



wwPDB EM Validation Summary Report ⓘ

Oct 20, 2024 – 10:51 AM EDT

PDB ID : 7N4V
EMDB ID : EMD-24179
Title : Structure of cholesterol-bound human NPC1L1
Authors : Li, X.; Long, T.
Deposited on : 2021-06-04
Resolution : 3.58 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
buster-report	:	1.1.7 (2018)
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

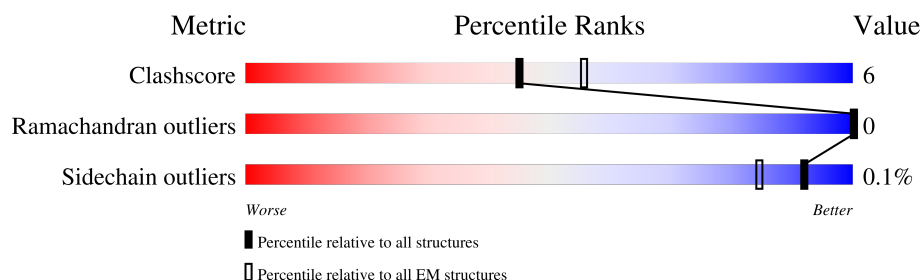
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.58 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	1332	
1	B	1332	
2	C	2	
2	D	2	
2	E	2	
2	F	2	
2	G	2	
2	H	2	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	C	2	X	-	-	-
2	NAG	F	2	X	-	-	-
3	NAG	A	1403	X	-	-	-
3	NAG	B	1604	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15390 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 Isoform 2 of NPC1-like intracellular cholesterol transporter 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	953	Total	C	N	O	S	0	0
			7426	4836	1206	1339	45		
1	B	953	Total	C	N	O	S	0	0
			7426	4836	1206	1339	45		

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



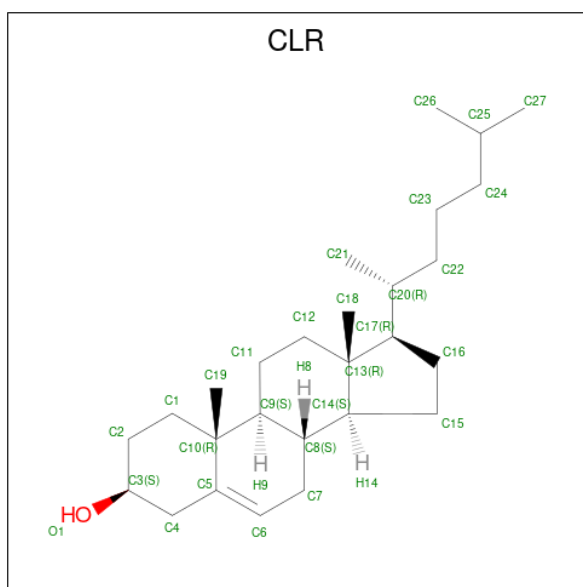
Mol	Chain	Residues	Atoms				AltConf	Trace
2	C	2	Total	C	N	O	0	0
			28	16	2	10		
2	D	2	Total	C	N	O	0	0
			28	16	2	10		
2	E	2	Total	C	N	O	0	0
			28	16	2	10		
2	F	2	Total	C	N	O	0	0
			28	16	2	10		
2	G	2	Total	C	N	O	0	0
			28	16	2	10		
2	H	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



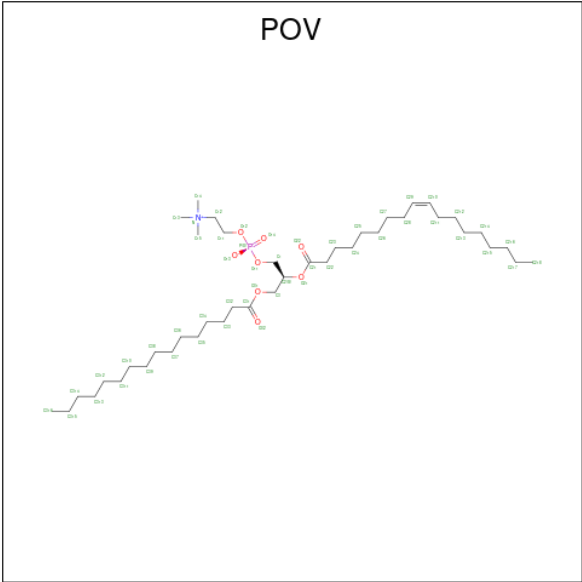
Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 4 is CHOLESTEROL (three-letter code: CLR) (formula: C₂₇H₄₆O).



Mol	Chain	Residues	Atoms			AltConf
4	A	1	Total	C	O	0
			28	27	1	
4	A	1	Total	C	O	0
			28	27	1	
4	A	1	Total	C	O	0
			28	27	1	
4	B	1	Total	C	O	0
			28	27	1	
4	B	1	Total	C	O	0
			28	27	1	
4	B	1	Total	C	O	0
			28	27	1	

- Molecule 5 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylamm onio)ethyl phosphate (three-letter code: POV) (formula: C₄₂H₈₂NO₈P).

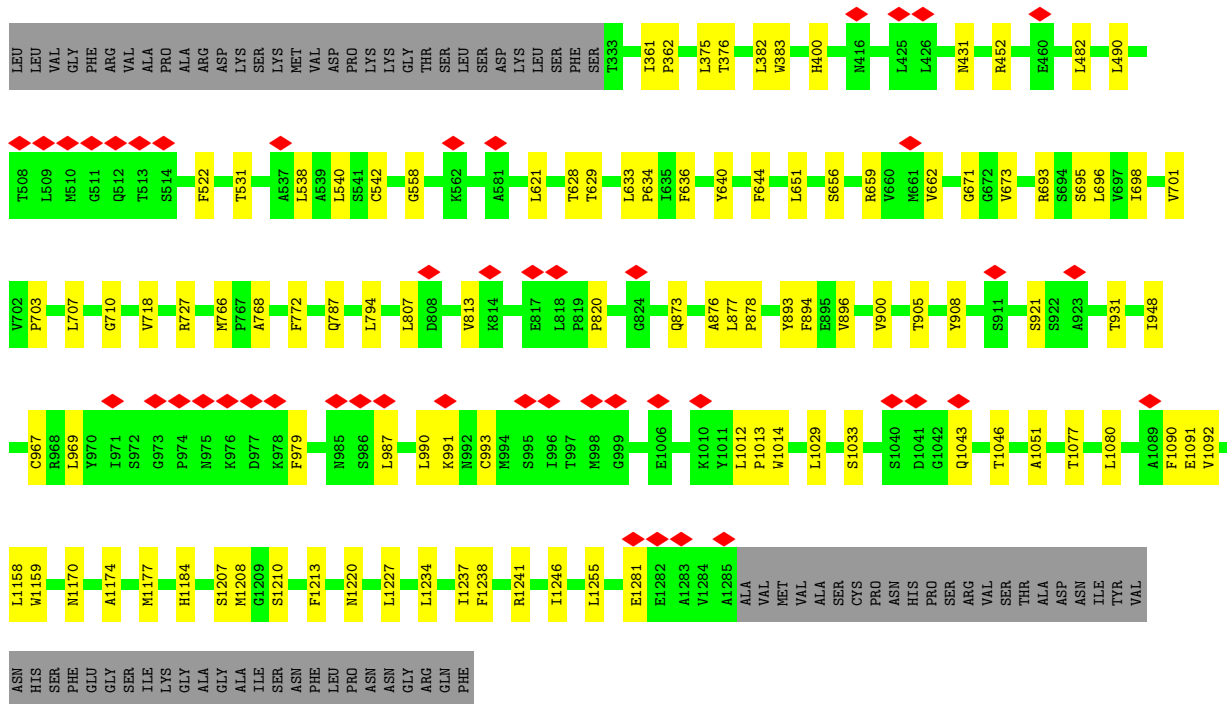


Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	N	O	P	0
			45	35	1	8	1	
5	B	1	Total	C	N	O	P	0
			45	35	1	8	1	

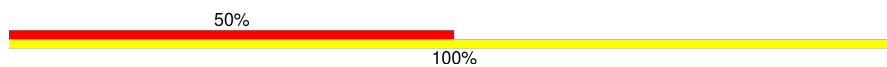
- Chain B:



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

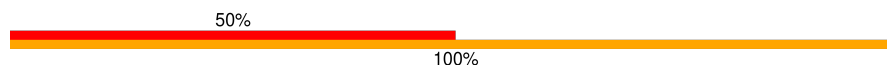


- Chain C:



NAG1
NAG2

- Chain D:





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



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



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



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	251678	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	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	2.341	Depositor
Minimum map value	-1.233	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.246	Depositor
Map size (Å)	299.88, 299.88, 299.88	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.833, 0.833, 0.833	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.70	0/7610	0.74	0/10367
1	B	0.70	0/7610	0.74	0/10367
All	All	0.70	0/15220	0.74	0/20734

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7426	0	7463	78	0
1	B	7426	0	7465	80	0
2	C	28	0	25	0	0
2	D	28	0	25	3	0
2	E	28	0	25	0	0
2	F	28	0	25	0	0
2	G	28	0	25	3	0
2	H	28	0	25	0	0
3	A	56	0	52	4	0
3	B	56	0	52	4	0
4	A	84	0	138	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	84	0	138	31	0
5	A	45	0	65	1	0
5	B	45	0	65	1	0
All	All	15390	0	15588	188	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 6.

The worst 5 of 188 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:1234:LEU:HD21	4:A:1405:CLR:C21	1.72	1.17
1:B:1234:LEU:HD21	4:B:1606:CLR:C21	1.77	1.13
1:B:431:ASN:ND2	3:B:1602:NAG:H82	1.68	1.09
1:B:1234:LEU:CD2	4:B:1606:CLR:H213	1.82	1.08
1:A:431:ASN:ND2	3:A:1401:NAG:H82	1.68	1.07

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	951/1332 (71%)	877 (92%)	74 (8%)	0	100	100
1	B	951/1332 (71%)	877 (92%)	74 (8%)	0	100	100
All	All	1902/2664 (71%)	1754 (92%)	148 (8%)	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	811/1122 (72%)	810 (100%)	1 (0%)	92	97
1	B	811/1122 (72%)	810 (100%)	1 (0%)	92	97
All	All	1622/2244 (72%)	1620 (100%)	2 (0%)	92	97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	894	PHE
1	B	894	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	577	ASN
1	A	1017	ASN
1	A	1043	GLN
1	B	1017	ASN
1	B	1043	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

12 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	$\# Z > 2$
2	NAG	C	1	1,2	14,14,15	0.43	0	17,19,21	1.69	6 (35%)
2	NAG	C	2	2	14,14,15	0.33	0	17,19,21	1.24	1 (5%)
2	NAG	D	1	1,2	14,14,15	0.49	0	17,19,21	1.36	2 (11%)
2	NAG	D	2	2	14,14,15	0.37	0	17,19,21	1.72	3 (17%)
2	NAG	E	1	1,2	14,14,15	0.55	0	17,19,21	1.24	2 (11%)
2	NAG	E	2	2	14,14,15	0.24	0	17,19,21	0.67	0
2	NAG	F	1	1,2	14,14,15	0.43	0	17,19,21	1.69	6 (35%)
2	NAG	F	2	2	14,14,15	0.33	0	17,19,21	1.24	1 (5%)
2	NAG	G	1	1,2	14,14,15	0.48	0	17,19,21	1.35	2 (11%)
2	NAG	G	2	2	14,14,15	0.37	0	17,19,21	1.72	3 (17%)
2	NAG	H	1	1,2	14,14,15	0.55	0	17,19,21	1.23	2 (11%)
2	NAG	H	2	2	14,14,15	0.25	0	17,19,21	0.67	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
2	NAG	C	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	C	2	2	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	D	2	2	-	4/6/23/26	0/1/1/1
2	NAG	E	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	F	2	2	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	G	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	G	2	2	-	4/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	H	2	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	G	2	NAG	C2-N2-C7	4.54	128.98	122.90
2	D	2	NAG	C2-N2-C7	4.50	128.93	122.90
2	D	2	NAG	C8-C7-N2	4.27	123.20	116.12
2	G	2	NAG	C8-C7-N2	4.27	123.19	116.12
2	C	2	NAG	C1-O5-C5	4.04	117.61	112.19

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	2	NAG	C1
2	F	2	NAG	C1

5 of 28 torsion outliers are listed below:

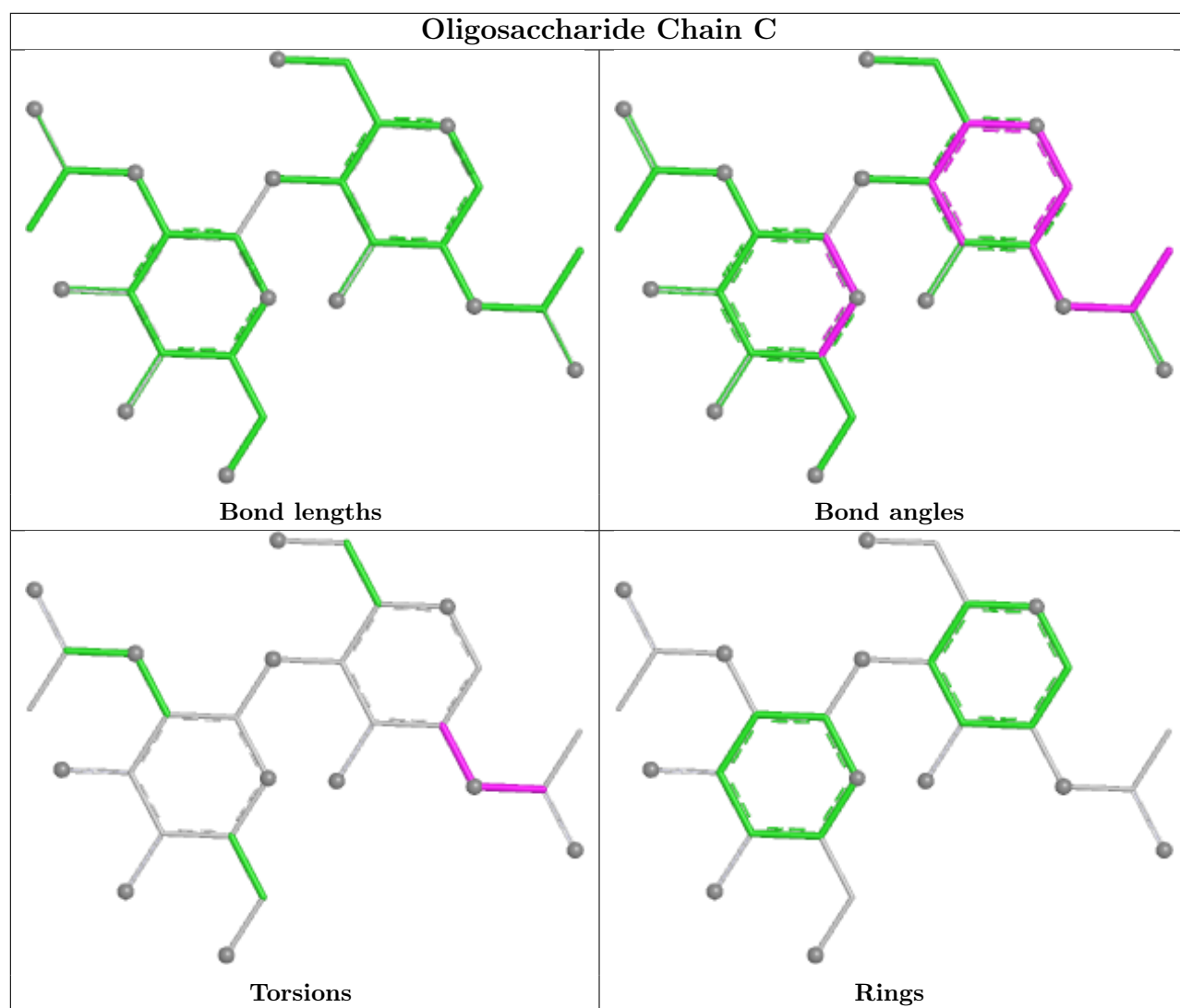
Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C1-C2-N2-C7
2	G	1	NAG	C1-C2-N2-C7
2	C	1	NAG	C8-C7-N2-C2
2	F	1	NAG	C8-C7-N2-C2
2	D	1	NAG	C8-C7-N2-C2

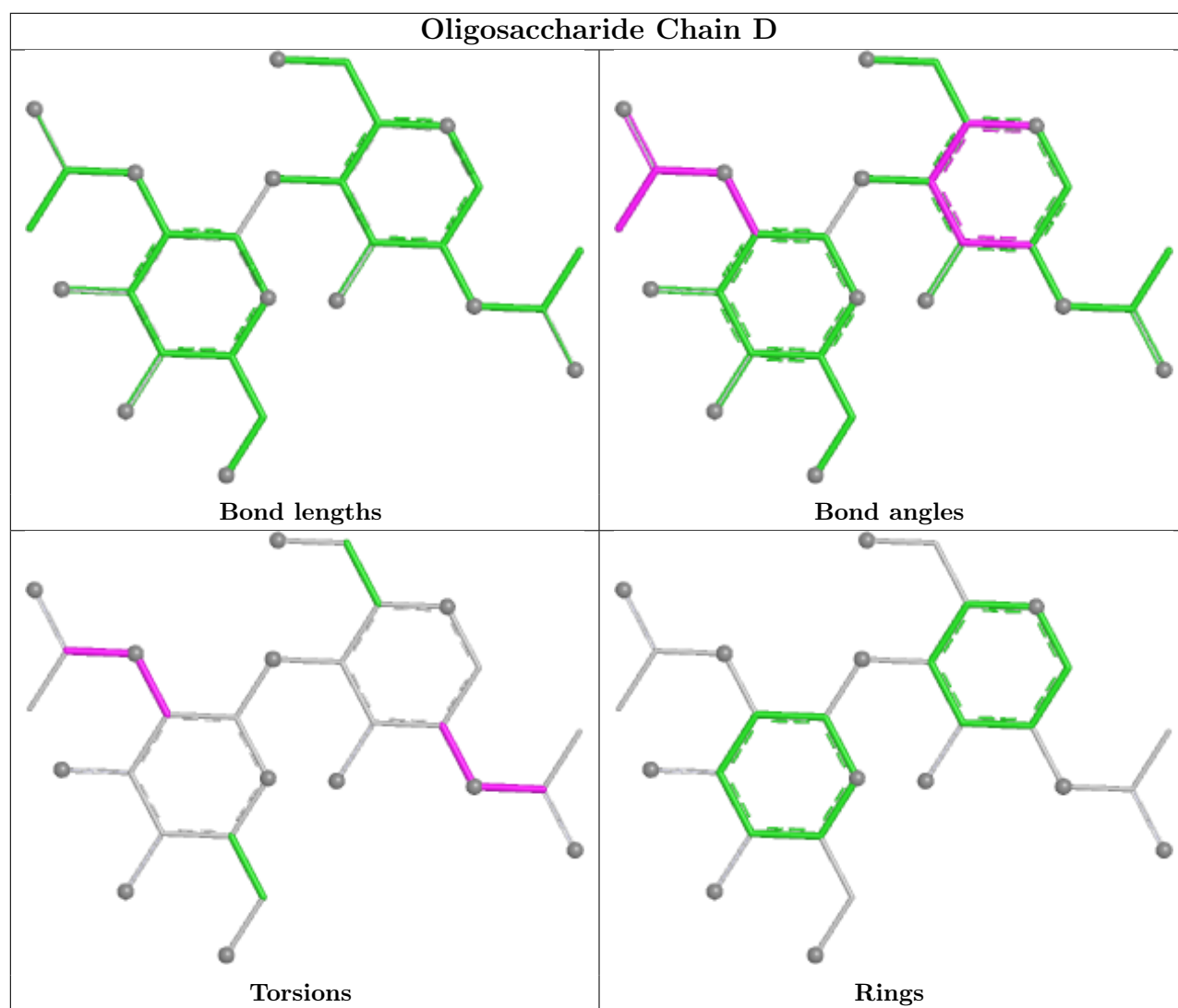
There are no ring outliers.

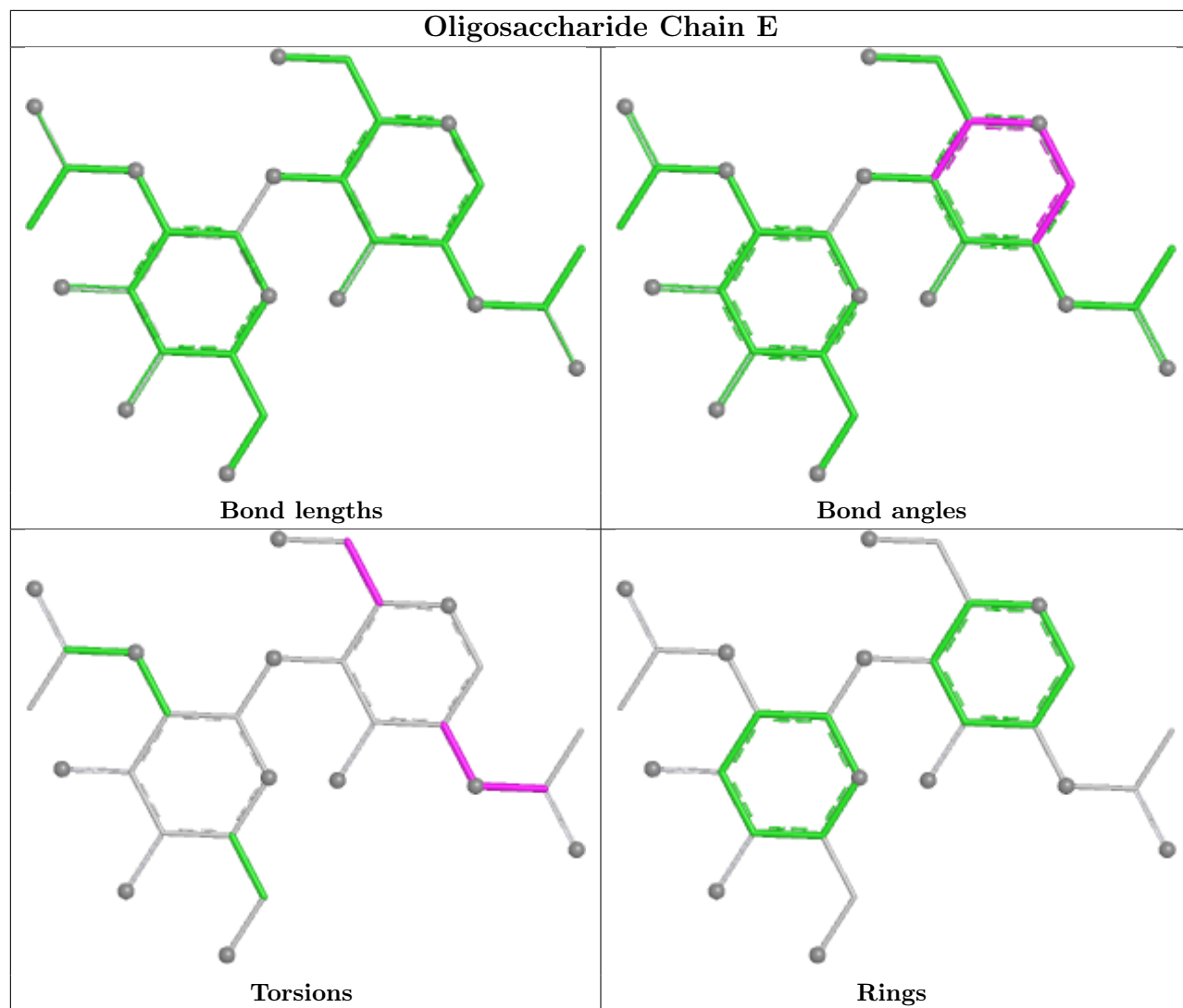
4 monomers are involved in 6 short contacts:

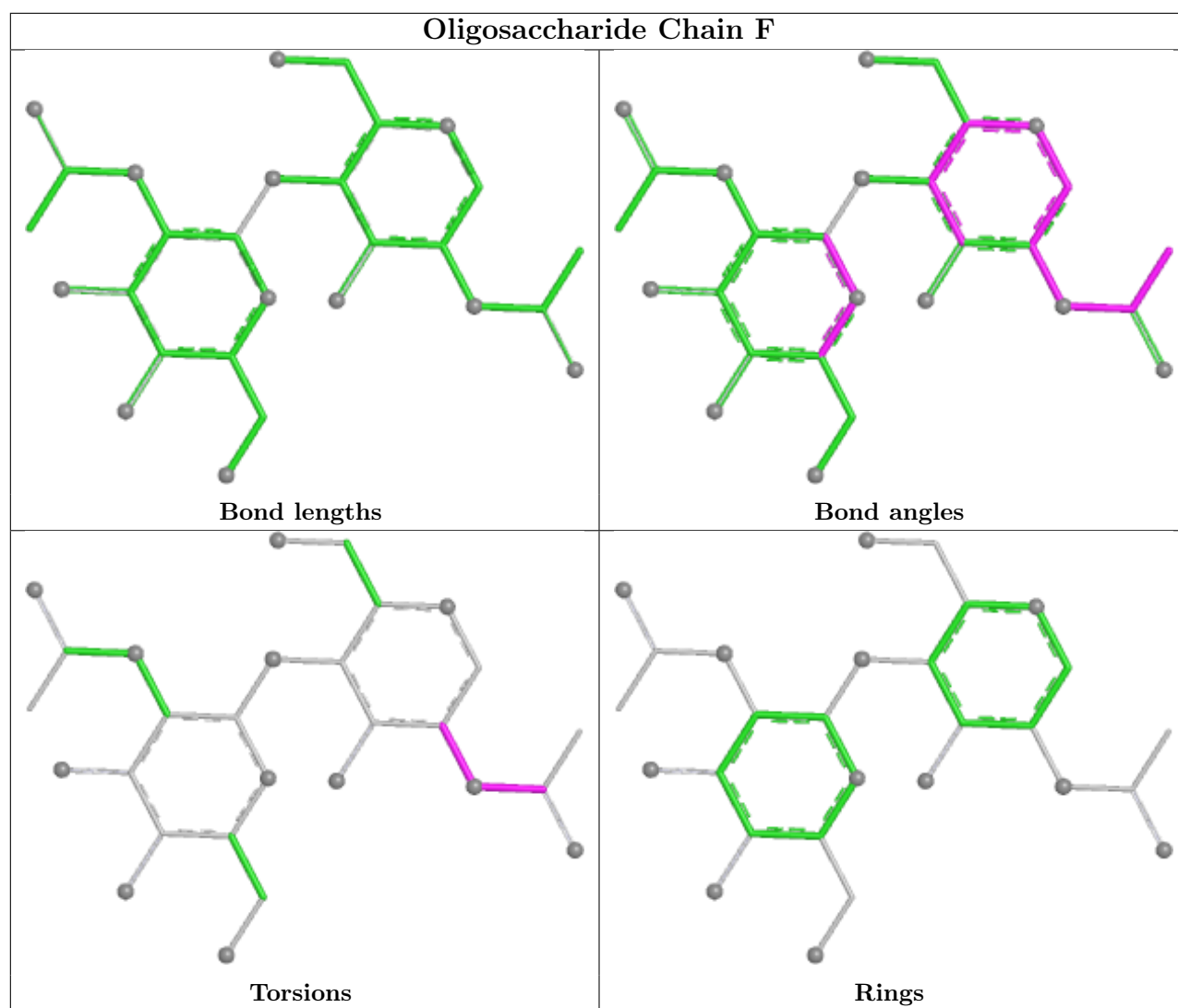
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	1	NAG	2	0
2	D	2	NAG	1	0
2	G	2	NAG	1	0
2	D	1	NAG	2	0

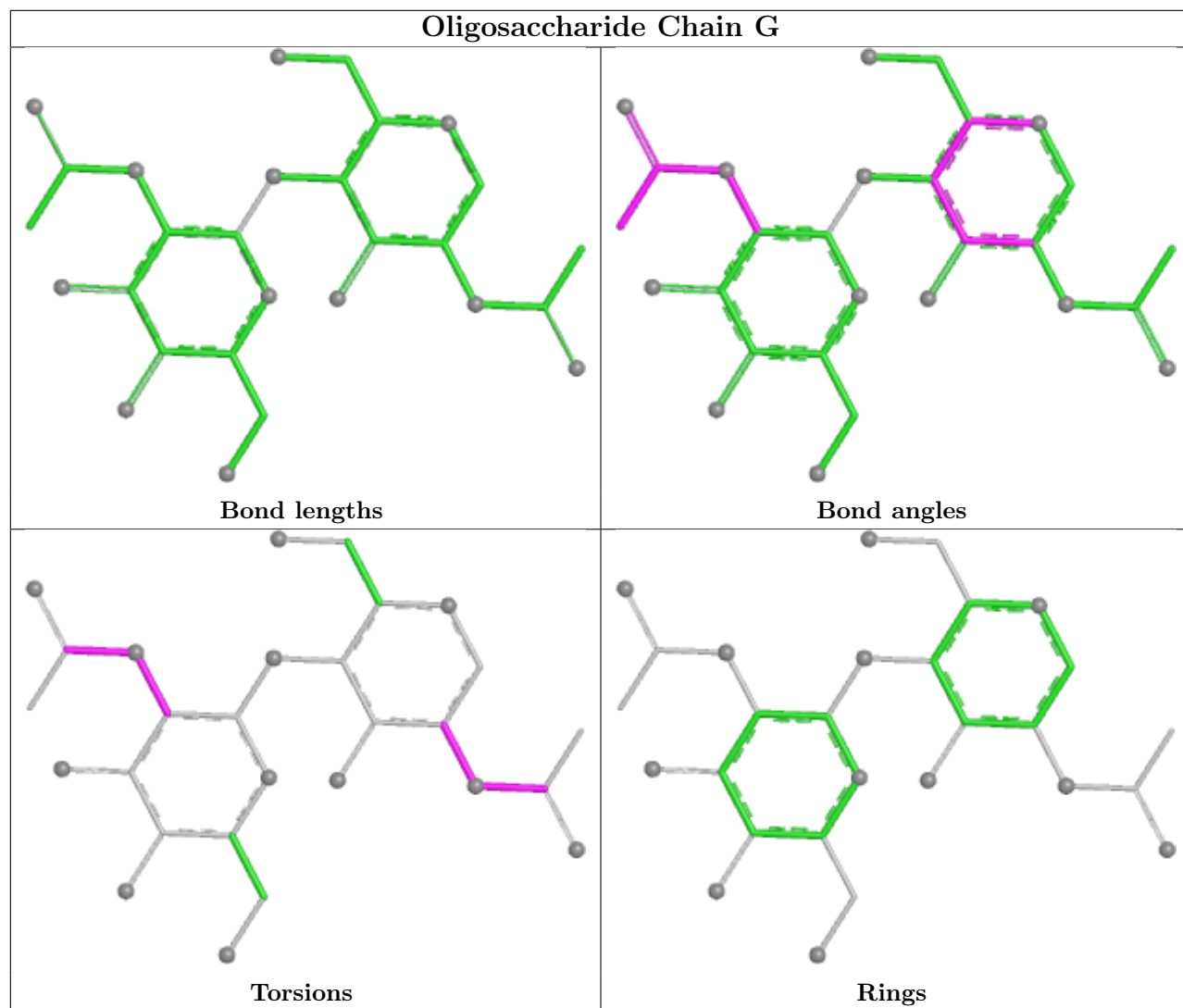
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

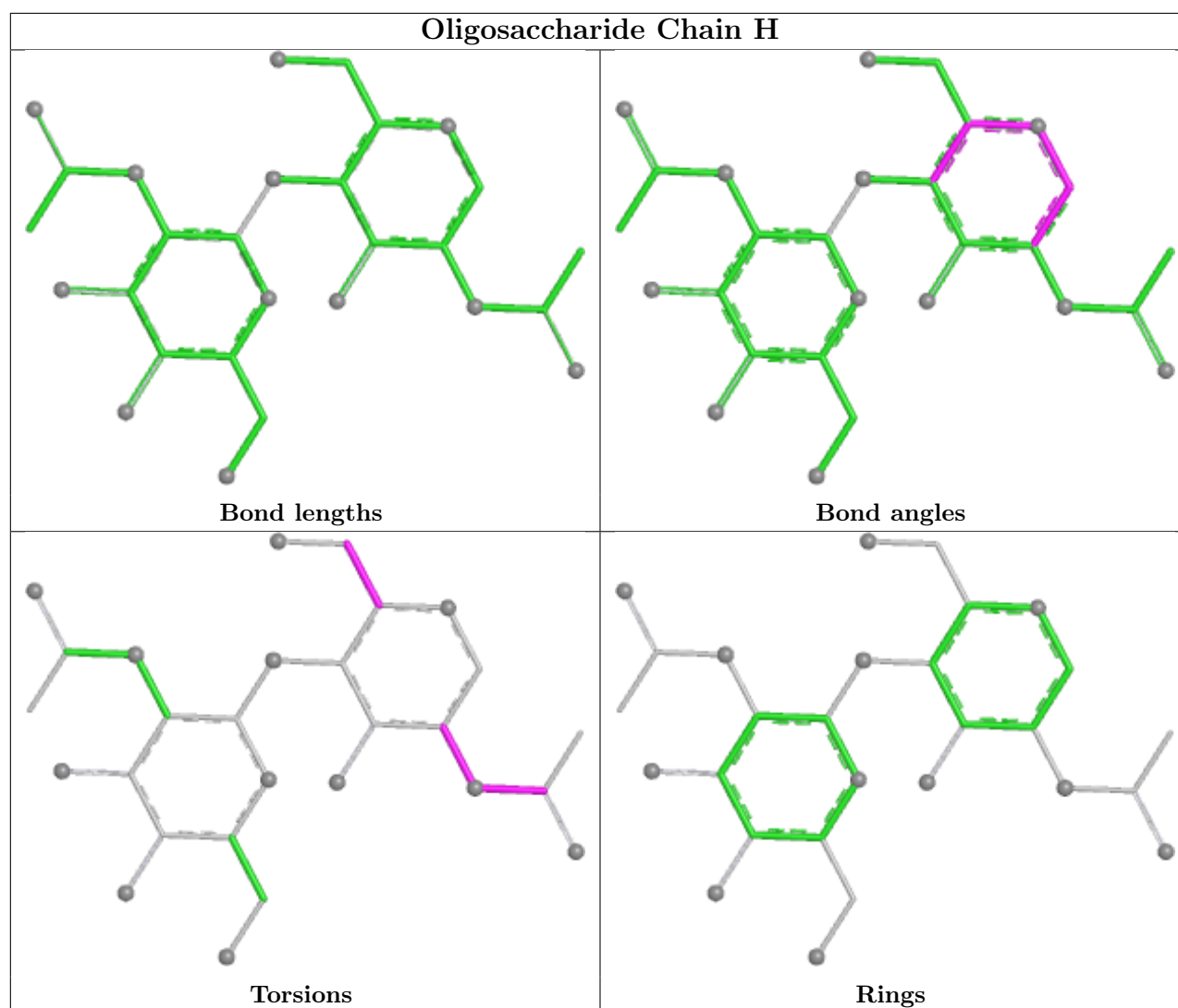












5.6 Ligand geometry [i](#)

16 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	$\# Z > 2$
3	NAG	B	1604	1	14,14,15	0.56	0	17,19,21	1.29	2 (11%)
3	NAG	A	1401	1	14,14,15	0.30	0	17,19,21	0.56	0
3	NAG	A	1403	1	14,14,15	0.57	0	17,19,21	1.28	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CLR	B	1606	-	31,31,31	0.77	0	48,48,48	1.70	9 (18%)
4	CLR	B	1608	-	31,31,31	0.82	2 (6%)	48,48,48	1.52	6 (12%)
4	CLR	A	1407	-	31,31,31	0.82	2 (6%)	48,48,48	1.52	7 (14%)
4	CLR	A	1406	-	31,31,31	0.83	2 (6%)	48,48,48	1.58	8 (16%)
4	CLR	B	1607	-	31,31,31	0.83	2 (6%)	48,48,48	1.58	6 (12%)
5	POV	A	1408	-	44,44,51	1.06	4 (9%)	50,52,59	0.94	2 (4%)
4	CLR	A	1405	-	31,31,31	0.78	0	48,48,48	1.70	8 (16%)
3	NAG	A	1404	1	14,14,15	0.34	0	17,19,21	0.79	0
5	POV	B	1601	-	44,44,51	1.06	4 (9%)	50,52,59	0.94	2 (4%)
3	NAG	B	1603	1	14,14,15	0.39	0	17,19,21	0.90	1 (5%)
3	NAG	B	1602	1	14,14,15	0.29	0	17,19,21	0.57	0
3	NAG	B	1605	1	14,14,15	0.33	0	17,19,21	0.79	0
3	NAG	A	1402	1	14,14,15	0.39	0	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
3	NAG	B	1604	1	1/1/5/7	2/6/23/26	0/1/1/1
3	NAG	A	1401	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1403	1	1/1/5/7	2/6/23/26	0/1/1/1
4	CLR	B	1606	-	-	6/10/68/68	0/4/4/4
4	CLR	B	1608	-	-	7/10/68/68	0/4/4/4
4	CLR	A	1407	-	-	7/10/68/68	0/4/4/4
4	CLR	A	1406	-	-	5/10/68/68	0/4/4/4
4	CLR	B	1607	-	-	5/10/68/68	0/4/4/4
5	POV	A	1408	-	-	29/48/48/55	-
4	CLR	A	1405	-	-	3/10/68/68	0/4/4/4
3	NAG	A	1404	1	-	2/6/23/26	0/1/1/1
5	POV	B	1601	-	-	29/48/48/55	-
3	NAG	B	1603	1	-	1/6/23/26	0/1/1/1
3	NAG	B	1602	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1605	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1402	1	-	1/6/23/26	0/1/1/1

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1601	POV	O21-C2	-2.72	1.40	1.46
5	A	1408	POV	O21-C2	-2.69	1.40	1.46
5	B	1601	POV	O31-C31	2.43	1.40	1.33
5	A	1408	POV	O31-C31	2.40	1.40	1.33
4	B	1607	CLR	C10-C9	-2.17	1.52	1.56

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1607	CLR	C13-C17-C20	-4.92	111.90	119.50
4	A	1406	CLR	C13-C17-C20	-4.91	111.92	119.50
4	A	1405	CLR	C13-C17-C20	-4.89	111.94	119.50
4	B	1606	CLR	C13-C17-C20	-4.86	112.00	119.50
4	A	1406	CLR	C13-C14-C8	-4.30	108.30	114.41

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1403	NAG	C1
3	B	1604	NAG	C1

5 of 105 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1401	NAG	C8-C7-N2-C2
3	A	1401	NAG	O7-C7-N2-C2
3	B	1602	NAG	C8-C7-N2-C2
3	B	1602	NAG	O7-C7-N2-C2
4	A	1407	CLR	C13-C17-C20-C22

There are no ring outliers.

10 monomers are involved in 74 short contacts:

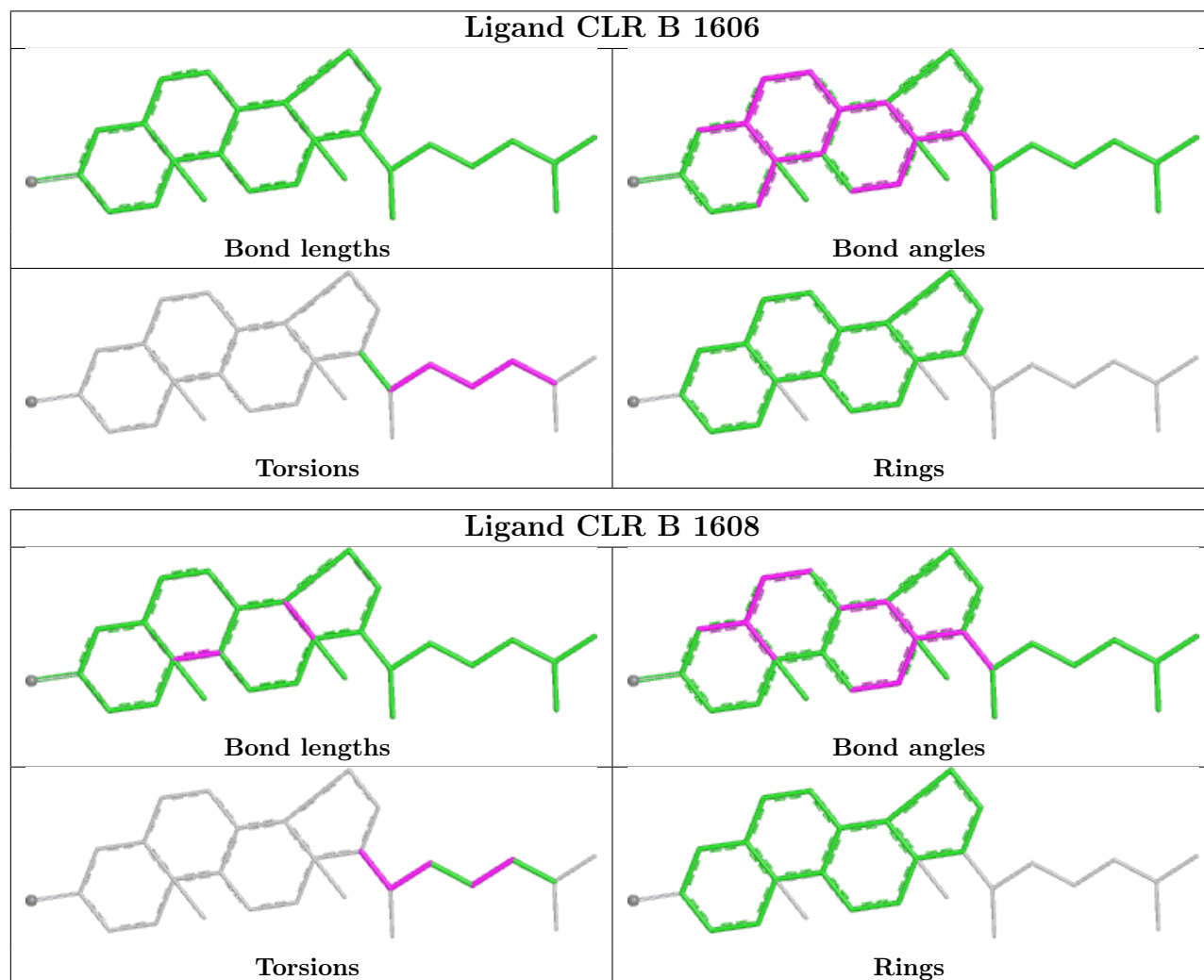
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1401	NAG	4	0
4	B	1606	CLR	17	0
4	B	1608	CLR	12	0
4	A	1407	CLR	15	0
4	A	1406	CLR	1	0
4	B	1607	CLR	2	0
5	A	1408	POV	1	0

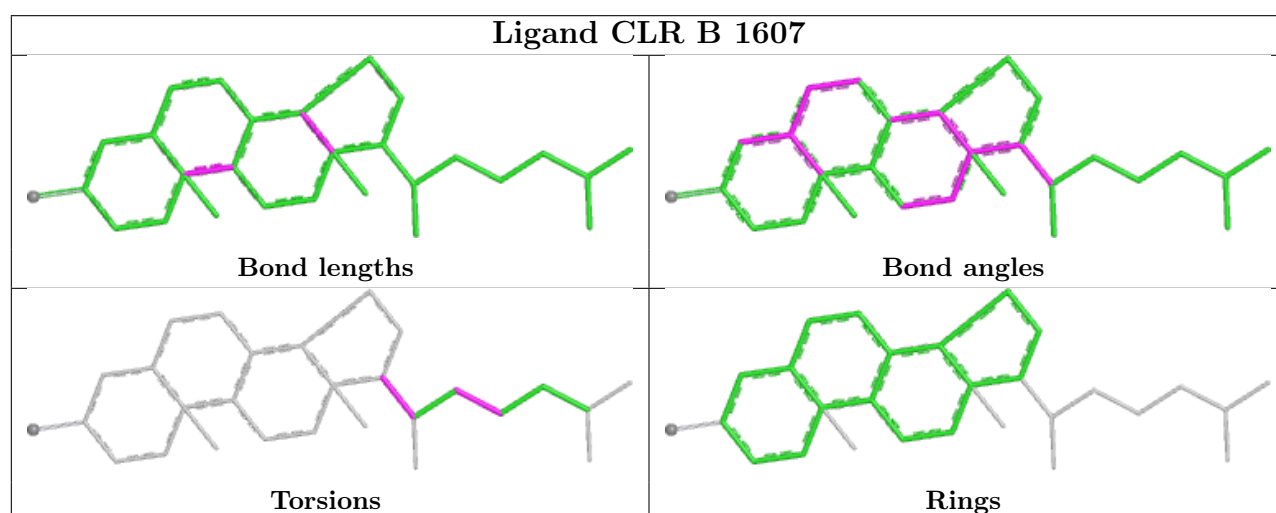
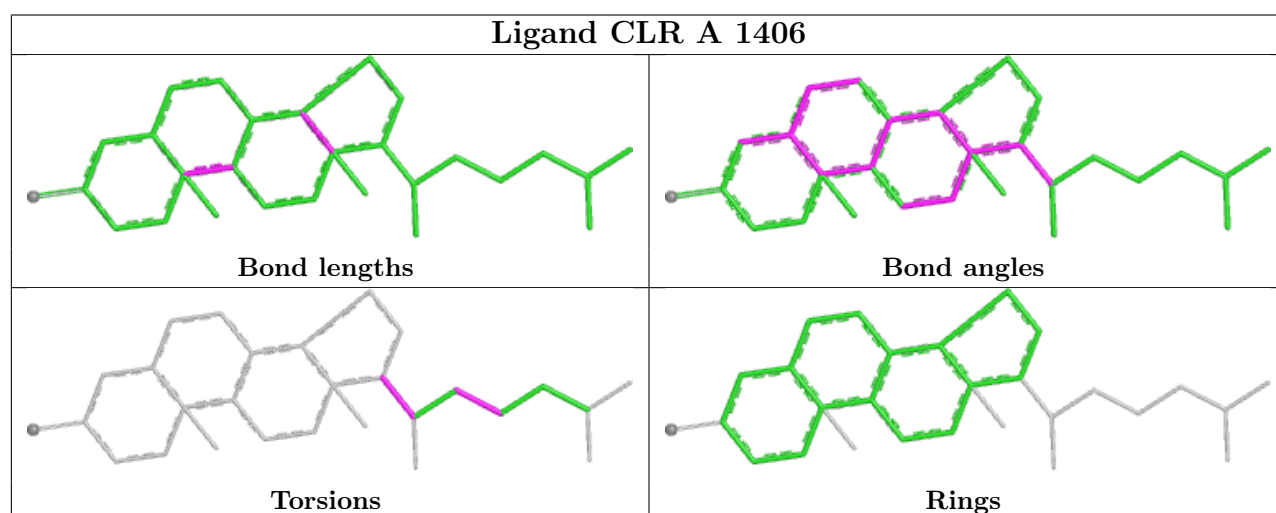
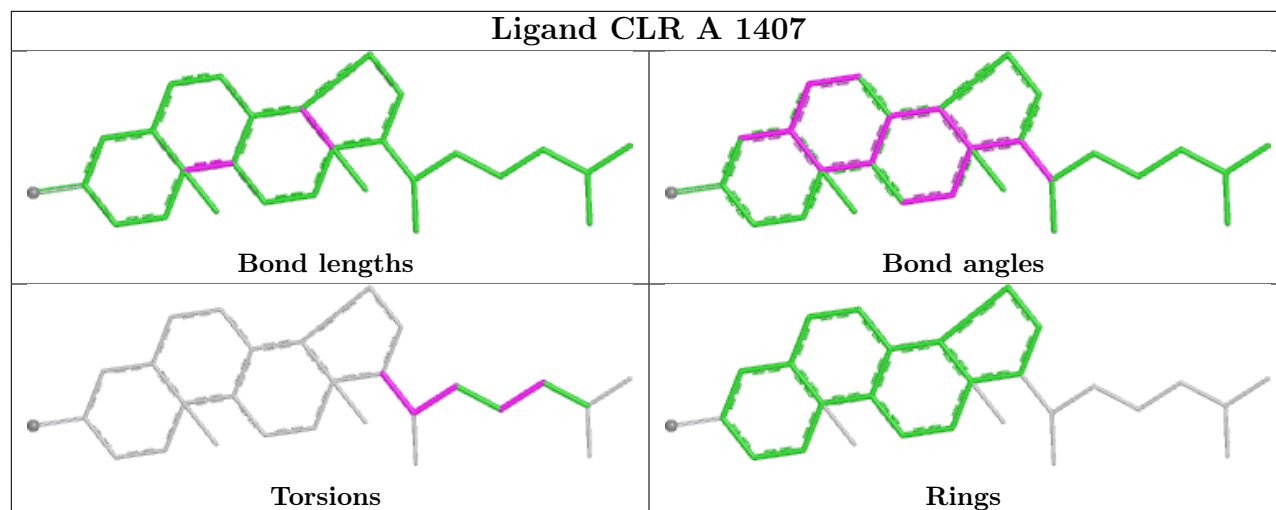
Continued on next page...

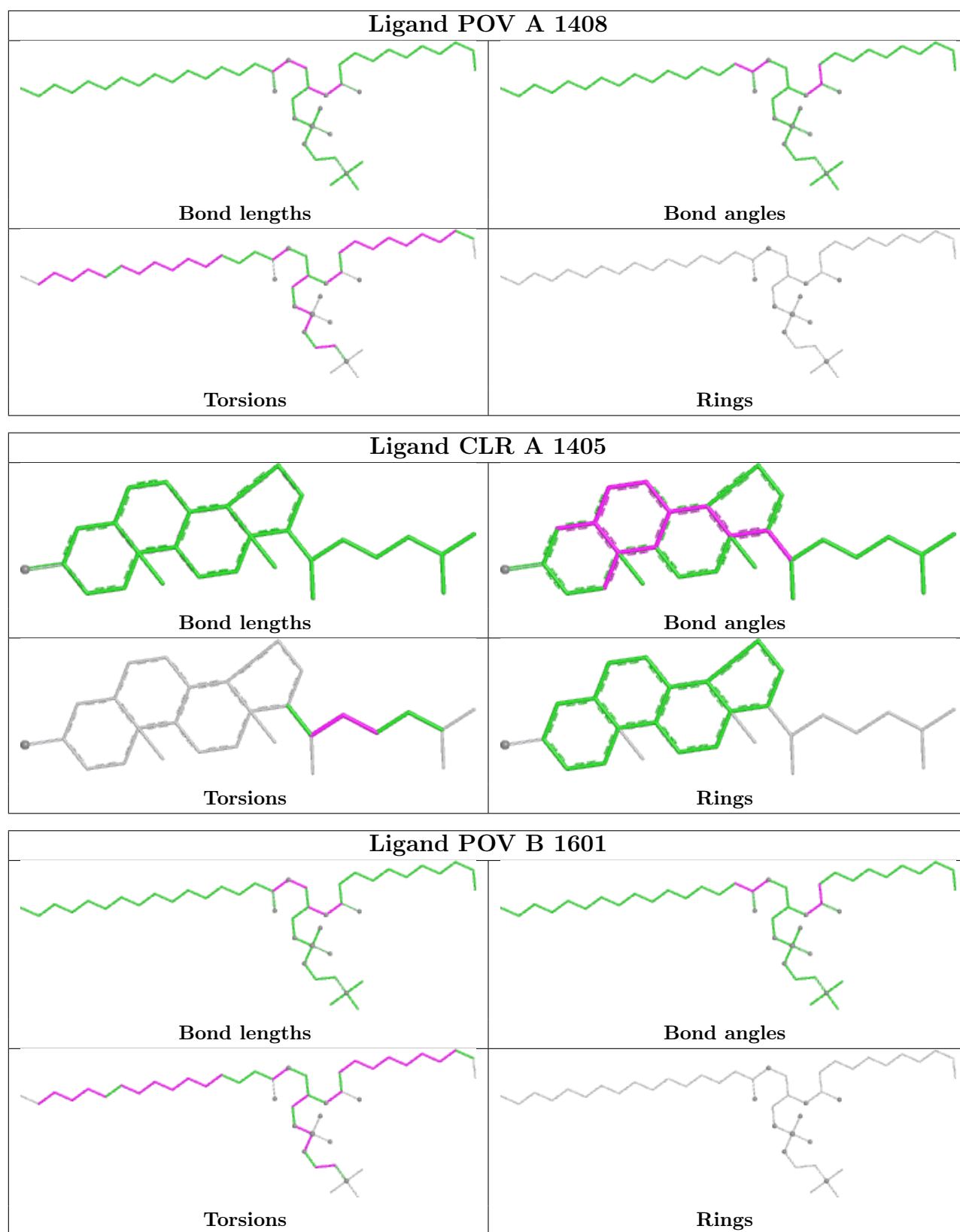
Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1405	CLR	17	0
5	B	1601	POV	1	0
3	B	1602	NAG	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

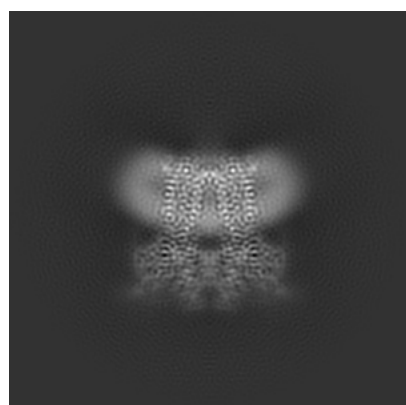
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24179. These allow visual inspection of the internal detail of the map and identification of artifacts.

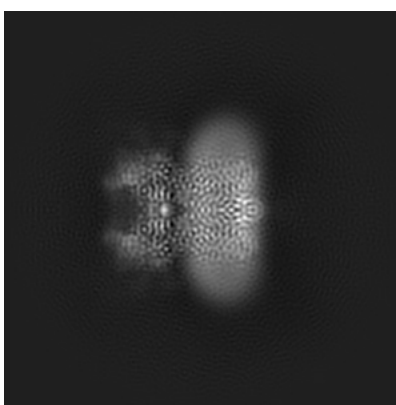
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

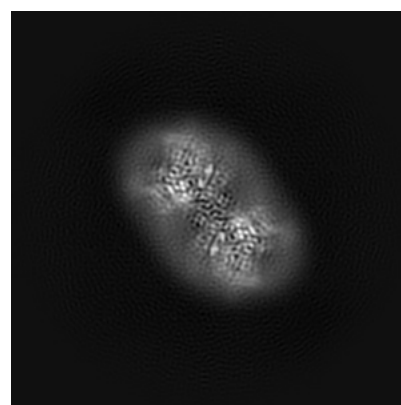
6.1.1 Primary map



X



Y

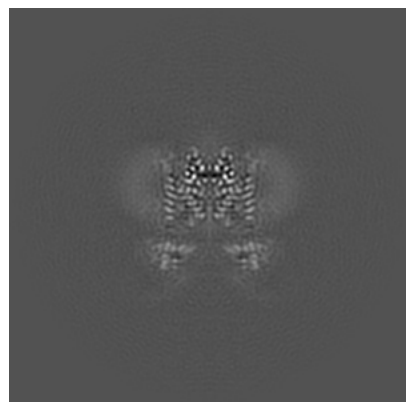


Z

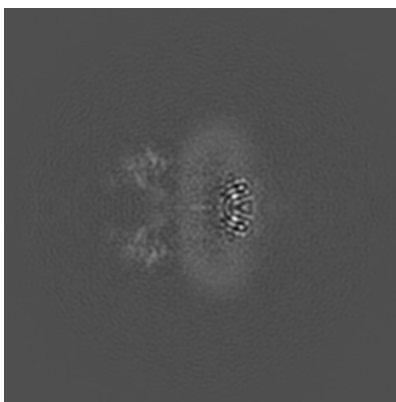
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

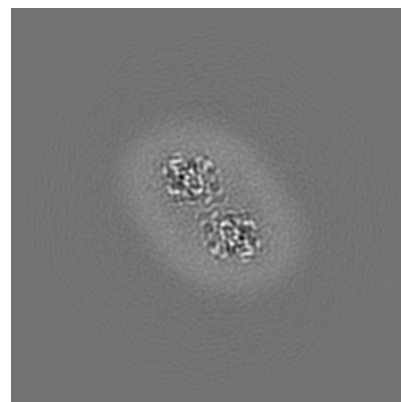
6.2.1 Primary map



X Index: 180



Y Index: 180

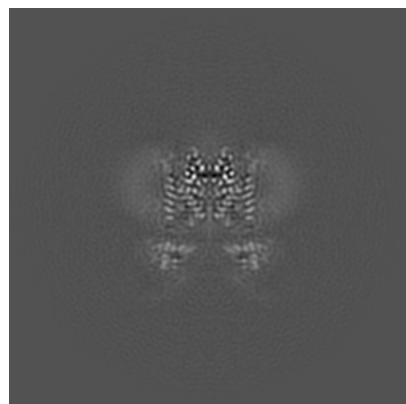


Z Index: 180

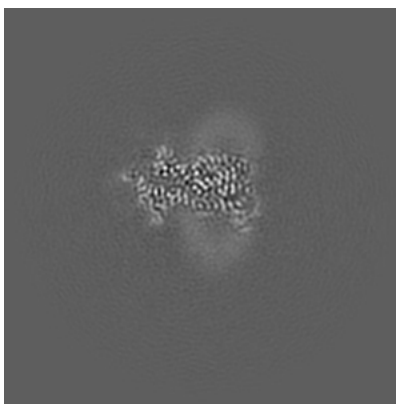
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

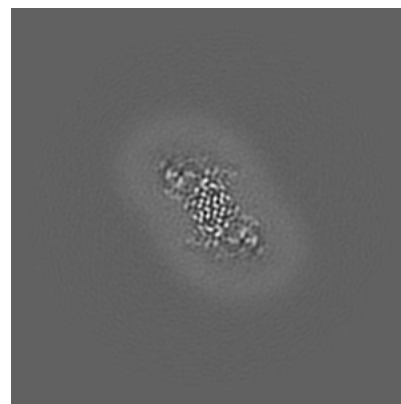
6.3.1 Primary map



X Index: 180



Y Index: 147

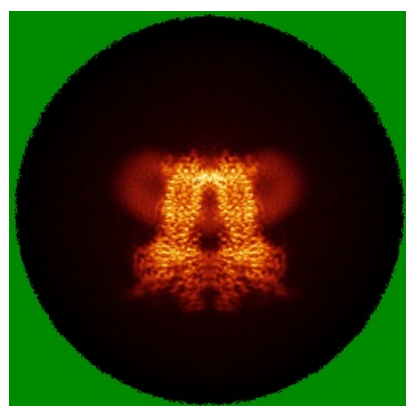


Z Index: 210

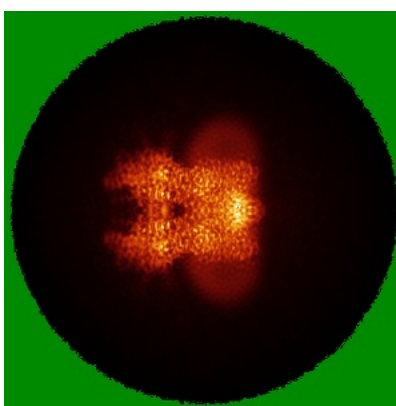
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

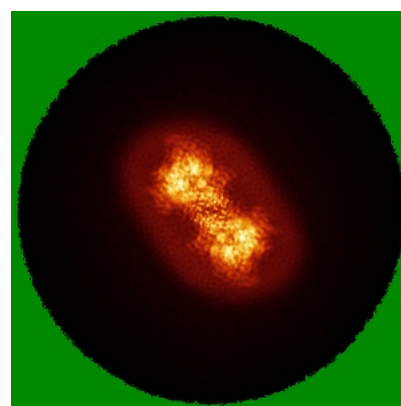
6.4.1 Primary map



X



Y

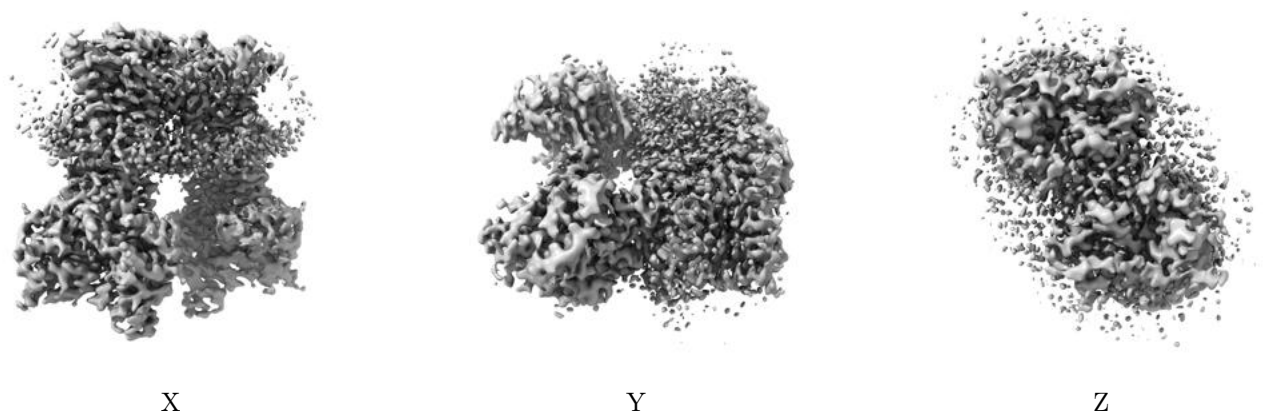


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.246. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

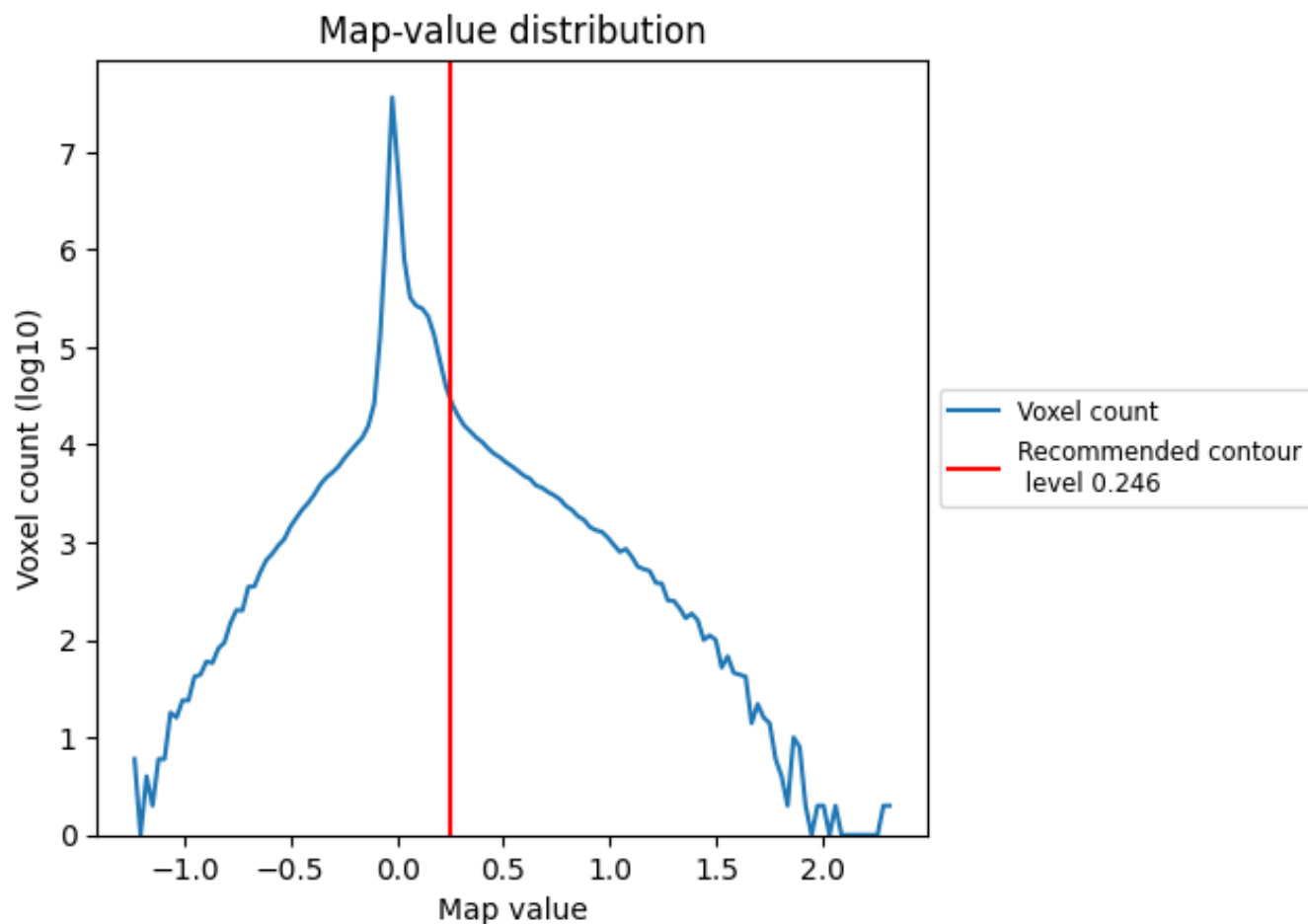
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

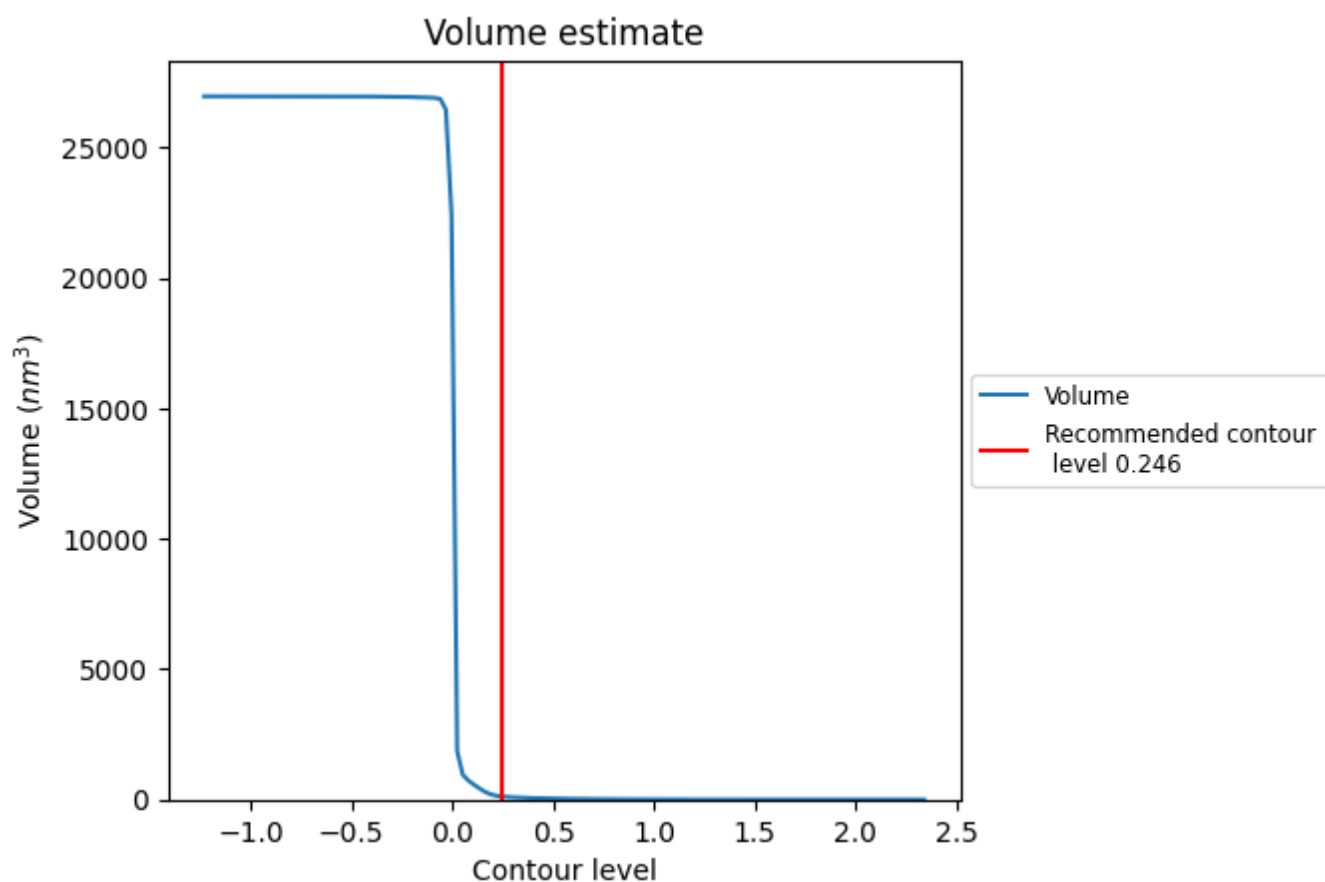
This section contains the results of statistical analysis of the map.

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.

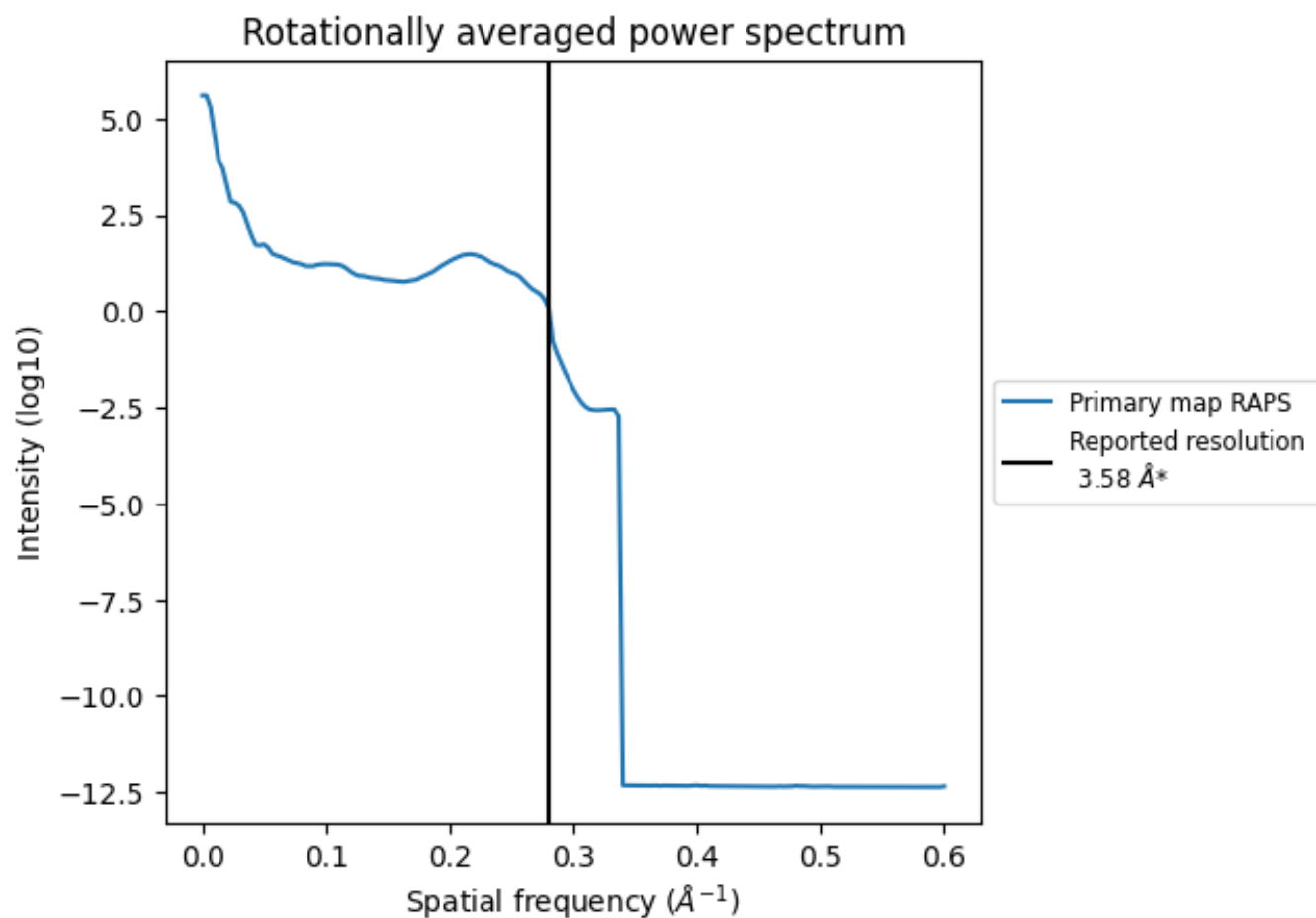
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 117 nm³; this corresponds to an approximate mass of 106 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 0.279 \AA^{-1}

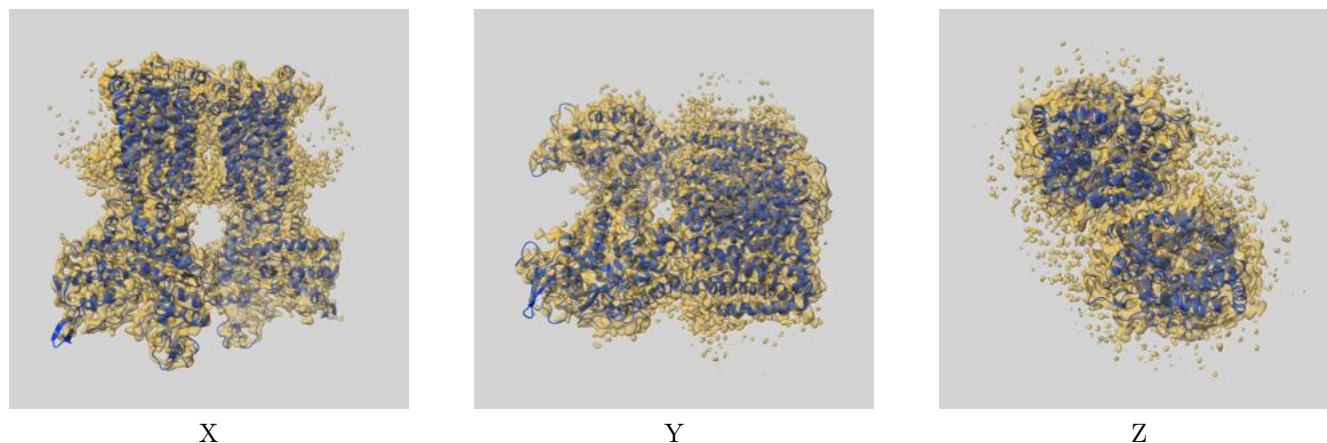
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

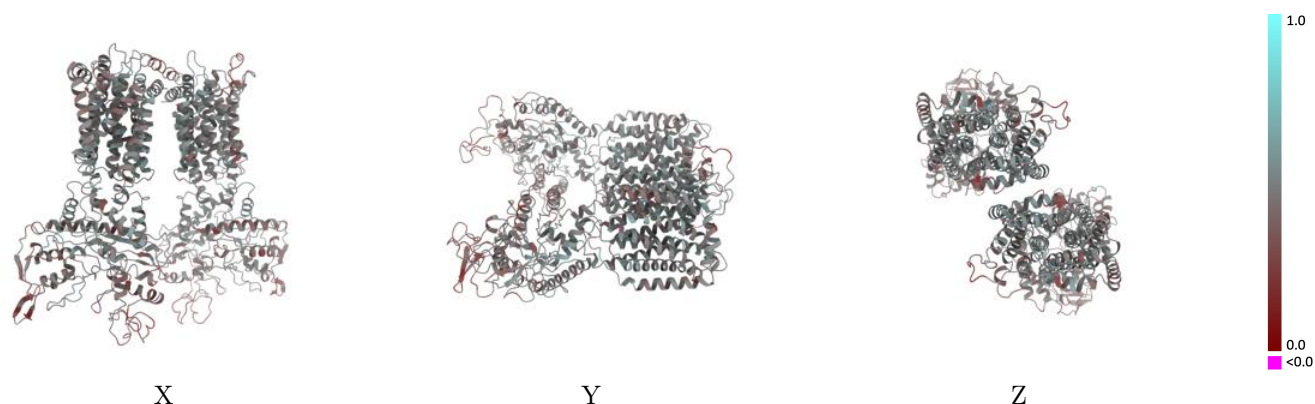
This section contains information regarding the fit between EMDB map EMD-24179 and PDB model 7N4V. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



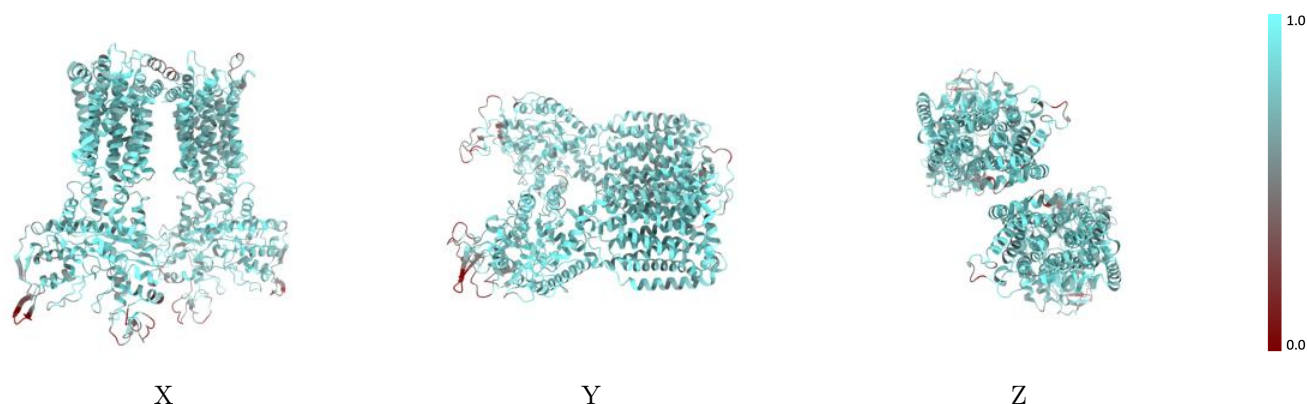
The images above show the 3D surface view of the map at the recommended contour level 0.246 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



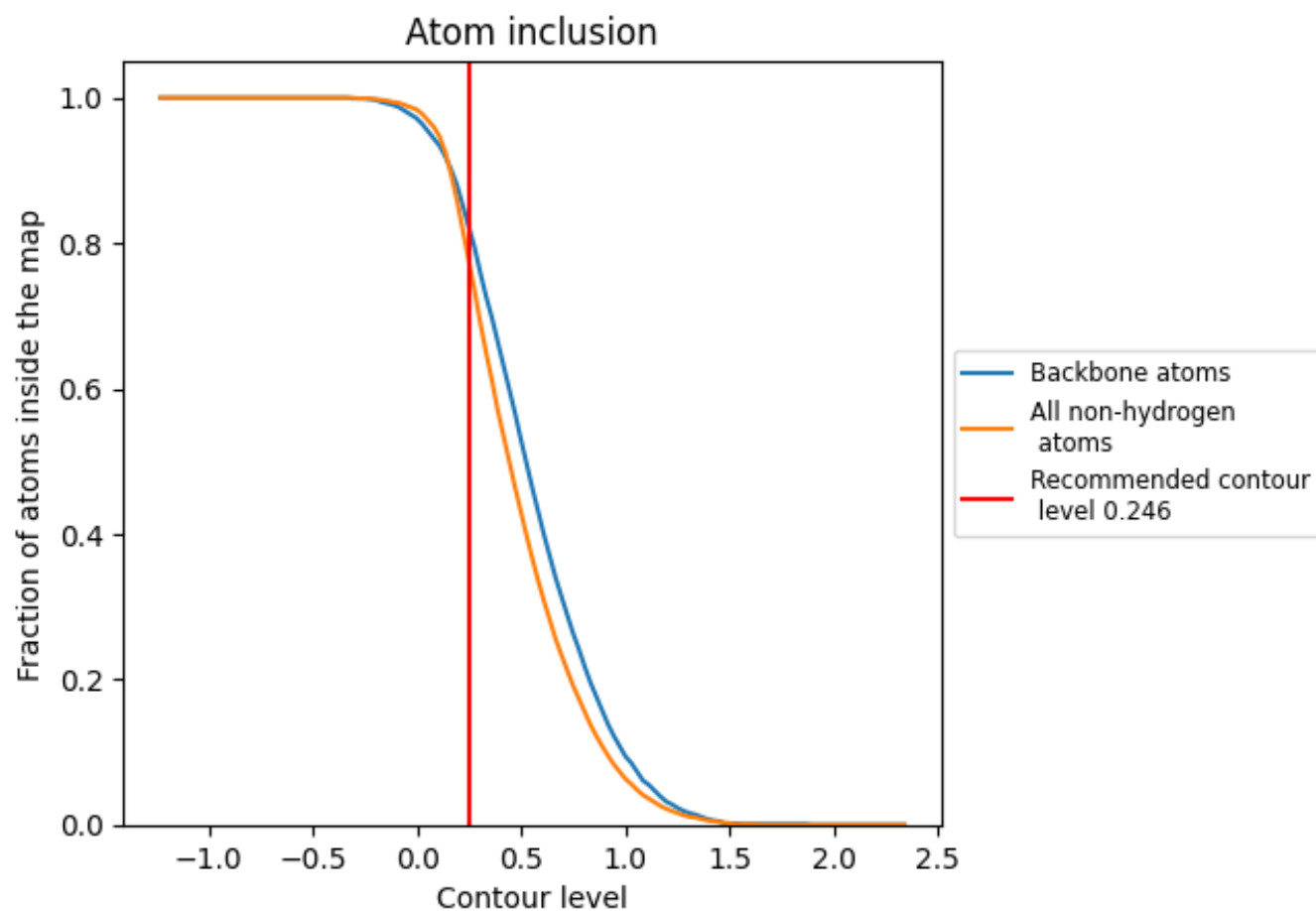
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.246).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 78% 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 (0.246) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7790	<div></div> 0.4530
A	<div></div> 0.7820	<div></div> 0.4550
B	<div></div> 0.7840	<div></div> 0.4540
C	<div></div> 0.4640	<div></div> 0.3620
D	<div></div> 0.3930	<div></div> 0.3420
E	<div></div> 0.5710	<div></div> 0.3440
F	<div></div> 0.4640	<div></div> 0.3350
G	<div></div> 0.3210	<div></div> 0.2950
H	<div></div> 0.5710	<div></div> 0.3240

1.0

0.0

<0.0