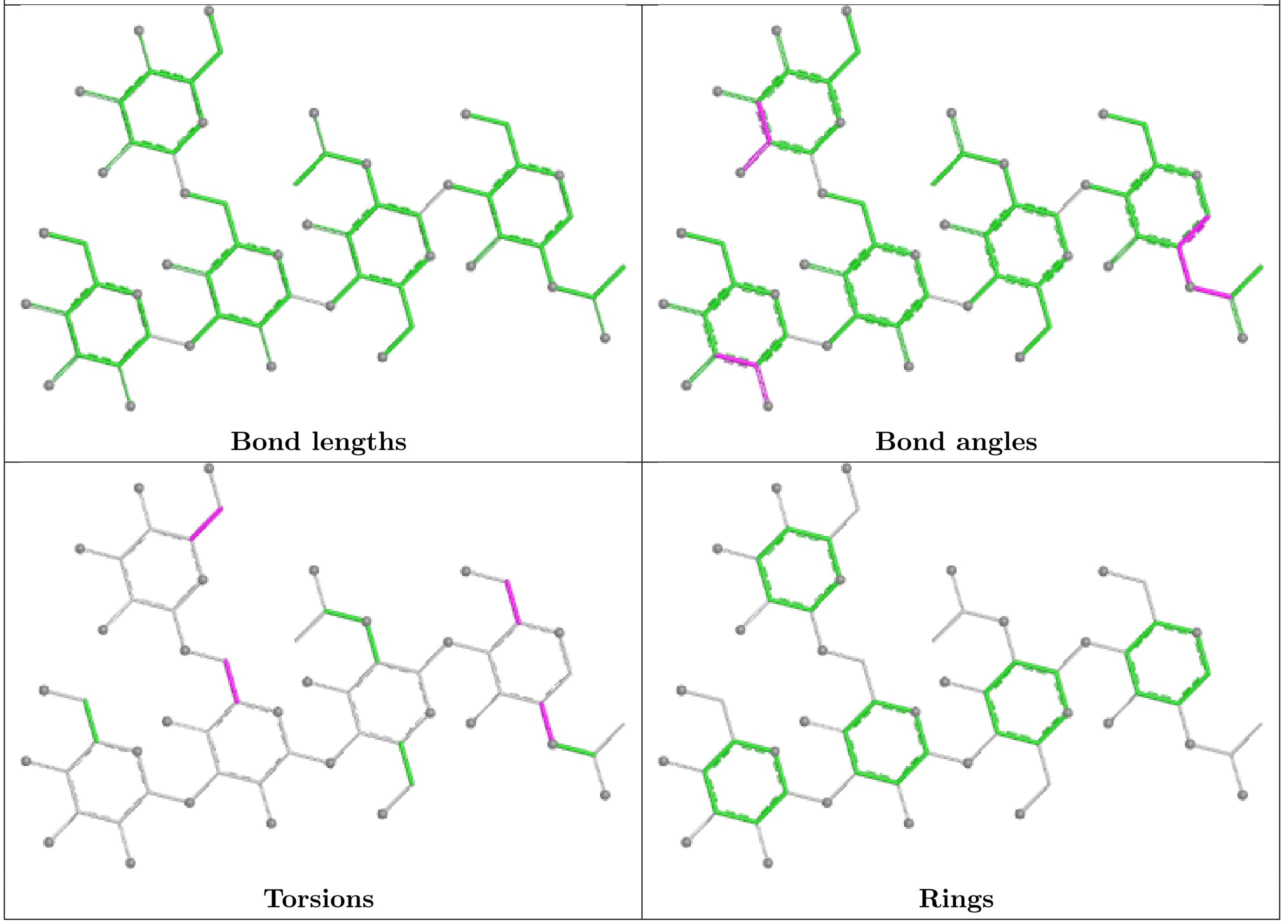


Bond lengths Bond angles

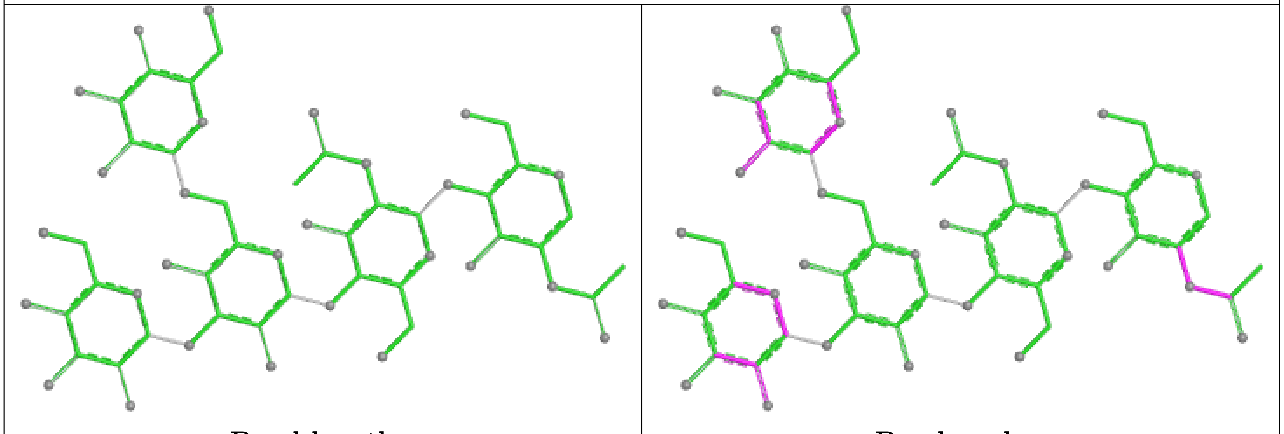


Torsions Rings

Oligosaccharide Chain P

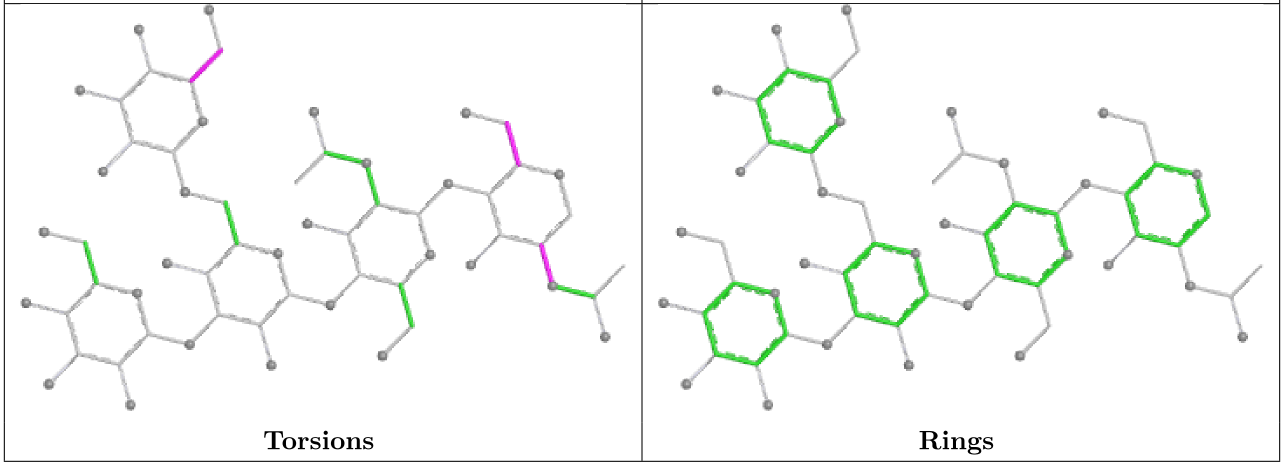


Oligosaccharide Chain U



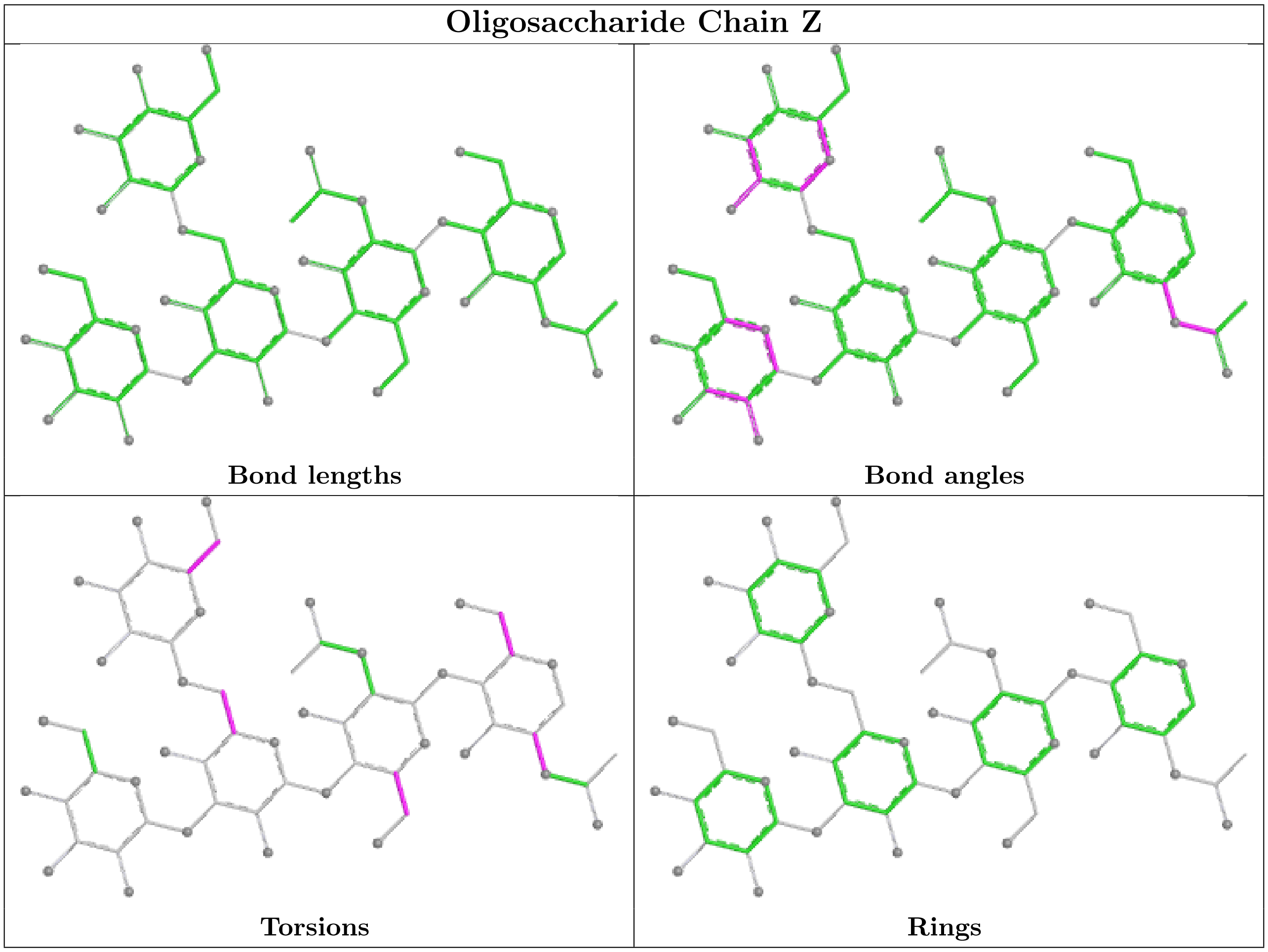
Bond lengths

Bond angles



Torsions

Rings



Oligosaccharide Chain Z

5.6 Ligand geometry ⓘ

45 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	$\#\|Z\| > 2$
8	NAG	B	701	2	14,14,15	0.56	0	17,19,21	1.02	1 (5%)
8	NAG	F	612	1	14,14,15	0.26	0	17,19,21	0.44	0
8	NAG	E	602	1	14,14,15	0.39	0	17,19,21	0.51	0
8	NAG	F	607	1	14,14,15	0.29	0	17,19,21	0.44	0
8	NAG	E	606	1	14,14,15	0.47	0	17,19,21	0.53	0
8	NAG	E	605	1	14,14,15	0.41	0	17,19,21	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
8	NAG	D	610	1	14,14,15	0.37	0	17,19,21	0.45	0
8	NAG	E	601	1	14,14,15	0.40	0	17,19,21	0.51	0
8	NAG	A	702	2	14,14,15	0.49	0	17,19,21	0.53	0
8	NAG	F	613	1	14,14,15	0.29	0	17,19,21	0.54	0
8	NAG	A	701	2	14,14,15	0.28	0	17,19,21	0.39	0
8	NAG	E	611	1	14,14,15	0.38	0	17,19,21	0.54	0
8	NAG	D	607	1	14,14,15	0.30	0	17,19,21	0.43	0
8	NAG	D	602	1	14,14,15	0.33	0	17,19,21	0.49	0
8	NAG	D	606	1	14,14,15	0.30	0	17,19,21	0.47	0
8	NAG	E	612	1	14,14,15	0.37	0	17,19,21	0.50	0
8	NAG	D	605	1	14,14,15	0.29	0	17,19,21	0.44	0
8	NAG	F	610	1	14,14,15	0.35	0	17,19,21	0.40	0
8	NAG	E	609	1	14,14,15	0.46	0	17,19,21	0.52	0
8	NAG	F	602	1	14,14,15	0.31	0	17,19,21	0.50	0
8	NAG	D	601	1	14,14,15	0.24	0	17,19,21	0.46	0
8	NAG	E	604	1	14,14,15	0.41	0	17,19,21	1.01	1 (5%)
8	NAG	C	702	2	14,14,15	0.60	1 (7%)	17,19,21	0.40	0
8	NAG	D	609	1	14,14,15	0.29	0	17,19,21	0.45	0
8	NAG	D	613	1	14,14,15	0.30	0	17,19,21	0.56	0
8	NAG	E	608	1	14,14,15	0.41	0	17,19,21	0.53	0
8	NAG	E	613	1	14,14,15	0.39	0	17,19,21	0.50	0
8	NAG	F	605	1	14,14,15	0.31	0	17,19,21	0.43	0
8	NAG	F	604	1	14,14,15	0.34	0	17,19,21	0.96	1 (5%)
8	NAG	F	606	1	14,14,15	0.31	0	17,19,21	0.48	0
8	NAG	D	612	1	14,14,15	0.25	0	17,19,21	0.46	0
8	NAG	C	701	2	14,14,15	0.51	0	17,19,21	0.44	0
8	NAG	E	607	1	14,14,15	0.40	0	17,19,21	0.49	0
8	NAG	F	609	1	14,14,15	0.33	0	17,19,21	0.48	0
8	NAG	D	611	1	14,14,15	0.27	0	17,19,21	0.50	0
8	NAG	E	603	1	14,14,15	0.42	0	17,19,21	0.52	0
8	NAG	B	702	2	14,14,15	0.24	0	17,19,21	0.74	0
8	NAG	F	601	1	14,14,15	0.35	0	17,19,21	0.46	0
8	NAG	E	610	1	14,14,15	0.50	0	17,19,21	0.51	0
8	NAG	D	604	1	14,14,15	0.39	0	17,19,21	0.97	1 (5%)
8	NAG	F	611	1	14,14,15	0.29	0	17,19,21	0.51	0
8	NAG	F	608	1	14,14,15	0.33	0	17,19,21	0.52	0
8	NAG	D	608	1	14,14,15	0.41	0	17,19,21	0.52	0
8	NAG	F	603	1	14,14,15	0.45	0	17,19,21	0.54	0
8	NAG	D	603	1	14,14,15	0.51	0	17,19,21	0.49	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
8	NAG	B	701	2	-	2/6/23/26	0/1/1/1
8	NAG	F	612	1	-	1/6/23/26	0/1/1/1
8	NAG	E	602	1	-	0/6/23/26	0/1/1/1
8	NAG	F	607	1	-	1/6/23/26	0/1/1/1
8	NAG	E	606	1	-	1/6/23/26	0/1/1/1
8	NAG	E	605	1	-	1/6/23/26	0/1/1/1
8	NAG	D	610	1	-	2/6/23/26	0/1/1/1
8	NAG	E	601	1	-	0/6/23/26	0/1/1/1
8	NAG	A	702	2	-	0/6/23/26	0/1/1/1
8	NAG	F	613	1	-	0/6/23/26	0/1/1/1
8	NAG	A	701	2	-	2/6/23/26	0/1/1/1
8	NAG	E	611	1	-	1/6/23/26	0/1/1/1
8	NAG	D	607	1	-	1/6/23/26	0/1/1/1
8	NAG	D	602	1	-	0/6/23/26	0/1/1/1
8	NAG	D	606	1	-	1/6/23/26	0/1/1/1
8	NAG	E	612	1	-	1/6/23/26	0/1/1/1
8	NAG	D	605	1	-	2/6/23/26	0/1/1/1
8	NAG	F	610	1	-	1/6/23/26	0/1/1/1
8	NAG	E	609	1	-	0/6/23/26	0/1/1/1
8	NAG	F	602	1	-	0/6/23/26	0/1/1/1
8	NAG	D	601	1	-	0/6/23/26	0/1/1/1
8	NAG	E	604	1	-	2/6/23/26	0/1/1/1
8	NAG	C	702	2	-	2/6/23/26	0/1/1/1
8	NAG	D	609	1	-	2/6/23/26	0/1/1/1
8	NAG	D	613	1	-	0/6/23/26	0/1/1/1
8	NAG	E	608	1	-	1/6/23/26	0/1/1/1
8	NAG	E	613	1	-	0/6/23/26	0/1/1/1
8	NAG	F	605	1	-	1/6/23/26	0/1/1/1
8	NAG	F	604	1	-	2/6/23/26	0/1/1/1
8	NAG	F	606	1	-	1/6/23/26	0/1/1/1
8	NAG	D	612	1	-	2/6/23/26	0/1/1/1
8	NAG	C	701	2	-	2/6/23/26	0/1/1/1
8	NAG	E	607	1	-	1/6/23/26	0/1/1/1
8	NAG	F	609	1	-	0/6/23/26	0/1/1/1
8	NAG	D	611	1	-	2/6/23/26	0/1/1/1
8	NAG	E	603	1	-	0/6/23/26	0/1/1/1
8	NAG	B	702	2	-	4/6/23/26	0/1/1/1
8	NAG	F	601	1	-	1/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	E	610	1	-	1/6/23/26	0/1/1/1
8	NAG	D	604	1	-	2/6/23/26	0/1/1/1
8	NAG	F	611	1	-	2/6/23/26	0/1/1/1
8	NAG	F	608	1	-	2/6/23/26	0/1/1/1
8	NAG	D	608	1	-	2/6/23/26	0/1/1/1
8	NAG	F	603	1	-	2/6/23/26	0/1/1/1
8	NAG	D	603	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	702	NAG	C1-C2	2.08	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	B	701	NAG	C2-N2-C7	3.20	127.19	122.90
8	E	604	NAG	C2-N2-C7	3.06	127.01	122.90
8	F	604	NAG	C2-N2-C7	3.04	126.98	122.90
8	D	604	NAG	C2-N2-C7	3.03	126.96	122.90

There are no chirality outliers.

5 of 51 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	B	702	NAG	C3-C2-N2-C7
8	B	702	NAG	C8-C7-N2-C2
8	B	702	NAG	O7-C7-N2-C2
8	D	609	NAG	O5-C5-C6-O6
8	D	611	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	702	NAG	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

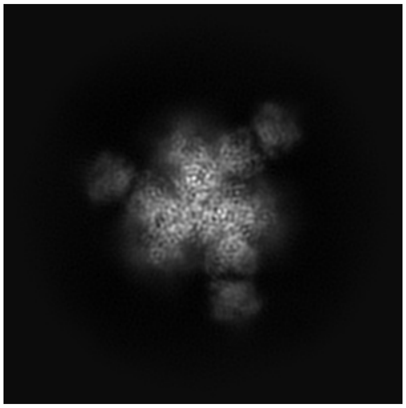
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-41438. These allow visual inspection of the internal detail of the map and identification of artifacts.

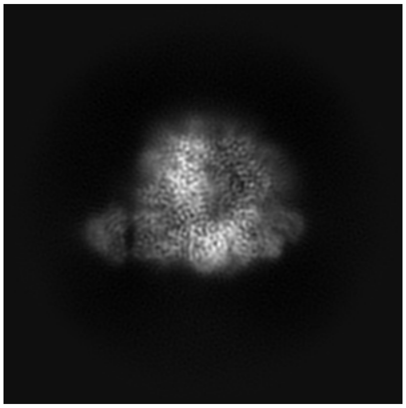
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

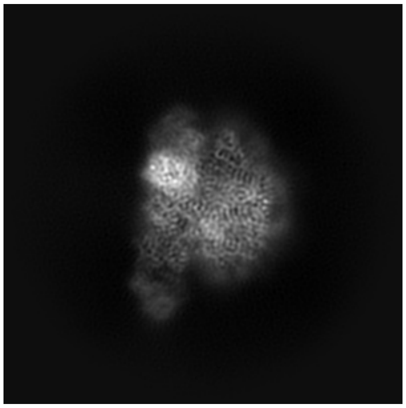
6.1.1 Primary map



X

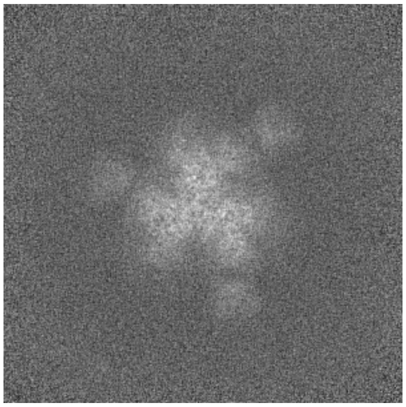


Y

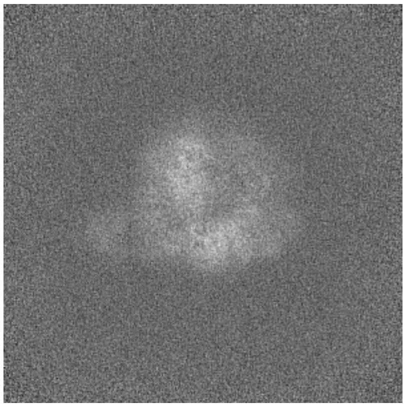


Z

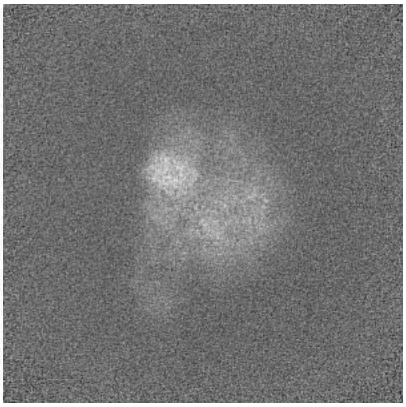
6.1.2 Raw map



X



Y

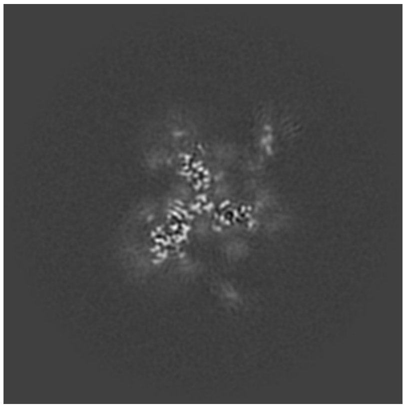


Z

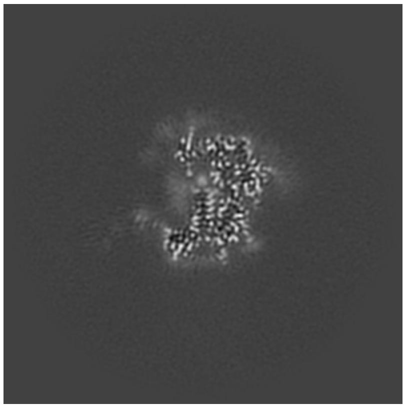
The images above show the map projected in three orthogonal directions.

6.2 Central slices

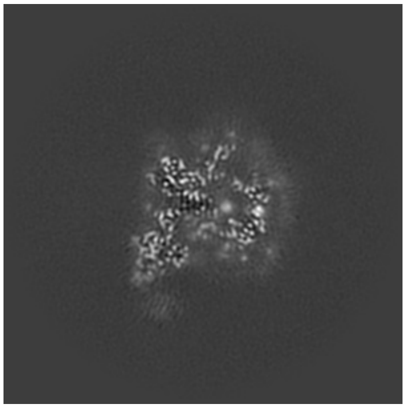
6.2.1 Primary map



X Index: 384

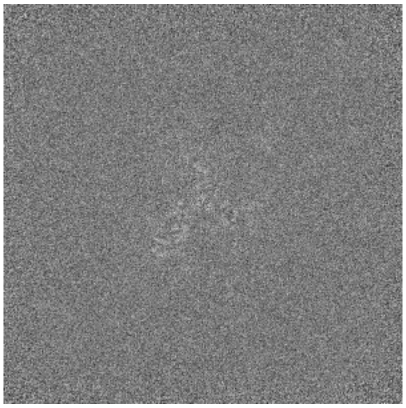


Y Index: 384

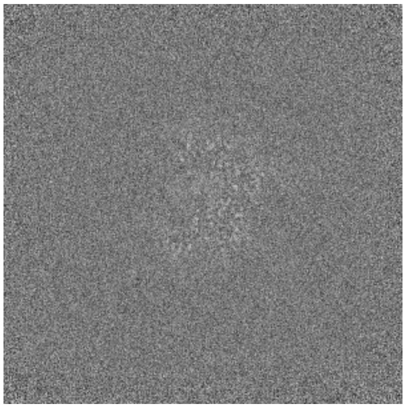


Z Index: 384

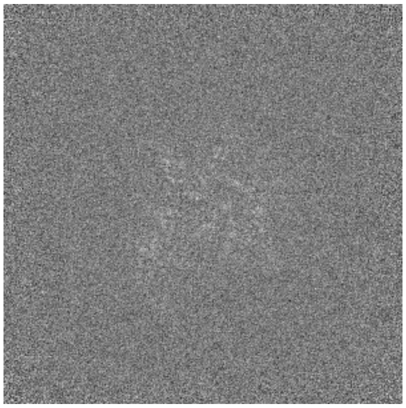
6.2.2 Raw map



X Index: 384



Y Index: 384

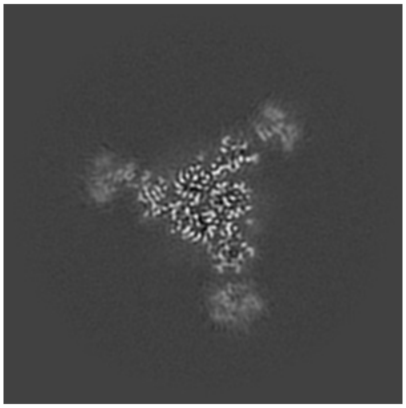


Z Index: 384

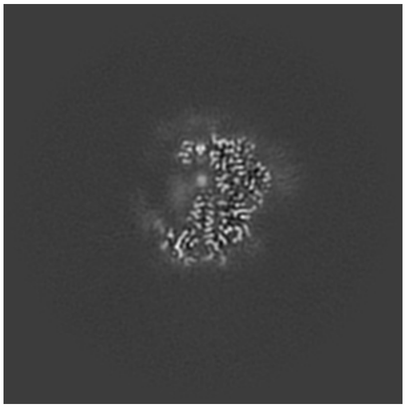
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices ⓘ

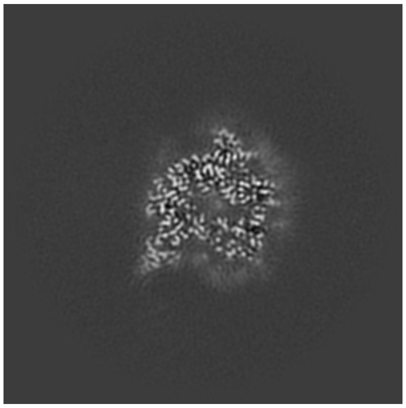
6.3.1 Primary map



X Index: 322

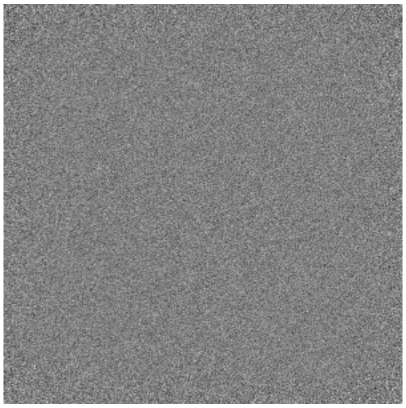


Y Index: 375

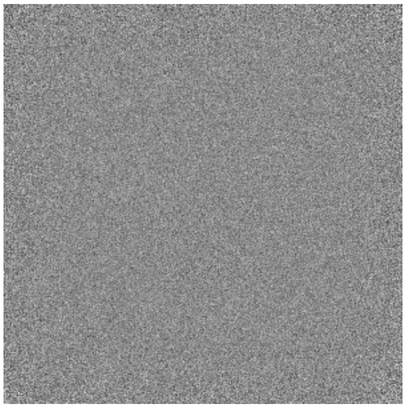


Z Index: 361

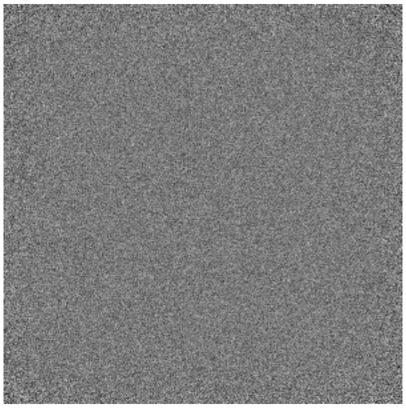
6.3.2 Raw map



X Index: 0



Y Index: 0

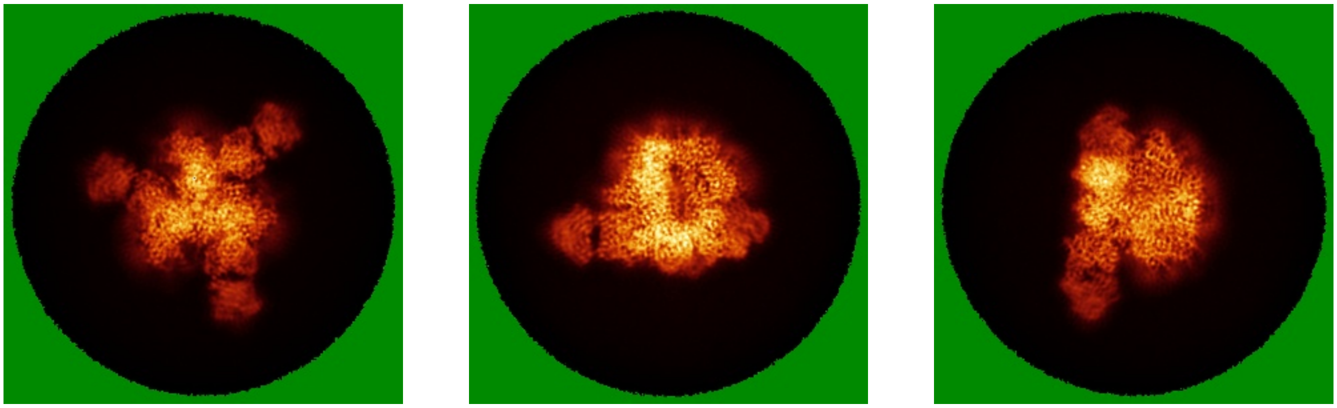


Z Index: 767

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

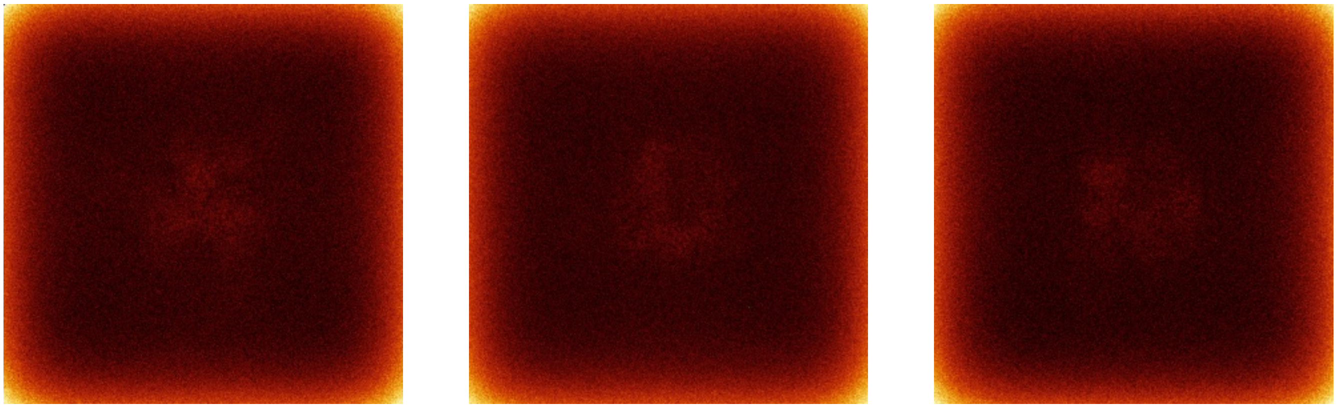
6.4 Orthogonal standard-deviation projections (False-color)

6.4.1 Primary map



X Y Z

6.4.2 Raw map



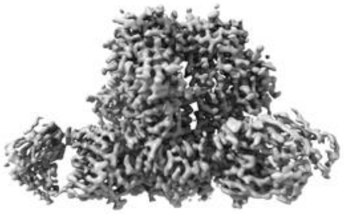
X Y Z

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

6.5 Orthogonal surface views

6.5.1 Primary map

X

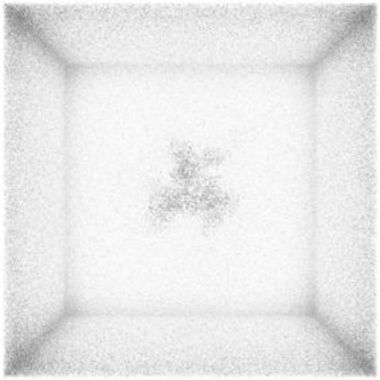


Y

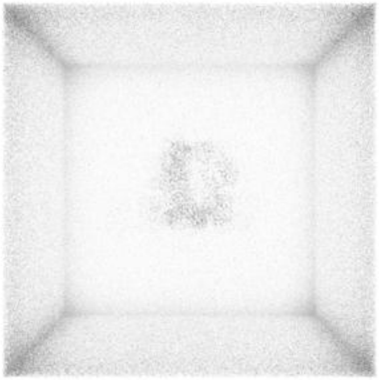
Z

The images above show the 3D surface view of the map at the recommended contour level 0.027. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

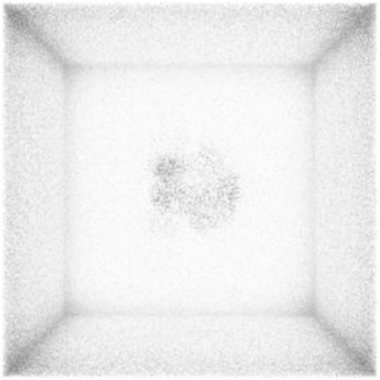
6.5.2 Raw map



X



Y



Z

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

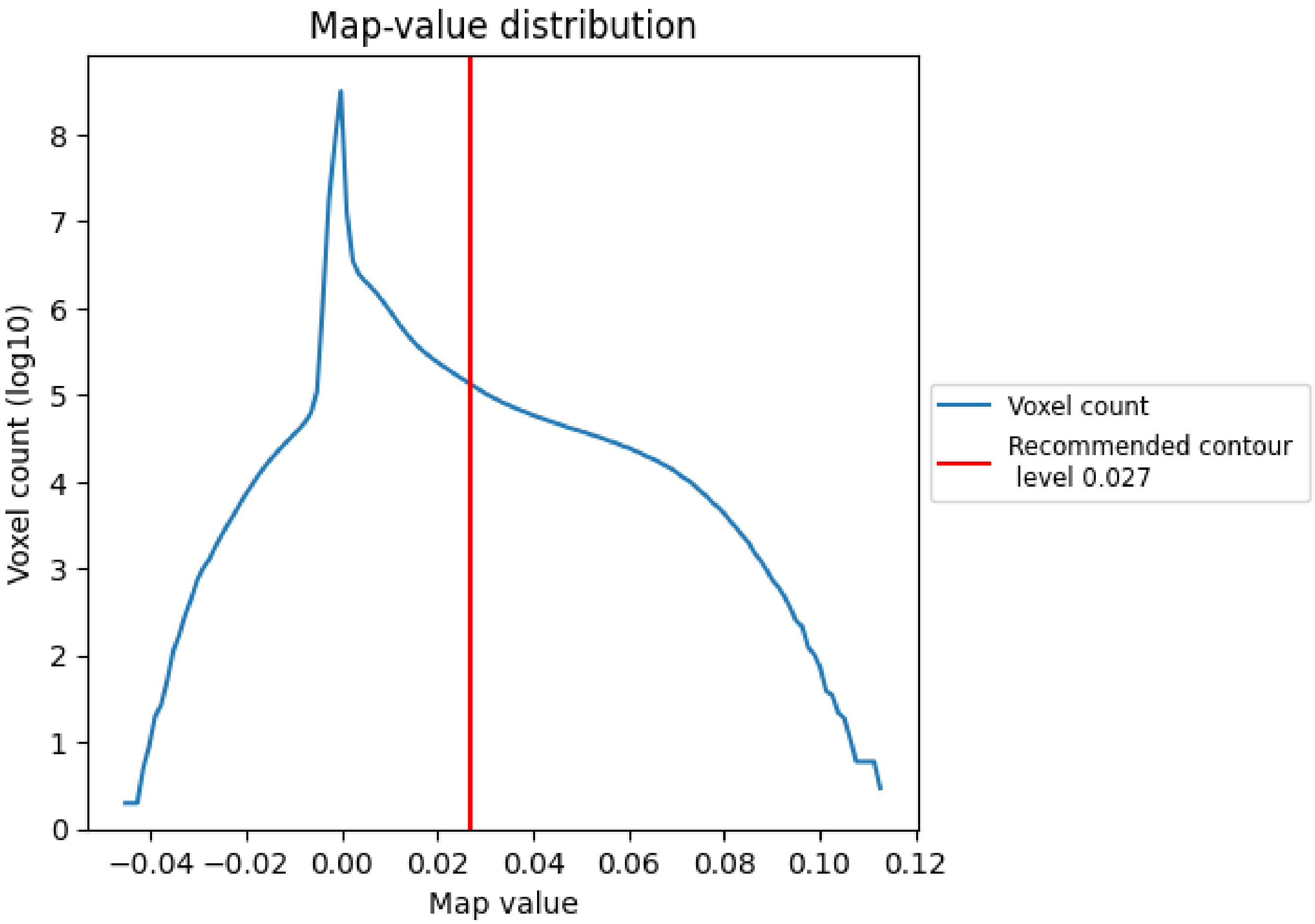
6.6 Mask visualisation

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

7 Map analysis ⓘ

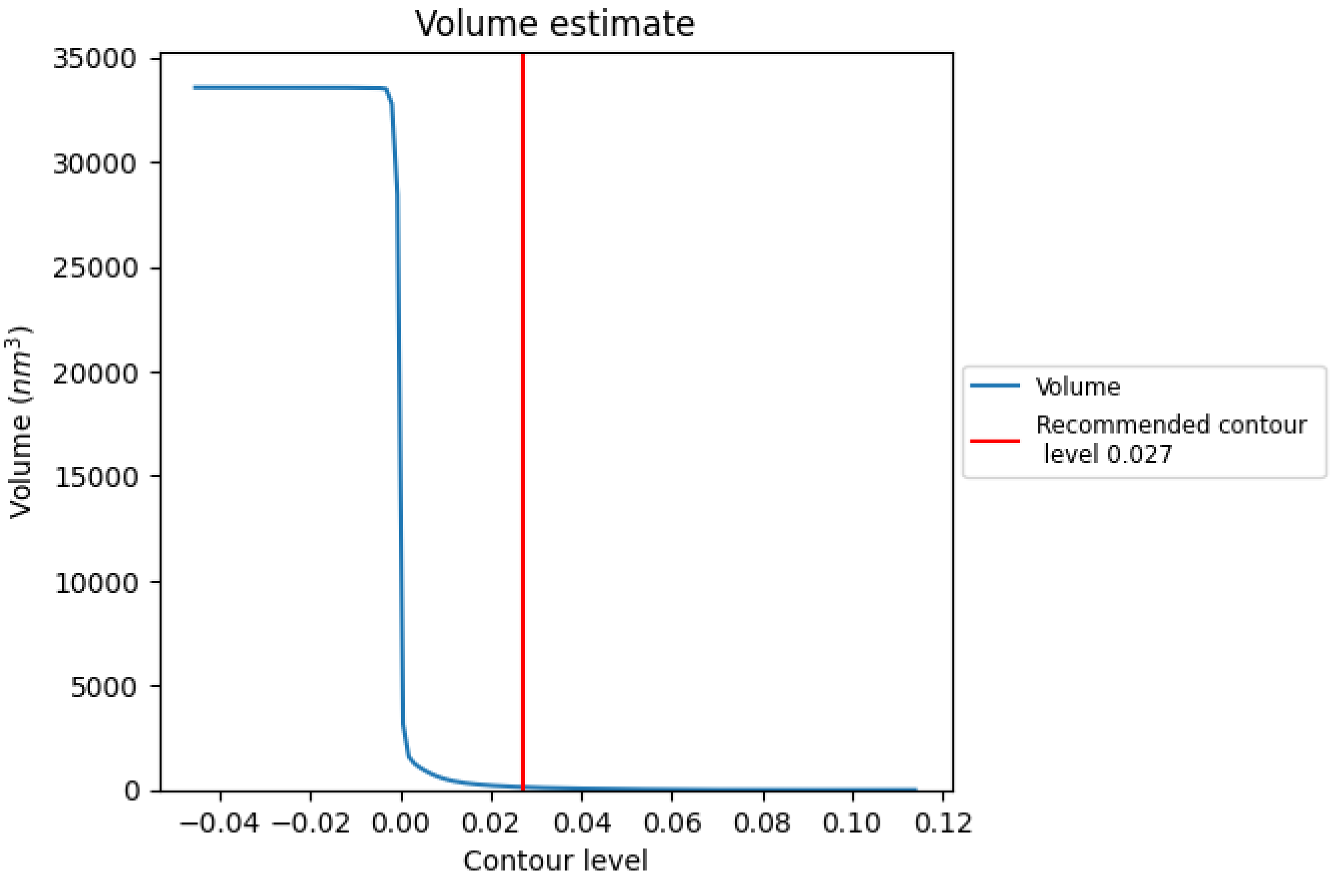
This section contains the results of statistical analysis of the map.

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.

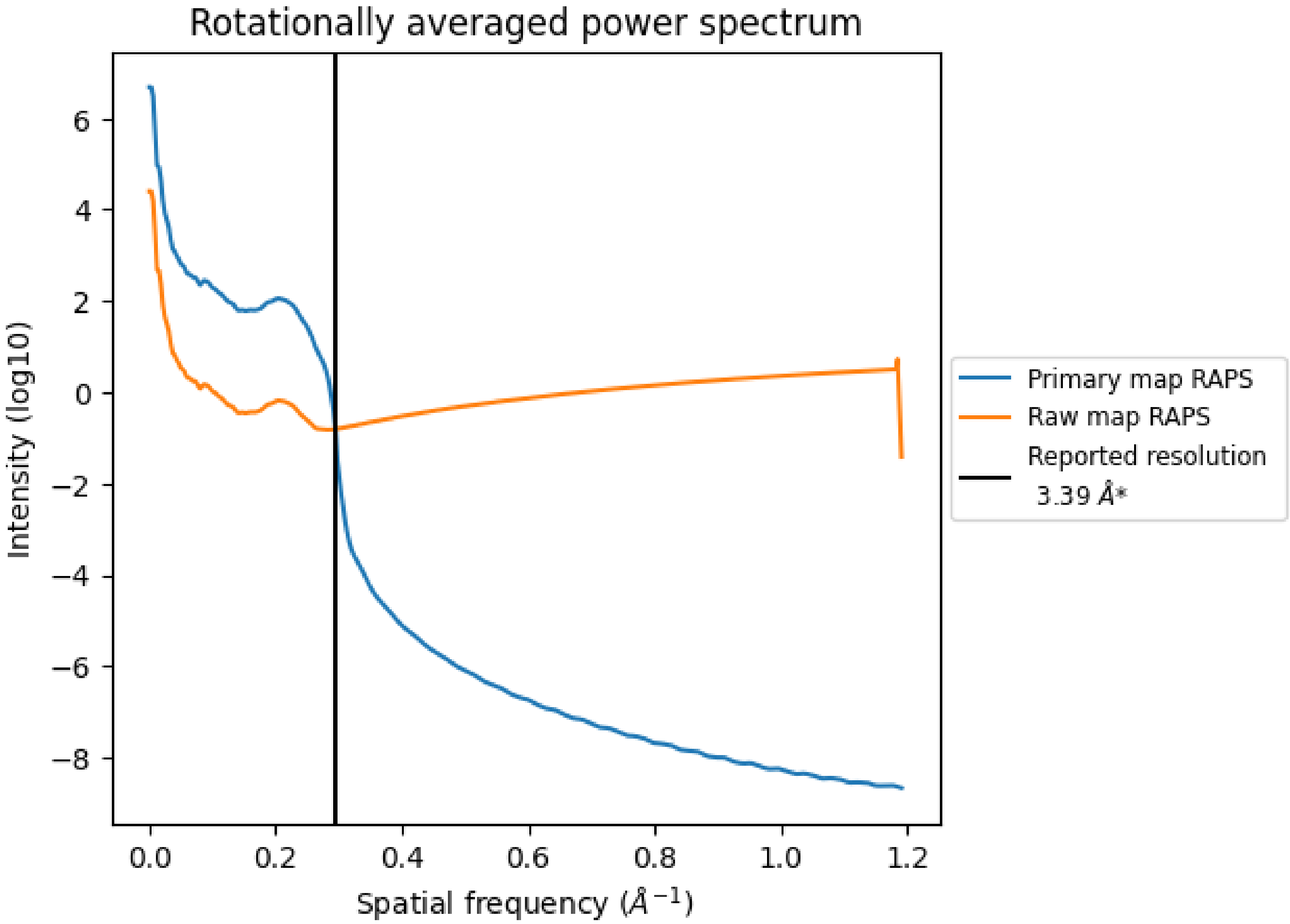
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 136 nm^3; this corresponds to an approximate mass of 123 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 ⓘ

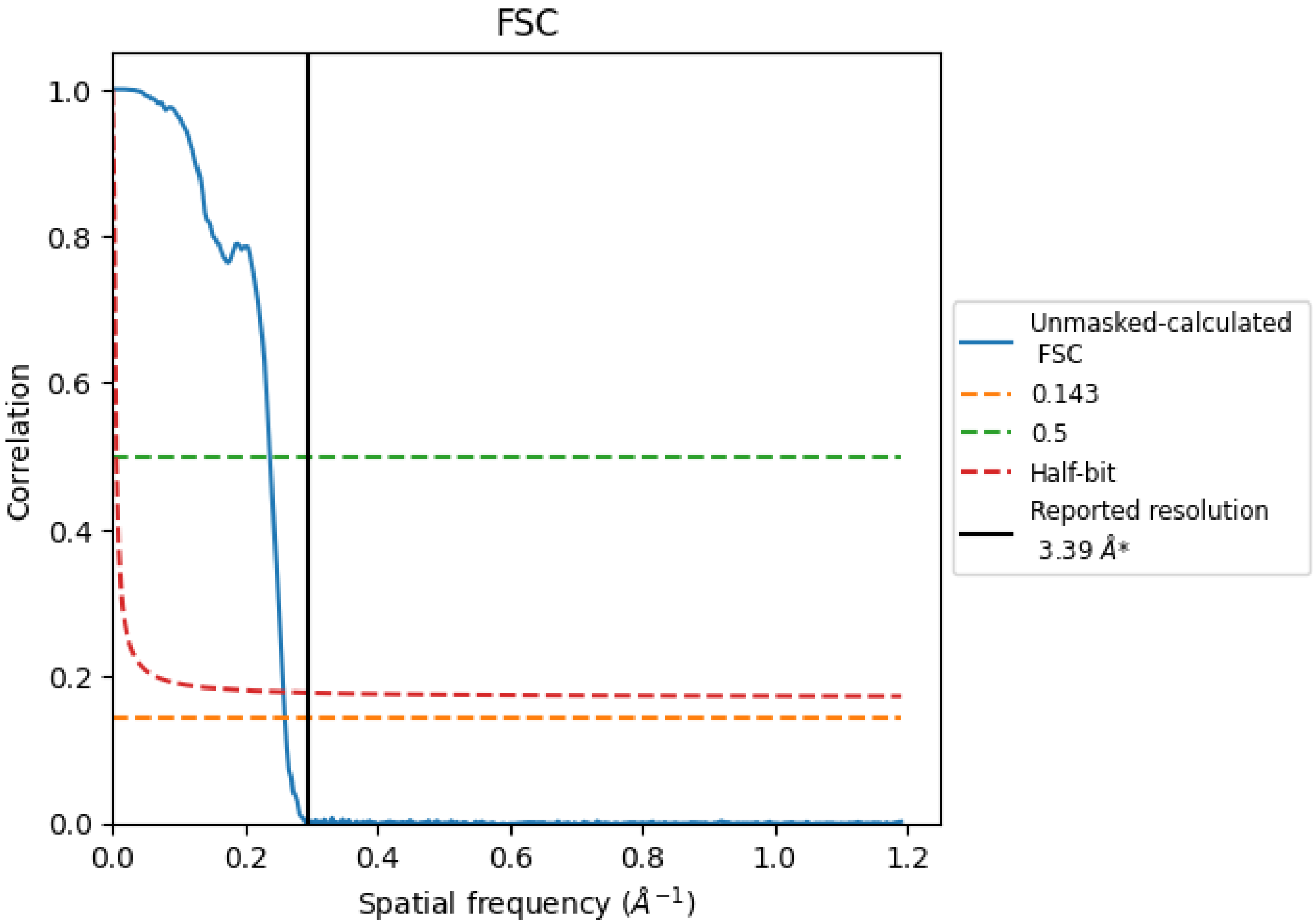


*Reported resolution corresponds to spatial frequency of 0.295 $Å^{-1}$

8 Fourier-Shell correlation ⓘ

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC ⓘ



*Reported resolution corresponds to spatial frequency of 0.295 Å^{-1}

8.2 Resolution estimates ⓘ

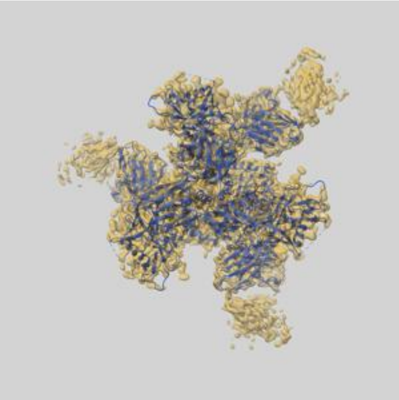
Resolution estimate (Å)	**Estimation criterion (FSC cut-off)**		
	0.143	0.5	Half-bit
Reported by author	3.39	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.84	4.21	3.87

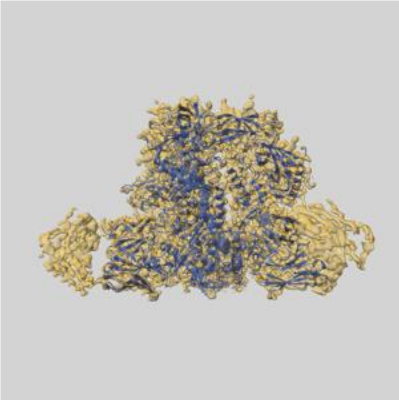
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.84 differs from the reported value 3.39 by more than 10 %

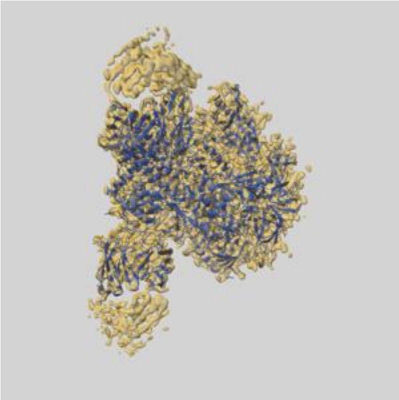
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-41438 and PDB model 8TO7. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay

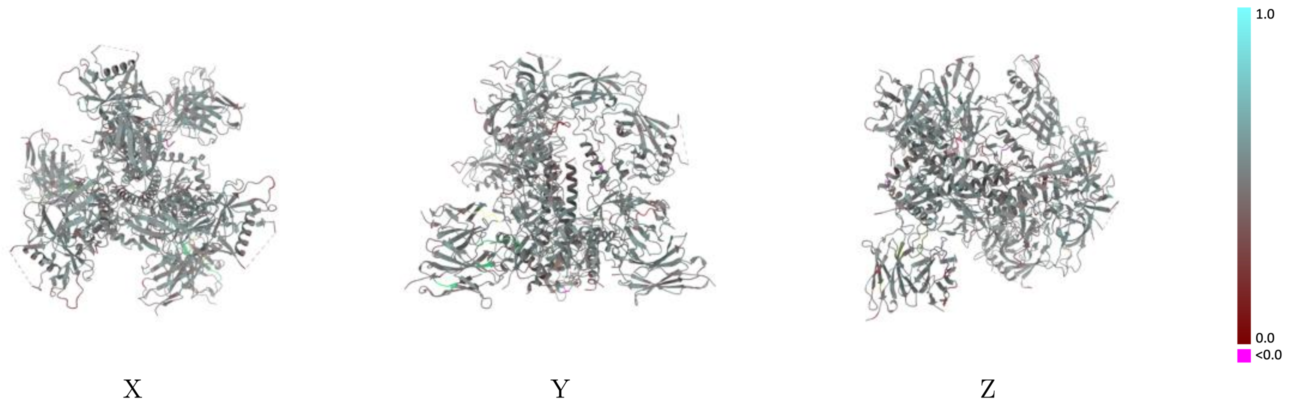

X


Y


Z

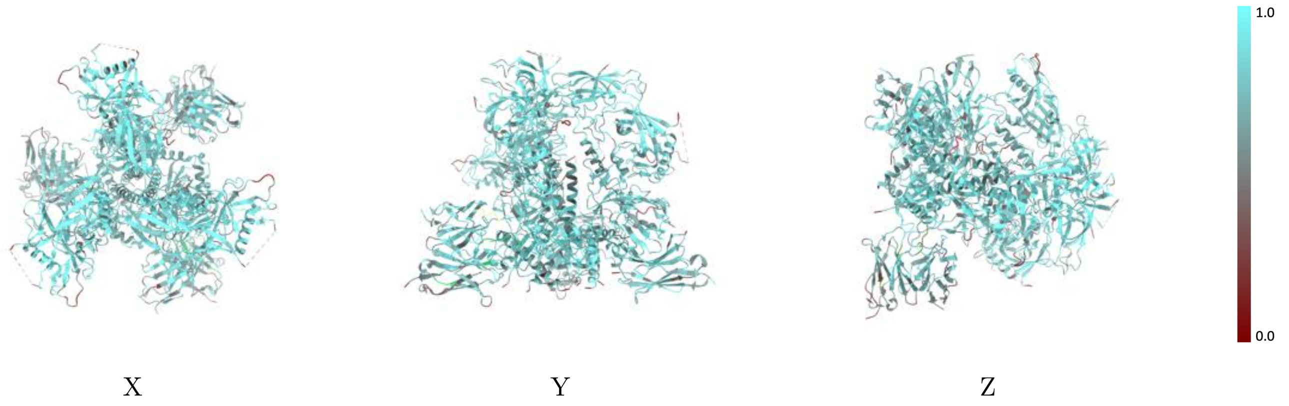
The images above show the 3D surface view of the map at the recommended contour level 0.027 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model ⓘ



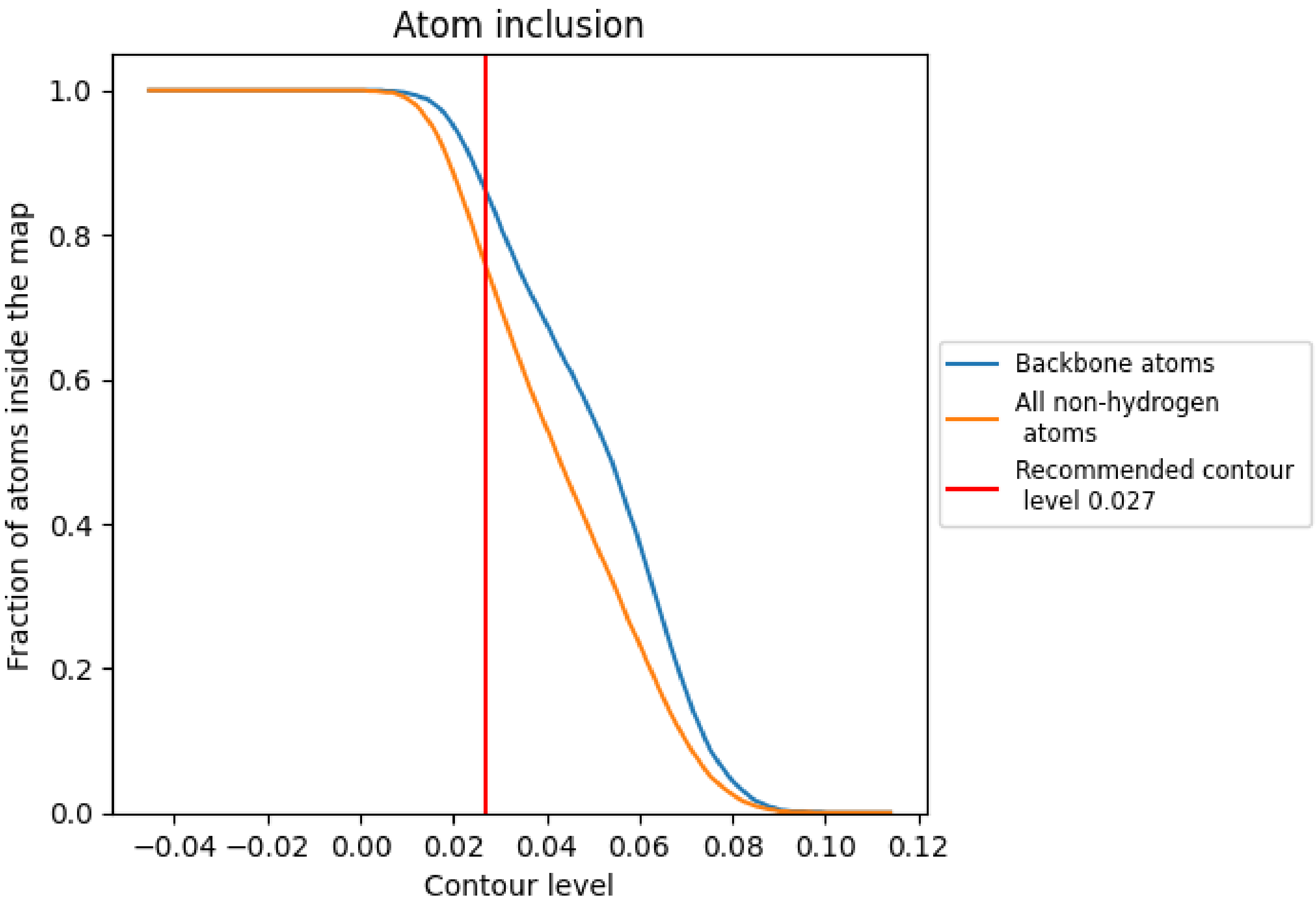
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 ⓘ



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 (0.027).

9.4 Atom inclusion ⓘ



At the recommended contour level, 86% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.027) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7560	0.4830
A	0.7660	0.4760
B	0.7740	0.4850
C	0.7860	0.4870
D	0.7810	0.4840
E	0.7790	0.4870
F	0.7800	0.4840
G	0.6660	0.4780
H	0.7580	0.4970
I	0.7040	0.4720
J	0.7090	0.4790
K	0.7490	0.4770
L	0.7720	0.5060
M	0.4360	0.4190
N	0.6790	0.4330
O	0.5000	0.4460
P	0.6230	0.4480
Q	0.2050	0.4120
R	0.4360	0.3890
S	0.6790	0.4580
T	0.5000	0.4540
U	0.5570	0.4510
V	0.3330	0.4200
W	0.4100	0.4290
X	0.6790	0.4820
Y	0.5710	0.4630
Z	0.6230	0.4890
a	0.3080	0.4400