



wwPDB EM Validation Summary Report ⓘ

Nov 11, 2024 – 01:33 AM EST

PDB ID : 7T2P
EMDB ID : EMD-25621
Title : The Envelope Glycoprotein SIVmac239.K180S SOSIP trimer in complex with
3 copies of the neutralizing antibody K11
Authors : Berndsen, Z.T.; Ward, A.B.
Deposited on : 2021-12-06
Resolution : 3.47 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.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

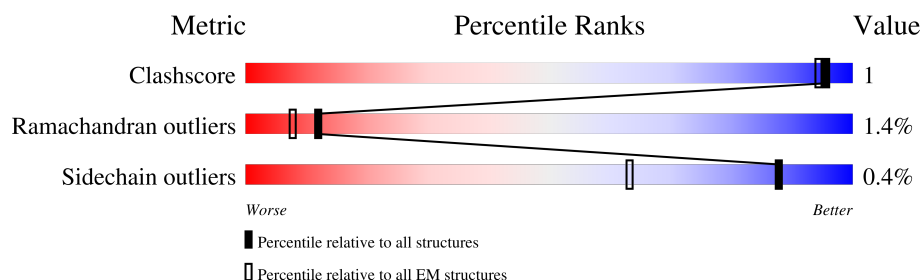
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.47 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.



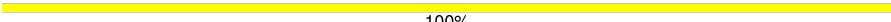




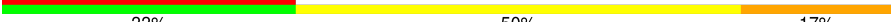
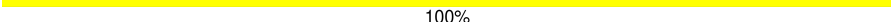
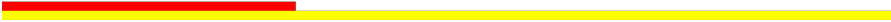
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 $\leq 5\%$. 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	527	<div> <div>6%</div> <div>84%</div> <div>9%</div> <div>6%</div> </div>
2	B	159	<div> <div>48%</div> <div>87%</div> <div>11%</div> </div>
3	H	485	<div> <div>6%</div> <div>26%</div> <div>73%</div> </div>
4	L	232	<div> <div>15%</div> <div>43%</div> <div>54%</div> </div>
5	C	8	<div> <div>38%</div> <div>12%</div> <div>88%</div> </div>
6	D	2	<div> <div>100%</div> </div>
6	K	2	<div> <div>100%</div> </div>
6	M	2	<div> <div>50%</div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
6	O	2	 100%
6	P	2	 50% 100%
7	E	3	 67% 100%
7	F	3	 67% 100%
7	G	3	 33% 100%
8	I	6	 33% 33% 50% 17%
9	J	5	 60% 100%
10	N	3	 33% 100%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 7632 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 Envelope glycoprotein gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	493	Total	C	N	O	S	0	0
			3953	2477	688	751	37		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	180	SER	LYS	engineered mutation	UNP A0A5C0E975
A	511	SER	ASP	conflict	UNP A0A5C0E975
A	512	CYS	VAL	conflict	UNP A0A5C0E975
A	523	ARG	ASN	conflict	UNP A0A5C0E975
A	526	ARG	-	expression tag	UNP A0A5C0E975
A	527	ARG	-	expression tag	UNP A0A5C0E975

- Molecule 2 is a protein called Envelope glycoprotein gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	142	Total	C	N	O	S	0	0
			1138	724	198	212	4		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	574	PRO	VAL	conflict	UNP L7XFX7
B	620	CYS	HIS	conflict	UNP L7XFX7
B	676	GLY	-	expression tag	UNP L7XFX7
B	677	SER	-	expression tag	UNP L7XFX7
B	678	GLY	-	expression tag	UNP L7XFX7
B	679	HIS	-	expression tag	UNP L7XFX7
B	680	HIS	-	expression tag	UNP L7XFX7
B	681	HIS	-	expression tag	UNP L7XFX7
B	682	HIS	-	expression tag	UNP L7XFX7
B	683	HIS	-	expression tag	UNP L7XFX7
B	684	HIS	-	expression tag	UNP L7XFX7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	685	HIS	-	expression tag	UNP L7XFX7
B	686	HIS	-	expression tag	UNP L7XFX7

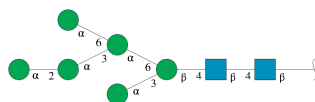
- Molecule 3 is a protein called K11 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	132	Total	C	N	O	S	0	0
			1028	650	173	199	6		

- Molecule 4 is a protein called K11 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	106	Total	C	N	O	S	0	0
			811	512	135	162	2		

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
5	C	8	Total	C	N	O	0	0
			94	52	2	40		

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



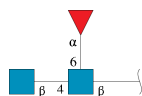
Mol	Chain	Residues	Atoms				AltConf	Trace
6	D	2	Total	C	N	O	0	0
			28	16	2	10		
6	K	2	Total	C	N	O	0	0
			28	16	2	10		

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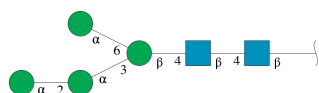
Mol	Chain	Residues	Atoms				AltConf	Trace
6	M	2	Total	C	N	O	0	0
			28	16	2	10		
6	O	2	Total	C	N	O	0	0
			28	16	2	10		
6	P	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 7 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



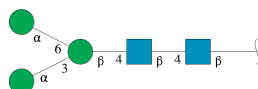
Mol	Chain	Residues	Atoms				AltConf	Trace
7	E	3	Total	C	N	O	0	0
			38	22	2	14		
7	F	3	Total	C	N	O	0	0
			38	22	2	14		
7	G	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-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.



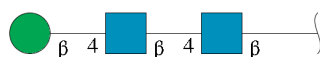
Mol	Chain	Residues	Atoms				AltConf	Trace
8	I	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 9 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.



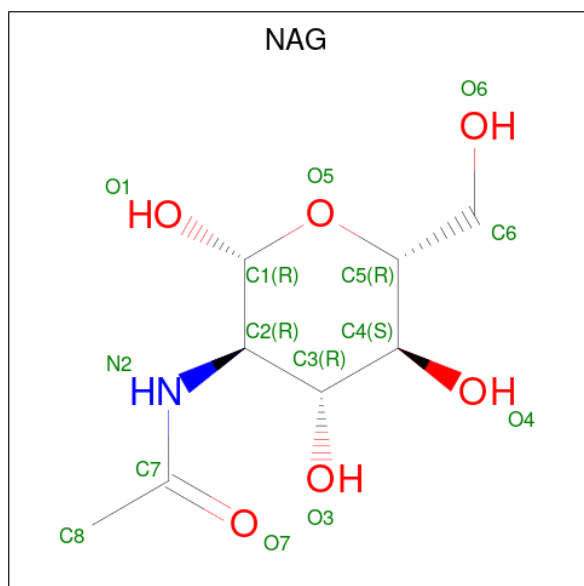
Mol	Chain	Residues	Atoms				AltConf	Trace
9	J	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 10 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
10	N	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

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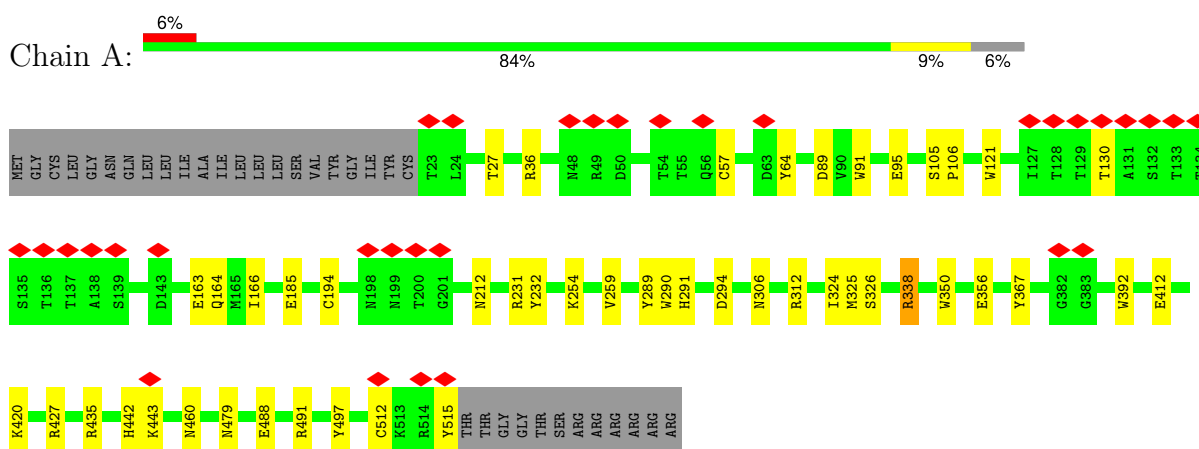
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Mol	Chain	Residues	Atoms				AltConf
11	A	1	Total	C	N	O	0
			14	8	1	5	
11	A	1	Total	C	N	O	0
			14	8	1	5	
11	A	1	Total	C	N	O	0
			14	8	1	5	
11	A	1	Total	C	N	O	0
			14	8	1	5	
11	A	1	Total	C	N	O	0
			14	8	1	5	
11	B	1	Total	C	N	O	0
			14	8	1	5	
11	B	1	Total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

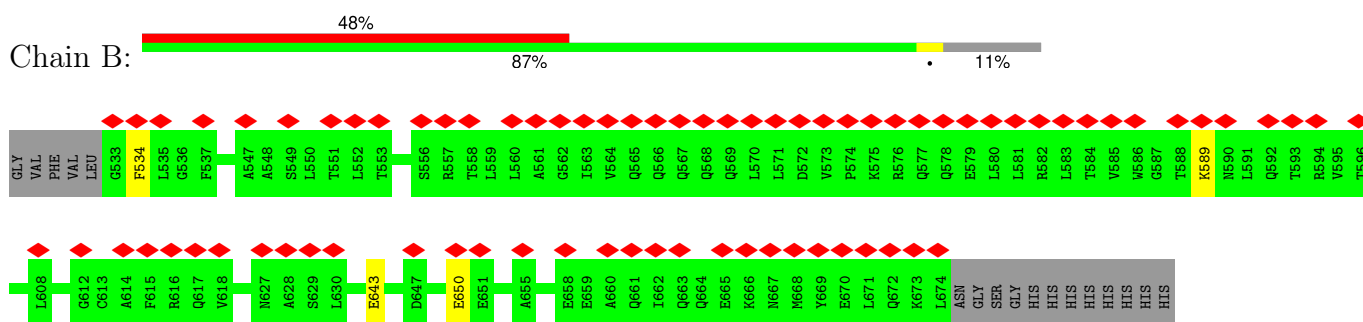
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

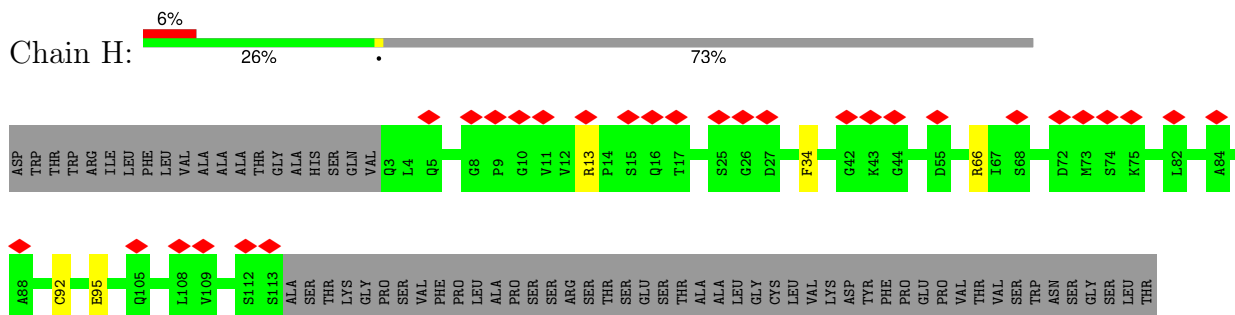
• Molecule 1: Envelope glycoprotein gp120



• Molecule 2: Envelope glycoprotein gp41



• Molecule 3: K11 Fab heavy chain



GLY	GLY	GLN	ALA	LYS	SER
SER	SER	PRO	GLU	PRO	GLY
THR	THR	ARG	VAL	PRO	THR
PHE	PHE	GLU	HIS	THR	HIS
LEU	LEU	PRO	HIS	CYS	THR
TYR	TYR	GLN	ALA	PRO	PHE
SER	SER	VAL	GLN	PRO	PRO
LYS	LYS	TYR	THR	CYS	ALA
LEU	LEU	THR	THR	THR	VAL
THR	THR	LEU	LYS	SER	GLN
VAL	VAL	PRO	ARG	PRO	VAL
GLY	GLY	PRO	GLU	GLU	SER
ASP	ASP	PRO	THR	LEU	GLY
LYS	LYS	SER	THR	LEU	SER
SER	SER	ARG	GLN	LEU	GLY
ARG	ARG	GLU	ASN	GLY	TYR
TRP	TRP	GLU	ASN	PRO	SER
GLN	GLN	LEU	SER	PRO	SER
GLN	GLN	THR	THR	SER	LEU
GLY	GLY	LYS	TYR	VAL	SER
ASN	ASN	ASN	ARG	PHE	SER
VAL	VAL	GLN	VAL	LEU	VAL
PHE	PHE	VAL	VAL	PHE	VAL
SER	SER	SER	SER	PRO	THR
CYS	CYS	LEU	VAL	PRO	VAL
SER	SER	THR	LEU	LYS	PRO
VAL	VAL	CYS	THR	PRO	SER
MET	LEU	ASP	GLN	THR	GLY
ILE	LEU	THR	ASP	ILE	THR
SER	ASN	PRO	LEU	SER	GLN
ARG	ASN	THR	ASN	ARG	THR
VAL	THR	GLY	LYS	THR	VAL
CYS	CYS	ILE	LYS	PRO	CYS
ASN	ASN	VAL	VAL	GLJ	ASN
VAL	VAL	THR	THR	VAL	VAL
HIS	HIS	TRP	CYS	CYS	HIS
LYS	LYS	GLU	LYS	VAL	LYS
PRO	PRO	SER	VAL	VAL	PRO
SER	SER	SER	ASN	VAL	SER
PRO	PRO	GLY	ASN	ASP	ASN
GLY	GLY	GLN	LYS	VAL	THR
LYS	LYS	PRO	ALA	SER	LYS
ASP	ASP	GLJ	LEU	GLN	VAL
VAL	VAL	THR	PRO	ASP	ASP
THR	THR	ALA	ALA	GLJ	LYS
TYR	TYR	LYS	ILE	VAL	ARG
LEU	LEU	THR	GLN	VAL	VAL
ASP	ASP	PRO	LYS	LYS	GLJ
THR	THR	THR	THR	PHE	ILE
PRO	PRO	PRO	THR	ASN	LYS
VAL	VAL	VAL	ILE	THR	THR
LEU	LEU	LYS	LYS	TRP	CYS
ASP	ASP	THR	ASP	VAL	GLY
SER	SER	GLY	LYS	ASN	GLY
ASP	ASP	THR	GLY	GLY	SER

- Molecule 4: K11 Fab light chain

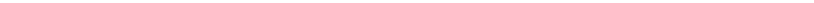
Chain L:  15% 43% 42%

- Molecule 5: α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] α -D-mannopyranose-(1-6)-[α -D-mannopyranose-(1-3)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain C:  12% 38% 88%

NAG1	NAG2	BMA3	MAN4	MAN5	MAN6	MAN7	MAN8
------	------	------	------	------	------	------	------

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

Chain D:  100%

NAG1
NAG2

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

Chain K:  100%

MAG1
MAG2

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

Chain M:  50%
100%

MAG1
MAG2

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

Chain O:  100%

MAG1
MAG2

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

Chain P:  50%
100%

MAG1
MAG2

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

Chain E:  67%
100%

MAG1
MAG2
FUC3

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

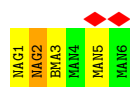
Chain F:  67%
100%

MAG1
MAG2
FUC3

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



- Molecule 8: α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose



- Molecule 9: α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose



- Molecule 10: β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	177365	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.371	Depositor
Minimum map value	-1.460	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.049	Depositor
Recommended contour level	0.33	Depositor
Map size (Å)	345.0, 345.0, 345.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.15, 1.15, 1.15	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: FUC, MAN, BMA, 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	1.15	22/4050 (0.5%)	0.95	6/5506 (0.1%)
2	B	0.99	2/1159 (0.2%)	0.83	0/1574
3	H	1.12	4/1052 (0.4%)	0.98	3/1429 (0.2%)
4	L	0.95	1/829 (0.1%)	0.91	0/1124
All	All	1.10	29/7090 (0.4%)	0.93	9/9633 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	92	CYS	CB-SG	-9.39	1.66	1.82
1	A	515	TYR	CG-CD1	8.05	1.49	1.39
1	A	350	TRP	CB-CG	-7.63	1.36	1.50
1	A	515	TYR	CG-CD2	7.56	1.49	1.39
1	A	515	TYR	CE1-CZ	7.18	1.47	1.38

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	312	ARG	NE-CZ-NH2	-10.21	115.20	120.30
3	H	66	ARG	NE-CZ-NH2	-9.11	115.75	120.30
3	H	66	ARG	NE-CZ-NH1	7.03	123.81	120.30
1	A	427	ARG	NE-CZ-NH2	-6.92	116.84	120.30
3	H	13	ARG	NE-CZ-NH2	-6.35	117.12	120.30

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	3953	0	3788	13	0
2	B	1138	0	1139	1	0
3	H	1028	0	979	0	0
4	L	811	0	793	2	0
5	C	94	0	79	0	0
6	D	28	0	25	0	0
6	K	28	0	25	0	0
6	M	28	0	25	0	0
6	O	28	0	25	0	0
6	P	28	0	25	0	0
7	E	38	0	34	0	0
7	F	38	0	34	0	0
7	G	38	0	34	0	0
8	I	72	0	61	1	0
9	J	61	0	52	0	0
10	N	39	0	34	0	0
11	A	140	0	129	0	0
11	B	42	0	39	0	0
All	All	7632	0	7320	14	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 1.

The worst 5 of 14 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:TRP:HH2	1:A:435:ARG:HD3	1.24	1.01
1:A:392:TRP:CH2	1:A:435:ARG:HD3	2.16	0.76
1:A:89:ASP:OD1	2:B:589:LYS:NZ	2.37	0.57
1:A:254:LYS:NZ	4:L:92:ASP:OD2	2.39	0.55
1:A:121:TRP:HE1	1:A:338:ARG:NH2	2.05	0.55

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	A	491/527 (93%)	465 (95%)	18 (4%)	8 (2%)	8	37
2	B	140/159 (88%)	133 (95%)	6 (4%)	1 (1%)	19	53
3	H	126/485 (26%)	124 (98%)	2 (2%)	0	100	100
4	L	104/232 (45%)	100 (96%)	1 (1%)	3 (3%)	3	27
All	All	861/1403 (61%)	822 (96%)	27 (3%)	12 (1%)	12	40

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	325	MET
1	A	479	ASN
1	A	130	THR
1	A	212	ASN
2	B	534	PHE

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	A	443/471 (94%)	440 (99%)	3 (1%)	81	88
2	B	120/135 (89%)	120 (100%)	0	100	100
3	H	116/436 (27%)	116 (100%)	0	100	100
4	L	91/205 (44%)	91 (100%)	0	100	100
All	All	770/1247 (62%)	767 (100%)	3 (0%)	88	94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	ILE
1	A	306	ASN
1	A	338	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

41 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	C	1	5,1	14,14,15	2.14	5 (35%)	17,19,21	0.98	1 (5%)
5	NAG	C	2	5	14,14,15	1.87	6 (42%)	17,19,21	1.41	2 (11%)
5	BMA	C	3	5	11,11,12	1.41	2 (18%)	15,15,17	0.58	0
5	MAN	C	4	5	11,11,12	1.41	2 (18%)	15,15,17	0.76	0
5	MAN	C	5	5	11,11,12	0.80	0	15,15,17	0.90	0
5	MAN	C	6	5	11,11,12	1.97	5 (45%)	15,15,17	0.64	0
5	MAN	C	7	5	11,11,12	1.93	5 (45%)	15,15,17	0.66	0
5	MAN	C	8	5	11,11,12	1.99	6 (54%)	15,15,17	0.66	0
6	NAG	D	1	6,1	14,14,15	2.07	5 (35%)	17,19,21	1.21	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	D	2	6	14,14,15	2.06	5 (35%)	17,19,21	0.84	1 (5%)
7	NAG	E	1	7,1	14,14,15	1.52	2 (14%)	17,19,21	1.01	2 (11%)
7	NAG	E	2	7	14,14,15	2.09	7 (50%)	17,19,21	0.85	0
7	FUC	E	3	7	10,10,11	1.92	5 (50%)	14,14,16	0.67	0
7	NAG	F	1	7,1	14,14,15	1.58	2 (14%)	17,19,21	1.01	1 (5%)
7	NAG	F	2	7	14,14,15	2.13	6 (42%)	17,19,21	0.88	1 (5%)
7	FUC	F	3	7	10,10,11	1.98	5 (50%)	14,14,16	0.66	0
7	NAG	G	1	7,1	14,14,15	1.56	2 (14%)	17,19,21	1.08	1 (5%)
7	NAG	G	2	7	14,14,15	2.02	5 (35%)	17,19,21	0.97	1 (5%)
7	FUC	G	3	7	10,10,11	1.83	5 (50%)	14,14,16	0.66	0
8	NAG	I	1	8,1	14,14,15	1.93	2 (14%)	17,19,21	1.24	1 (5%)
8	NAG	I	2	8	14,14,15	1.86	5 (35%)	17,19,21	0.86	1 (5%)
8	BMA	I	3	8	11,11,12	1.32	2 (18%)	15,15,17	0.64	0
8	MAN	I	4	8	11,11,12	0.69	0	15,15,17	0.70	0
8	MAN	I	5	8	11,11,12	0.65	0	15,15,17	0.90	1 (6%)
8	MAN	I	6	8	11,11,12	0.81	0	15,15,17	0.85	0
9	NAG	J	1	9,1	14,14,15	2.04	4 (28%)	17,19,21	1.00	1 (5%)
9	NAG	J	2	9	14,14,15	2.04	6 (42%)	17,19,21	0.93	1 (5%)
9	BMA	J	3	9	11,11,12	1.47	3 (27%)	15,15,17	0.57	0
9	MAN	J	4	9	11,11,12	1.97	5 (45%)	15,15,17	0.66	0
9	MAN	J	5	9	11,11,12	1.95	5 (45%)	15,15,17	0.67	0
6	NAG	K	1	6,1	14,14,15	1.89	4 (28%)	17,19,21	1.08	1 (5%)
6	NAG	K	2	6	14,14,15	1.99	6 (42%)	17,19,21	1.05	1 (5%)
6	NAG	M	1	6,1	14,14,15	2.33	7 (50%)	17,19,21	0.99	1 (5%)
6	NAG	M	2	6	14,14,15	2.01	6 (42%)	17,19,21	0.92	1 (5%)
10	NAG	N	1	1,10	14,14,15	2.02	4 (28%)	17,19,21	1.13	2 (11%)
10	NAG	N	2	10	14,14,15	2.01	6 (42%)	17,19,21	1.11	2 (11%)
10	BMA	N	3	10	11,11,12	2.00	6 (54%)	15,15,17	0.66	0
6	NAG	O	1	6,1	14,14,15	2.13	6 (42%)	17,19,21	1.65	3 (17%)
6	NAG	O	2	6	14,14,15	2.03	6 (42%)	17,19,21	0.89	1 (5%)
6	NAG	P	1	6,1	14,14,15	2.12	6 (42%)	17,19,21	1.13	2 (11%)
6	NAG	P	2	6	14,14,15	2.02	6 (42%)	17,19,21	0.90	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	C	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	C	2	5	-	0/6/23/26	0/1/1/1
5	BMA	C	3	5	-	0/2/19/22	0/1/1/1
5	MAN	C	4	5	-	2/2/19/22	0/1/1/1
5	MAN	C	5	5	-	2/2/19/22	0/1/1/1
5	MAN	C	6	5	-	2/2/19/22	0/1/1/1
5	MAN	C	7	5	-	1/2/19/22	0/1/1/1
5	MAN	C	8	5	-	0/2/19/22	0/1/1/1
6	NAG	D	1	6,1	-	0/6/23/26	0/1/1/1
6	NAG	D	2	6	-	0/6/23/26	0/1/1/1
7	NAG	E	1	7,1	-	0/6/23/26	0/1/1/1
7	NAG	E	2	7	-	0/6/23/26	0/1/1/1
7	FUC	E	3	7	-	-	0/1/1/1
7	NAG	F	1	7,1	-	0/6/23/26	0/1/1/1
7	NAG	F	2	7	-	0/6/23/26	0/1/1/1
7	FUC	F	3	7	-	-	0/1/1/1
7	NAG	G	1	7,1	-	2/6/23/26	0/1/1/1
7	NAG	G	2	7	-	0/6/23/26	0/1/1/1
7	FUC	G	3	7	-	-	0/1/1/1
8	NAG	I	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	I	2	8	-	0/6/23/26	0/1/1/1
8	BMA	I	3	8	-	0/2/19/22	0/1/1/1
8	MAN	I	4	8	-	1/2/19/22	0/1/1/1
8	MAN	I	5	8	-	2/2/19/22	0/1/1/1
8	MAN	I	6	8	-	2/2/19/22	0/1/1/1
9	NAG	J	1	9,1	-	0/6/23/26	0/1/1/1
9	NAG	J	2	9	-	0/6/23/26	0/1/1/1
9	BMA	J	3	9	-	0/2/19/22	0/1/1/1
9	MAN	J	4	9	-	1/2/19/22	0/1/1/1
9	MAN	J	5	9	-	0/2/19/22	0/1/1/1
6	NAG	K	1	6,1	-	0/6/23/26	0/1/1/1
6	NAG	K	2	6	-	0/6/23/26	0/1/1/1
6	NAG	M	1	6,1	-	0/6/23/26	0/1/1/1
6	NAG	M	2	6	-	0/6/23/26	0/1/1/1
10	NAG	N	1	1,10	-	0/6/23/26	0/1/1/1
10	NAG	N	2	10	-	0/6/23/26	0/1/1/1
10	BMA	N	3	10	-	0/2/19/22	0/1/1/1
6	NAG	O	1	6,1	-	1/6/23/26	0/1/1/1
6	NAG	O	2	6	-	0/6/23/26	0/1/1/1
6	NAG	P	1	6,1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	P	2	6	-	0/6/23/26	0/1/1/1

The worst 5 of 175 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	M	1	NAG	C1-C2	6.14	1.60	1.52
10	N	1	NAG	C1-C2	5.60	1.60	1.52
8	I	1	NAG	C1-C2	5.60	1.60	1.52
6	D	1	NAG	C1-C2	5.52	1.59	1.52
9	J	1	NAG	C1-C2	5.47	1.59	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	O	1	NAG	C2-N2-C7	4.70	129.20	122.90
5	C	2	NAG	C8-C7-N2	3.39	121.74	116.12
8	I	1	NAG	C8-C7-N2	2.73	120.65	116.12
6	O	1	NAG	O7-C7-C8	-2.72	117.22	122.05
6	D	1	NAG	C1-O5-C5	2.66	115.75	112.19

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

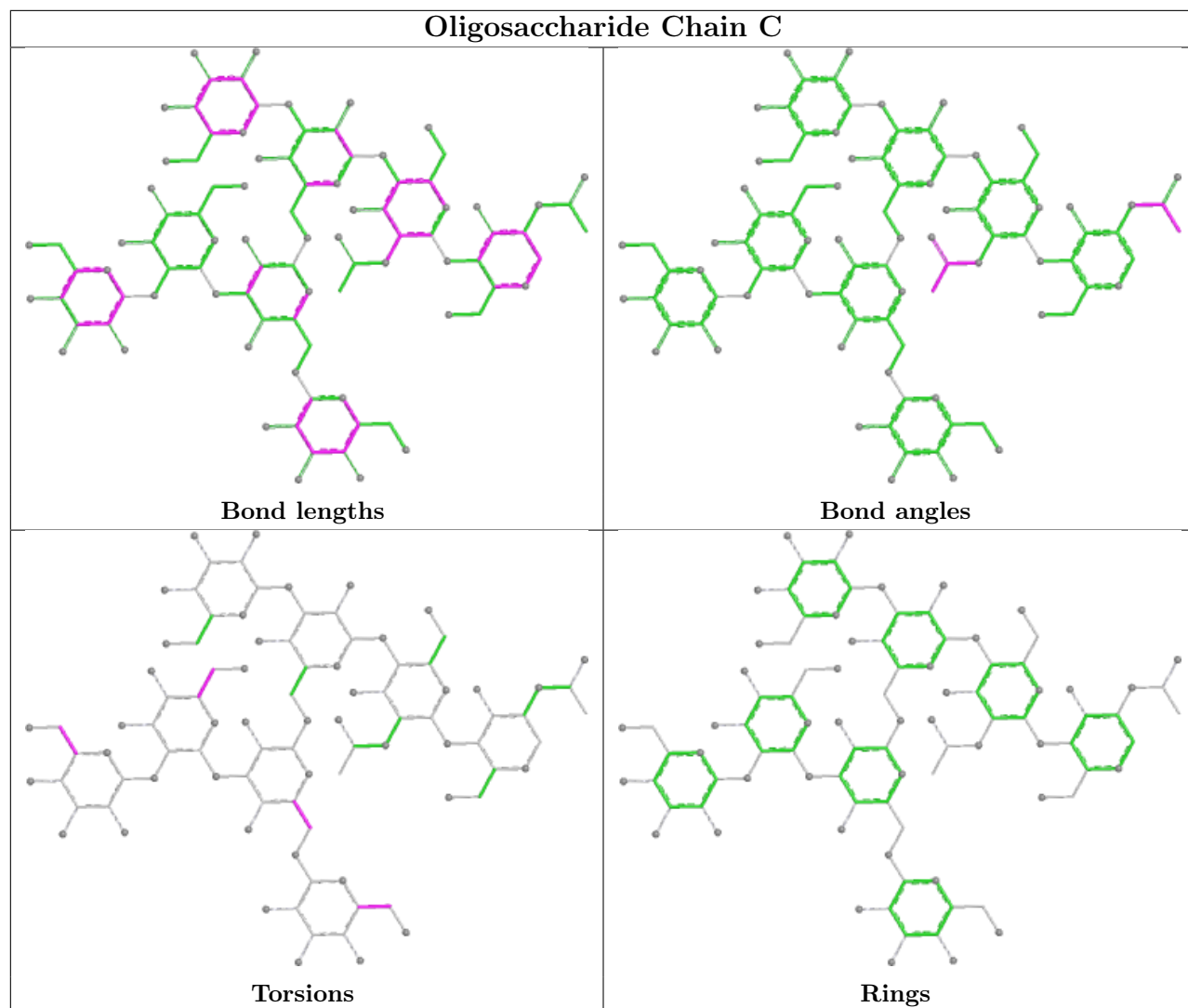
Mol	Chain	Res	Type	Atoms
6	O	1	NAG	C3-C2-N2-C7
5	C	4	MAN	O5-C5-C6-O6
5	C	5	MAN	O5-C5-C6-O6
5	C	4	MAN	C4-C5-C6-O6
8	I	6	MAN	O5-C5-C6-O6

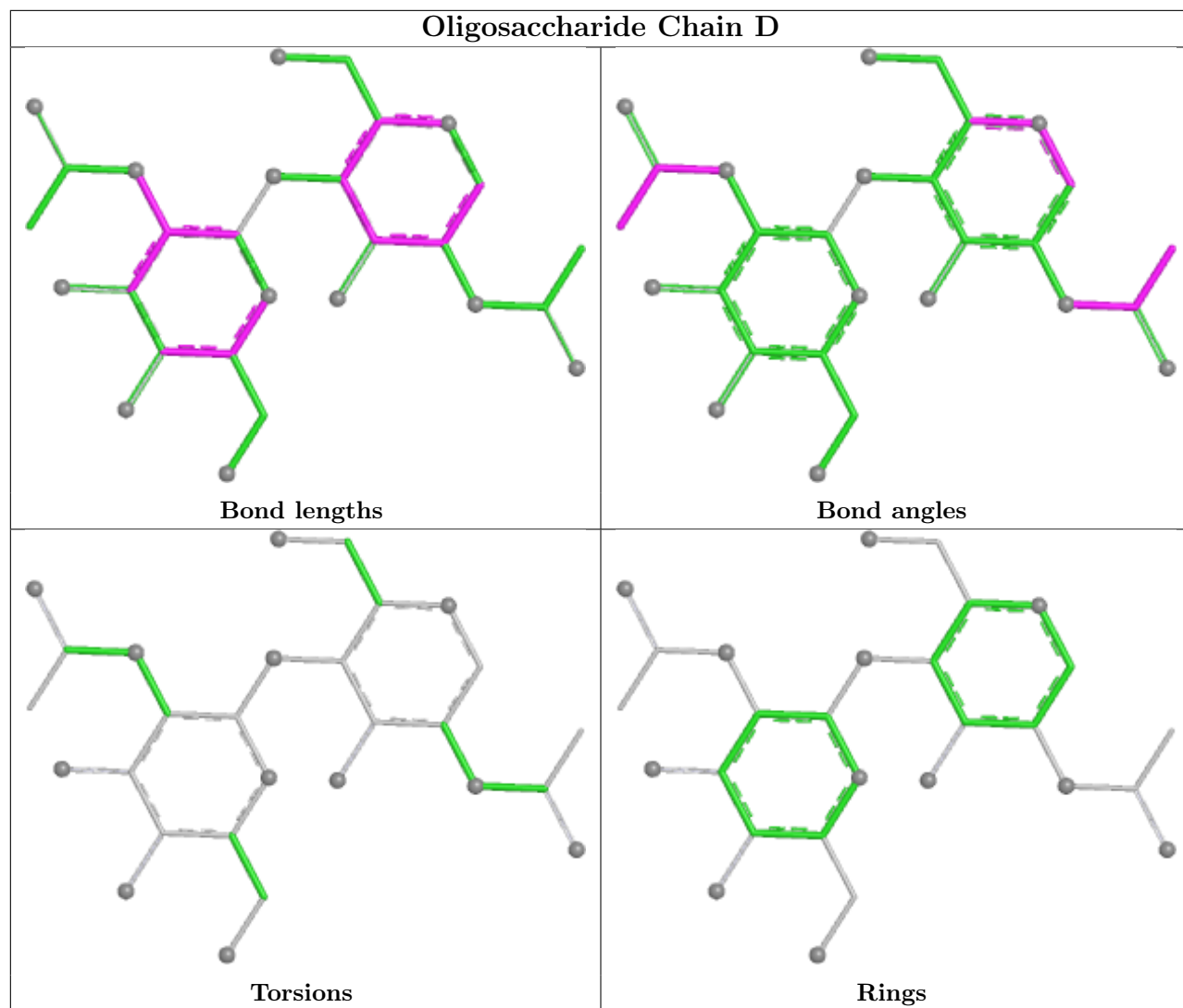
There are no ring outliers.

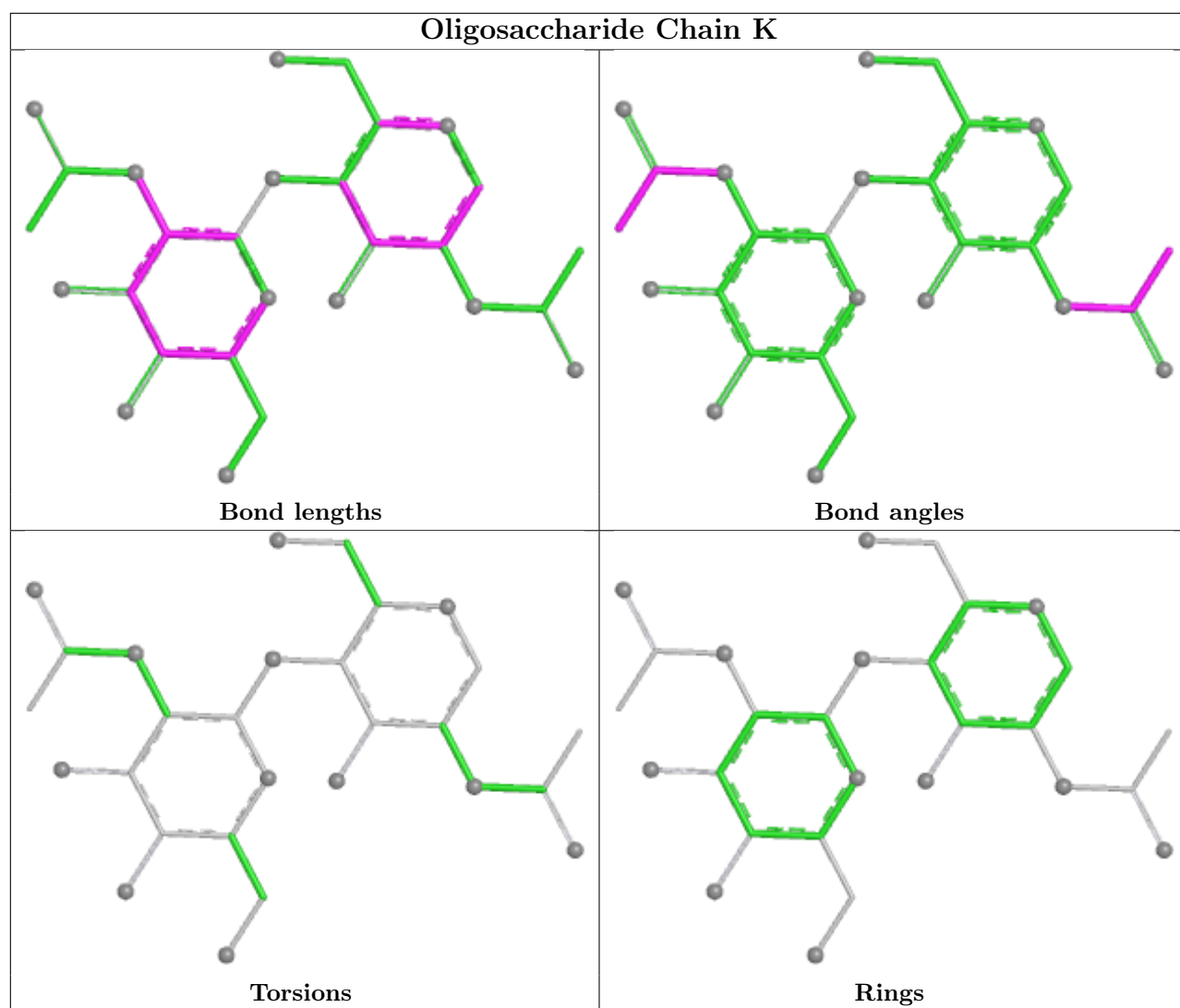
1 monomer is involved in 1 short contact:

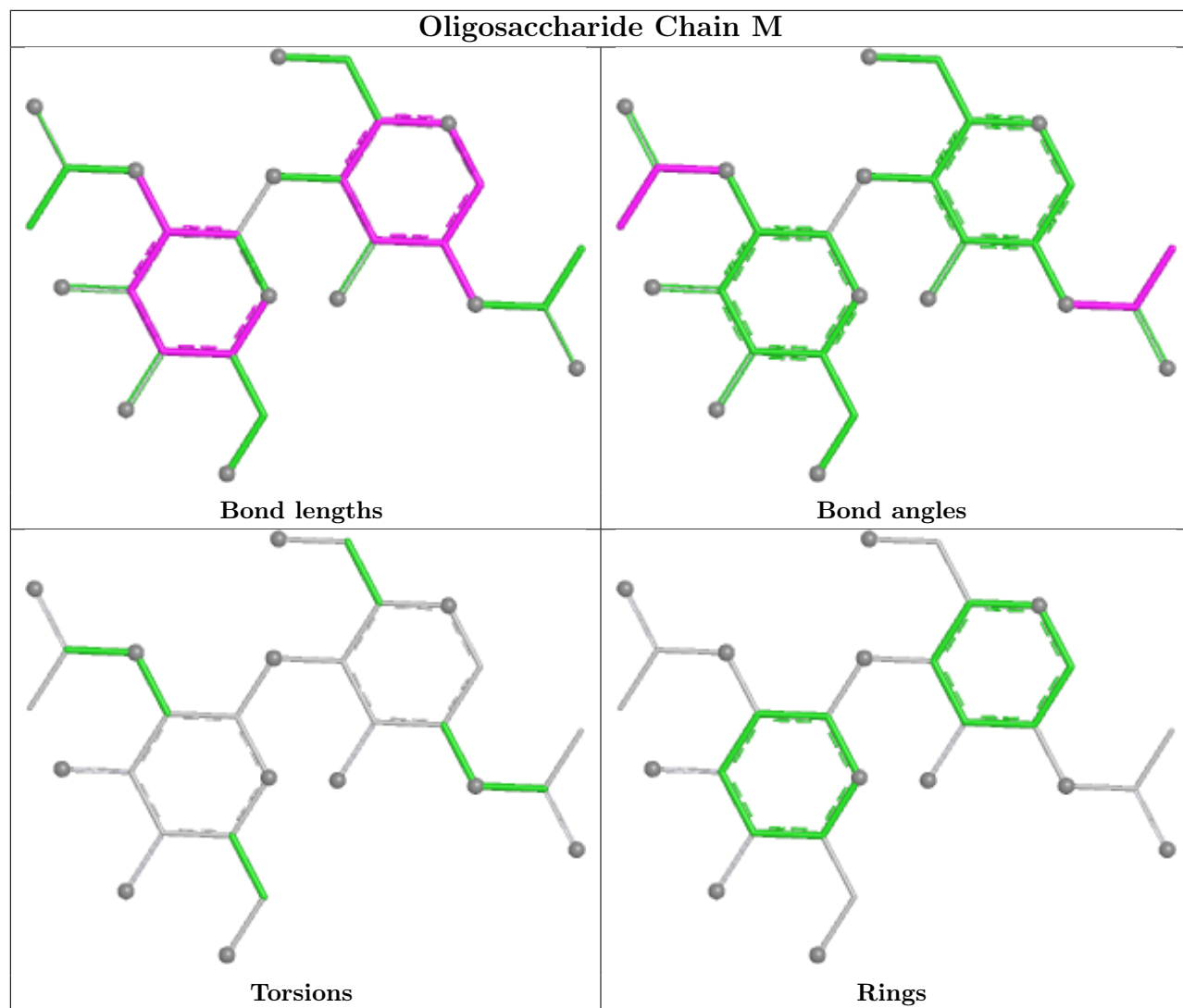
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	I	2	NAG	1	0

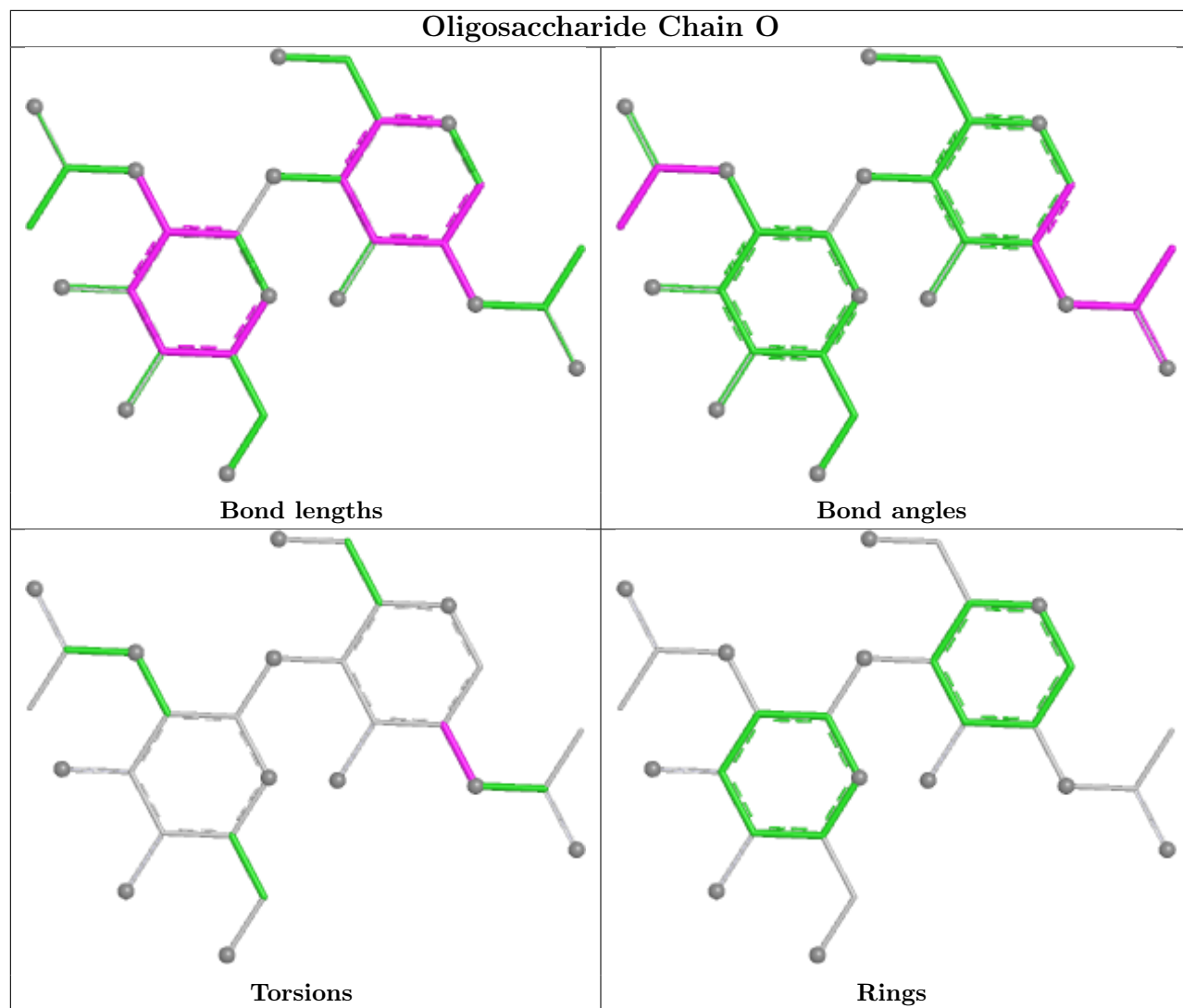
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

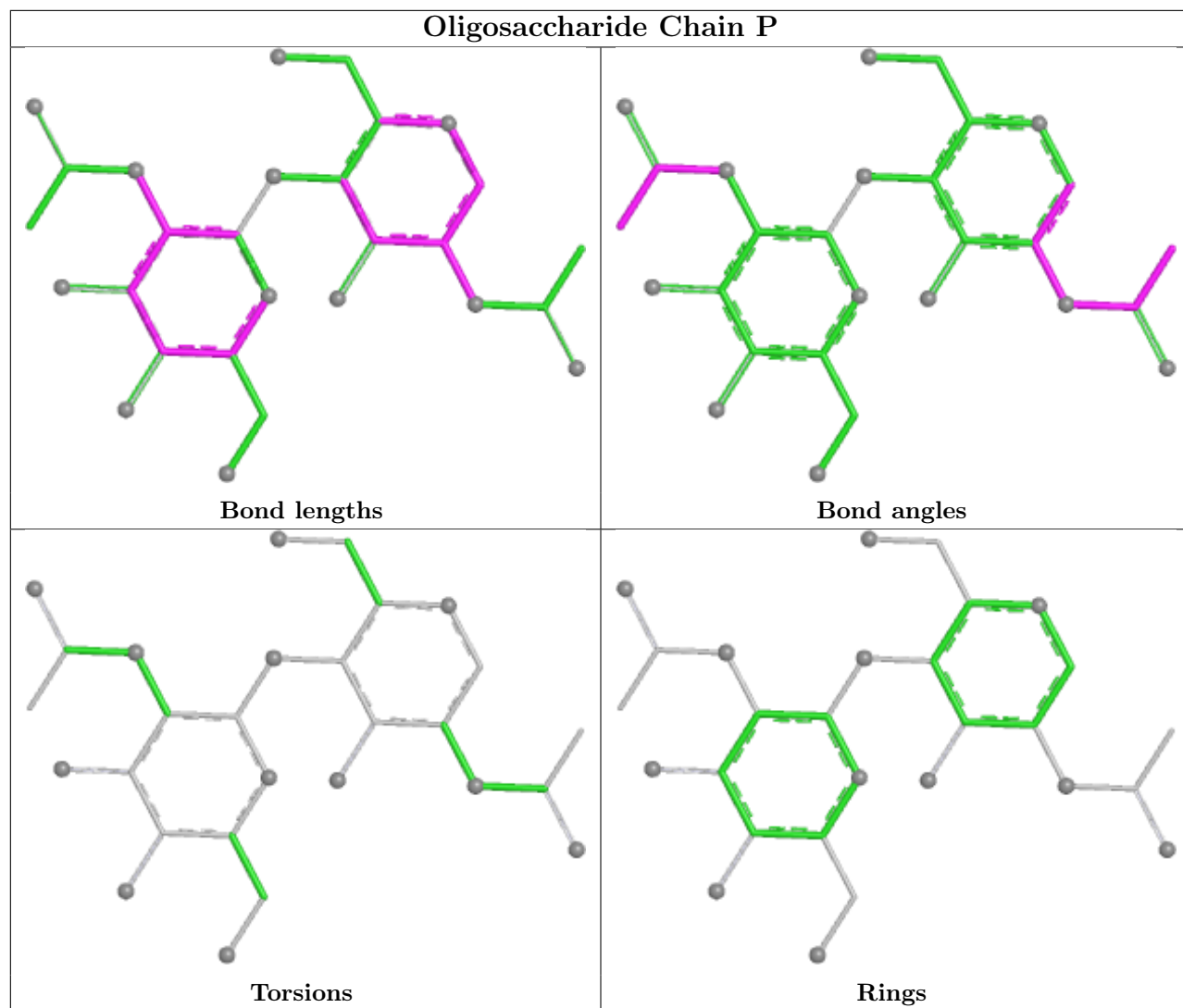


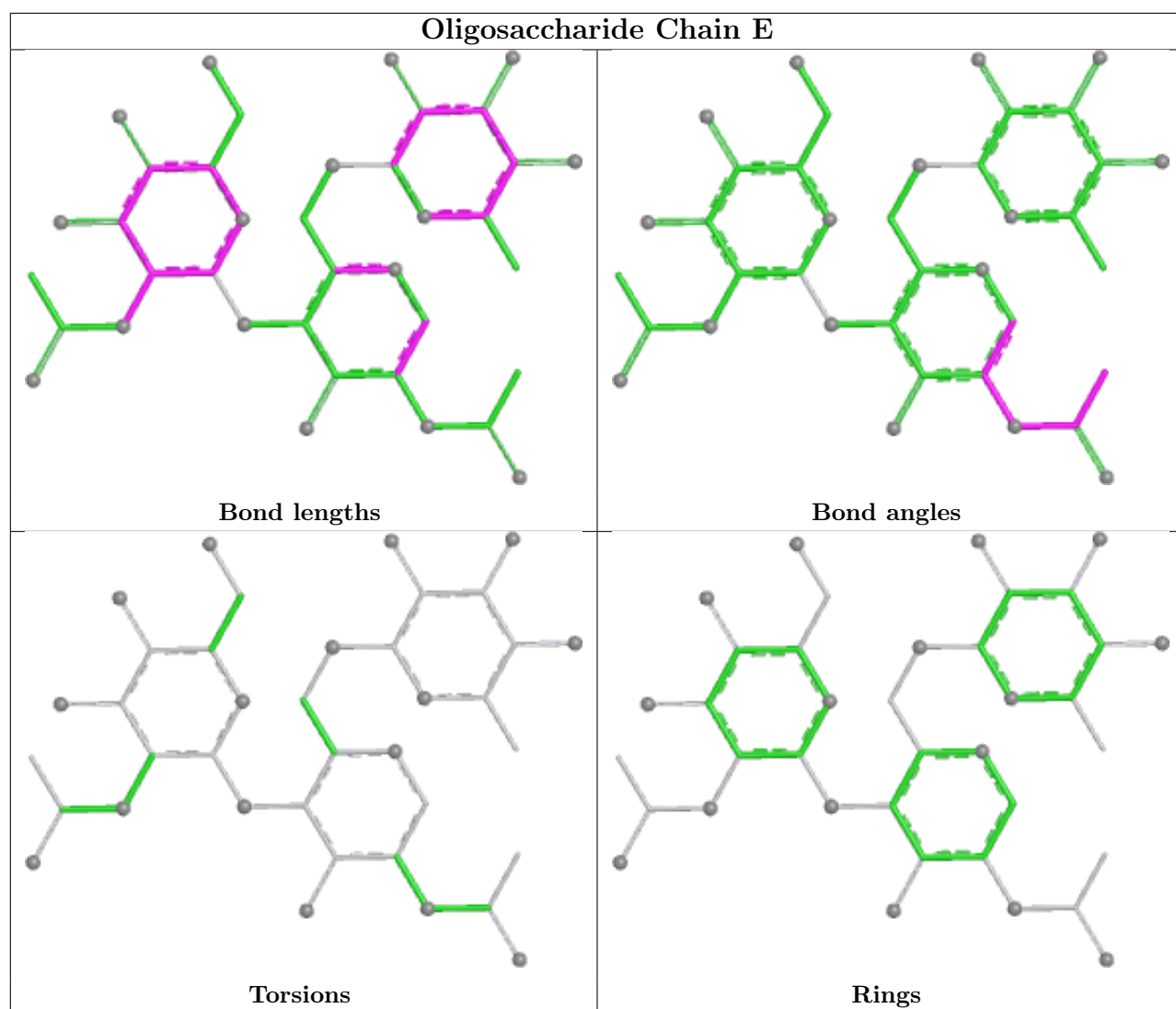


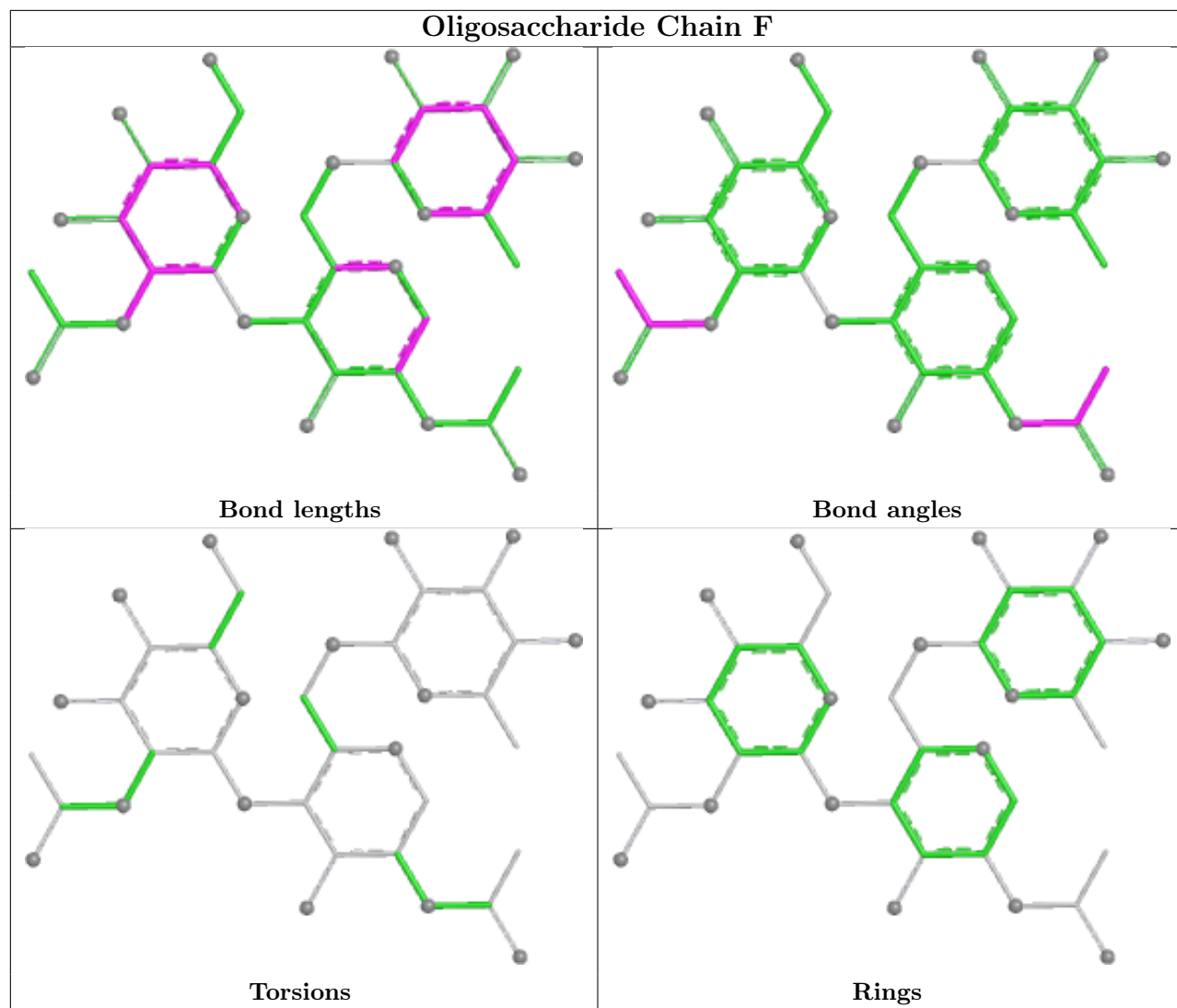


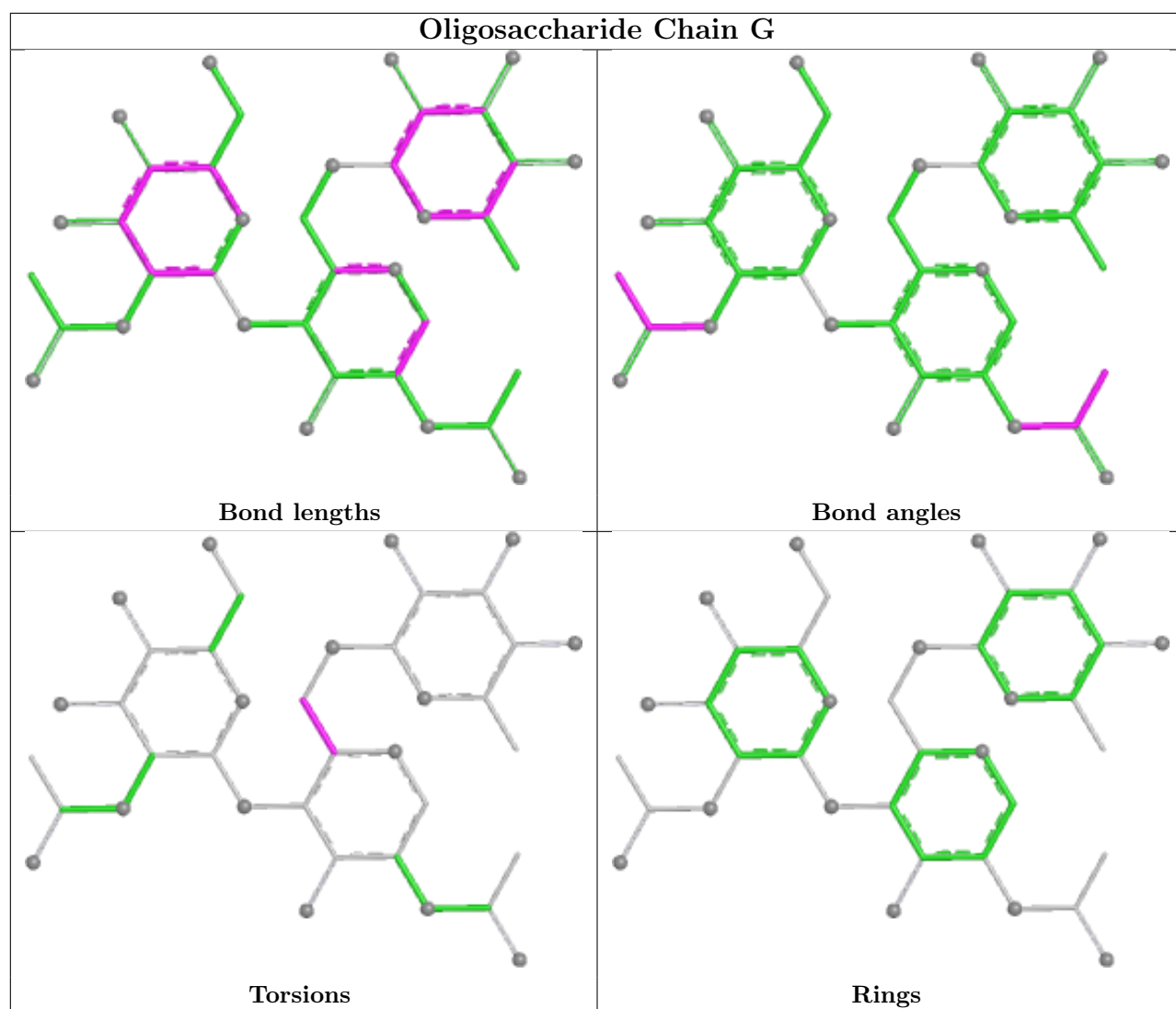


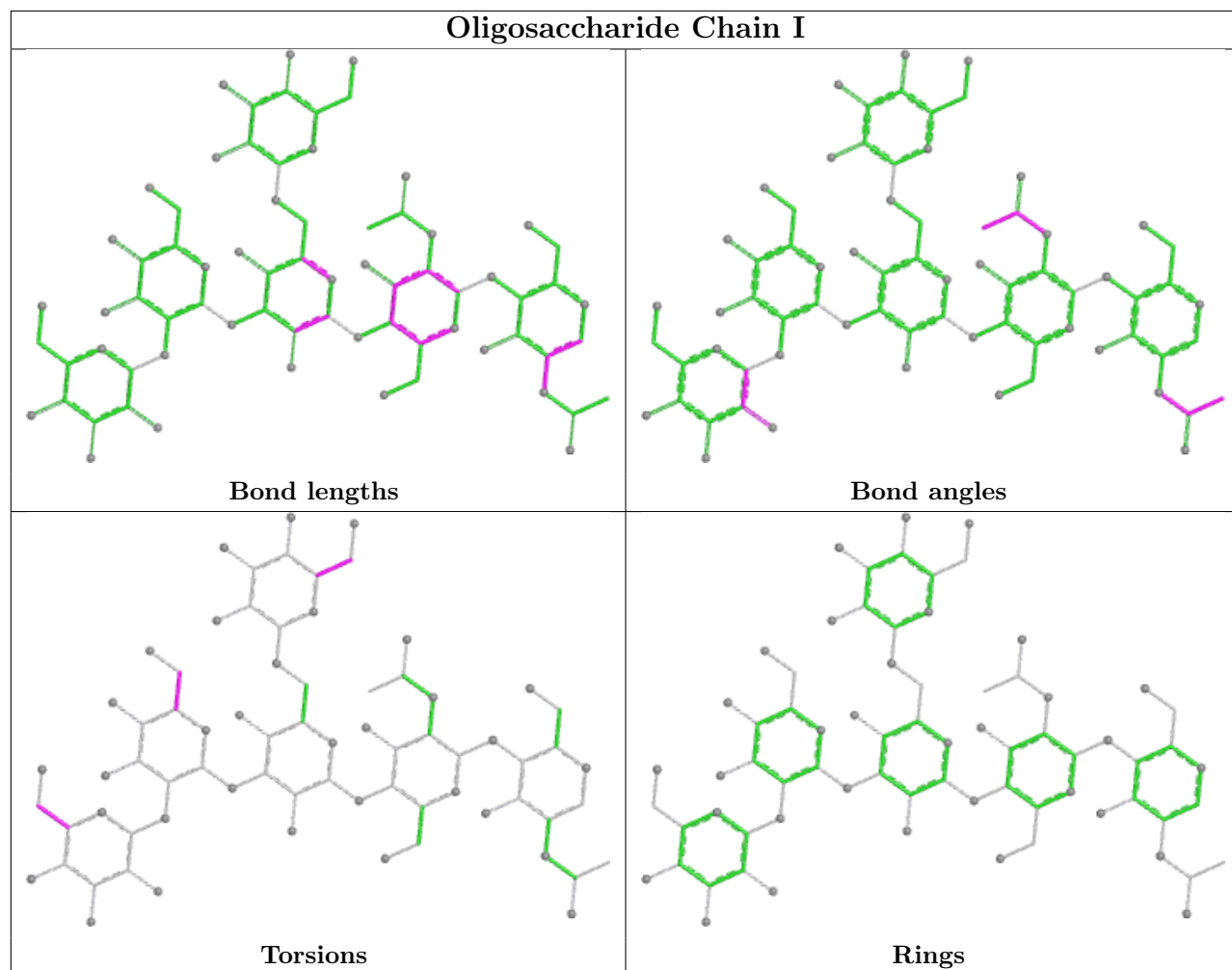


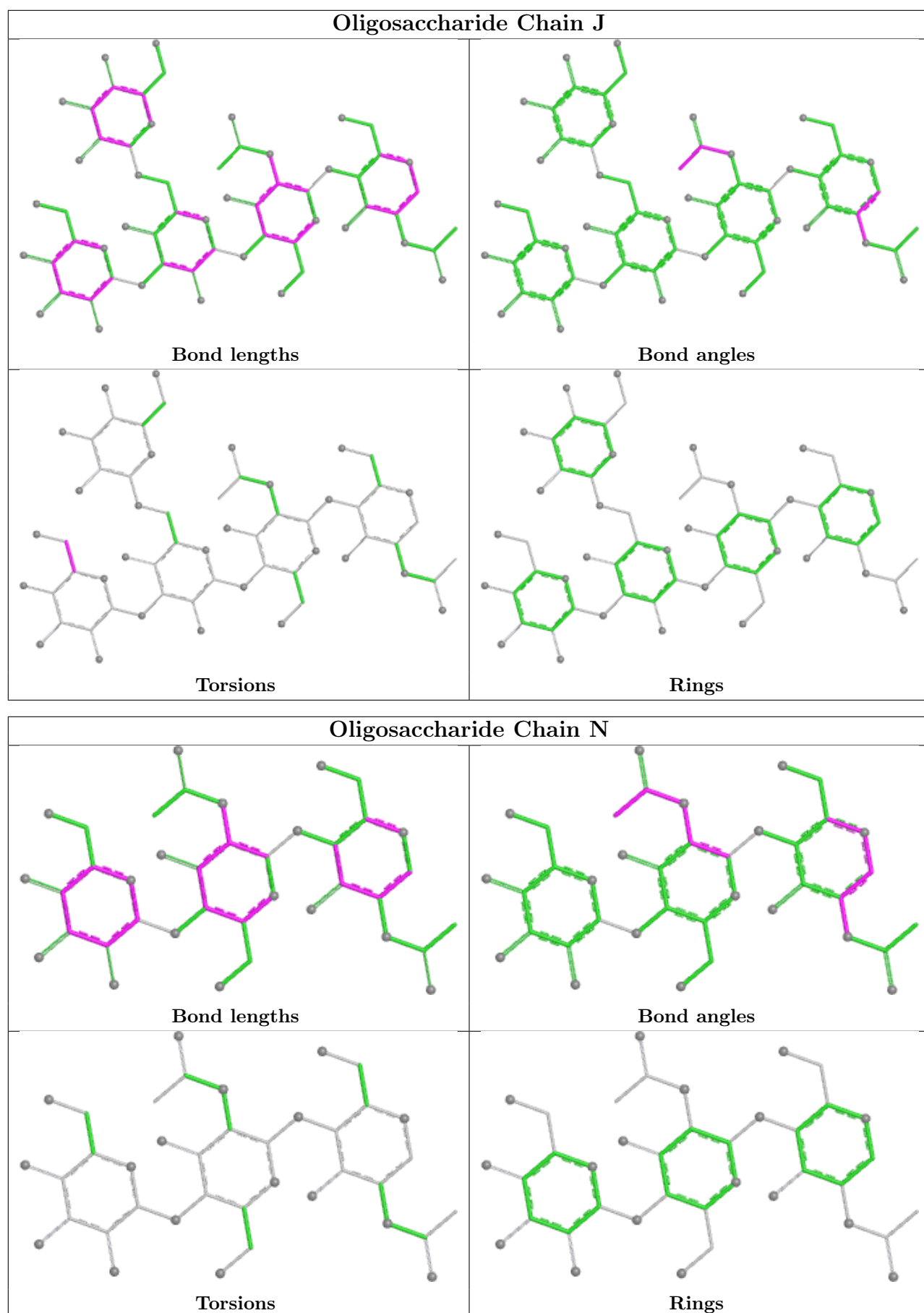












5.6 Ligand geometry

13 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
11	NAG	A	610	1	14,14,15	2.08	5 (35%)	17,19,21	6.83	2 (11%)
11	NAG	A	607	1	14,14,15	2.14	5 (35%)	17,19,21	1.14	2 (11%)
11	NAG	A	609	1	14,14,15	2.38	6 (42%)	17,19,21	0.94	1 (5%)
11	NAG	A	602	1	14,14,15	0.30	0	17,19,21	0.59	0
11	NAG	A	605	1	14,14,15	2.33	6 (42%)	17,19,21	0.97	1 (5%)
11	NAG	B	701	2	14,14,15	2.17	7 (50%)	17,19,21	1.04	1 (5%)
11	NAG	A	604	1	14,14,15	2.22	5 (35%)	17,19,21	1.05	1 (5%)
11	NAG	A	601	1	14,14,15	2.32	6 (42%)	17,19,21	1.08	2 (11%)
11	NAG	A	603	1	14,14,15	2.22	5 (35%)	17,19,21	1.11	3 (17%)
11	NAG	A	606	1	14,14,15	2.30	6 (42%)	17,19,21	0.92	1 (5%)
11	NAG	B	703	2	14,14,15	2.33	6 (42%)	17,19,21	1.01	1 (5%)
11	NAG	B	702	2	14,14,15	2.28	6 (42%)	17,19,21	1.00	1 (5%)
11	NAG	A	608	1	14,14,15	2.15	6 (42%)	17,19,21	1.07	2 (11%)

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
11	NAG	A	610	1	-	0/6/23/26	0/1/1/1
11	NAG	A	607	1	-	0/6/23/26	0/1/1/1
11	NAG	A	609	1	-	0/6/23/26	0/1/1/1
11	NAG	A	602	1	-	2/6/23/26	0/1/1/1
11	NAG	A	605	1	-	0/6/23/26	0/1/1/1
11	NAG	B	701	2	-	1/6/23/26	0/1/1/1
11	NAG	A	604	1	-	0/6/23/26	0/1/1/1
11	NAG	A	601	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	NAG	A	603	1	-	0/6/23/26	0/1/1/1
11	NAG	A	606	1	-	0/6/23/26	0/1/1/1
11	NAG	B	703	2	-	0/6/23/26	0/1/1/1
11	NAG	B	702	2	-	0/6/23/26	0/1/1/1
11	NAG	A	608	1	-	1/6/23/26	0/1/1/1

The worst 5 of 69 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	609	NAG	C1-C2	6.36	1.61	1.52
11	A	605	NAG	C1-C2	6.08	1.60	1.52
11	B	703	NAG	C1-C2	6.03	1.60	1.52
11	A	603	NAG	C1-C2	6.02	1.60	1.52
11	A	604	NAG	C1-C2	5.97	1.60	1.52

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	610	NAG	C2-N2-C7	27.81	160.16	122.90
11	A	607	NAG	C8-C7-N2	2.88	120.89	116.12
11	A	601	NAG	C8-C7-N2	2.80	120.77	116.12
11	A	610	NAG	C8-C7-N2	2.65	120.52	116.12
11	B	701	NAG	C8-C7-N2	2.59	120.41	116.12

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	602	NAG	C8-C7-N2-C2
11	A	602	NAG	O7-C7-N2-C2
11	B	701	NAG	C4-C5-C6-O6
11	A	608	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	H	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	52:SER	C	52(A):TYR	N	5.54
1	H	51:ILE	C	52:SER	N	3.95
1	H	52(A):TYR	C	53:ASP	N	3.35

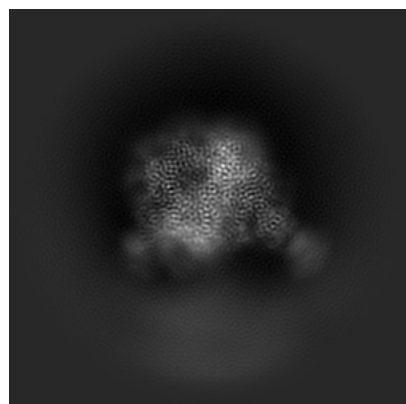
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25621. These allow visual inspection of the internal detail of the map and identification of artifacts.

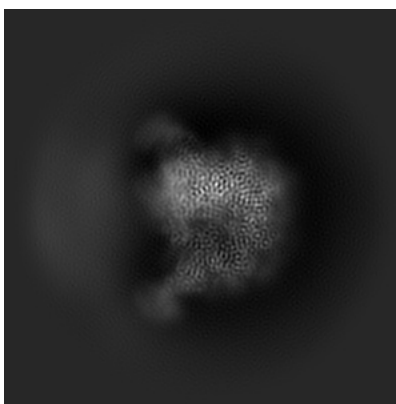
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

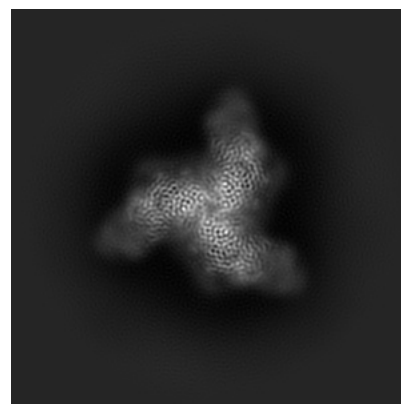
6.1.1 Primary map



X

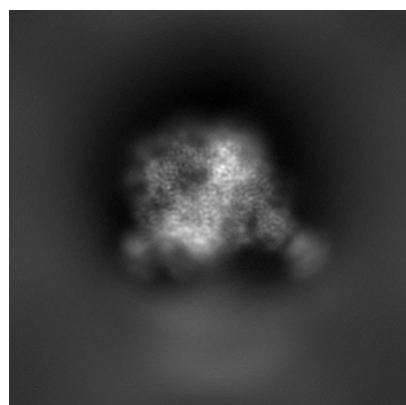


Y

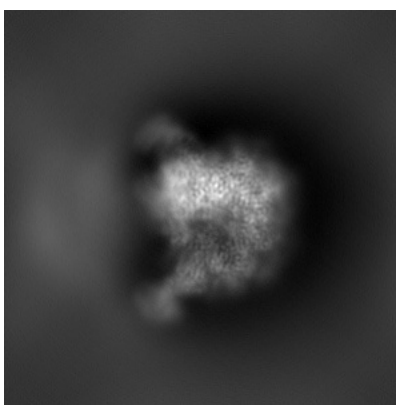


Z

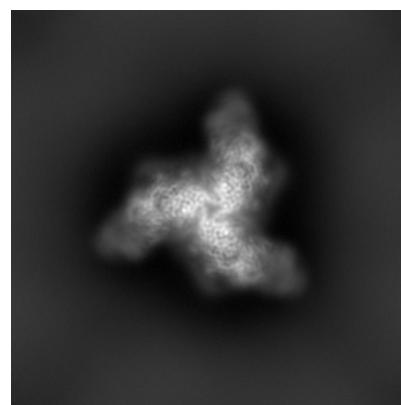
6.1.2 Raw map



X



Y

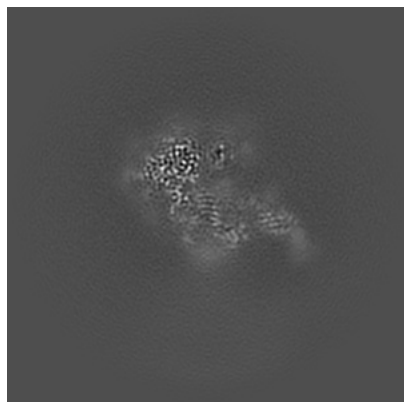


Z

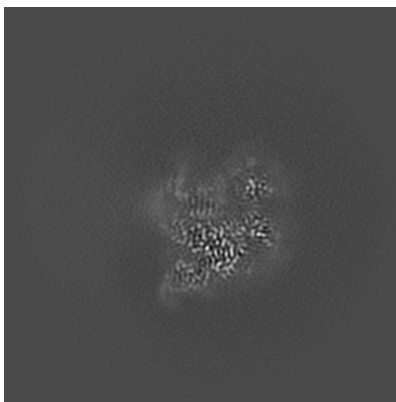
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

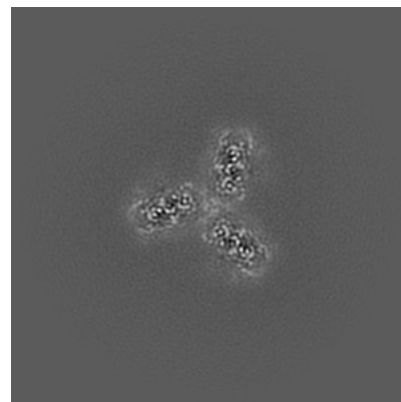
6.2.1 Primary map



X Index: 150

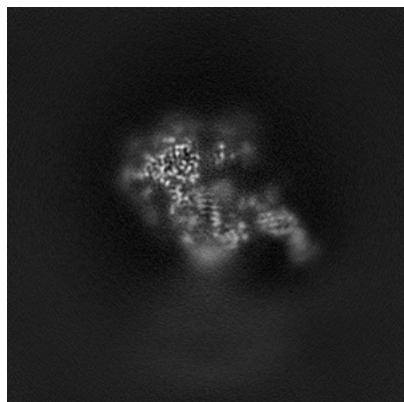


Y Index: 150

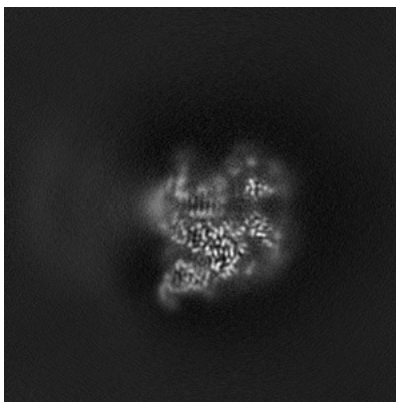


Z Index: 150

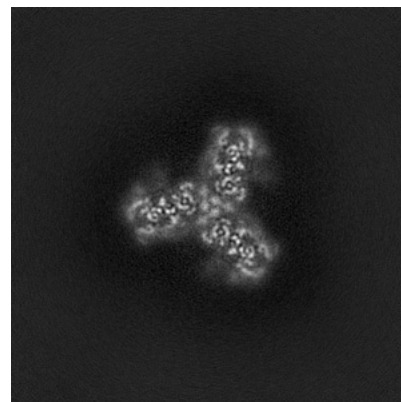
6.2.2 Raw map



X Index: 150



Y Index: 150

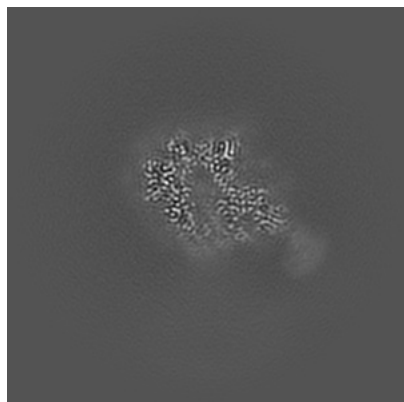


Z Index: 150

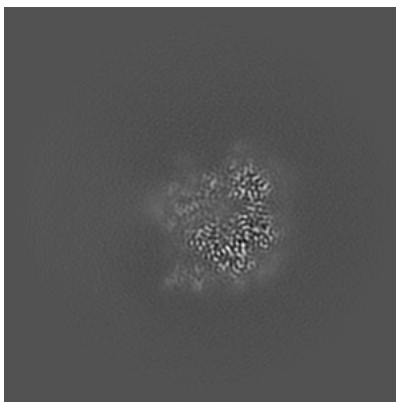
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

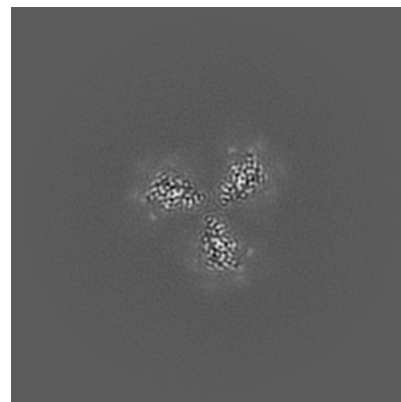
6.3.1 Primary map



X Index: 160

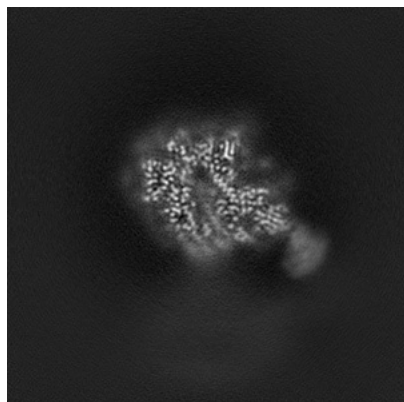


Y Index: 157

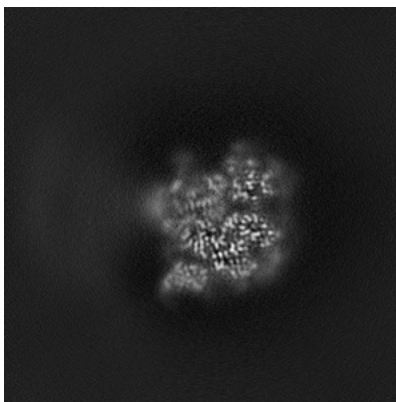


Z Index: 178

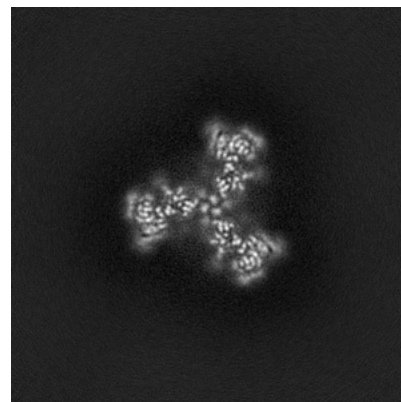
6.3.2 Raw map



X Index: 160



Y Index: 154

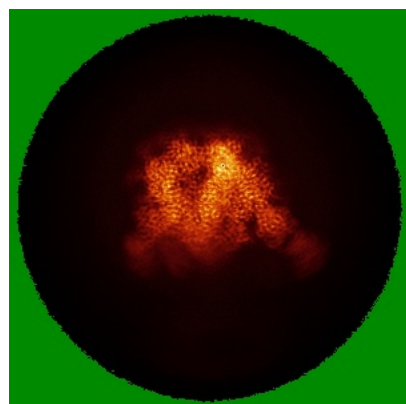


Z Index: 145

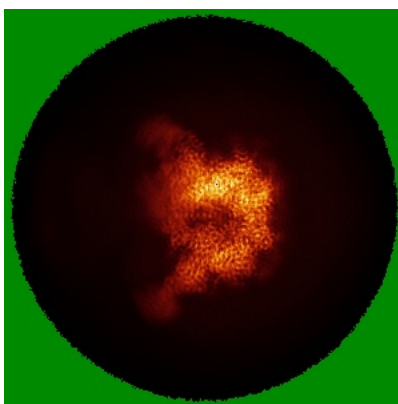
The images above show the largest variance slices of the map in three orthogonal directions.

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

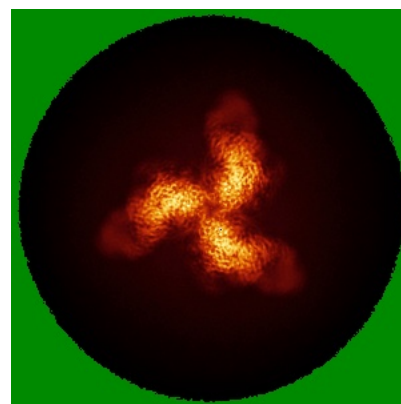
6.4.1 Primary map



X

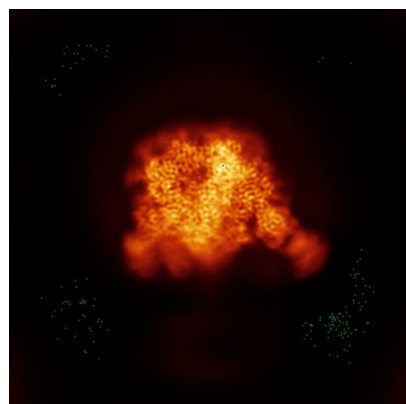


Y

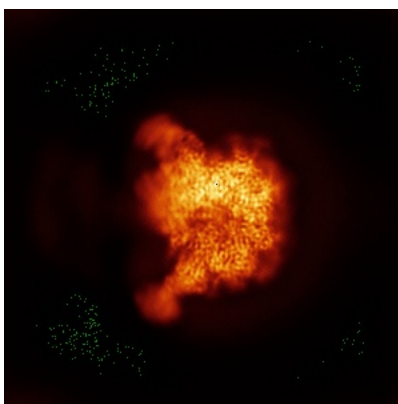


Z

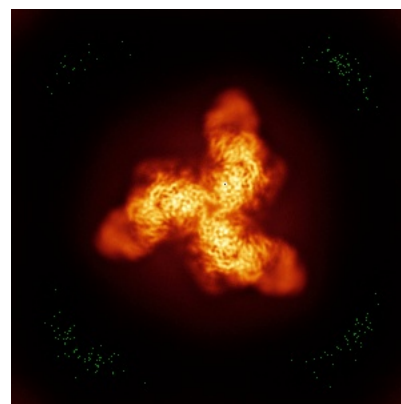
6.4.2 Raw map



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.

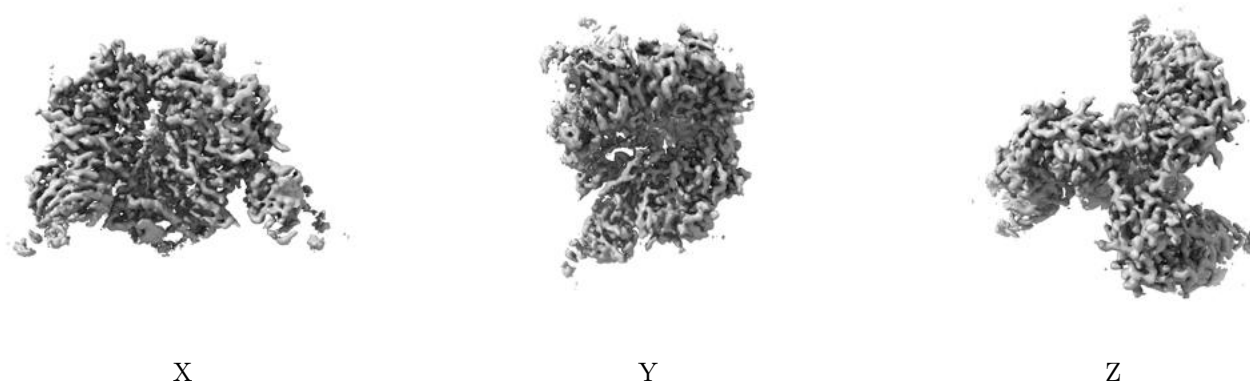
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.33. 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



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.

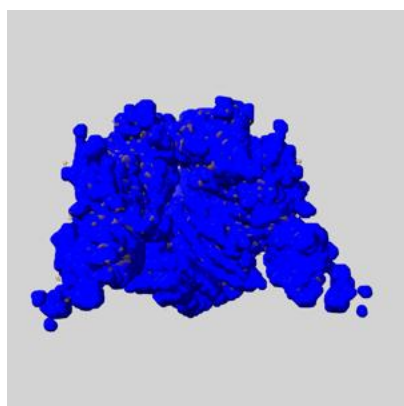
6.6 Mask visualisation [i](#)

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

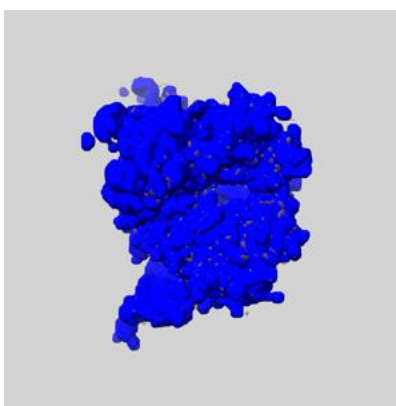
A mask typically either:

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

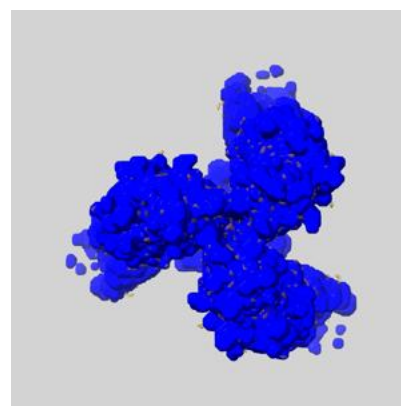
6.6.1 emd_25621_msk_1.map [i](#)



X



Y

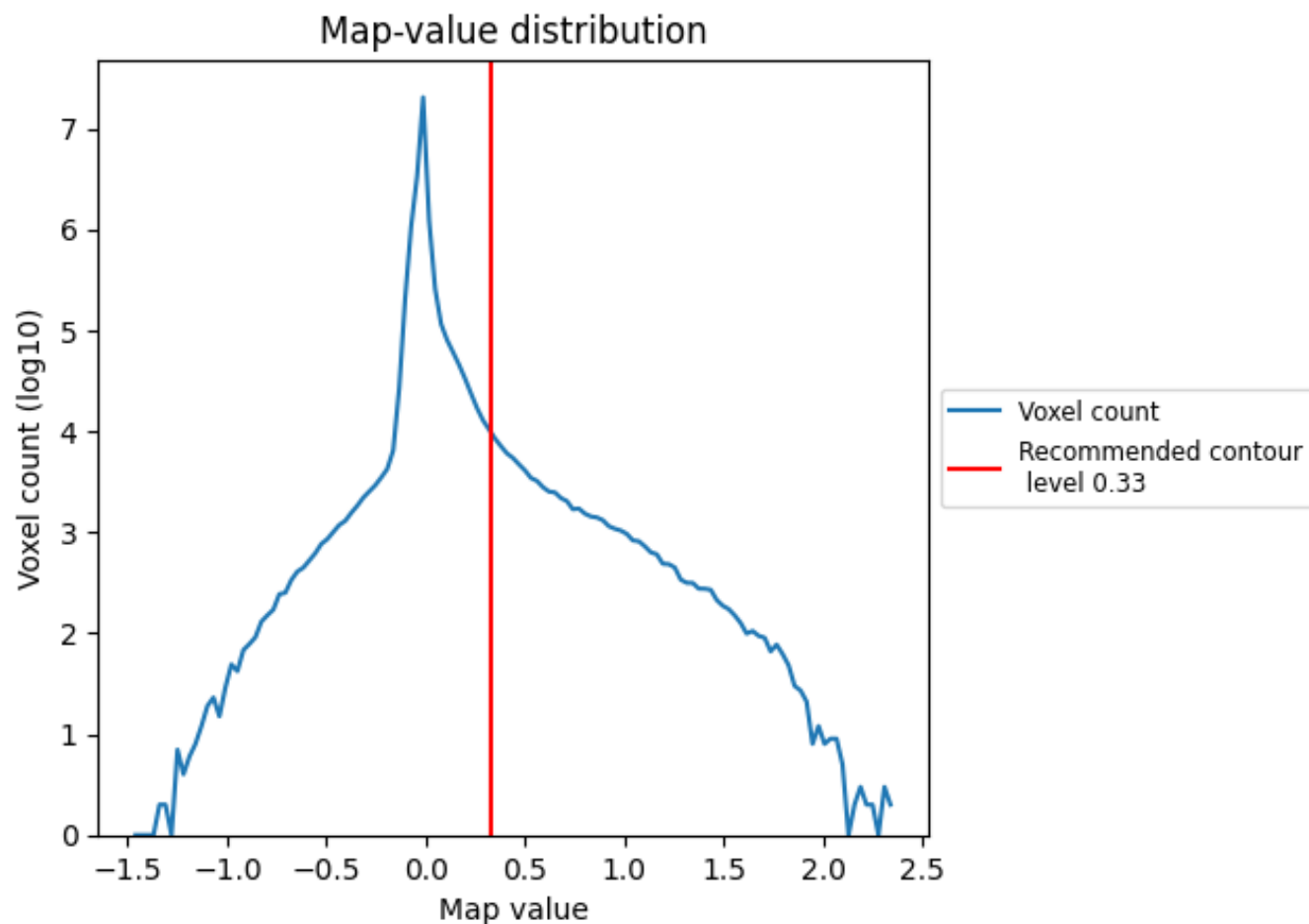


Z

7 Map analysis [i](#)

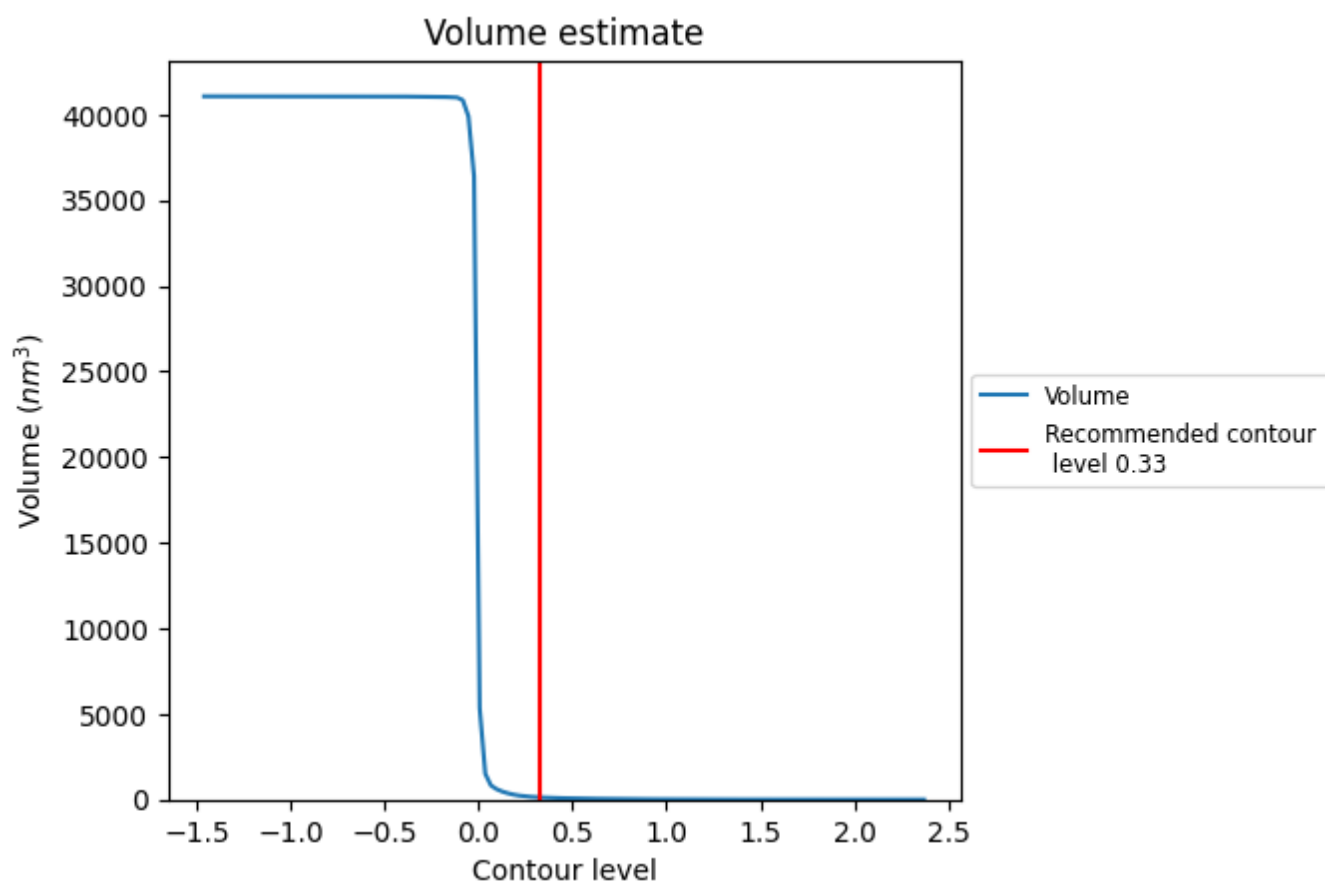
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

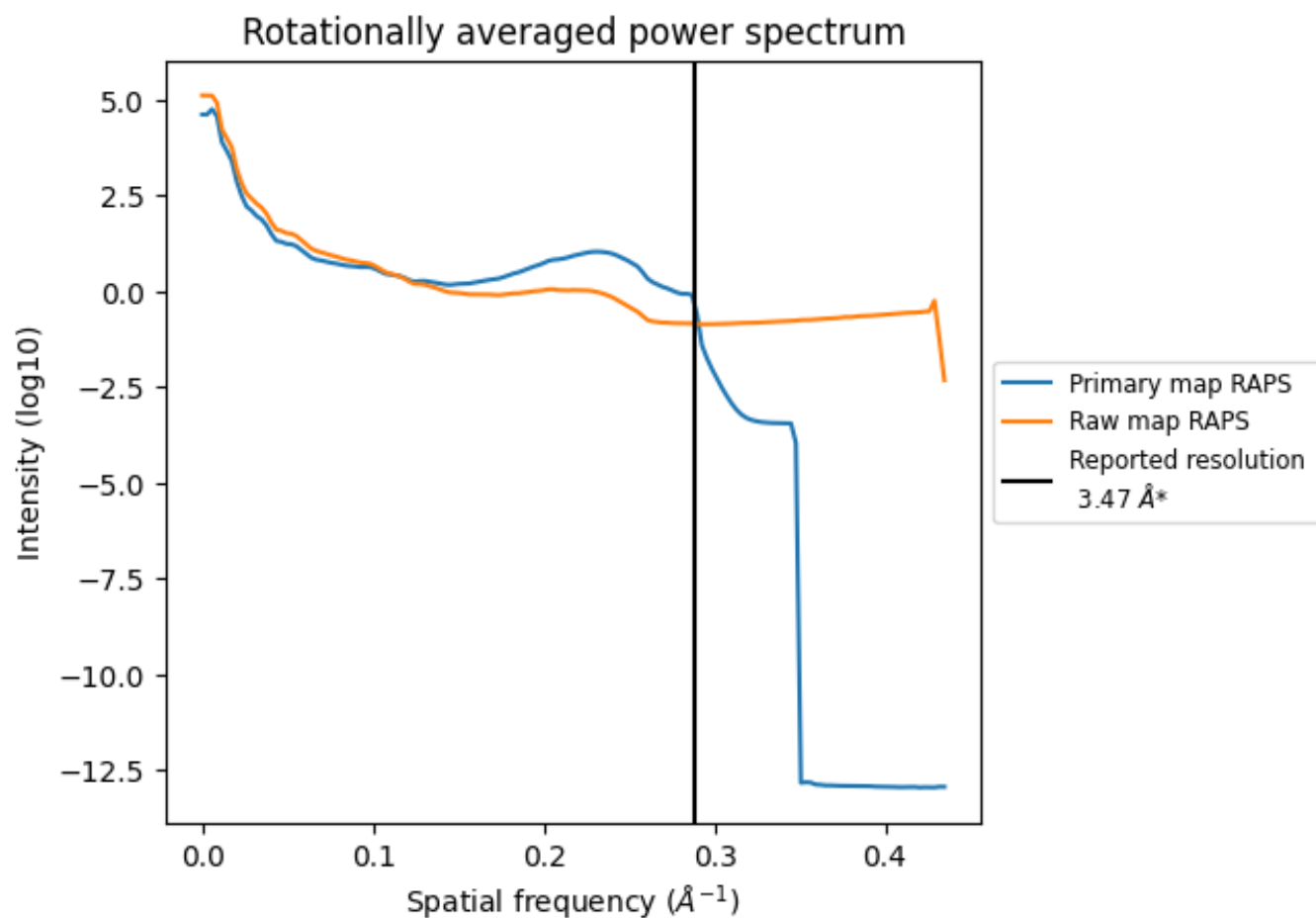
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 126 nm^3 ; this corresponds to an approximate mass of 114 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 ⓘ

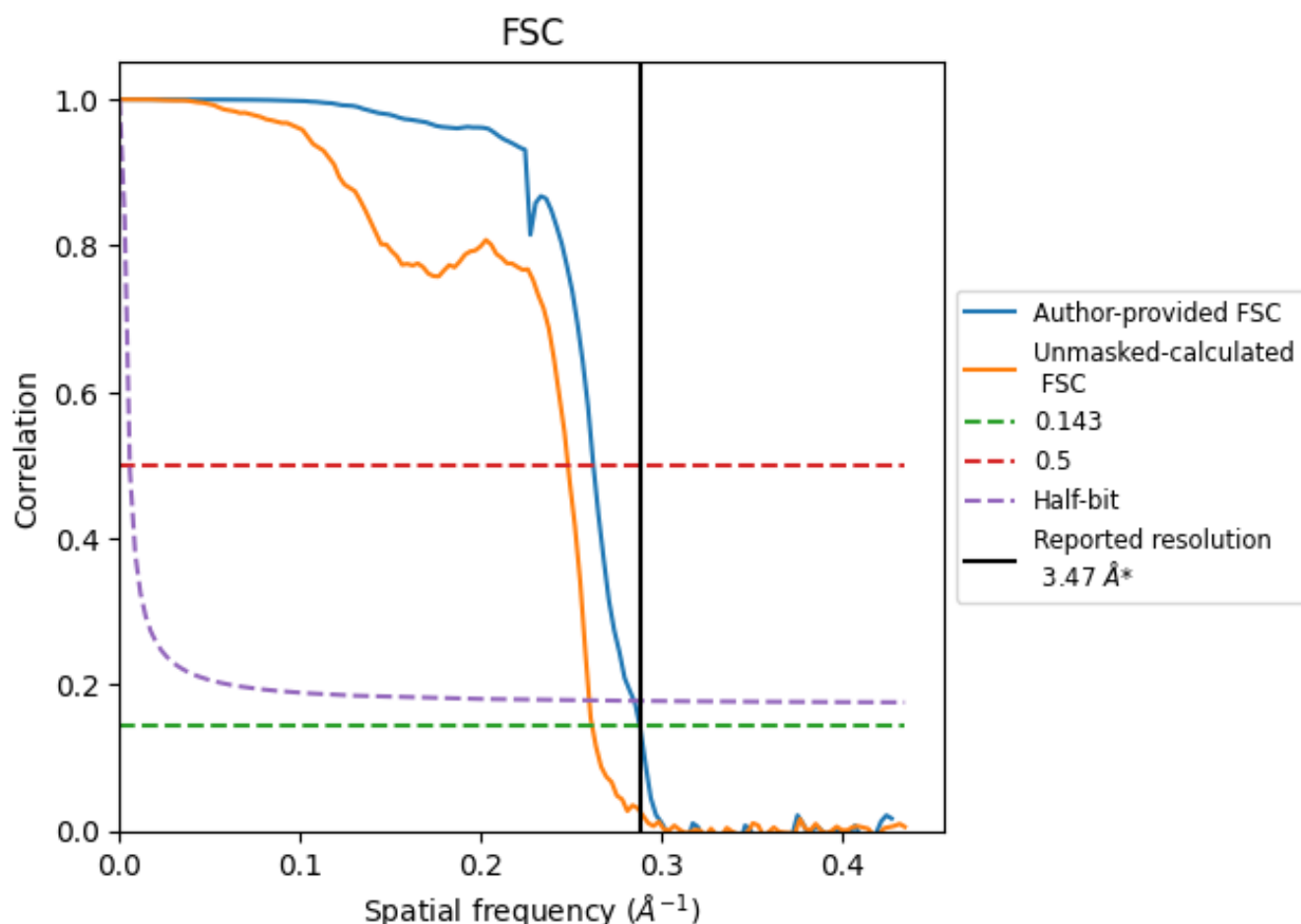


*Reported resolution corresponds to spatial frequency of 0.288 Å⁻¹

8 Fourier-Shell correlation [i](#)

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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.288 \AA^{-1}

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.47	-	-
Author-provided FSC curve	3.47	3.81	3.51
Unmasked-calculated*	3.82	4.03	3.84

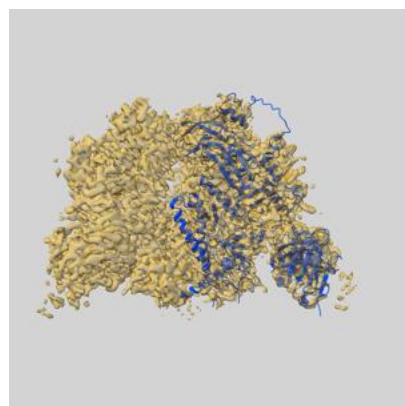
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.82 differs from the reported value 3.47 by more than 10 %

9 Map-model fit [i](#)

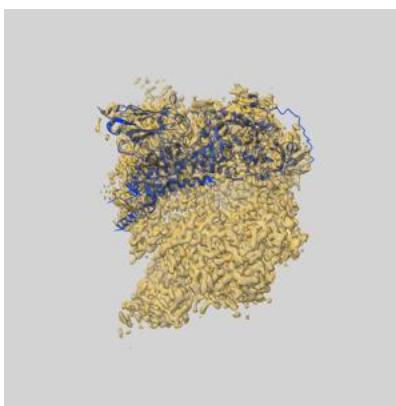
This section contains information regarding the fit between EMDB map EMD-25621 and PDB model 7T2P. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlays

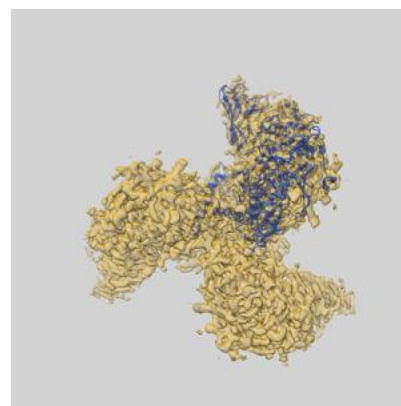
9.1.1 Map-model overlay [i](#)



X

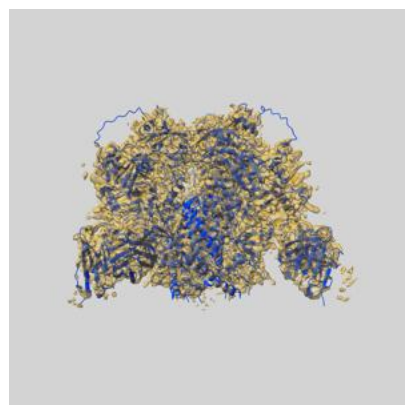


Y

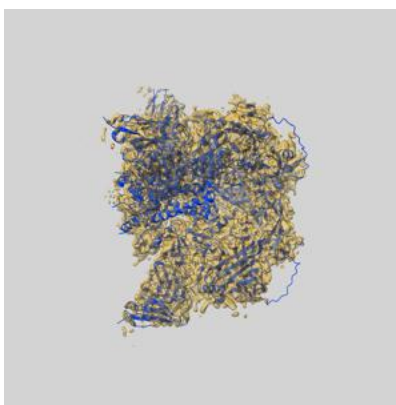


Z

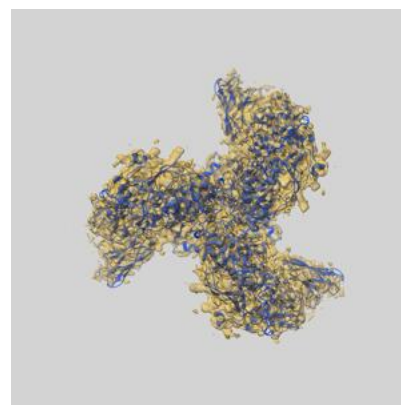
9.1.2 Map-model assembly overlay [i](#)



X



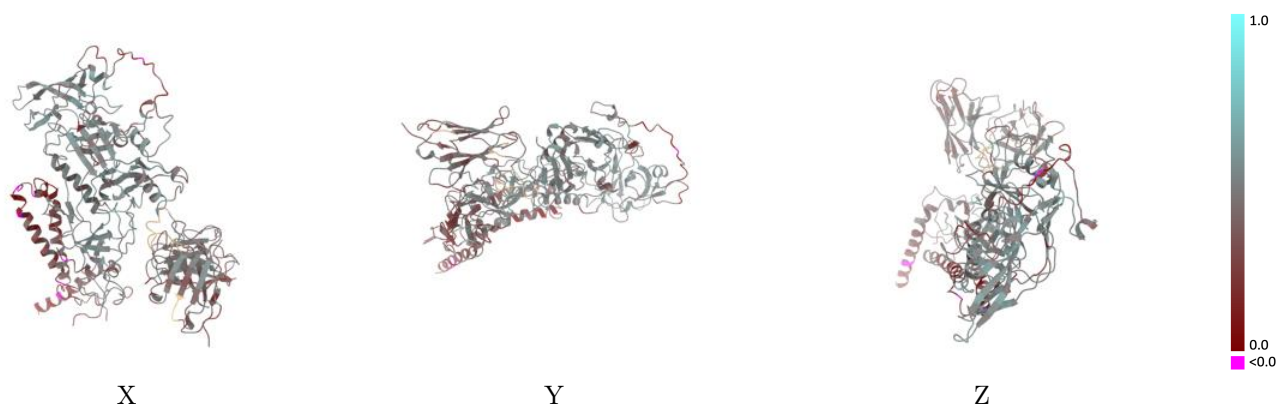
Y



Z

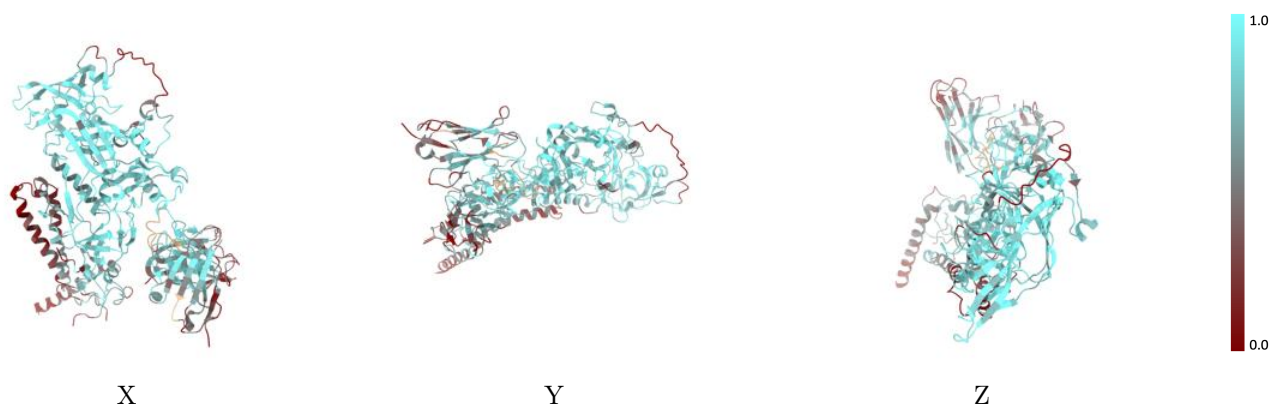
The images above show the 3D surface view of the map at the recommended contour level 0.33 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



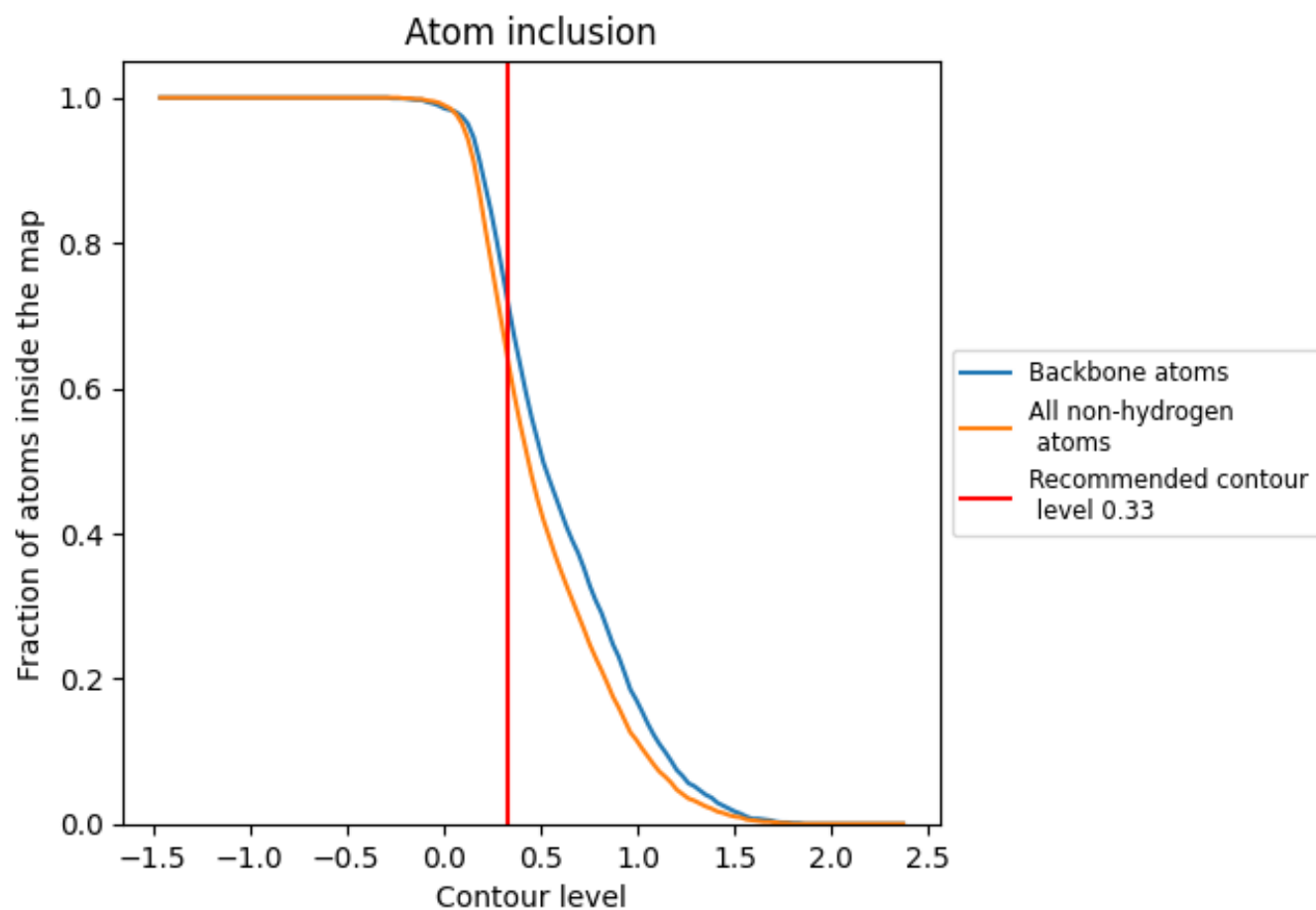
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.33).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 64% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.33) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6430	<div></div> 0.4220
A	<div></div> 0.7590	<div></div> 0.4700
B	<div></div> 0.3780	<div></div> 0.2770
C	<div></div> 0.5320	<div></div> 0.4370
D	<div></div> 0.5360	<div></div> 0.4600
E	<div></div> 0.2370	<div></div> 0.3100
F	<div></div> 0.2100	<div></div> 0.3390
G	<div></div> 0.6050	<div></div> 0.4120
H	<div></div> 0.6330	<div></div> 0.4310
I	<div></div> 0.5560	<div></div> 0.4250
J	<div></div> 0.2950	<div></div> 0.3360
K	<div></div> 0.7500	<div></div> 0.4190
L	<div></div> 0.5670	<div></div> 0.4060
M	<div></div> 0.2860	<div></div> 0.2290
N	<div></div> 0.5900	<div></div> 0.4180
O	<div></div> 0.7500	<div></div> 0.4530
P	<div></div> 0.5360	<div></div> 0.3450

1.0

0.0

<0.0