Full wwPDB EM Validation Report ⓘ

Mar 10, 2022 – 12:52 am GMT

PDB ID	:	7PVD
EMDB ID	:	EMD-13667
Title	:	Structure of the membrane soluble spike complex from the Lassa virus in a C1-symmetric map focused on the ectodomain
Authors	:	Diskin, R.; Katz, M.
Deposited on	:	2021-10-02
Resolution	:	3.70 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 following versions of software and data (see references ⓘ) were used in the production of this report:

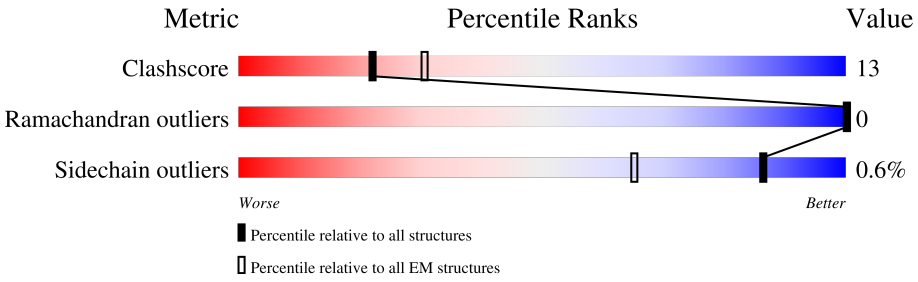
EMDB validation analysis	:	0.0.0.dev97
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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 3.70 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	244	6% 65% · 34%
1	b	244	5% 65% · 34%
1	c	244	· 65% · 34%
2	A	259	5% 49% 23% 29%
2	B	259	· 50% 22% 29%
2	C	259	· 50% 22% 29%
3	D	2	50% 50%
3	E	2	50% 50%

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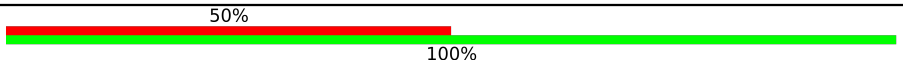
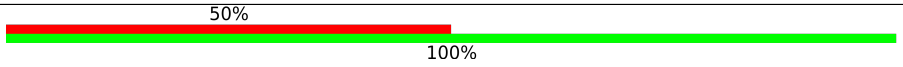
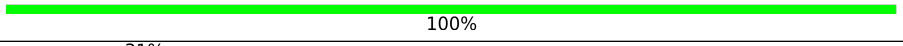
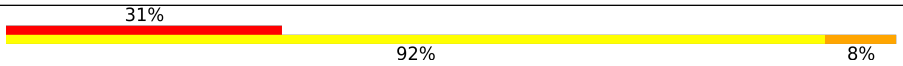
Mol	Chain	Length	Quality of chain
3	F	2	
3	G	2	
3	H	2	
3	I	2	
3	J	2	
3	K	2	
3	L	2	
4	M	13	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8902 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 Glycoprotein G2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	160	Total	C	N	O	S	0	0
			1298	818	218	249	13		
1	b	160	Total	C	N	O	S	0	0
			1298	818	218	249	13		
1	c	160	Total	C	N	O	S	0	0
			1298	818	218	249	13		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	492	GLY	-	expression tag	UNP P08669
a	493	GLY	-	expression tag	UNP P08669
a	494	GLY	-	expression tag	UNP P08669
a	495	SER	-	expression tag	UNP P08669
a	496	ASP	-	expression tag	UNP P08669
a	497	TYR	-	expression tag	UNP P08669
a	498	LYS	-	expression tag	UNP P08669
a	499	ASP	-	expression tag	UNP P08669
a	500	ASP	-	expression tag	UNP P08669
a	501	ASP	-	expression tag	UNP P08669
a	502	ASP	-	expression tag	UNP P08669
a	503	LYS	-	expression tag	UNP P08669
b	492	GLY	-	expression tag	UNP P08669
b	493	GLY	-	expression tag	UNP P08669
b	494	GLY	-	expression tag	UNP P08669
b	495	SER	-	expression tag	UNP P08669
b	496	ASP	-	expression tag	UNP P08669
b	497	TYR	-	expression tag	UNP P08669
b	498	LYS	-	expression tag	UNP P08669
b	499	ASP	-	expression tag	UNP P08669
b	500	ASP	-	expression tag	UNP P08669
b	501	ASP	-	expression tag	UNP P08669
b	502	ASP	-	expression tag	UNP P08669
b	503	LYS	-	expression tag	UNP P08669

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Chain	Residue	Modelled	Actual	Comment	Reference
c	492	GLY	-	expression tag	UNP P08669
c	493	GLY	-	expression tag	UNP P08669
c	494	GLY	-	expression tag	UNP P08669
c	495	SER	-	expression tag	UNP P08669
c	496	ASP	-	expression tag	UNP P08669
c	497	TYR	-	expression tag	UNP P08669
c	498	LYS	-	expression tag	UNP P08669
c	499	ASP	-	expression tag	UNP P08669
c	500	ASP	-	expression tag	UNP P08669
c	501	ASP	-	expression tag	UNP P08669
c	502	ASP	-	expression tag	UNP P08669
c	503	LYS	-	expression tag	UNP P08669

- Molecule 2 is a protein called Pre-glycoprotein polyprotein GP complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	185	Total	C	N	O	S	0	0
			1484	935	257	277	15		
2	B	185	Total	C	N	O	S	0	0
			1484	935	257	277	15		
2	C	185	Total	C	N	O	S	0	0
			1484	935	257	277	15		

- Molecule 3 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
3	D	2	Total	C	N	O	0	0
			28	16	2	10		
3	E	2	Total	C	N	O	0	0
			28	16	2	10		
3	F	2	Total	C	N	O	0	0
			28	16	2	10		
3	G	2	Total	C	N	O	0	0
			28	16	2	10		
3	H	2	Total	C	N	O	0	0
			28	16	2	10		

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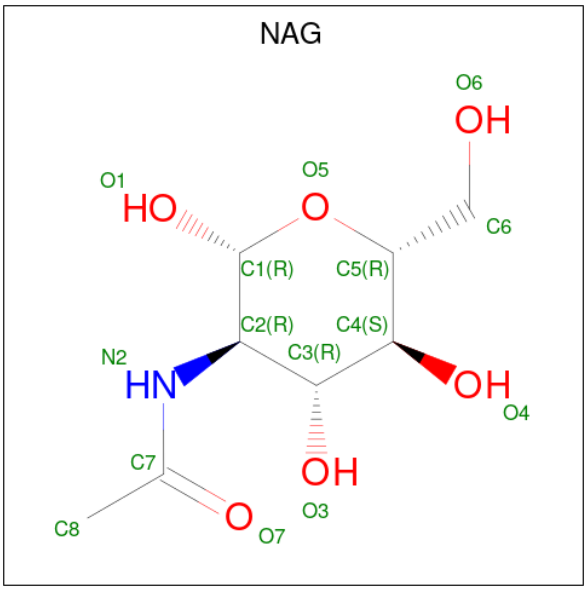
Mol	Chain	Residues	Atoms				AltConf	Trace
3	I	2	Total	C	N	O	0	0
			28	16	2	10		
3	J	2	Total	C	N	O	0	0
			28	16	2	10		
3	K	2	Total	C	N	O	0	0
			28	16	2	10		
3	L	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is an oligosaccharide called alpha-D-xylopyranose-(1-3)-beta-D-glucopyranuronic acid-(1-3)-alpha-D-xylopyranose-(1-3)-beta-D-glucopyranuronic acid-(1-3)-alpha-D-xylopyranose-(1-3)-beta-D-glucopyranuronic acid-(1-3)-alpha-D-xylopyranose-(1-3)-beta-D-glucopyranuronic acid-(1-3)-alpha-D-xylopyranose-(1-3)-beta-D-glucopyranuronic acid-(1-3)-alpha-D-xylopyranose.

Mol	Chain	Residues	Atoms			AltConf	Trace
4	M	13	Total	C	O	0	0
			136	71	65		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

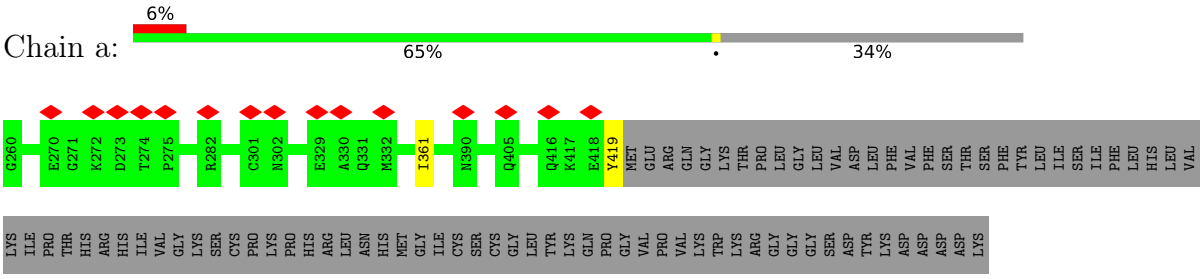


Mol	Chain	Residues	Atoms				AltConf
5	a	1	Total	C	N	O	0
			28	16	2	10	
5	a	1	Total	C	N	O	0
			28	16	2	10	
5	b	1	Total	C	N	O	0
			28	16	2	10	
5	b	1	Total	C	N	O	0
			28	16	2	10	
5	c	1	Total	C	N	O	0
			28	16	2	10	
5	c	1	Total	C	N	O	0
			28	16	2	10	
5	A	1	Total	C	N	O	0
			28	16	2	10	
5	A	1	Total	C	N	O	0
			28	16	2	10	
5	B	1	Total	C	N	O	0
			28	16	2	10	
5	B	1	Total	C	N	O	0
			28	16	2	10	
5	C	1	Total	C	N	O	0
			28	16	2	10	
5	C	1	Total	C	N	O	0
			28	16	2	10	

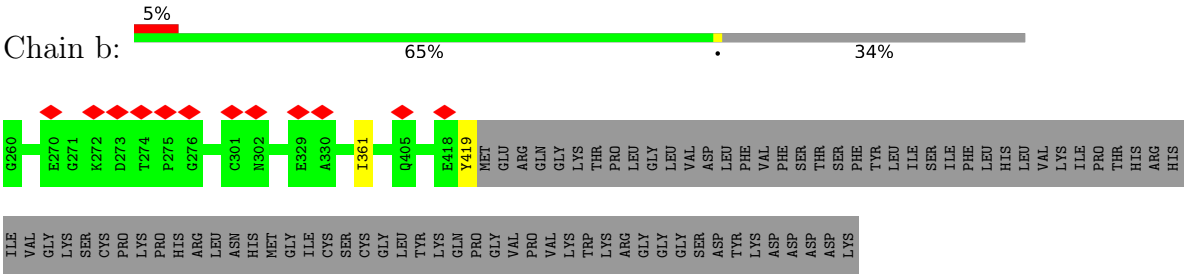
3 Residue-property plots (i)

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.

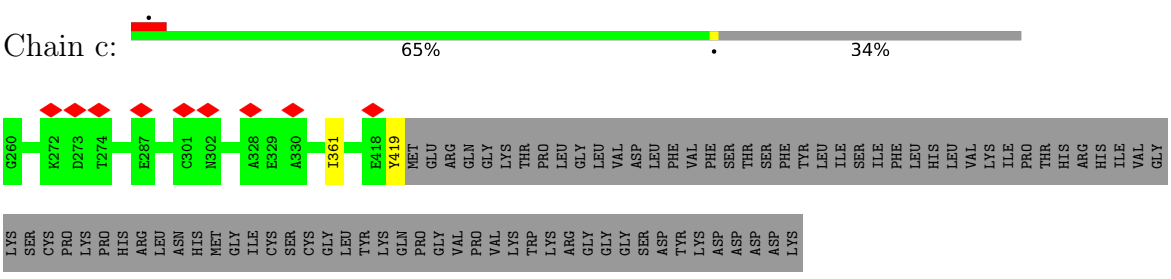
• Molecule 1: Glycoprotein G2



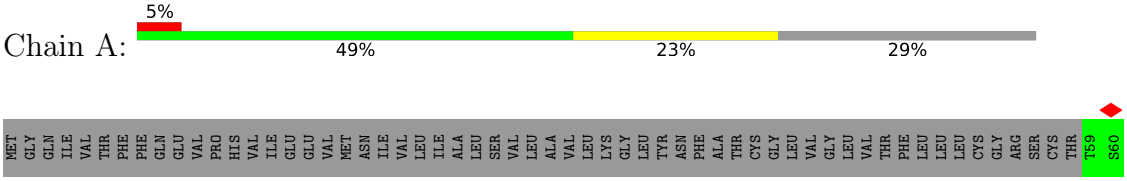
• Molecule 1: Glycoprotein G2

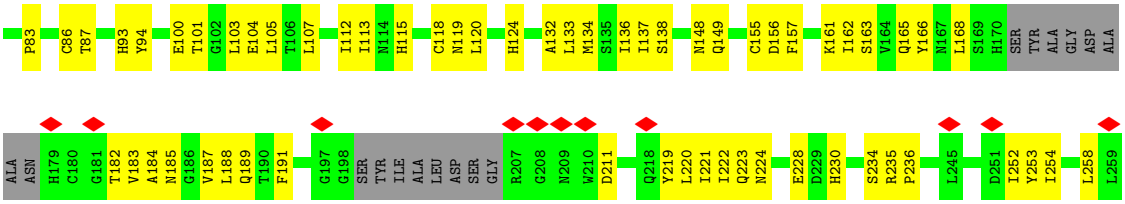


• Molecule 1: Glycoprotein G2



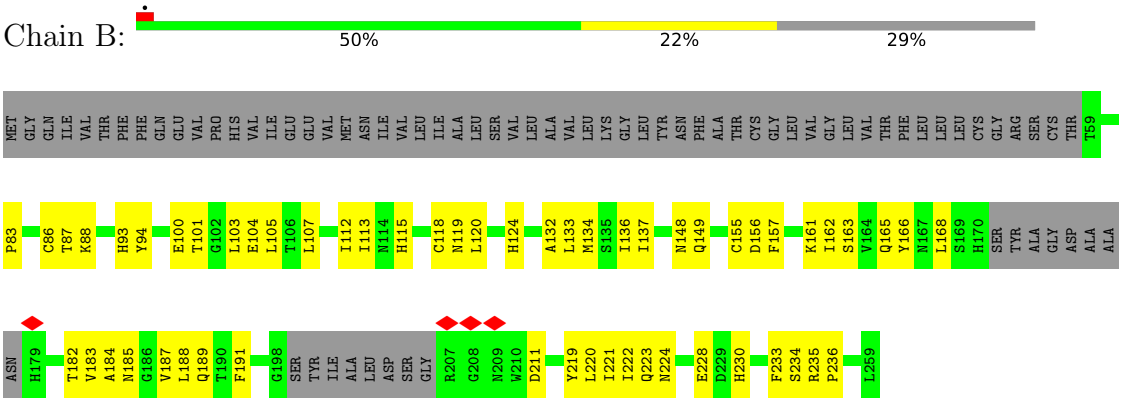
• Molecule 2: Pre-glycoprotein polyprotein GP complex





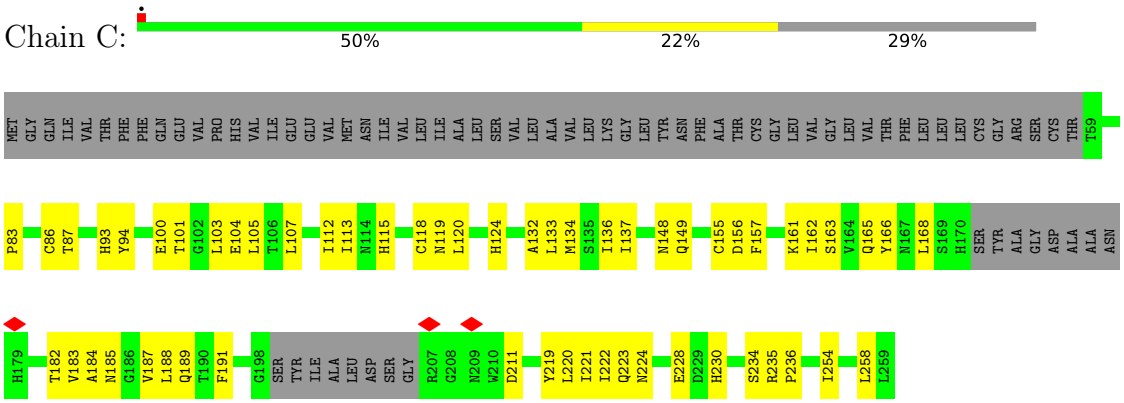
• Molecule 2: Pre-glycoprotein polyprotein GP complex

Chain B:



• Molecule 2: Pre-glycoprotein polyprotein GP complex

Chain C:



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

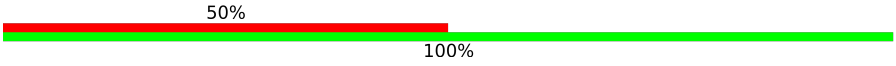
Chain D:

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

Chain E:

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

Chain F:



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

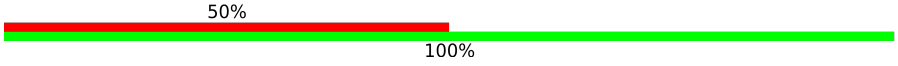
Chain G:

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

Chain H:

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

Chain I:



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

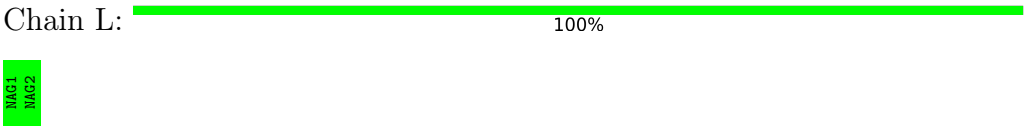
Chain J:

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

Chain K:

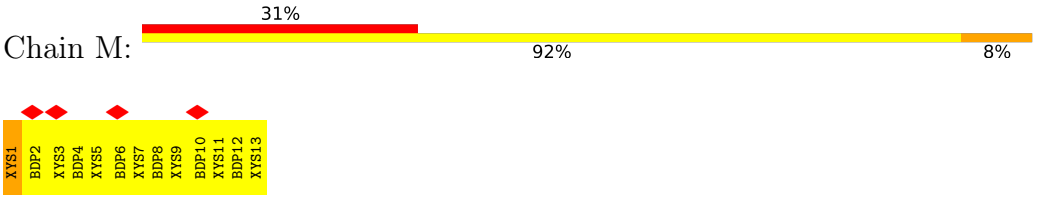
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:



• Molecule 4: alpha-D-xylopyranose-(1-3)-beta-D-glucopyranuronic acid-(1-3)-alpha-D-xylopyranose-(1-3)-beta-D-glucopyranuronic acid-(1-3)-alpha-D-xylopyranose-(1-3)-beta-D-glucopyranuronic acid-(1-3)-alpha-D-xylopyranose-(1-3)-beta-D-glucopyranuronic acid-(1-3)-alpha-D-xylopyranose-(1-3)-beta-D-glucopyranuronic acid-(1-3)-alpha-D-xylopyranose-(1-3)-beta-D-glucopyranuronic acid-(1-3)-alpha-D-xylopyranose

Chain M:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	103416	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	73	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.745	Depositor
Minimum map value	-0.375	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	265.728, 265.728, 265.728	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.038, 1.038, 1.038	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: XYS, BDP, 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	0.30	0/1325	0.50	0/1789
1	b	0.30	0/1325	0.49	0/1789
1	c	0.30	0/1325	0.49	0/1789
2	A	0.28	0/1516	0.53	0/2050
2	B	0.28	0/1516	0.53	0/2050
2	C	0.28	0/1516	0.53	0/2050
All	All	0.29	0/8523	0.51	0/11517

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

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	1298	0	1246	0	0
1	b	1298	0	1246	0	0
1	c	1298	0	1246	0	0
2	A	1484	0	1429	45	0
2	B	1484	0	1429	42	0
2	C	1484	0	1429	41	0
3	D	28	0	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	28	0	25	1	0
3	F	28	0	25	0	0
3	G	28	0	25	2	0
3	H	28	0	25	1	0
3	I	28	0	25	0	0
3	J	28	0	25	1	0
3	K	28	0	25	1	0
3	L	28	0	25	0	0
4	M	136	0	87	1	0
5	A	28	0	26	0	0
5	B	28	0	26	0	0
5	C	28	0	26	0	0
5	a	28	0	26	0	0
5	b	28	0	26	0	0
5	c	28	0	26	0	0
All	All	8902	0	8493	123	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 13.

All (123) 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:C:228:GLU:HB2	2:C:230:HIS:HD2	1.39	0.87
2:A:228:GLU:HB2	2:A:230:HIS:HD2	1.39	0.86
2:B:228:GLU:HB2	2:B:230:HIS:HD2	1.39	0.84
2:A:112:ILE:HG13	2:A:113:ILE:HG13	1.68	0.75
2:C:112:ILE:HG13	2:C:113:ILE:HG13	1.68	0.75
2:B:112:ILE:HG13	2:B:113:ILE:HG13	1.68	0.74
2:B:118:CYS:HA	2:B:155:CYS:HB2	1.75	0.68
2:A:93:HIS:HB2	2:A:105:LEU:HB2	1.76	0.68
2:C:118:CYS:HA	2:C:155:CYS:HB2	1.75	0.68
2:A:104:GLU:O	2:A:222:ILE:HA	1.95	0.67
2:B:93:HIS:HB2	2:B:105:LEU:HB2	1.76	0.67
2:A:118:CYS:HA	2:A:155:CYS:HB2	1.75	0.66
2:B:235:ARG:HD3	2:B:236:PRO:HD2	1.77	0.66
2:A:87:THR:H	2:A:234:SER:HB2	1.61	0.66
2:B:104:GLU:O	2:B:222:ILE:HA	1.95	0.66
2:C:93:HIS:HB2	2:C:105:LEU:HB2	1.76	0.66
2:B:87:THR:H	2:B:234:SER:HB2	1.61	0.65
2:C:235:ARG:HD3	2:C:236:PRO:HD2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:87:THR:H	2:C:234:SER:HB2	1.61	0.65
2:C:104:GLU:O	2:C:222:ILE:HA	1.95	0.65
2:A:235:ARG:HD3	2:A:236:PRO:HD2	1.77	0.65
2:C:228:GLU:HB2	2:C:230:HIS:CD2	2.29	0.64
2:A:228:GLU:HB2	2:A:230:HIS:CD2	2.29	0.63
2:A:100:GLU:OE1	2:A:101:THR:OG1	2.17	0.62
2:C:100:GLU:OE1	2:C:101:THR:OG1	2.17	0.61
2:B:100:GLU:OE1	2:B:101:THR:OG1	2.17	0.61
2:B:119:ASN:OD1	3:G:1:NAG:N2	2.36	0.59
2:C:119:ASN:OD1	3:J:1:NAG:N2	2.36	0.59
2:B:149:GLN:HB2	2:B:183:VAL:HG11	1.85	0.58
2:A:119:ASN:OD1	3:D:1:NAG:N2	2.36	0.58
2:A:191:PHE:CE2	2:A:220:LEU:HD13	2.39	0.58
2:A:149:GLN:HB2	2:A:183:VAL:HG11	1.85	0.58
2:B:228:GLU:HB2	2:B:230:HIS:CD2	2.29	0.58
2:C:191:PHE:CE2	2:C:220:LEU:HD13	2.39	0.57
2:B:191:PHE:CE2	2:B:220:LEU:HD13	2.39	0.57
2:C:149:GLN:HB2	2:C:183:VAL:HG11	1.85	0.56
2:A:189:GLN:NE2	2:A:211:ASP:OD1	2.38	0.56
2:C:189:GLN:NE2	2:C:211:ASP:OD1	2.38	0.56
2:B:189:GLN:NE2	2:B:211:ASP:OD1	2.38	0.56
2:A:219:TYR:OH	3:E:1:NAG:N2	2.29	0.55
2:A:112:ILE:HG12	2:A:221:ILE:HD12	1.89	0.54
2:C:112:ILE:HG12	2:C:221:ILE:HD12	1.89	0.54
3:G:1:NAG:H62	4:M:1:XYS:H3	1.90	0.54
2:B:112:ILE:HG12	2:B:221:ILE:HD12	1.89	0.53
2:A:101:THR:HG21	2:A:133:LEU:HD11	1.91	0.52
2:B:101:THR:HG21	2:B:133:LEU:HD11	1.91	0.52
2:C:219:TYR:OH	3:K:1:NAG:N2	2.29	0.52
2:C:168:LEU:HD13	2:C:188:LEU:HD11	1.91	0.52
2:B:156:ASP:HB3	2:B:163:SER:HB2	1.91	0.52
2:B:83:PRO:HG2	2:B:136:ILE:HD11	1.92	0.52
2:A:156:ASP:HB3	2:A:163:SER:HB2	1.91	0.52
2:B:219:TYR:OH	3:H:1:NAG:N2	2.29	0.51
2:A:168:LEU:HD13	2:A:188:LEU:HD11	1.91	0.51
2:C:156:ASP:HB3	2:C:163:SER:HB2	1.91	0.51
2:B:86:CYS:HB3	2:B:236:PRO:HA	1.92	0.51
2:B:168:LEU:HD13	2:B:188:LEU:HD11	1.91	0.51
2:C:101:THR:HG21	2:C:133:LEU:HD11	1.92	0.51
2:A:138:SER:OG	2:C:254:ILE:HG12	2.10	0.51
2:A:162:ILE:O	2:A:223:GLN:HA	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:83:PRO:HG2	2:C:136:ILE:HD11	1.92	0.51
2:C:162:ILE:O	2:C:223:GLN:HA	2.11	0.51
2:A:83:PRO:HG2	2:A:136:ILE:HD11	1.92	0.50
2:A:86:CYS:HB3	2:A:236:PRO:HA	1.92	0.50
2:C:86:CYS:HB3	2:C:236:PRO:HA	1.92	0.50
2:B:157:PHE:HA	2:B:161:LYS:O	2.13	0.49
2:B:162:ILE:O	2:B:223:GLN:HA	2.11	0.49
2:C:157:PHE:HA	2:C:161:LYS:O	2.13	0.49
2:A:103:LEU:HD23	2:A:224:ASN:HA	1.94	0.49
2:C:103:LEU:HD23	2:C:224:ASN:HA	1.94	0.49
2:A:253:TYR:HB3	2:B:124:HIS:NE2	2.27	0.48
2:B:103:LEU:HD23	2:B:224:ASN:HA	1.94	0.48
2:B:191:PHE:CZ	2:B:220:LEU:HD22	2.48	0.48
2:C:107:LEU:HG	2:C:220:LEU:HD12	1.96	0.48
2:C:191:PHE:CZ	2:C:220:LEU:HD22	2.48	0.48
2:A:107:LEU:HG	2:A:220:LEU:HD12	1.96	0.48
2:A:191:PHE:CZ	2:A:220:LEU:HD22	2.48	0.48
2:A:157:PHE:HA	2:A:161:LYS:O	2.13	0.47
2:B:107:LEU:HG	2:B:220:LEU:HD12	1.96	0.47
2:C:191:PHE:CZ	2:C:220:LEU:HD13	2.50	0.47
2:A:187:VAL:HG12	2:A:191:PHE:CE2	2.50	0.47
2:C:187:VAL:HG12	2:C:191:PHE:CE2	2.50	0.47
2:A:165:GLN:HG2	2:A:166:TYR:N	2.30	0.47
2:B:191:PHE:CZ	2:B:220:LEU:HD13	2.50	0.47
2:C:165:GLN:HG2	2:C:166:TYR:N	2.30	0.47
2:A:94:TYR:CE1	2:A:230:HIS:HE1	2.33	0.47
2:A:191:PHE:CZ	2:A:220:LEU:HD13	2.50	0.47
2:B:94:TYR:CE1	2:B:230:HIS:HE1	2.33	0.47
2:B:185:ASN:O	2:B:189:GLN:HG3	2.16	0.46
2:B:134:MET:SD	2:B:137:ILE:HD11	2.56	0.46
2:B:187:VAL:HG12	2:B:191:PHE:CE2	2.50	0.46
2:B:165:GLN:HG2	2:B:166:TYR:N	2.30	0.46
2:A:134:MET:SD	2:A:137:ILE:HD11	2.56	0.46
2:C:185:ASN:O	2:C:189:GLN:HG3	2.16	0.46
2:A:185:ASN:O	2:A:189:GLN:HG3	2.16	0.46
2:B:120:LEU:O	2:B:124:HIS:ND1	2.49	0.46
2:C:94:TYR:CE1	2:C:230:HIS:HE1	2.33	0.46
2:C:120:LEU:O	2:C:124:HIS:ND1	2.49	0.45
2:A:120:LEU:O	2:A:124:HIS:ND1	2.49	0.45
2:B:148:ASN:OD1	2:B:149:GLN:HG2	2.17	0.45
2:C:134:MET:SD	2:C:137:ILE:HD11	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:148:ASN:OD1	2:C:149:GLN:HG2	2.17	0.45
2:A:254:ILE:O	2:B:124:HIS:HE1	2.00	0.45
2:A:252:ILE:HD11	2:C:258:LEU:O	2.17	0.44
2:A:148:ASN:OD1	2:A:149:GLN:HG2	2.17	0.44
2:A:258:LEU:HD23	2:A:258:LEU:HA	1.89	0.44
2:B:120:LEU:HD23	2:B:157:PHE:HE2	1.83	0.43
2:A:120:LEU:HD23	2:A:157:PHE:HE2	1.83	0.42
2:C:113:ILE:HB	2:C:165:GLN:OE1	2.20	0.42
2:C:120:LEU:HD23	2:C:157:PHE:HE2	1.83	0.42
2:A:138:SER:HA	2:C:254:ILE:HD13	2.02	0.42
2:A:113:ILE:HG23	2:A:115:HIS:CD2	2.55	0.42
2:C:182:THR:HG22	2:C:184:ALA:H	1.85	0.42
2:B:182:THR:HG22	2:B:184:ALA:H	1.85	0.41
2:B:113:ILE:HG23	2:B:115:HIS:CD2	2.55	0.41
2:B:132:ALA:O	2:B:136:ILE:HG12	2.20	0.41
2:A:182:THR:HG22	2:A:184:ALA:H	1.85	0.41
2:A:113:ILE:HB	2:A:165:GLN:OE1	2.20	0.41
2:B:113:ILE:HB	2:B:165:GLN:OE1	2.20	0.41
2:C:132:ALA:O	2:C:136:ILE:HG12	2.20	0.41
2:A:132:ALA:O	2:A:136:ILE:HG12	2.20	0.41
2:B:88:LYS:O	2:B:233:PHE:HB2	2.21	0.41
2:A:253:TYR:HB3	2:B:124:HIS:HE2	1.85	0.40
2:C:113:ILE:HG23	2:C:115:HIS:CD2	2.55	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	158/244 (65%)	153 (97%)	5 (3%)	0	100	100
1	b	158/244 (65%)	153 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	c	158/244 (65%)	153 (97%)	5 (3%)	0	100	100
2	A	179/259 (69%)	171 (96%)	8 (4%)	0	100	100
2	B	179/259 (69%)	171 (96%)	8 (4%)	0	100	100
2	C	179/259 (69%)	171 (96%)	8 (4%)	0	100	100
All	All	1011/1509 (67%)	972 (96%)	39 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	143/218 (66%)	141 (99%)	2 (1%)	67	82
1	b	143/218 (66%)	141 (99%)	2 (1%)	67	82
1	c	143/218 (66%)	141 (99%)	2 (1%)	67	82
2	A	168/228 (74%)	168 (100%)	0	100	100
2	B	168/228 (74%)	168 (100%)	0	100	100
2	C	168/228 (74%)	168 (100%)	0	100	100
All	All	933/1338 (70%)	927 (99%)	6 (1%)	86	93

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	a	361	ILE
1	a	419	TYR
1	b	361	ILE
1	b	419	TYR
1	c	361	ILE
1	c	419	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	a	305	HIS
2	A	127	ASN
2	A	230	HIS
2	B	127	ASN
2	B	131	HIS
2	B	230	HIS
2	C	127	ASN
2	C	230	HIS

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

31 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	D	1	2,3	14,14,15	0.38	0	17,19,21	0.51	0
3	NAG	D	2	3	14,14,15	0.20	0	17,19,21	0.40	0
3	NAG	E	1	2,3	14,14,15	0.20	0	17,19,21	0.43	0
3	NAG	E	2	3	14,14,15	0.18	0	17,19,21	0.41	0
3	NAG	F	1	2,3	14,14,15	0.42	0	17,19,21	0.51	0
3	NAG	F	2	3	14,14,15	0.29	0	17,19,21	0.42	0
3	NAG	G	1	2,3	14,14,15	0.38	0	17,19,21	0.51	0
3	NAG	G	2	3	14,14,15	0.21	0	17,19,21	0.42	0
3	NAG	H	1	2,3	14,14,15	0.21	0	17,19,21	0.44	0
3	NAG	H	2	3	14,14,15	0.20	0	17,19,21	0.41	0
3	NAG	I	1	2,3	14,14,15	0.44	0	17,19,21	0.50	0
3	NAG	I	2	3	14,14,15	0.29	0	17,19,21	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	NAG	J	1	2,3	14,14,15	0.38	0	17,19,21	0.50	0
3	NAG	J	2	3	14,14,15	0.18	0	17,19,21	0.40	0
3	NAG	K	1	2,3	14,14,15	0.19	0	17,19,21	0.43	0
3	NAG	K	2	3	14,14,15	0.19	0	17,19,21	0.41	0
3	NAG	L	1	2,3	14,14,15	0.42	0	17,19,21	0.51	0
3	NAG	L	2	3	14,14,15	0.28	0	17,19,21	0.41	0
4	XYS	M	1	4	10,10,10	1.94	2 (20%)	14,14,14	0.98	1 (7%)
4	BDP	M	10	4	9,12,13	2.13	3 (33%)	12,17,19	2.50	5 (41%)
4	XYS	M	11	4	9,9,10	1.77	2 (22%)	10,12,14	1.25	1 (10%)
4	BDP	M	12	4	9,12,13	2.42	4 (44%)	12,17,19	1.05	0
4	XYS	M	13	4	9,9,10	1.78	2 (22%)	10,12,14	1.08	1 (10%)
4	BDP	M	2	4	9,12,13	2.44	4 (44%)	12,17,19	0.97	1 (8%)
4	XYS	M	3	4	9,9,10	1.60	2 (22%)	10,12,14	3.19	4 (40%)
4	BDP	M	4	4	9,12,13	2.38	4 (44%)	12,17,19	1.69	1 (8%)
4	XYS	M	5	4	9,9,10	1.78	2 (22%)	10,12,14	0.95	0
4	BDP	M	6	4	9,12,13	2.32	3 (33%)	12,17,19	1.75	1 (8%)
4	XYS	M	7	4	9,9,10	1.94	3 (33%)	10,12,14	1.22	1 (10%)
4	BDP	M	8	4	9,12,13	2.41	4 (44%)	12,17,19	1.14	1 (8%)
4	XYS	M	9	4	9,9,10	1.84	3 (33%)	10,12,14	0.72	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
3	NAG	D	1	2,3	-	1/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	NAG	E	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	NAG	F	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	2/6/23/26	0/1/1/1
3	NAG	G	1	2,3	-	1/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
3	NAG	H	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	J	1	2,3	-	1/6/23/26	0/1/1/1
3	NAG	J	2	3	-	2/6/23/26	0/1/1/1
3	NAG	K	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	K	2	3	-	0/6/23/26	0/1/1/1
3	NAG	L	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	L	2	3	-	2/6/23/26	0/1/1/1
4	XYS	M	1	4	-	-	0/1/1/1
4	BDP	M	10	4	-	0/0/21/24	0/1/1/1
4	XYS	M	11	4	-	-	0/1/1/1
4	BDP	M	12	4	-	0/0/21/24	0/1/1/1
4	XYS	M	13	4	-	-	0/1/1/1
4	BDP	M	2	4	-	0/0/21/24	0/1/1/1
4	XYS	M	3	4	-	-	0/1/1/1
4	BDP	M	4	4	-	0/0/21/24	0/1/1/1
4	XYS	M	5	4	-	-	0/1/1/1
4	BDP	M	6	4	-	0/0/21/24	0/1/1/1
4	XYS	M	7	4	-	-	0/1/1/1
4	BDP	M	8	4	-	0/0/21/24	0/1/1/1
4	XYS	M	9	4	-	-	0/1/1/1

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	M	1	XYS	O5-C1	4.95	1.49	1.43
4	M	2	BDP	C2-C3	-4.30	1.46	1.52
4	M	8	BDP	C2-C3	-4.22	1.46	1.52
4	M	12	BDP	C2-C3	-4.21	1.46	1.52
4	M	7	XYS	O5-C1	4.07	1.50	1.42
4	M	4	BDP	C2-C3	-4.05	1.46	1.52
4	M	6	BDP	O3-C3	4.02	1.52	1.43
4	M	10	BDP	O3-C3	3.96	1.52	1.43
4	M	6	BDP	C2-C3	-3.93	1.46	1.52
4	M	2	BDP	O3-C3	3.90	1.52	1.43
4	M	4	BDP	O3-C3	3.88	1.52	1.43
4	M	8	BDP	O3-C3	3.83	1.52	1.43
4	M	12	BDP	O3-C3	3.77	1.51	1.43
4	M	11	XYS	O5-C1	3.72	1.50	1.42
4	M	13	XYS	O5-C1	3.71	1.50	1.42
4	M	9	XYS	O5-C1	3.70	1.50	1.42
4	M	5	XYS	O5-C1	3.59	1.49	1.42
4	M	10	BDP	C2-C3	-3.59	1.47	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	M	3	XYS	O5-C1	3.53	1.49	1.42
4	M	12	BDP	O5-C1	3.28	1.49	1.43
4	M	8	BDP	O5-C1	3.17	1.48	1.43
4	M	4	BDP	O5-C1	3.11	1.48	1.43
4	M	2	BDP	O5-C1	3.02	1.48	1.43
4	M	6	BDP	O5-C1	2.90	1.48	1.43
4	M	9	XYS	O5-C5	2.78	1.48	1.42
4	M	5	XYS	O5-C5	2.72	1.48	1.42
4	M	7	XYS	O5-C5	2.69	1.48	1.42
4	M	11	XYS	O5-C5	2.60	1.47	1.42
4	M	1	XYS	O5-C5	2.58	1.47	1.43
4	M	13	XYS	O5-C5	2.58	1.47	1.42
4	M	10	BDP	O5-C1	2.50	1.47	1.43
4	M	2	BDP	O5-C5	2.47	1.46	1.43
4	M	8	BDP	O5-C5	2.33	1.46	1.43
4	M	3	XYS	O5-C5	2.28	1.47	1.42
4	M	12	BDP	O5-C5	2.27	1.46	1.43
4	M	4	BDP	O5-C5	2.21	1.46	1.43
4	M	7	XYS	C2-C3	-2.01	1.49	1.52
4	M	9	XYS	C2-C3	-2.01	1.49	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	M	3	XYS	C1-C2-C3	7.05	118.34	109.67
4	M	10	BDP	C1-C2-C3	5.77	116.75	109.67
4	M	3	XYS	C4-C3-C2	5.33	117.25	110.92
4	M	6	BDP	C1-C2-C3	4.78	115.54	109.67
4	M	4	BDP	C1-C2-C3	4.27	114.91	109.67
4	M	10	BDP	C2-C3-C4	4.04	117.89	110.89
4	M	7	XYS	C1-C2-C3	3.43	113.88	109.67
4	M	3	XYS	C5-C4-C3	3.15	113.54	109.67
4	M	10	BDP	C3-C4-C5	3.10	115.40	109.02
4	M	11	XYS	C1-C2-C3	3.07	113.44	109.67
4	M	3	XYS	C5-O5-C1	-2.90	107.07	111.52
4	M	8	BDP	C1-C2-C3	2.50	112.73	109.67
4	M	1	XYS	C5-O5-C1	-2.48	108.54	112.71
4	M	13	XYS	C1-C2-C3	2.33	112.52	109.67
4	M	10	BDP	O3-C3-C2	-2.05	106.07	109.99
4	M	10	BDP	C1-O5-C5	-2.03	108.59	112.17
4	M	2	BDP	C6-C5-C4	-2.00	108.04	113.04

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	2	NAG	O5-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6
3	J	2	NAG	O5-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6
3	L	2	NAG	O5-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6
3	I	1	NAG	O5-C5-C6-O6
3	L	1	NAG	O5-C5-C6-O6
3	F	1	NAG	C4-C5-C6-O6
3	I	1	NAG	C4-C5-C6-O6
3	L	1	NAG	C4-C5-C6-O6
3	E	1	NAG	O5-C5-C6-O6
3	K	1	NAG	O5-C5-C6-O6
3	J	2	NAG	C4-C5-C6-O6
3	H	1	NAG	O5-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	E	1	NAG	C4-C5-C6-O6
3	H	1	NAG	C4-C5-C6-O6
3	K	1	NAG	C4-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
3	I	2	NAG	C4-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	J	1	NAG	O5-C5-C6-O6

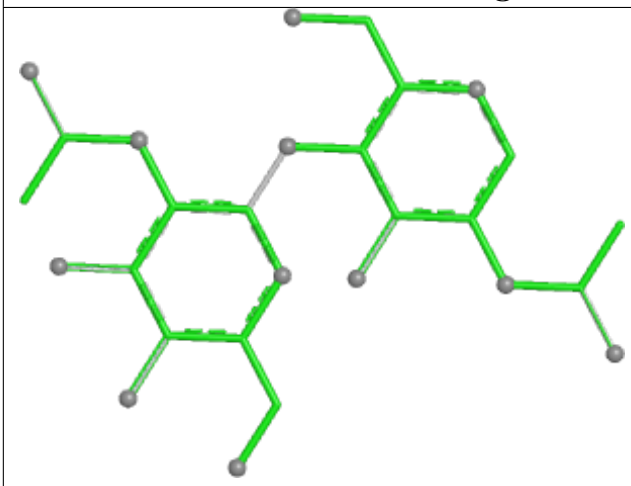
There are no ring outliers.

7 monomers are involved in 7 short contacts:

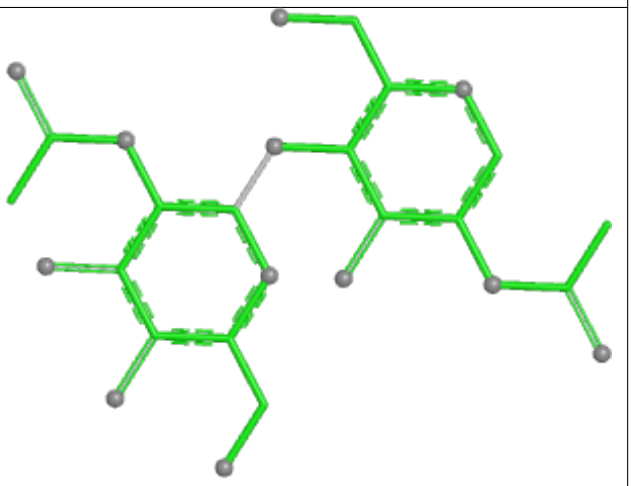
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1	NAG	1	0
3	E	1	NAG	1	0
3	H	1	NAG	1	0
3	K	1	NAG	1	0
4	M	1	XYS	1	0
3	J	1	NAG	1	0
3	G	1	NAG	2	0

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

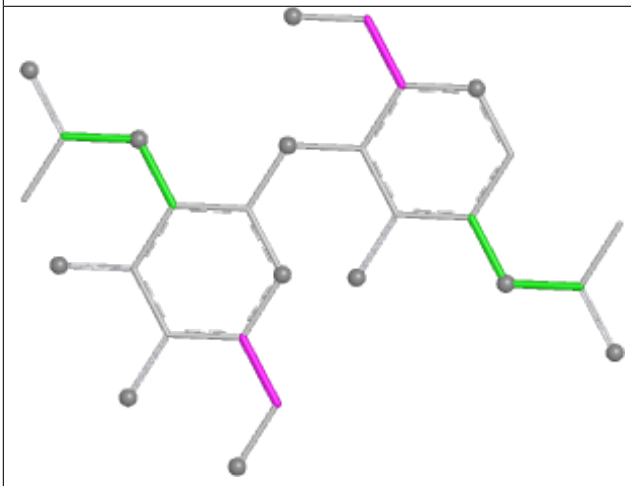
Oligosaccharide Chain D



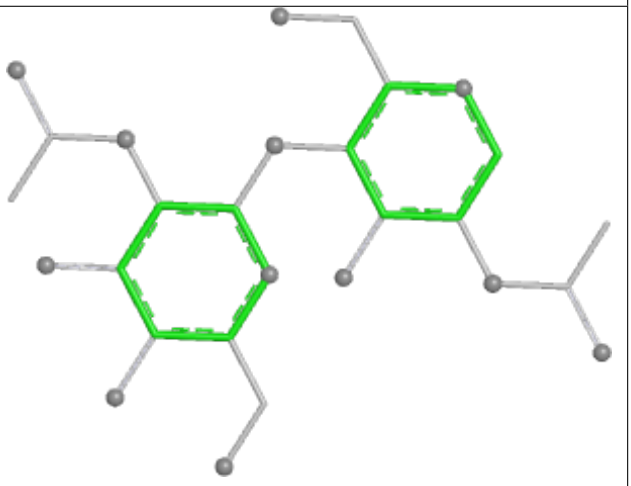
Bond lengths



Bond angles

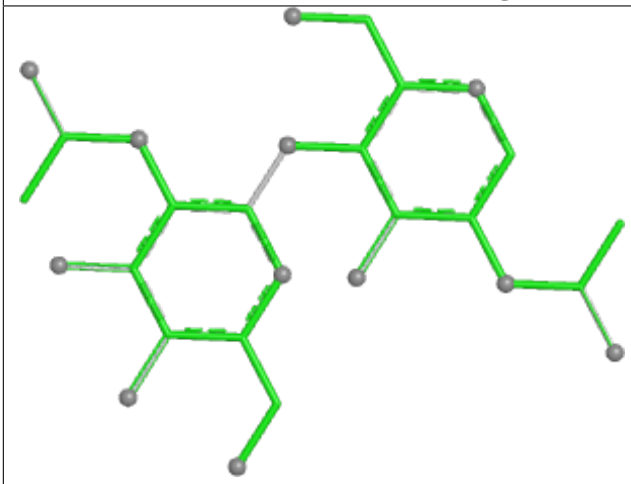


Torsions

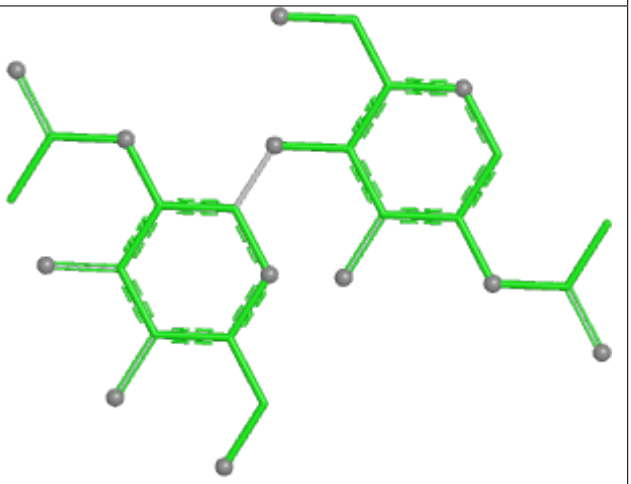


Rings

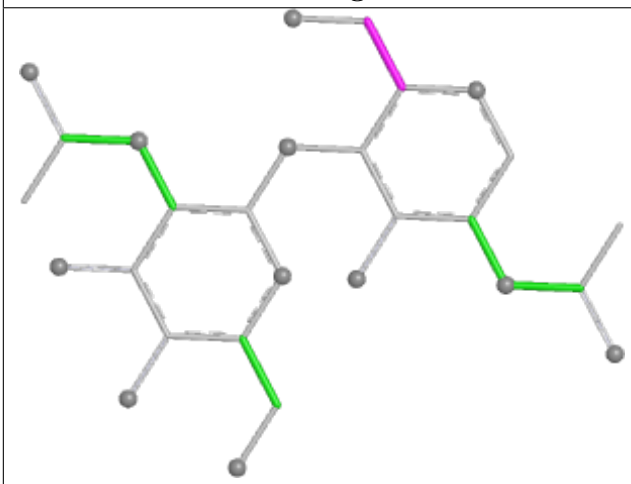
Oligosaccharide Chain E



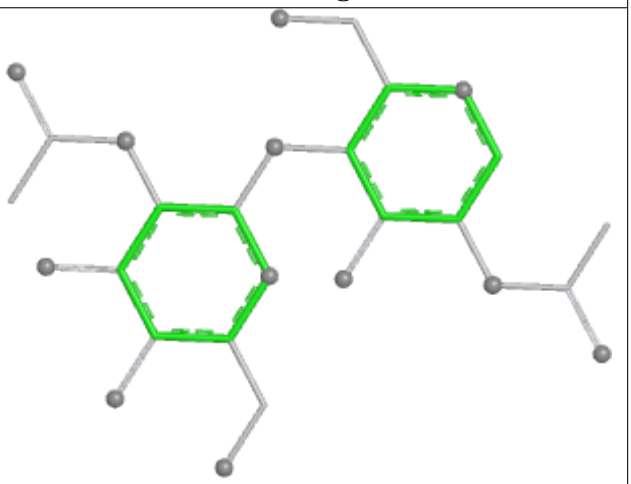
Bond lengths



Bond angles

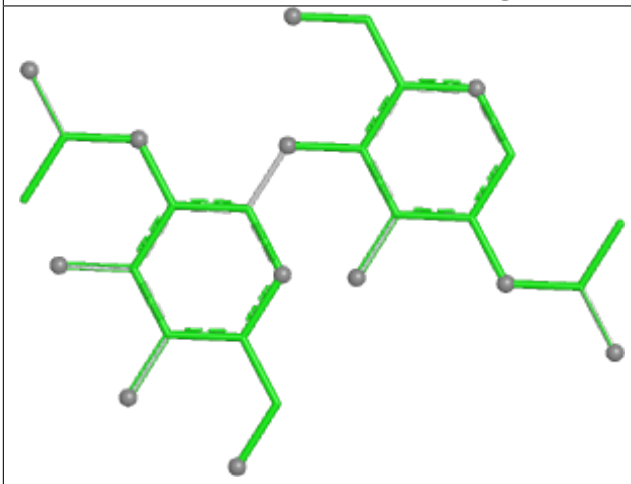


Torsions

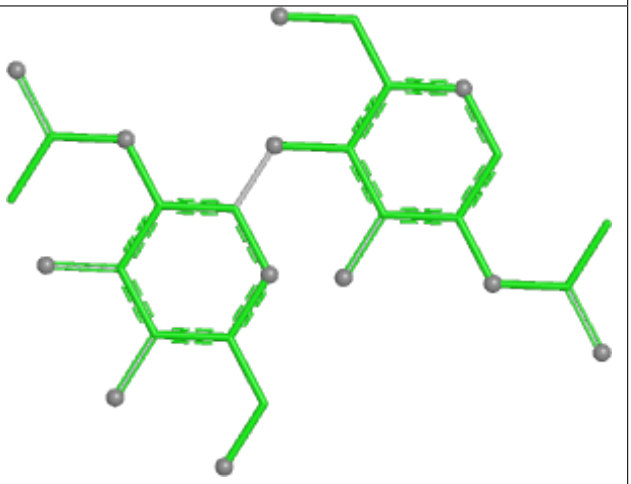


Rings

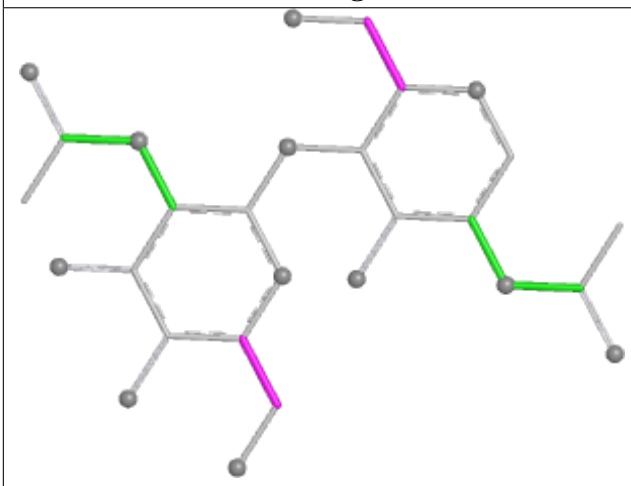
Oligosaccharide Chain F



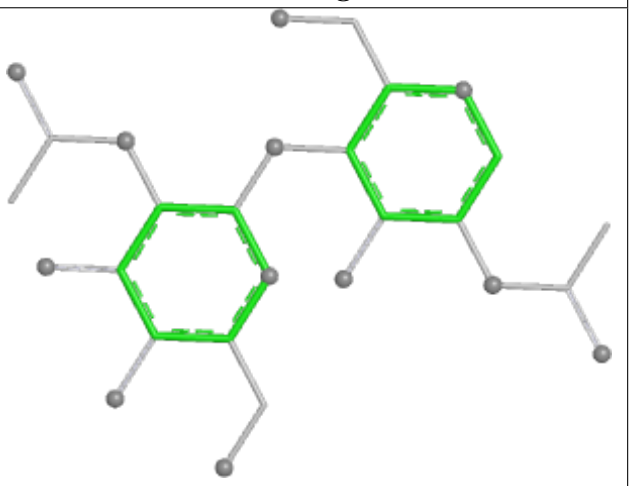
Bond lengths



Bond angles

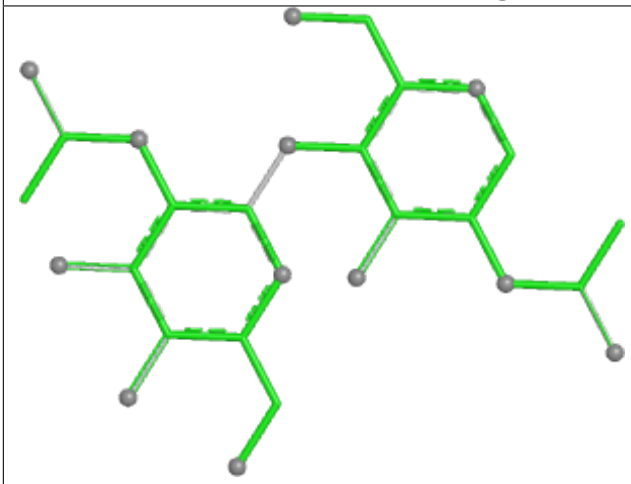


Torsions

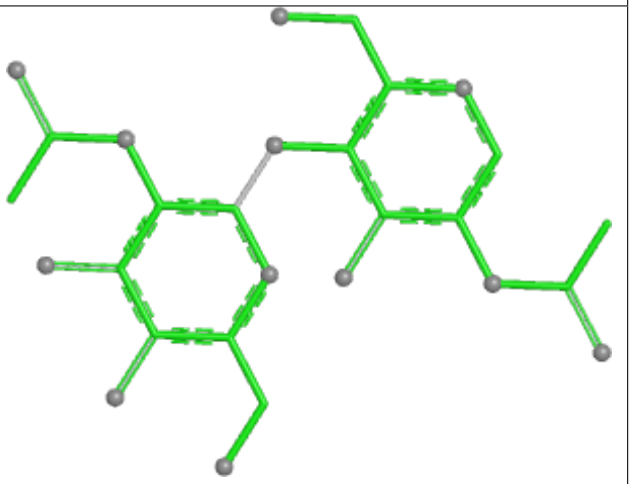


Rings

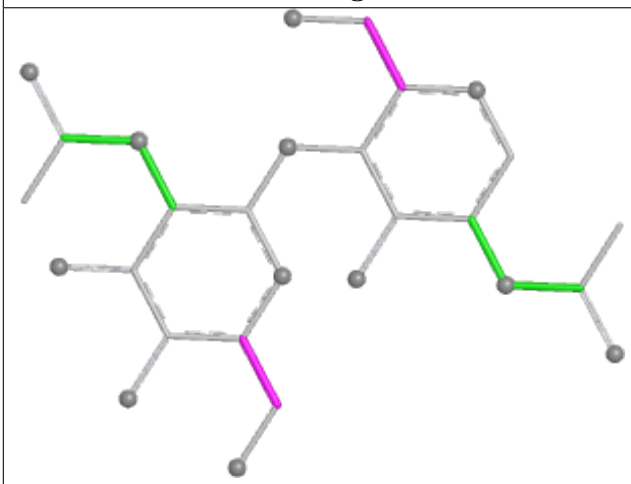
Oligosaccharide Chain G



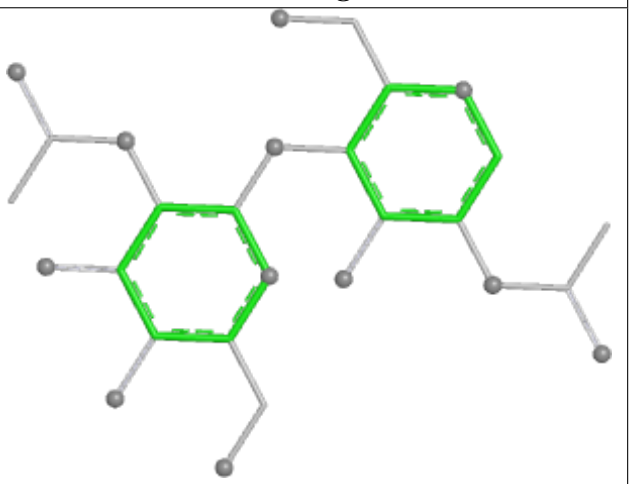
Bond lengths



Bond angles

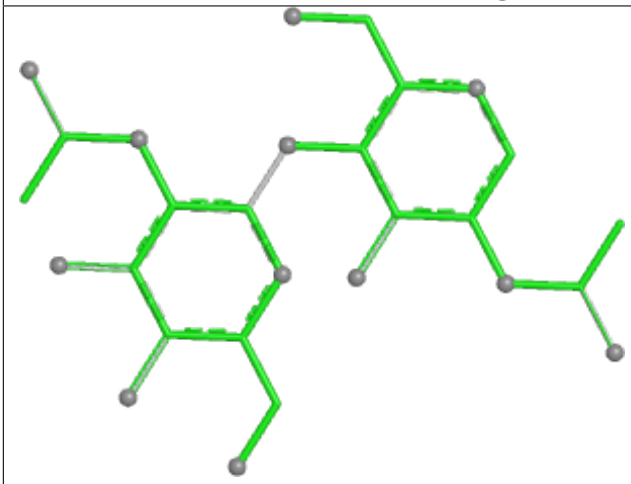


Torsions

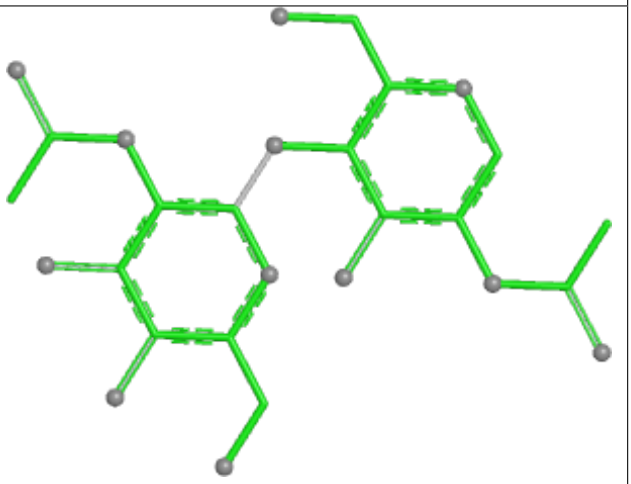


Rings

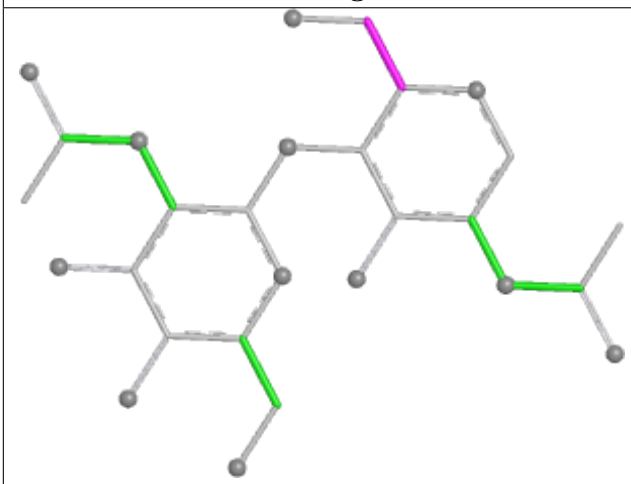
Oligosaccharide Chain H



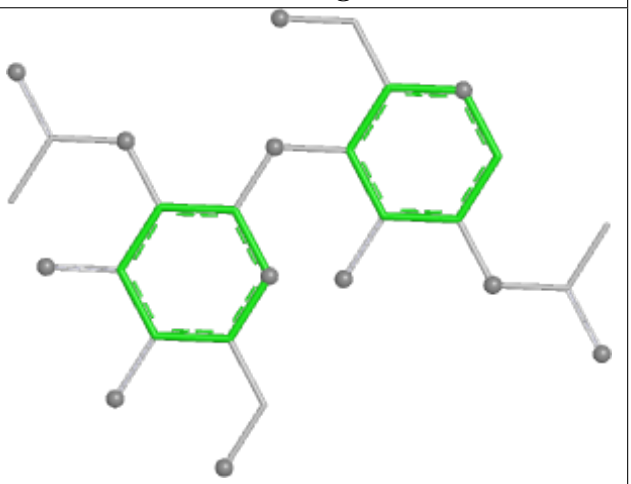
Bond lengths



Bond angles

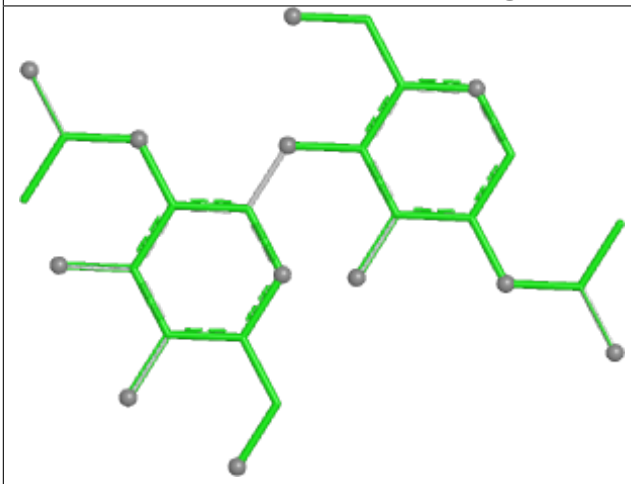


Torsions

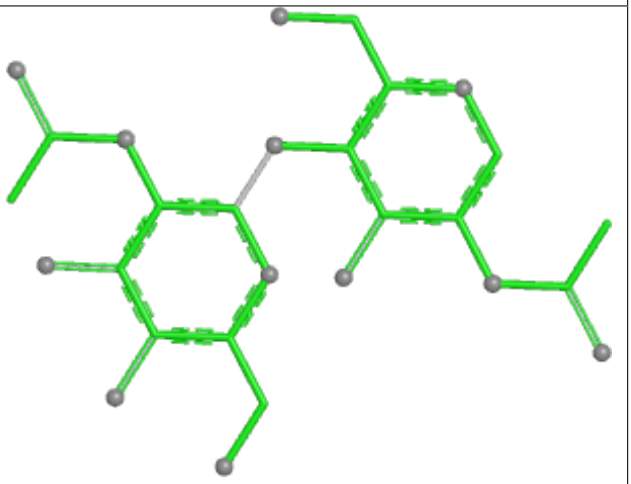


Rings

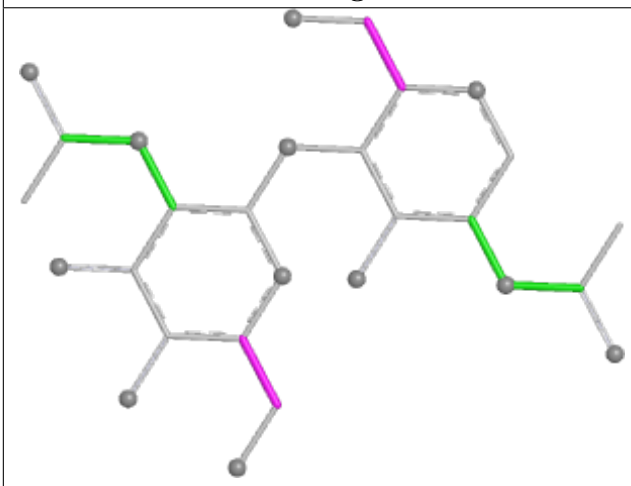
Oligosaccharide Chain I



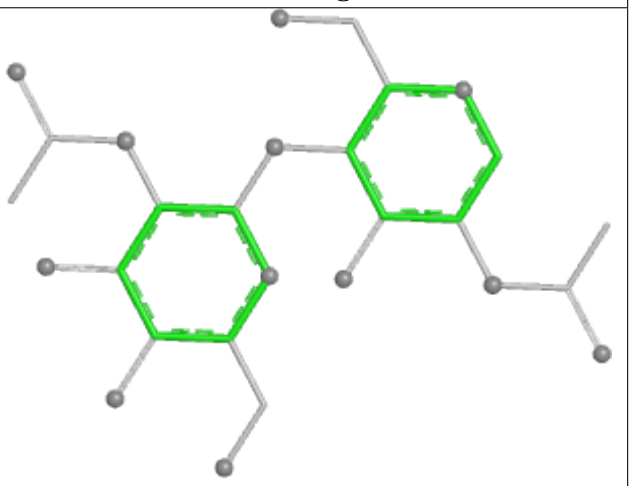
Bond lengths



Bond angles

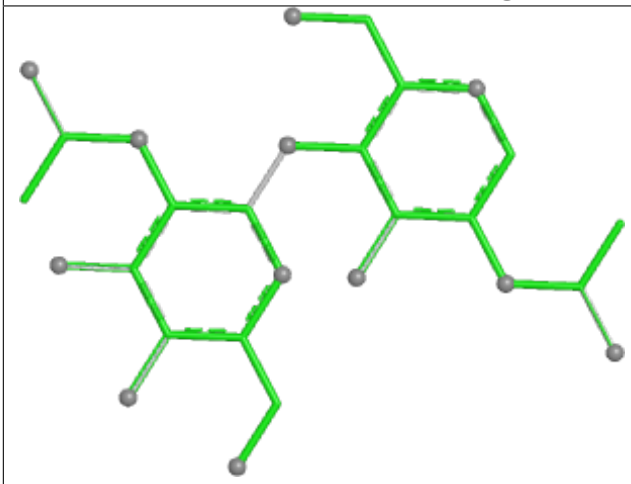


Torsions

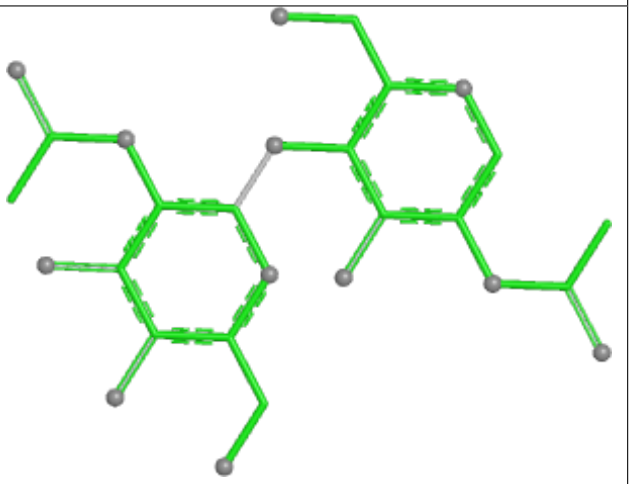


Rings

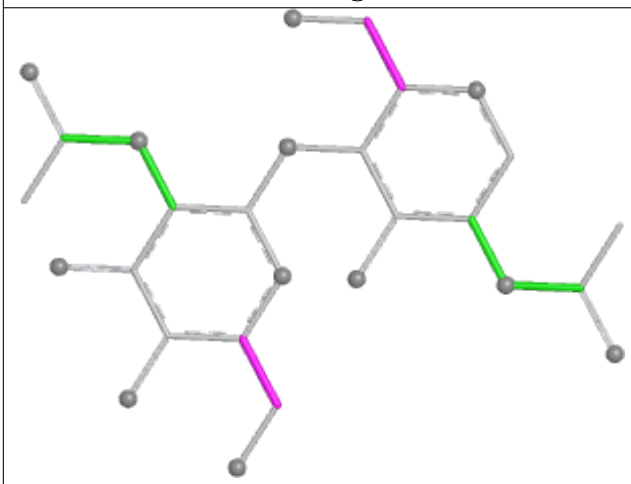
Oligosaccharide Chain J



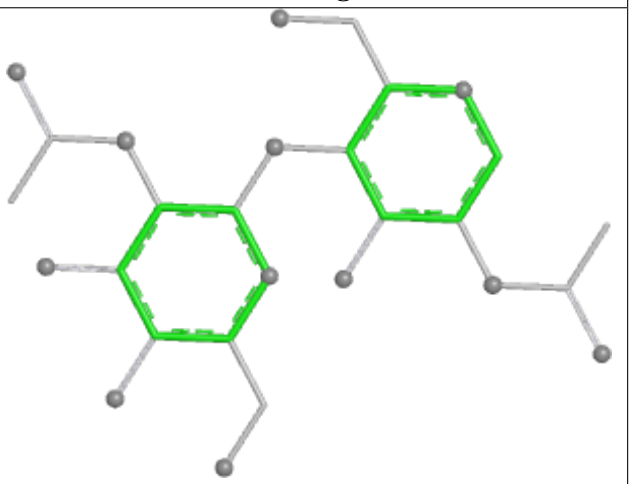
Bond lengths



Bond angles

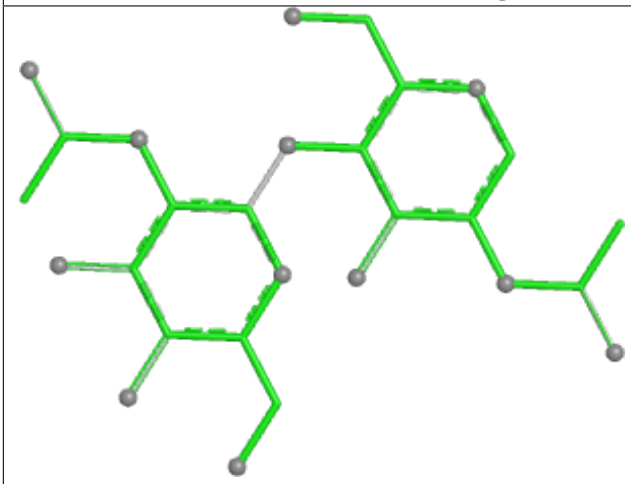


Torsions

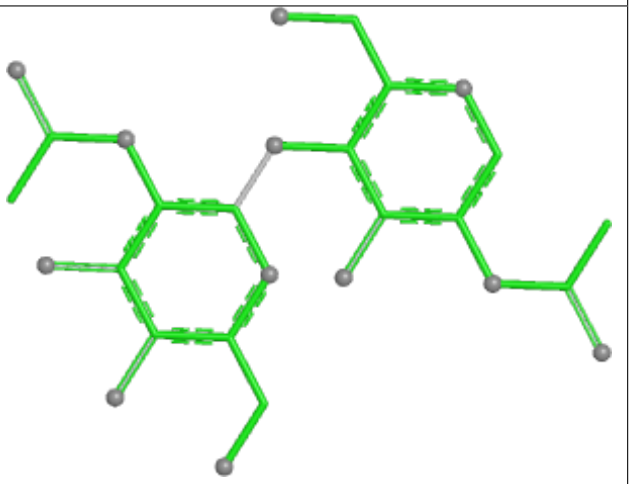


Rings

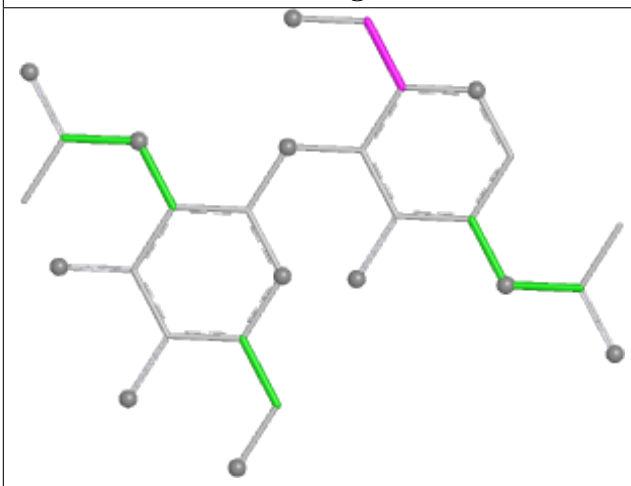
Oligosaccharide Chain K



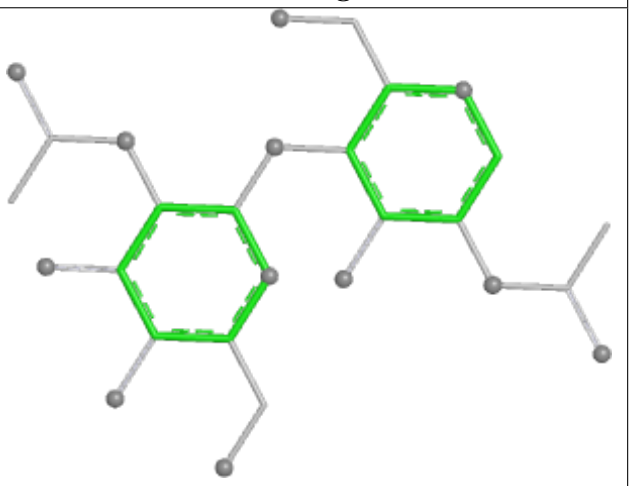
Bond lengths



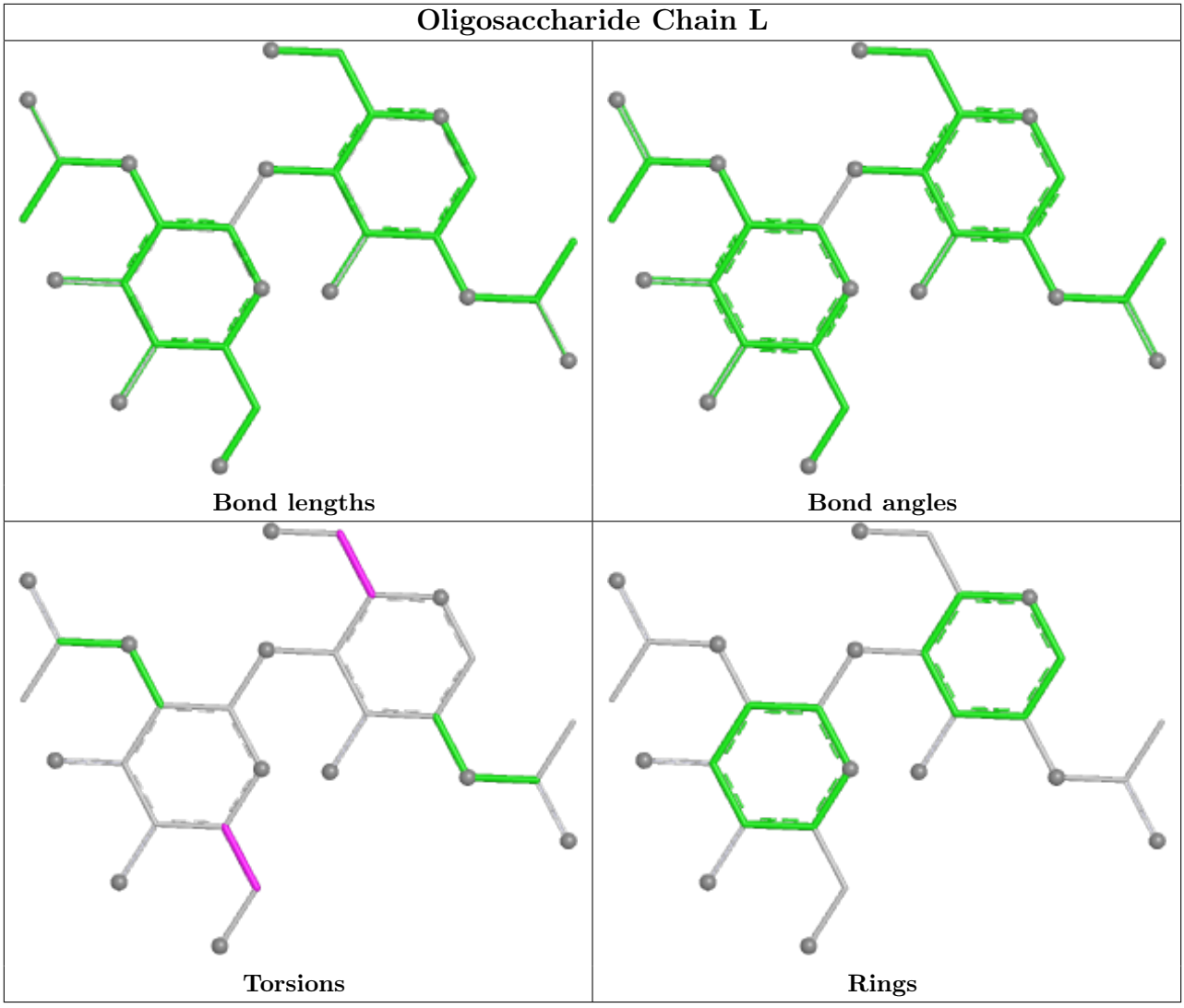
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

12 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	$\#\|Z\| > 2$
5	NAG	c	601	1	14,14,15	0.26	0	17,19,21	0.46	0
5	NAG	B	301	2	14,14,15	0.25	0	17,19,21	0.42	0
5	NAG	b	601	1	14,14,15	0.25	0	17,19,21	0.46	0
5	NAG	b	602	1	14,14,15	0.21	0	17,19,21	0.41	0
5	NAG	C	302	2	14,14,15	0.38	0	17,19,21	0.36	0
5	NAG	B	302	2	14,14,15	0.39	0	17,19,21	0.37	0
5	NAG	a	602	1	14,14,15	0.22	0	17,19,21	0.41	0
5	NAG	a	601	1	14,14,15	0.25	0	17,19,21	0.45	0
5	NAG	A	301	2	14,14,15	0.25	0	17,19,21	0.42	0
5	NAG	C	301	2	14,14,15	0.26	0	17,19,21	0.41	0
5	NAG	A	302	2	14,14,15	0.39	0	17,19,21	0.36	0
5	NAG	c	602	1	14,14,15	0.23	0	17,19,21	0.41	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
5	NAG	c	601	1	-	1/6/23/26	0/1/1/1
5	NAG	B	301	2	-	0/6/23/26	0/1/1/1
5	NAG	b	601	1	-	1/6/23/26	0/1/1/1
5	NAG	b	602	1	-	0/6/23/26	0/1/1/1
5	NAG	C	302	2	-	2/6/23/26	0/1/1/1
5	NAG	B	302	2	-	2/6/23/26	0/1/1/1
5	NAG	a	602	1	-	0/6/23/26	0/1/1/1
5	NAG	a	601	1	-	1/6/23/26	0/1/1/1
5	NAG	A	301	2	-	0/6/23/26	0/1/1/1
5	NAG	C	301	2	-	0/6/23/26	0/1/1/1
5	NAG	A	302	2	-	2/6/23/26	0/1/1/1
5	NAG	c	602	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	302	NAG	O5-C5-C6-O6
5	B	302	NAG	O5-C5-C6-O6
5	C	302	NAG	O5-C5-C6-O6
5	A	302	NAG	C4-C5-C6-O6
5	B	302	NAG	C4-C5-C6-O6
5	C	302	NAG	C4-C5-C6-O6
5	a	601	NAG	O5-C5-C6-O6
5	b	601	NAG	O5-C5-C6-O6
5	c	601	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

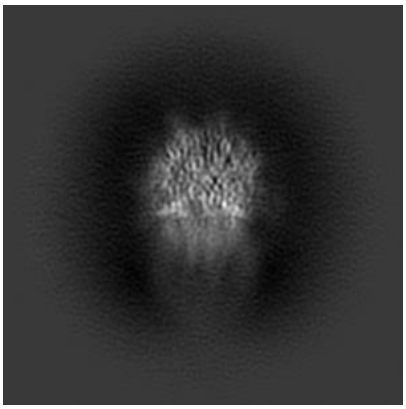
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13667. These allow visual inspection of the internal detail of the map and identification of artifacts.

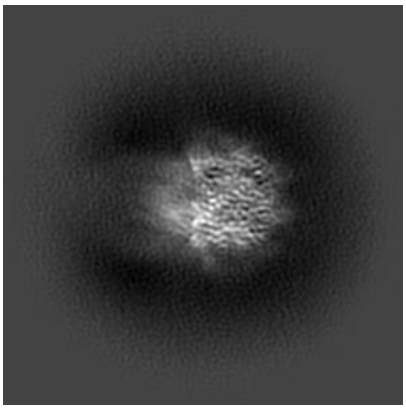
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

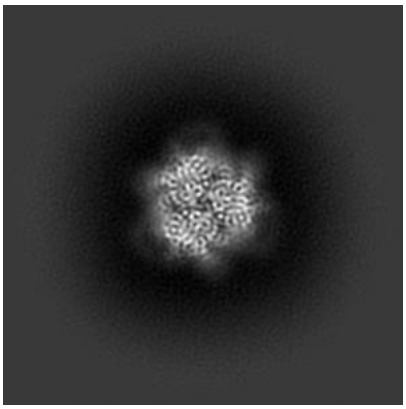
6.1.1 Primary map



X

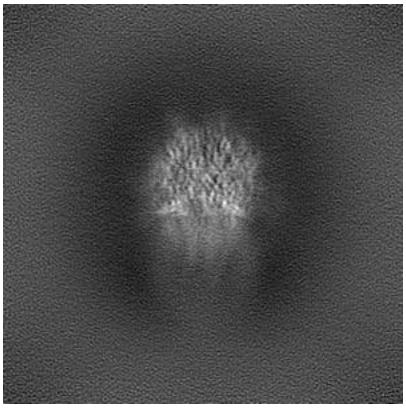


Y

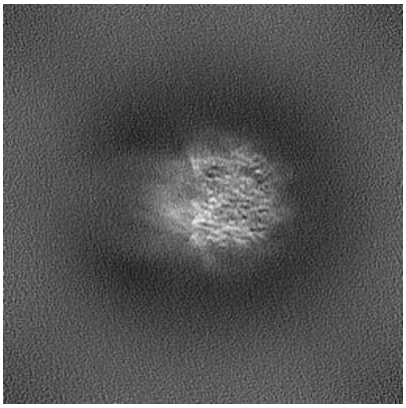


Z

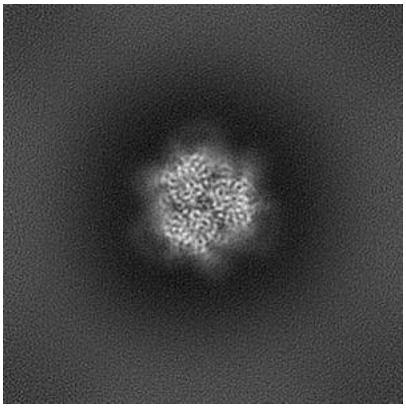
6.1.2 Raw map



X



Y

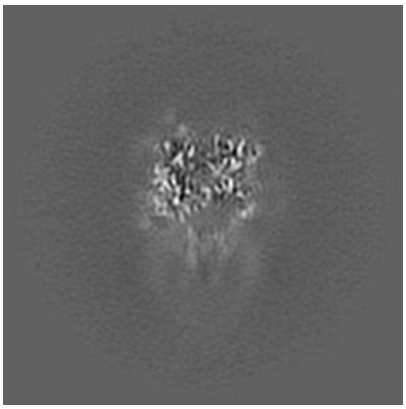


Z

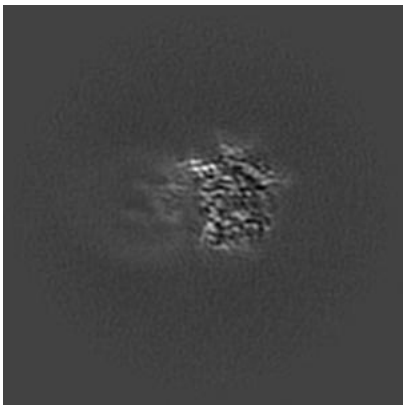
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

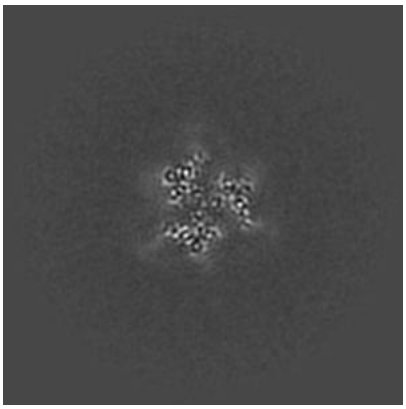
6.2.1 Primary map



X Index: 128

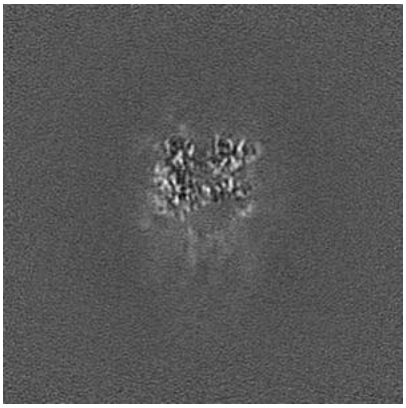


Y Index: 128

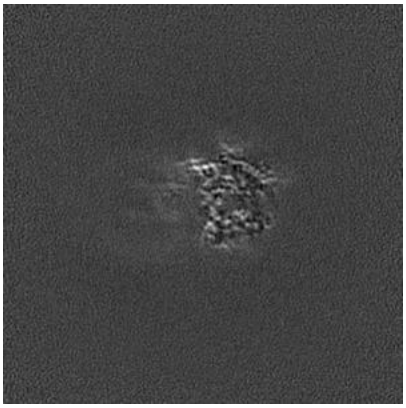


Z Index: 128

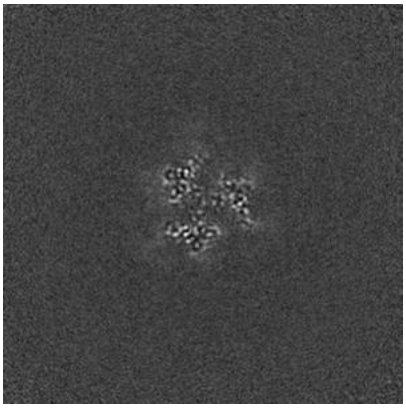
6.2.2 Raw map



X Index: 128



Y Index: 128

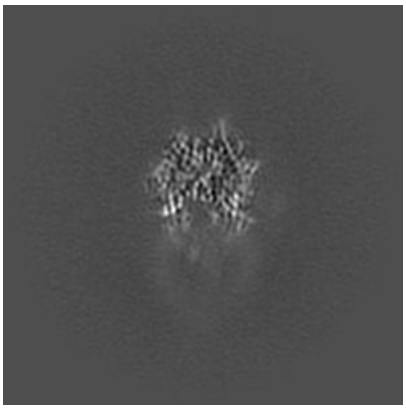


Z Index: 128

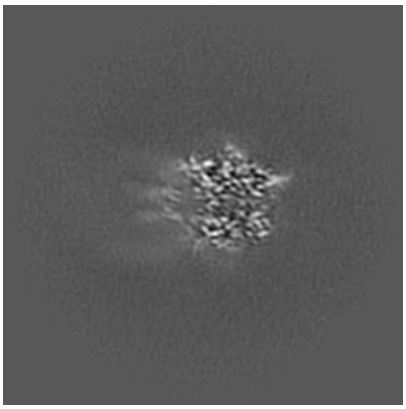
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

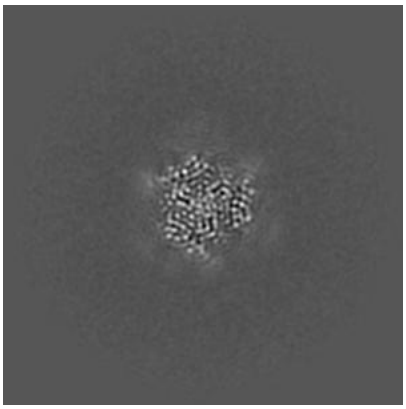
6.3.1 Primary map



X Index: 116

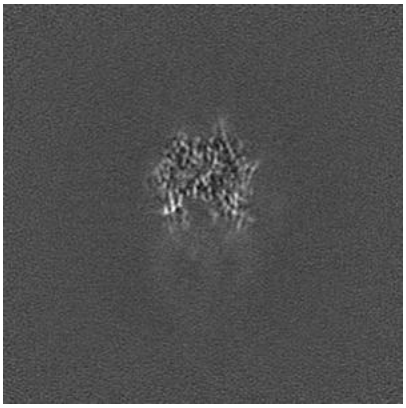


Y Index: 132

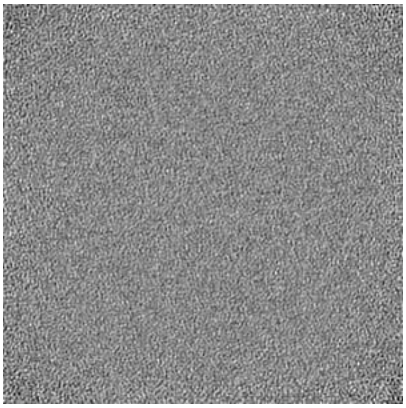


Z Index: 133

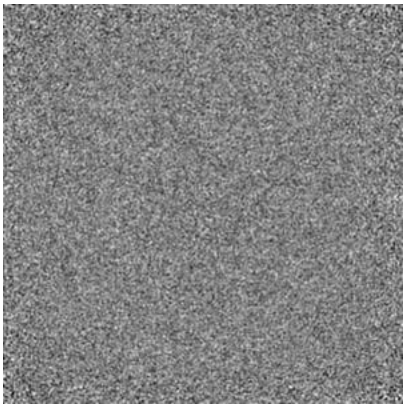
6.3.2 Raw map



X Index: 116



Y Index: 0

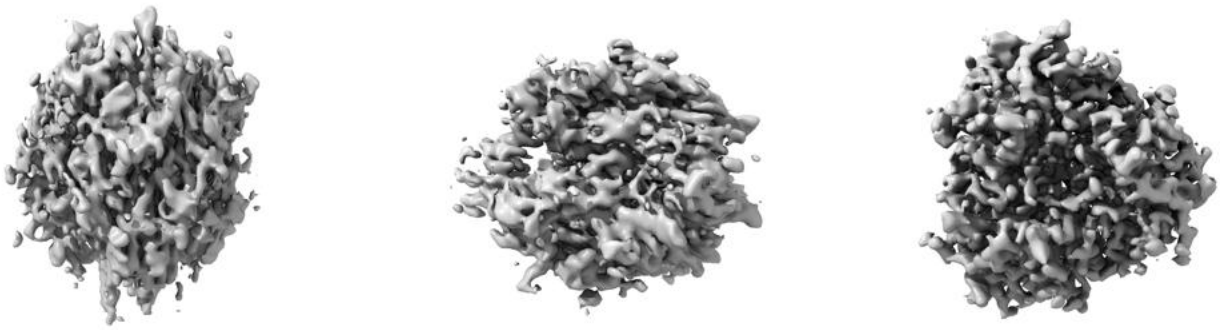


Z Index: 0

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

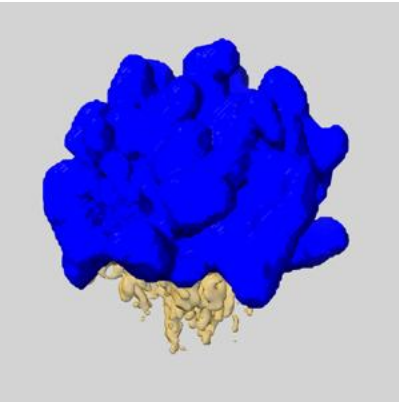
6.5 Mask visualisation (i)

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

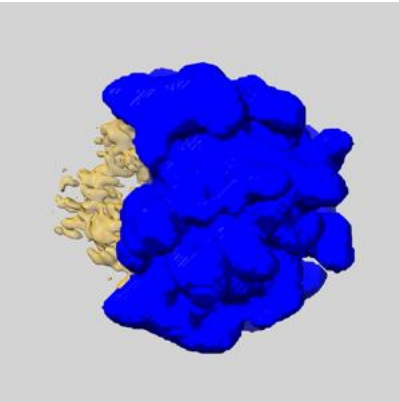
A mask typically either:

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

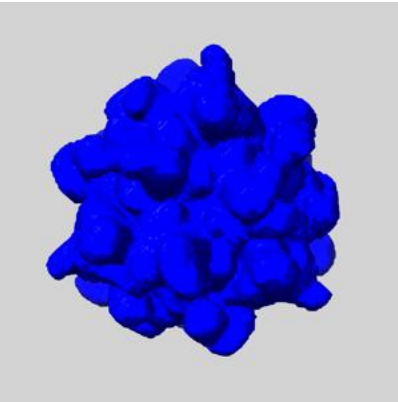
6.5.1 emd_13667_msk_1.map (i)



X



Y

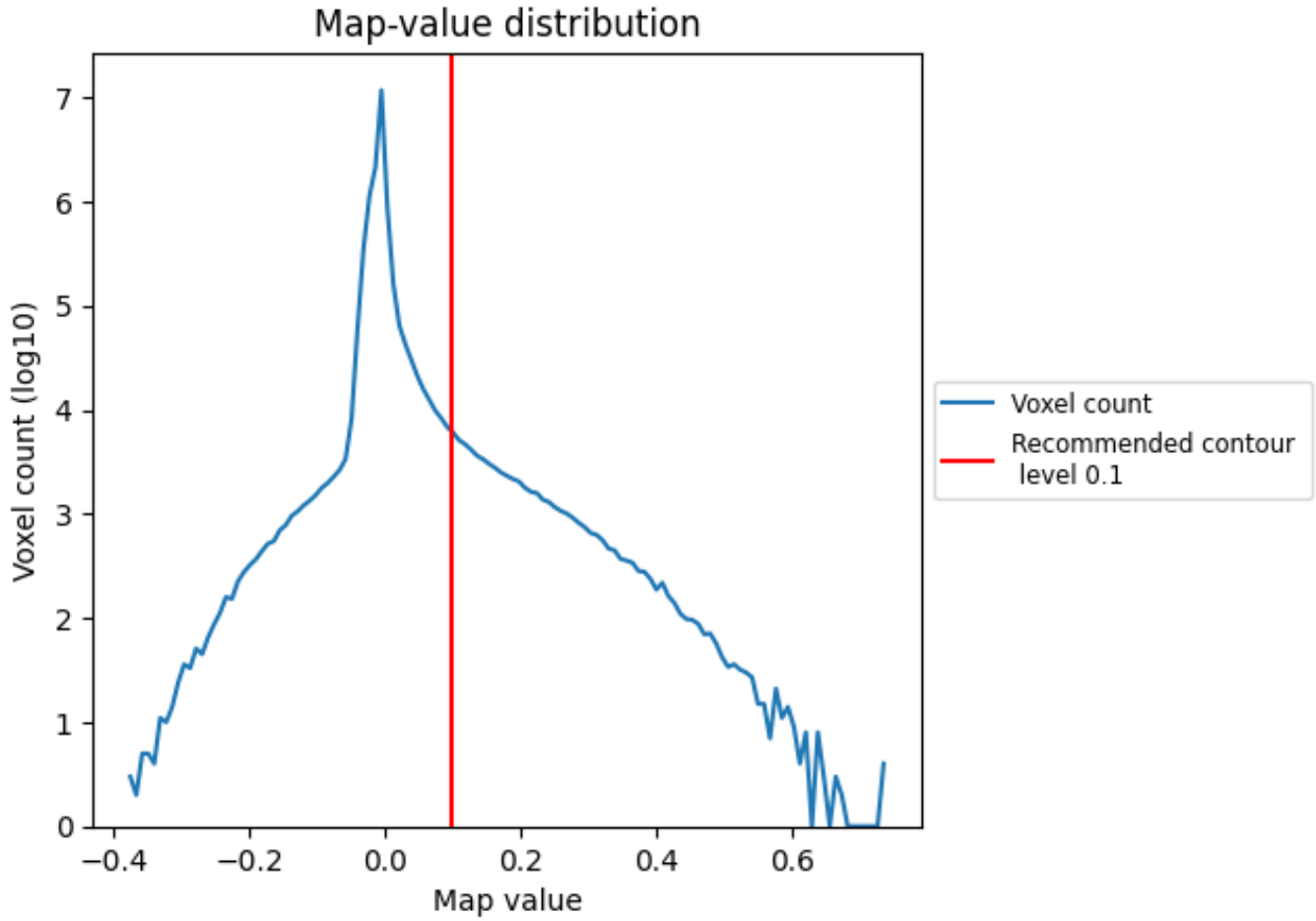


Z

7 Map analysis

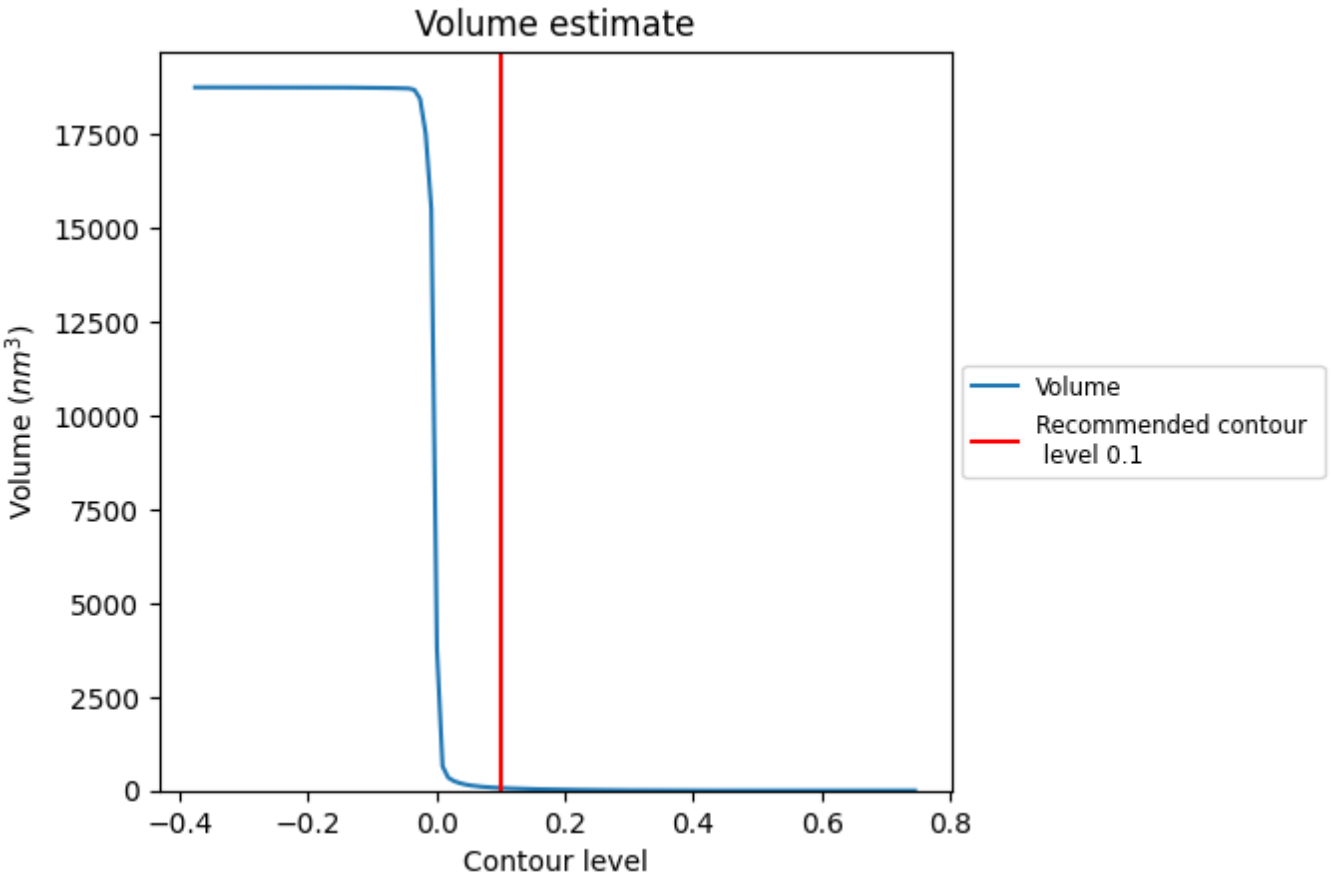
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

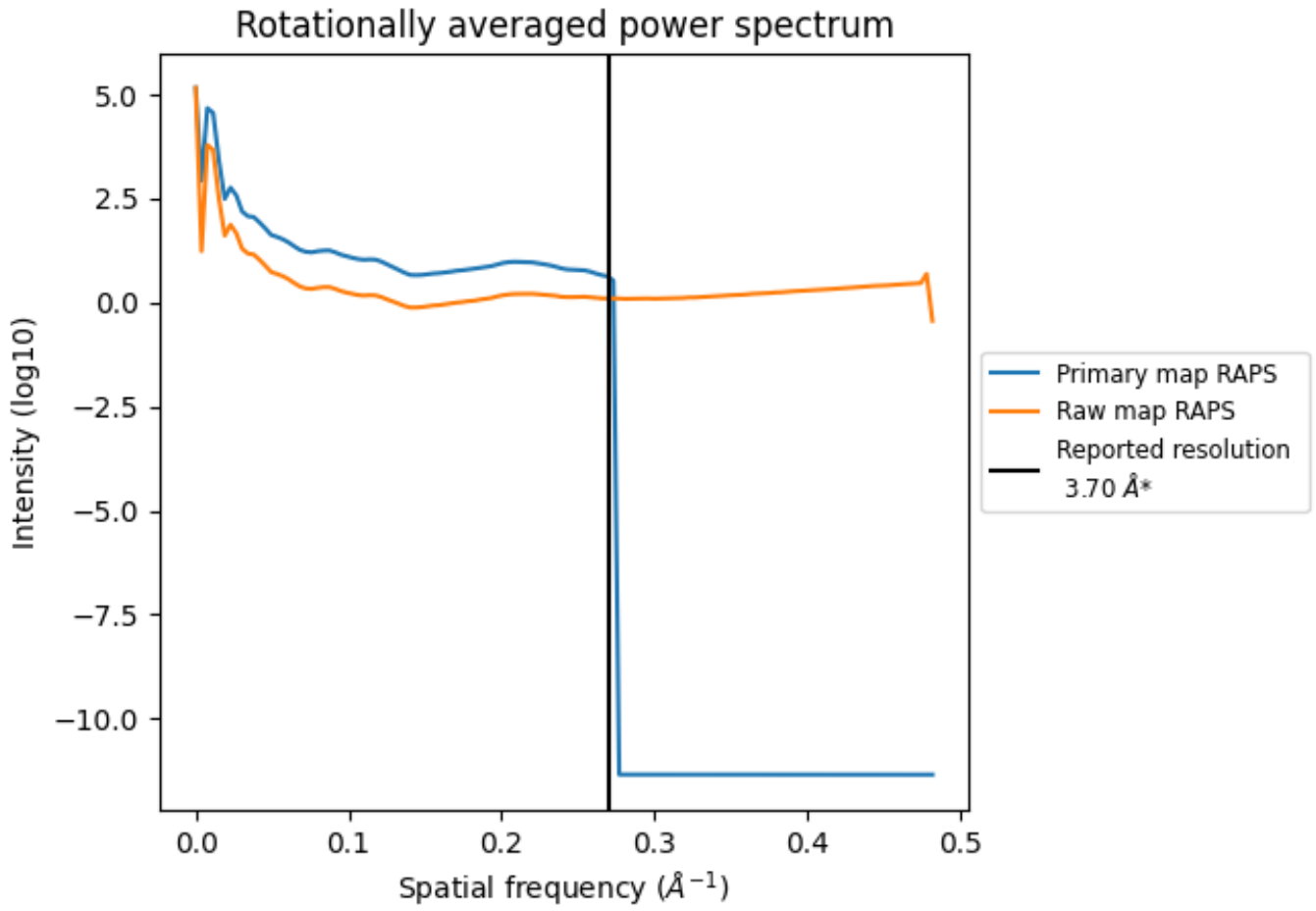
7.2 Volume estimate



The volume at the recommended contour level is 70 nm^3; this corresponds to an approximate mass of 63 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)

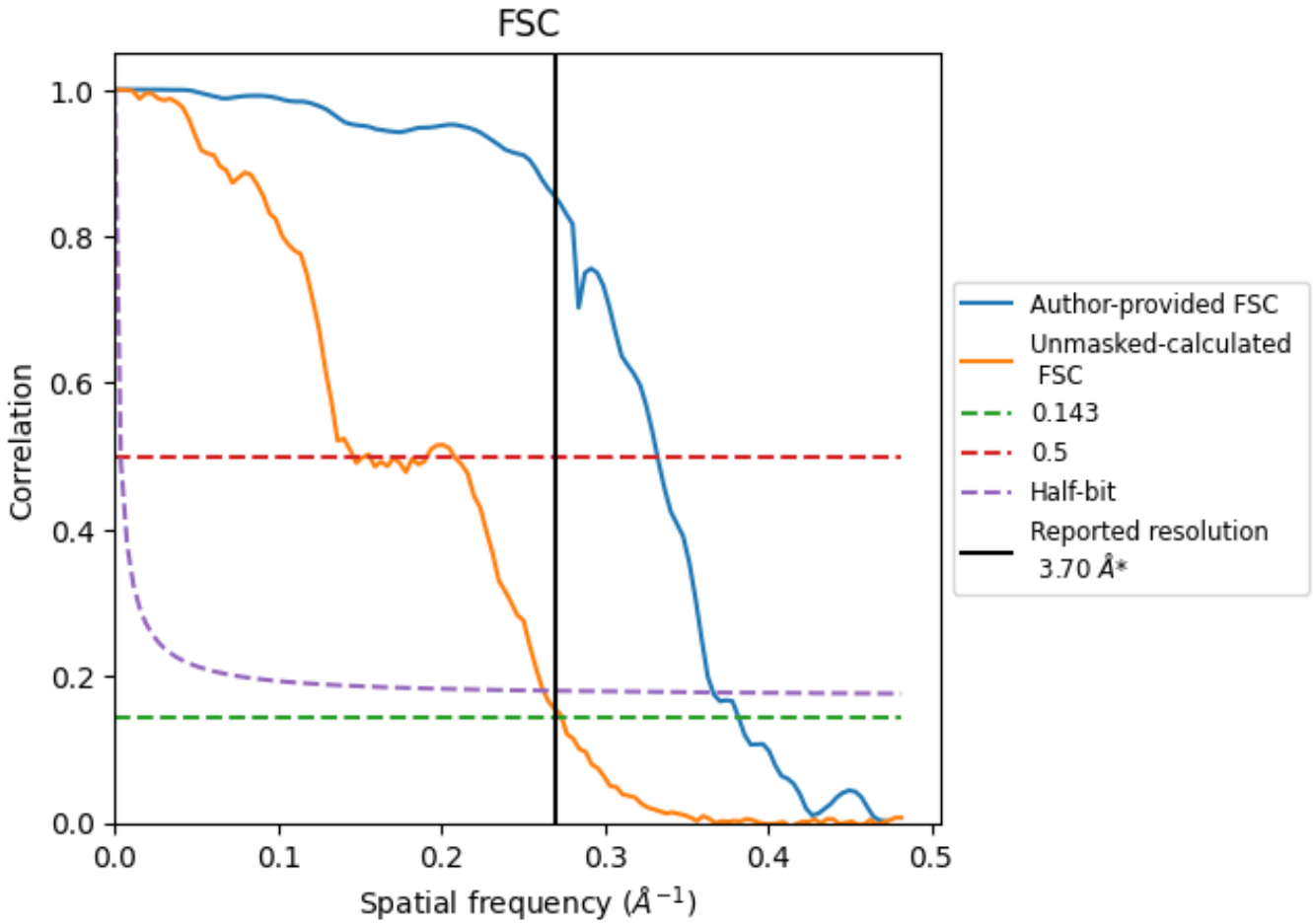


*Reported resolution corresponds to spatial frequency of 0.270 Å^{-1}

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 0.270 Å^{-1}

8.2 Resolution estimates (i)

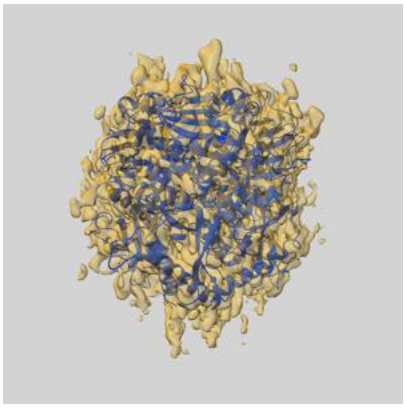
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	Other
Reported by author	-	-	-	3.70
Author-provided FSC curve	2.62	3.01	2.73	-
Unmasked-calculated*	3.65	6.85	3.81	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

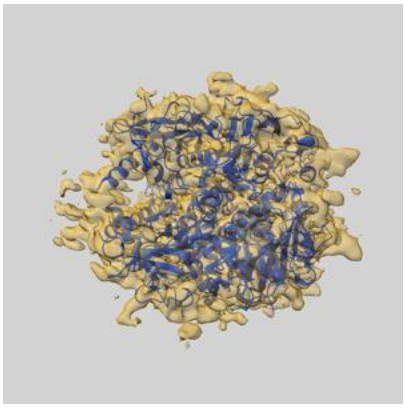
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-13667 and PDB model 7PVD. Per-residue inclusion information can be found in section 3 on page 8.

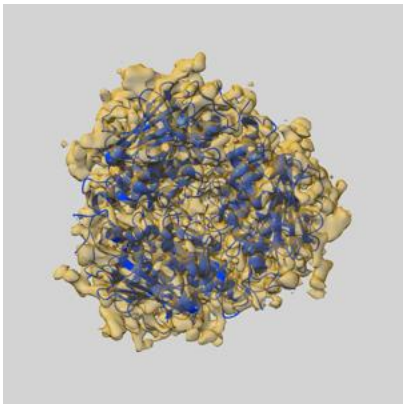
9.1 Map-model overlay



X



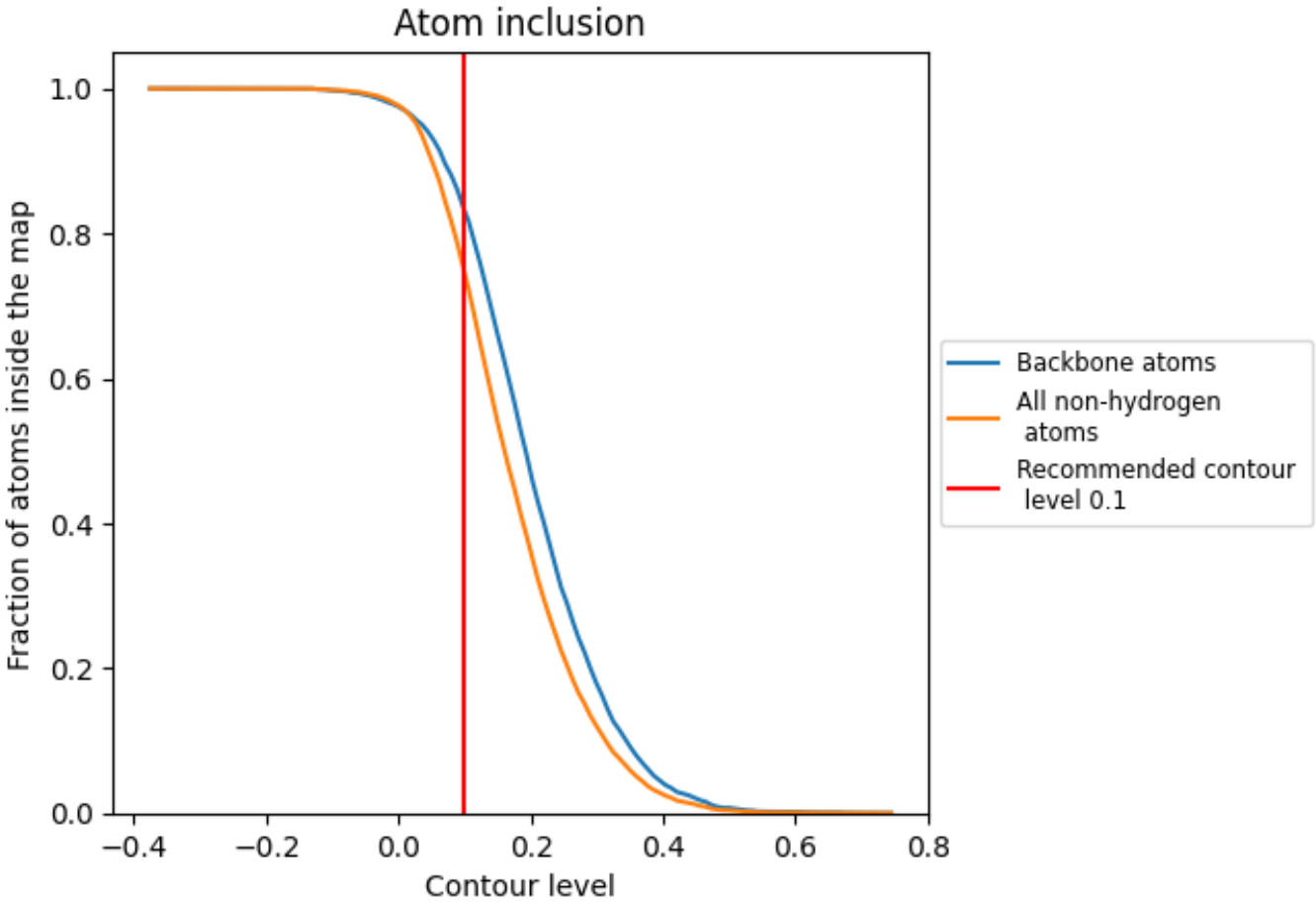
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1 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 Atom inclusion (i)



At the recommended contour level, 83% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.