



wwPDB EM Validation Summary Report ⓘ

Nov 30, 2022 – 06:23 AM JST

PDB ID : 7YE9
EMDB ID : EMD-33766
Title : SARS-CoV-2 Spike (6P) in complex with 3 R1-32 Fabs
Authors : Liu, B.; Gao, X.; Li, Z.; Chen, X.; He, J.; Chen, L.; Xiong, X.
Deposited on : 2022-07-05
Resolution : 4.17 Å(reported)

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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.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

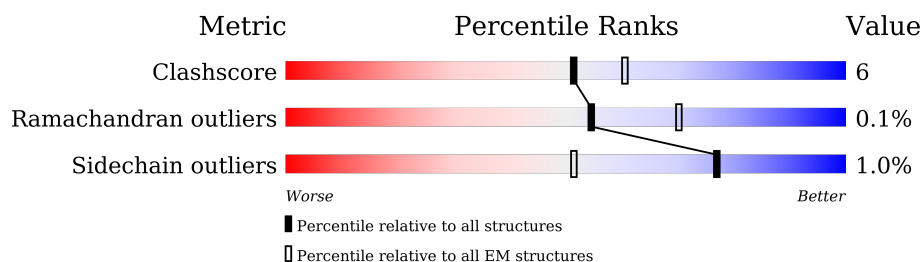
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.17 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.





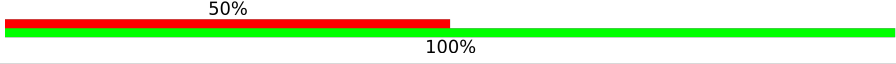

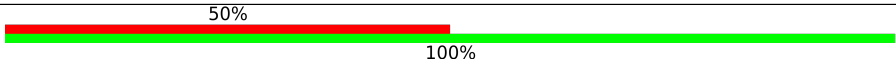

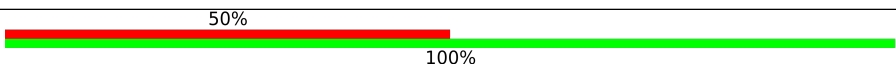
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 $\leq 5\%$. 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	1208	
1	B	1208	
1	C	1208	
2	G	228	
2	H	228	
2	N	228	
3	I	214	
3	L	214	

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Mol	Chain	Length	Quality of chain
3	O	214	 84% 79% 20%
4	D	2	 50% 50%
4	E	2	 50% 100%
4	F	2	 50% 50%
4	J	2	 50% 100%
4	K	2	 50% 50%
4	M	2	 50% 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 35208 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1066	Total	C	N	O	S	0	0
			8344	5324	1394	1588	38		
1	B	1066	Total	C	N	O	S	0	0
			8344	5324	1394	1588	38		
1	C	1066	Total	C	N	O	S	0	0
			8344	5324	1394	1588	38		

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	682	GLY	ARG	engineered mutation	UNP P0DTC2
A	683	SER	ARG	engineered mutation	UNP P0DTC2
A	685	SER	ARG	engineered mutation	UNP P0DTC2
A	817	PRO	PHE	engineered mutation	UNP P0DTC2
A	892	PRO	ALA	engineered mutation	UNP P0DTC2
A	899	PRO	ALA	engineered mutation	UNP P0DTC2
A	942	PRO	ALA	engineered mutation	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	682	GLY	ARG	engineered mutation	UNP P0DTC2
B	683	SER	ARG	engineered mutation	UNP P0DTC2
B	685	SER	ARG	engineered mutation	UNP P0DTC2
B	817	PRO	PHE	engineered mutation	UNP P0DTC2
B	892	PRO	ALA	engineered mutation	UNP P0DTC2
B	899	PRO	ALA	engineered mutation	UNP P0DTC2
B	942	PRO	ALA	engineered mutation	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	682	GLY	ARG	engineered mutation	UNP P0DTC2
C	683	SER	ARG	engineered mutation	UNP P0DTC2
C	685	SER	ARG	engineered mutation	UNP P0DTC2
C	817	PRO	PHE	engineered mutation	UNP P0DTC2
C	892	PRO	ALA	engineered mutation	UNP P0DTC2
C	899	PRO	ALA	engineered mutation	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	942	PRO	ALA	engineered mutation	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2

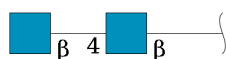
- Molecule 2 is a protein called Heavy chain of R1-32 Fab.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	227	Total	C	N	O	S	2	0
			1667	1049	277	332	9		
2	G	227	Total	C	N	O	S	2	0
			1667	1049	277	332	9		
2	N	227	Total	C	N	O	S	2	0
			1667	1049	277	332	9		

- Molecule 3 is a protein called Light chain of R1-32 Fab.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	213	Total	C	N	O	S	0	0
			1557	971	261	321	4		
3	I	213	Total	C	N	O	S	0	0
			1557	971	261	321	4		
3	O	213	Total	C	N	O	S	0	0
			1557	971	261	321	4		

- Molecule 4 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
4	D	2	Total	C	N	O		0	0
			28	16	2	10			
4	E	2	Total	C	N	O		0	0
			28	16	2	10			
4	F	2	Total	C	N	O		0	0
			28	16	2	10			
4	J	2	Total	C	N	O		0	0
			28	16	2	10			
4	K	2	Total	C	N	O		0	0
			28	16	2	10			

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

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
5	A	1	Total 112	64	8	40	0
5	A	1	Total 112	64	8	40	0
5	A	1	Total 112	64	8	40	0
5	A	1	Total 112	64	8	40	0
5	A	1	Total 112	64	8	40	0
5	A	1	Total 112	64	8	40	0
5	A	1	Total 112	64	8	40	0
5	A	1	Total 112	64	8	40	0
5	B	1	Total 112	64	8	40	0
5	B	1	Total 112	64	8	40	0


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Mol	Chain	Residues	Atoms				AltConf
5	B	1	Total	C	N	O	0
			112	64	8	40	
5	B	1	Total	C	N	O	0
			112	64	8	40	
5	B	1	Total	C	N	O	0
			112	64	8	40	
5	B	1	Total	C	N	O	0
			112	64	8	40	
5	B	1	Total	C	N	O	0
			112	64	8	40	
5	B	1	Total	C	N	O	0
			112	64	8	40	
5	C	1	Total	C	N	O	0
			112	64	8	40	
5	C	1	Total	C	N	O	0
			112	64	8	40	
5	C	1	Total	C	N	O	0
			112	64	8	40	
5	C	1	Total	C	N	O	0
			112	64	8	40	
5	C	1	Total	C	N	O	0
			112	64	8	40	
5	C	1	Total	C	N	O	0
			112	64	8	40	
5	C	1	Total	C	N	O	0
			112	64	8	40	


GLU	GLU	PHE	LEU	ASP	PHE	LEU	VAL	TYR	PHE	LYS	ASN	THR	SER	PRO	ASP	VAL	ASP	LEU	GLY	ILE	SER	GLY	ILE	ASN	ALA	SER	VAL	VAL	ASN	ILE	GLN	LYS	GLU	ILE	ASP	ARG	LEU	ASN	GLY	VAL	ASN	ALA	LYS	ASN	LEU	ASN	GLU	SER	LEU	ILE	GLY	LYS	TYR	GLN
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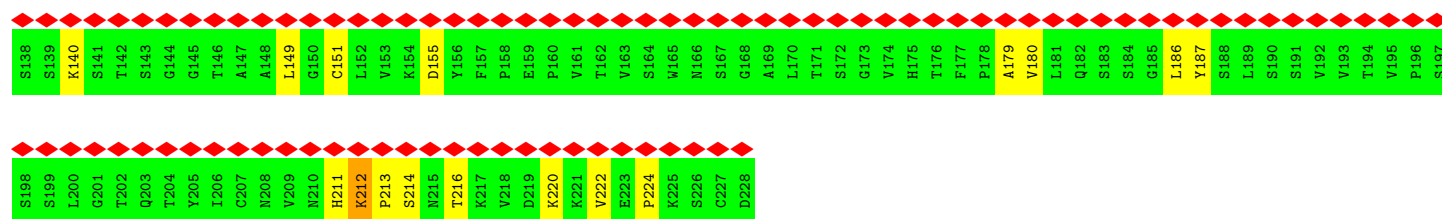
• Molecule 1: Spike glycoprotein

Chain B: 

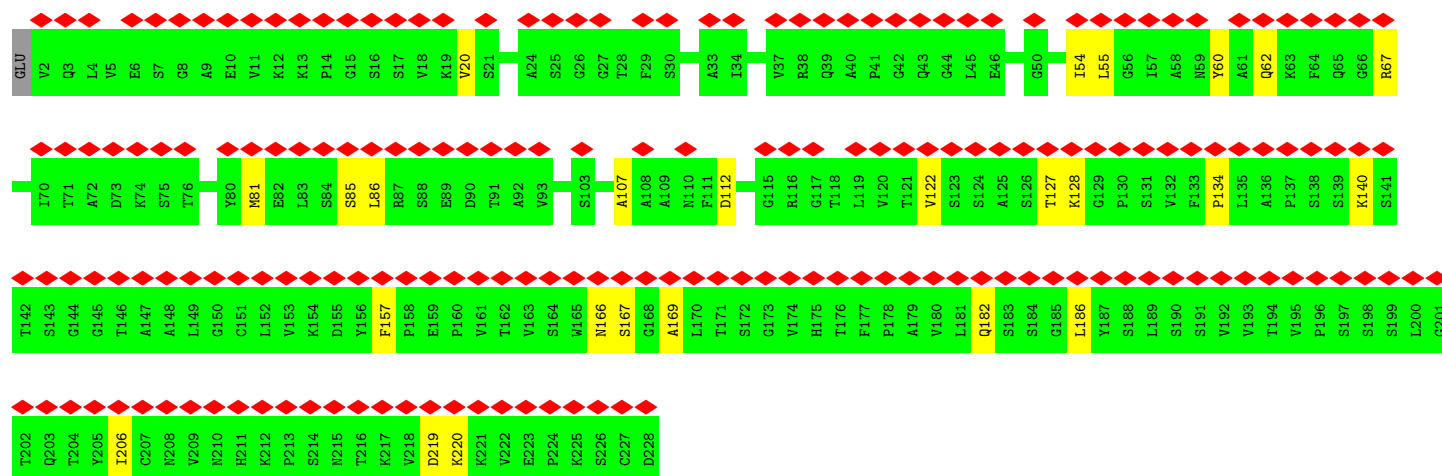
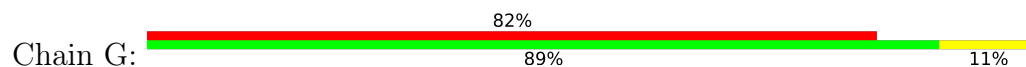
TYR	GLU	GLN
D1146	SER	PHE
L894	LYS	GLU
F898	GLU	GLU
P899	LEU	ASP
Y917	ASP	LYS
L922	TYR	PHE
S940	LYS	THR
THR	ASN	PRO
PRO	HIS	SER
A944	THR	SER
K947	PRO	ASP
Y976	VAL	ASP
L977	ASP	LEU
N978	LEU	GLY
ASP	ASP	ILE
S1030	SER	SER
L1034	ILE	ASN
Y1047	ALA	SER
S1051	VAL	VAL
VAL	VAL	ASN
H1064	ASN	ILE
Y1067	GLN	LYS
Y1068	GLU	TYR
P1069	GLY	ASP
C1082	ASP	CYS
A1087	LEU	GLY
E1092	GLU	ASP
Q1106	VAL	ILE
R1107	ALA	ALA
N1108	ASN	ALA
F1109	ASN	ARG
D1118	LEU	ASP
N1125	GLU	ILE
C1126	LEU	ASP
V1129	GLN	LEU
Y1138	GLU	GLY
E1144	LYS	
L1145		
F490	P426	F347
F497	D427	A348
Q498	F429	S349
P499	T430	V350
T500	G431	Y351
N501	C432	A352
G502	V433	W353
V503	I434	N354
G504	A435	R355
Y505	W436	K356
Q506	N437	R357
Y508	S438	I358
R509	N439	S359
V510	N440	N360
W511	L441	C361
V512	D442	V362
L513	S443	A363
GLY	K444	D364
SER	V445	Y365
N641	G446	S366
V656	C447	V367
N657	N448	L368
N658	Y449	Y369
S659	N450	N370
Y660	Y451	S371
G667	R457	A372
S673	K458	S373
Y674	S459	F374
Q675	N460	S375
T676	L461	Y380
GLN	K462	T385
THR	P463	K386
ASN	F464	L387
PRO	E465	N388
GLY	R466	D389
ASP	N542	L390
ILE	L552	V327
ALA	P561	R328
ALA	F565	F329
SER	C566	P330
SER	D568	N331
SER	I569	C336
VAL	R577	F337
ALA	A701	F338
S689	A713	G339
Q690		E340
I693		R190
L864		E191
S884		F192
Q889		V193
P892		Y204
		R214
		D215

• Molecule 1: Spike glycoprotein

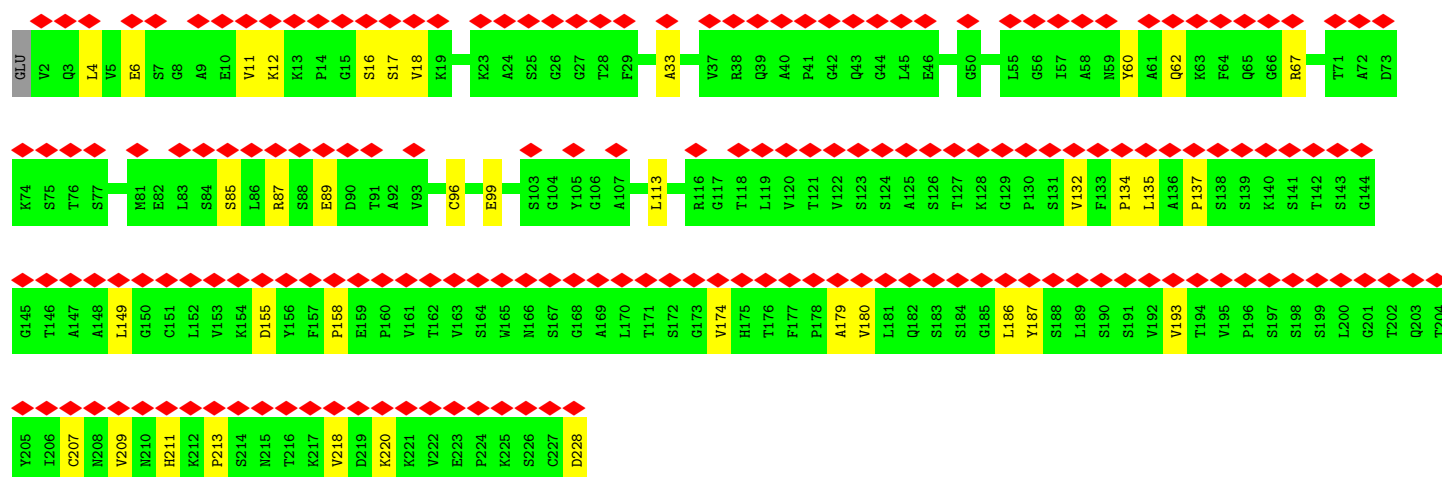
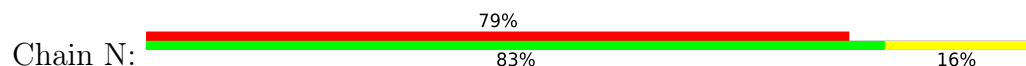
Chain C: 



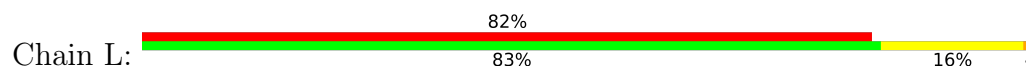
• Molecule 2: Heavy chain of R1-32 Fab

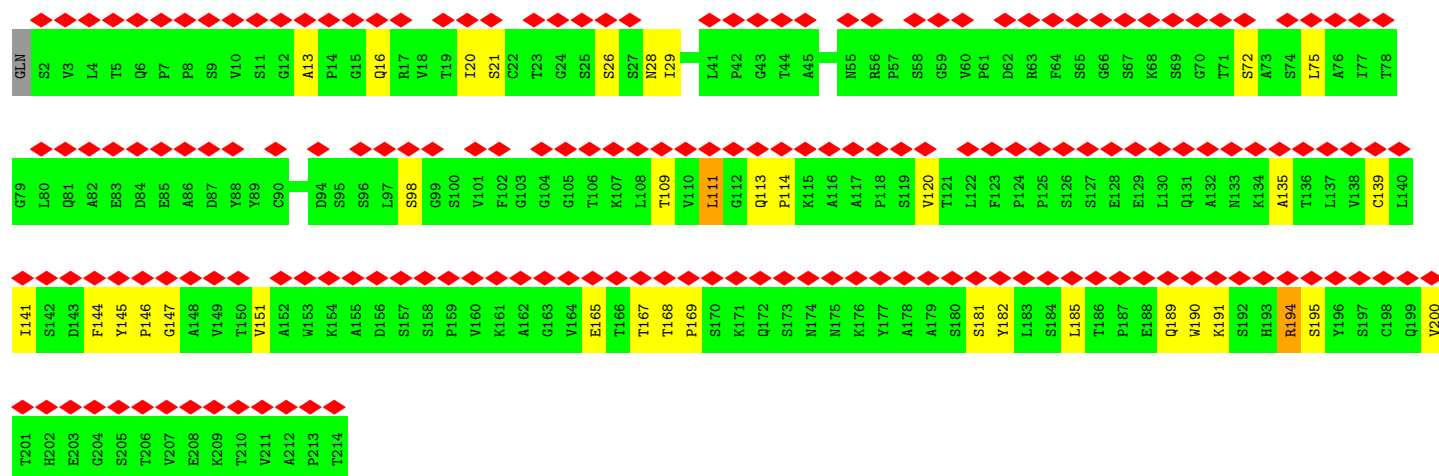


• Molecule 2: Heavy chain of R1-32 Fab

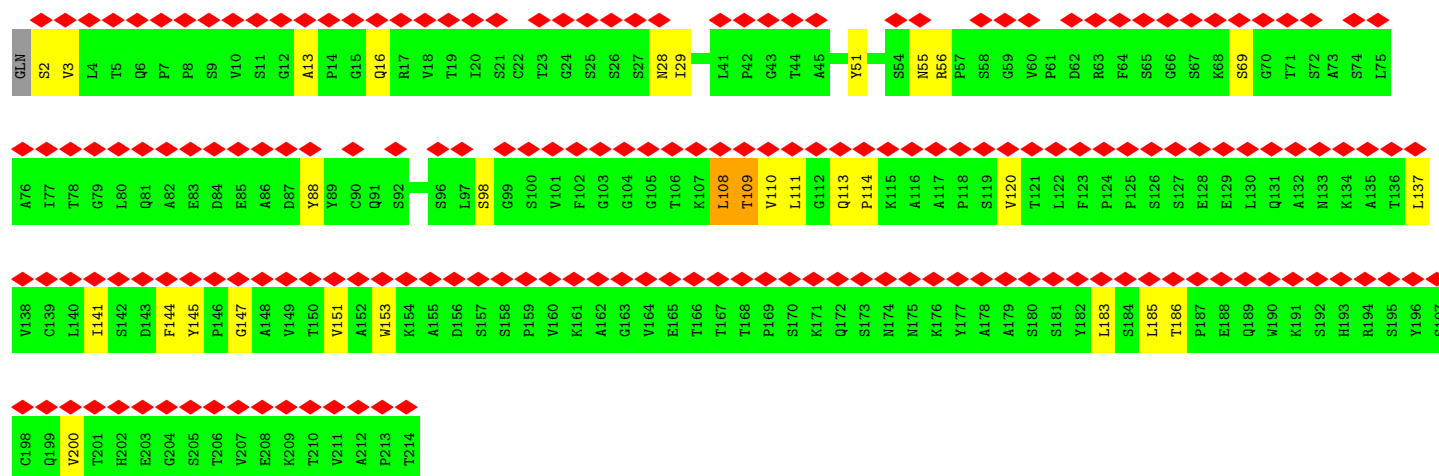
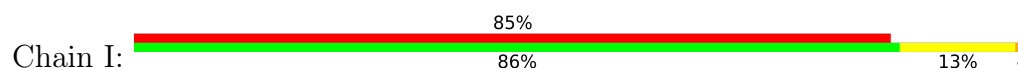


• Molecule 3: Light chain of R1-32 Fab

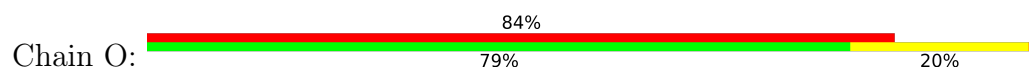




• Molecule 3: Light chain of R1-32 Fab



• Molecule 3: Light chain of R1-32 Fab





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

Chain D:



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

Chain E:



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

Chain F:



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

Chain J:



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

Chain K:



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

Chain M:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	56902	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 ($e^-/\text{\AA}^2$)	63	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	45000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.207	Depositor
Minimum map value	-0.091	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	337.91998, 337.91998, 337.91998	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7599999, 1.7599999, 1.7599999	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

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	0.25	0/8540	0.42	0/11624
1	B	0.25	0/8540	0.42	0/11624
1	C	0.25	0/8540	0.42	0/11624
2	G	0.25	0/1710	0.47	0/2328
2	H	0.25	0/1710	0.47	0/2328
2	N	0.25	0/1710	0.45	0/2328
3	I	0.25	0/1595	0.45	0/2181
3	L	0.25	0/1595	0.44	0/2181
3	O	0.25	0/1595	0.45	0/2181
All	All	0.25	0/35535	0.43	0/48399

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	8344	0	8128	93	0
1	B	8344	0	8128	103	0
1	C	8344	0	8128	114	0
2	G	1667	0	1639	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	1667	0	1639	26	0
2	N	1667	0	1639	21	0
3	I	1557	0	1498	22	0
3	L	1557	0	1498	28	0
3	O	1557	0	1498	36	0
4	D	28	0	25	1	0
4	E	28	0	25	0	0
4	F	28	0	25	1	0
4	J	28	0	25	0	0
4	K	28	0	25	1	0
4	M	28	0	25	0	0
5	A	112	0	104	0	0
5	B	112	0	104	0	0
5	C	112	0	104	0	0
All	All	35208	0	34257	404	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 404 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:B:1069:PRO:HG2	1:C:892:PRO:HD2	1.52	0.90
1:A:1069:PRO:HG2	1:B:892:PRO:HD2	1.52	0.89
3:I:113:GLN:HA	3:I:145:TYR:HE1	1.39	0.86
1:B:328:ARG:HG2	1:B:530:SER:HA	1.60	0.82
1:C:816:SER:HB3	1:C:817:PRO:HD2	1.64	0.78

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	1054/1208 (87%)	1017 (96%)	35 (3%)	2 (0%)	47	80
1	B	1054/1208 (87%)	1026 (97%)	28 (3%)	0	100	100
1	C	1054/1208 (87%)	1021 (97%)	32 (3%)	1 (0%)	51	85
2	G	227/228 (100%)	220 (97%)	7 (3%)	0	100	100
2	H	227/228 (100%)	223 (98%)	4 (2%)	0	100	100
2	N	227/228 (100%)	221 (97%)	6 (3%)	0	100	100
3	I	211/214 (99%)	202 (96%)	9 (4%)	0	100	100
3	L	211/214 (99%)	202 (96%)	9 (4%)	0	100	100
3	O	211/214 (99%)	201 (95%)	9 (4%)	1 (0%)	29	68
All	All	4476/4950 (90%)	4333 (97%)	139 (3%)	4 (0%)	54	85

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	529	LYS
3	O	111	LEU
1	C	522	ALA
1	A	527	PRO

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	934/1056 (88%)	927 (99%)	7 (1%)	84	90
1	B	934/1056 (88%)	924 (99%)	10 (1%)	73	84
1	C	934/1056 (88%)	928 (99%)	6 (1%)	86	92
2	G	186/186 (100%)	185 (100%)	1 (0%)	88	93
2	H	186/186 (100%)	184 (99%)	2 (1%)	73	84
2	N	186/186 (100%)	184 (99%)	2 (1%)	73	84
3	I	174/177 (98%)	170 (98%)	4 (2%)	50	69
3	L	174/177 (98%)	171 (98%)	3 (2%)	60	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	O	174/177 (98%)	168 (97%)	6 (3%)	37 60
All	All	3882/4257 (91%)	3841 (99%)	41 (1%)	77 84

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	140	LYS
3	O	107	LYS
3	I	108	LEU
3	I	111	LEU
3	O	109	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	613	GLN
2	G	39	GLN
1	C	137	ASN
3	L	189	GLN
3	O	199	GLN

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 ⓘ

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
4	NAG	D	1	4,1	14,14,15	0.20	0	17,19,21	0.39	0
4	NAG	D	2	4	14,14,15	0.20	0	17,19,21	0.42	0
4	NAG	E	1	4,1	14,14,15	0.20	0	17,19,21	0.41	0
4	NAG	E	2	4	14,14,15	0.23	0	17,19,21	0.43	0
4	NAG	F	1	4,1	14,14,15	0.22	0	17,19,21	0.40	0
4	NAG	F	2	4	14,14,15	0.23	0	17,19,21	0.43	0
4	NAG	J	1	4,1	14,14,15	0.20	0	17,19,21	0.41	0
4	NAG	J	2	4	14,14,15	0.23	0	17,19,21	0.42	0
4	NAG	K	1	4,1	14,14,15	0.21	0	17,19,21	0.42	0
4	NAG	K	2	4	14,14,15	0.22	0	17,19,21	0.41	0
4	NAG	M	1	4,1	14,14,15	0.22	0	17,19,21	0.40	0
4	NAG	M	2	4	14,14,15	0.24	0	17,19,21	0.42	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
4	NAG	D	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
4	NAG	E	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
4	NAG	F	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	NAG	J	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	J	2	4	-	2/6/23/26	0/1/1/1
4	NAG	K	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	K	2	4	-	2/6/23/26	0/1/1/1
4	NAG	M	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	M	2	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	J	1	NAG	O5-C5-C6-O6

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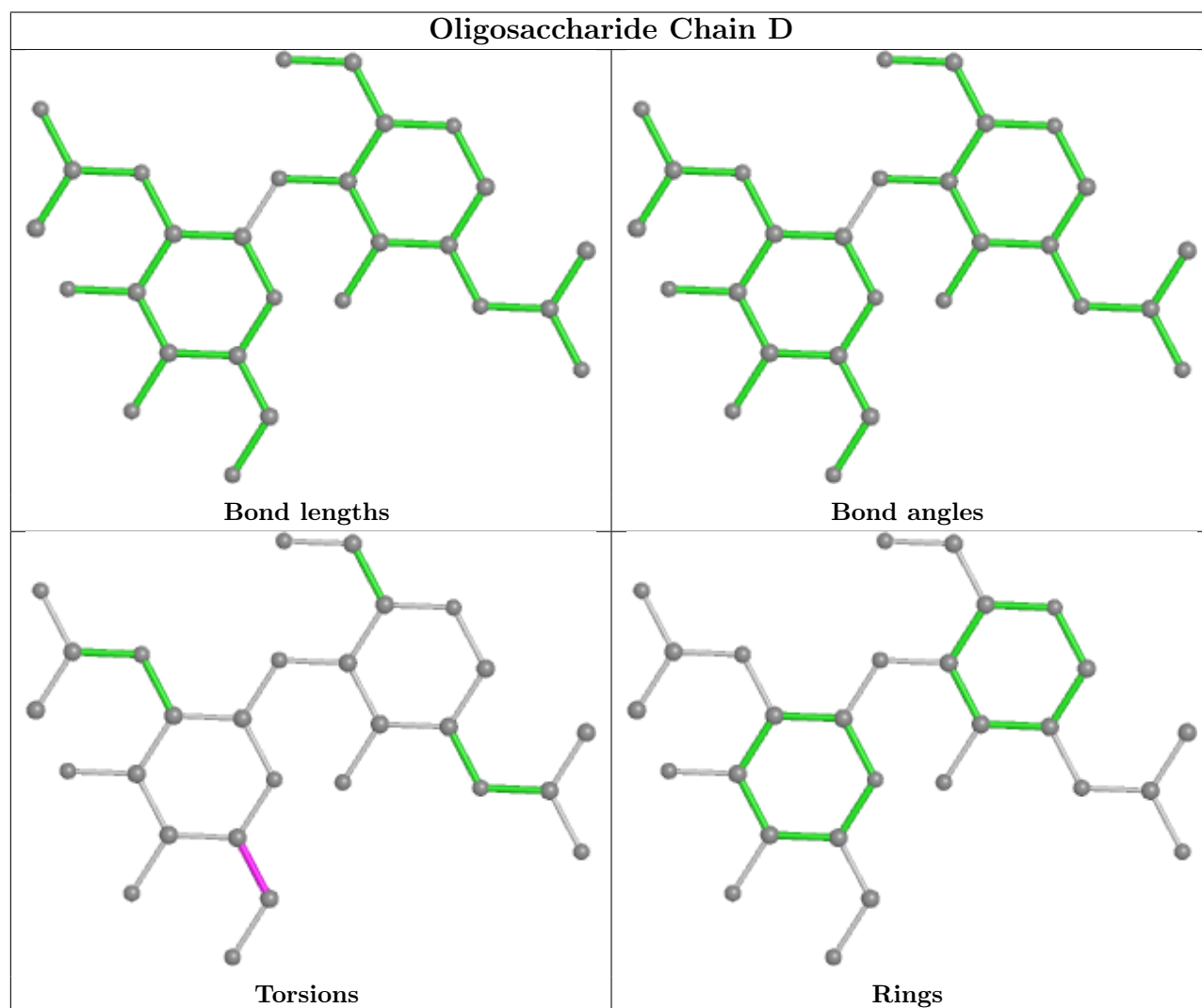
Mol	Chain	Res	Type	Atoms
4	M	1	NAG	O5-C5-C6-O6
4	E	1	NAG	O5-C5-C6-O6
4	D	2	NAG	O5-C5-C6-O6
4	K	2	NAG	O5-C5-C6-O6

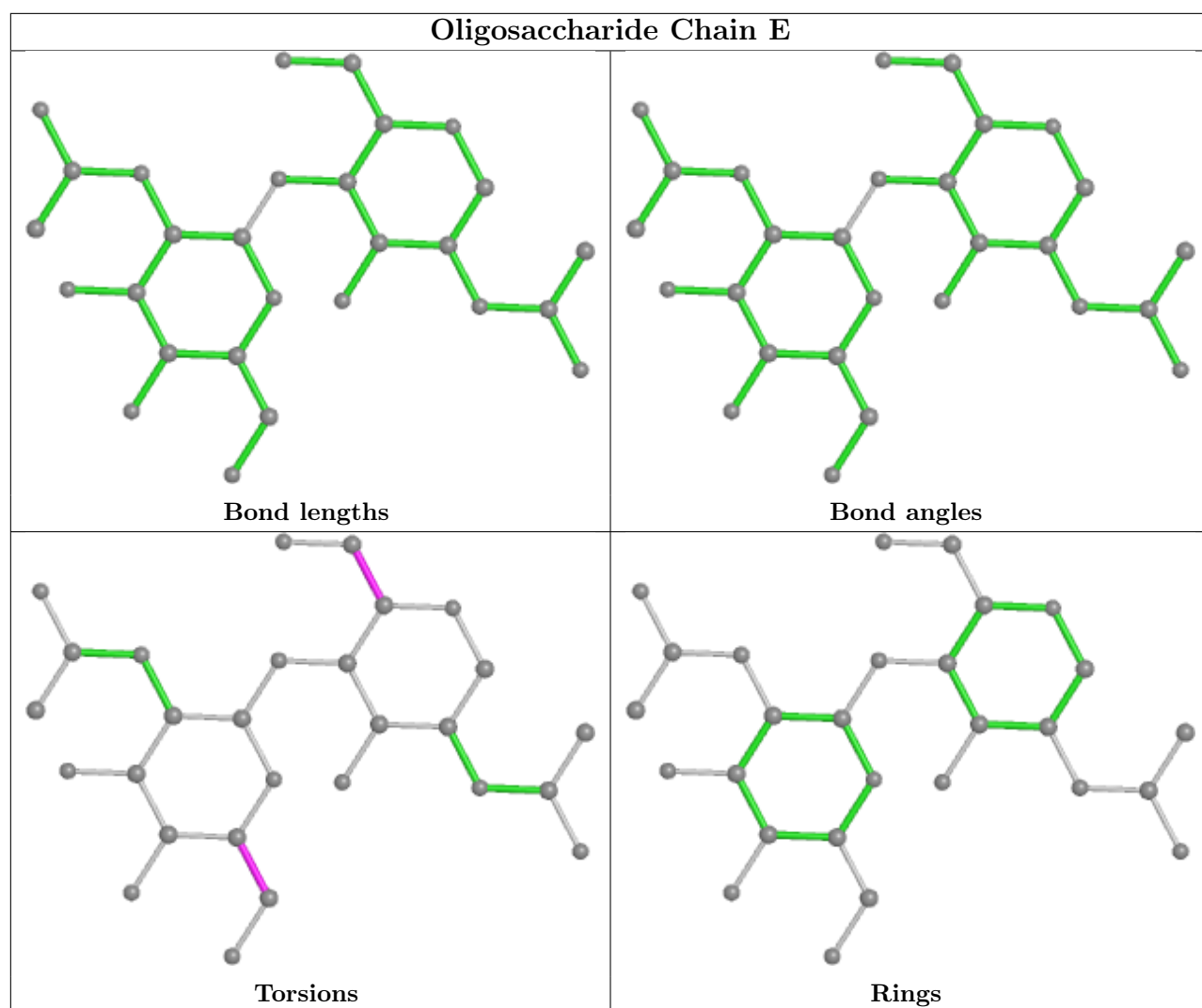
There are no ring outliers.

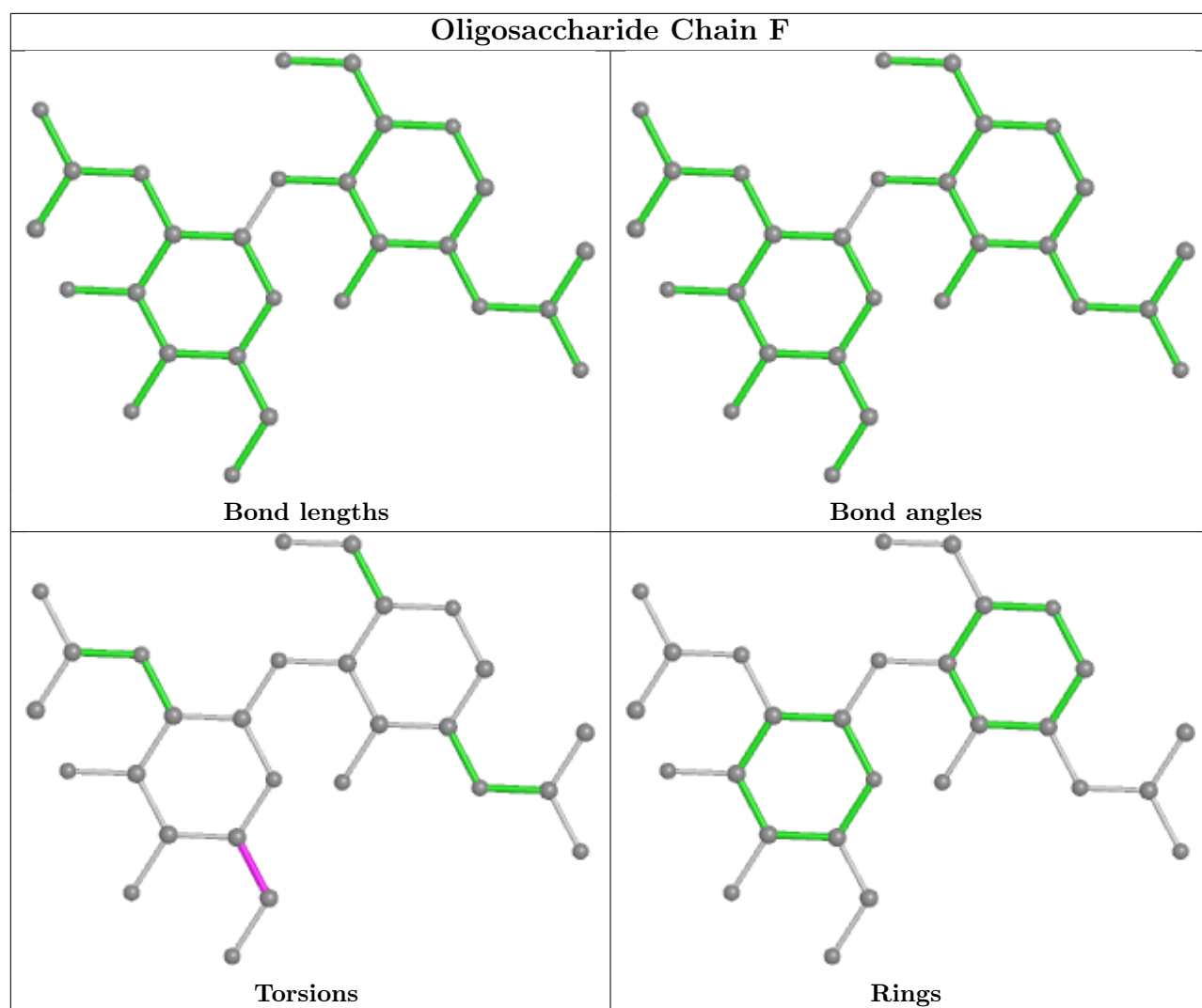
3 monomers are involved in 3 short contacts:

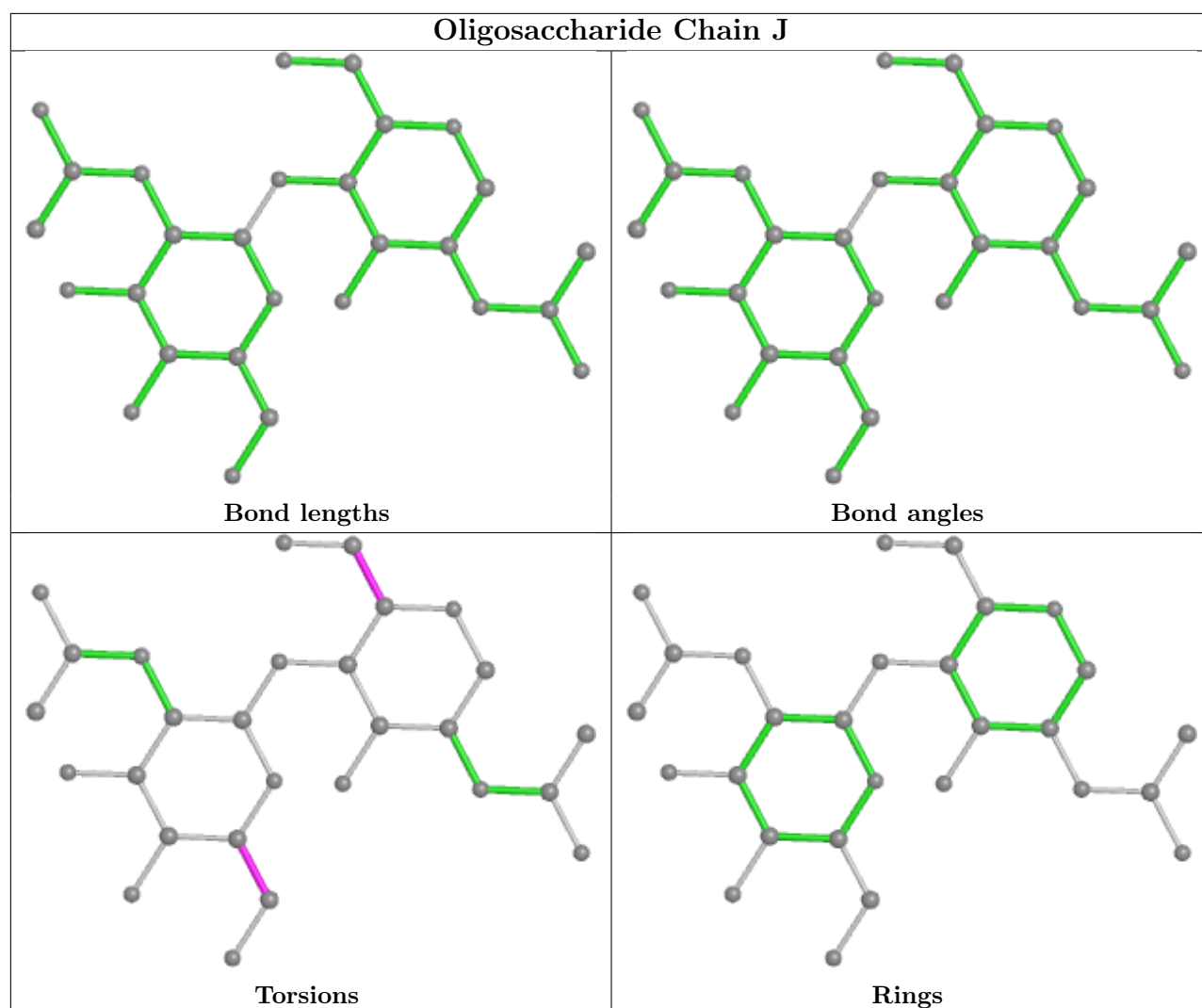
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	K	1	NAG	1	0
4	F	1	NAG	1	0
4	D	1	NAG	1	0

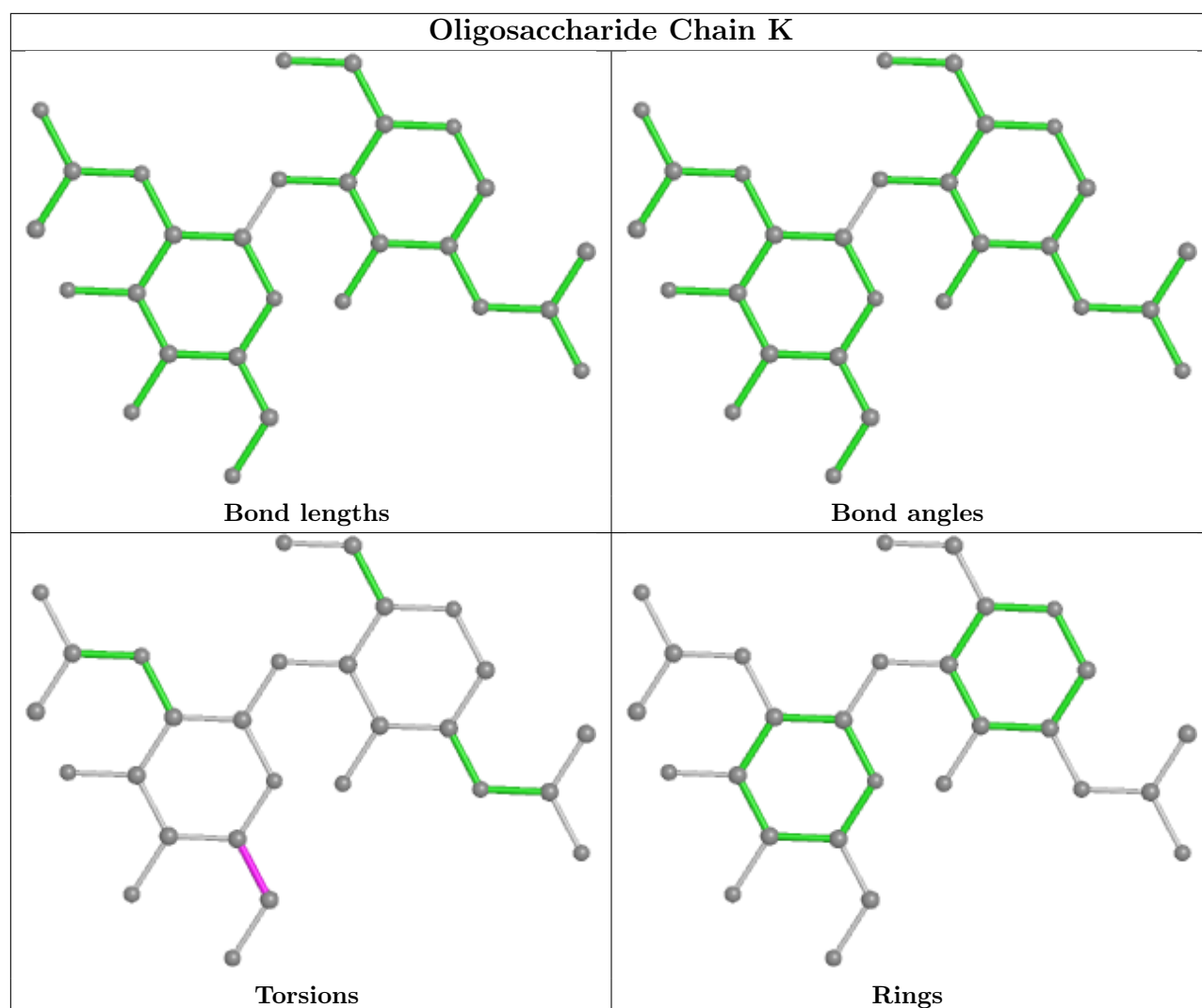
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

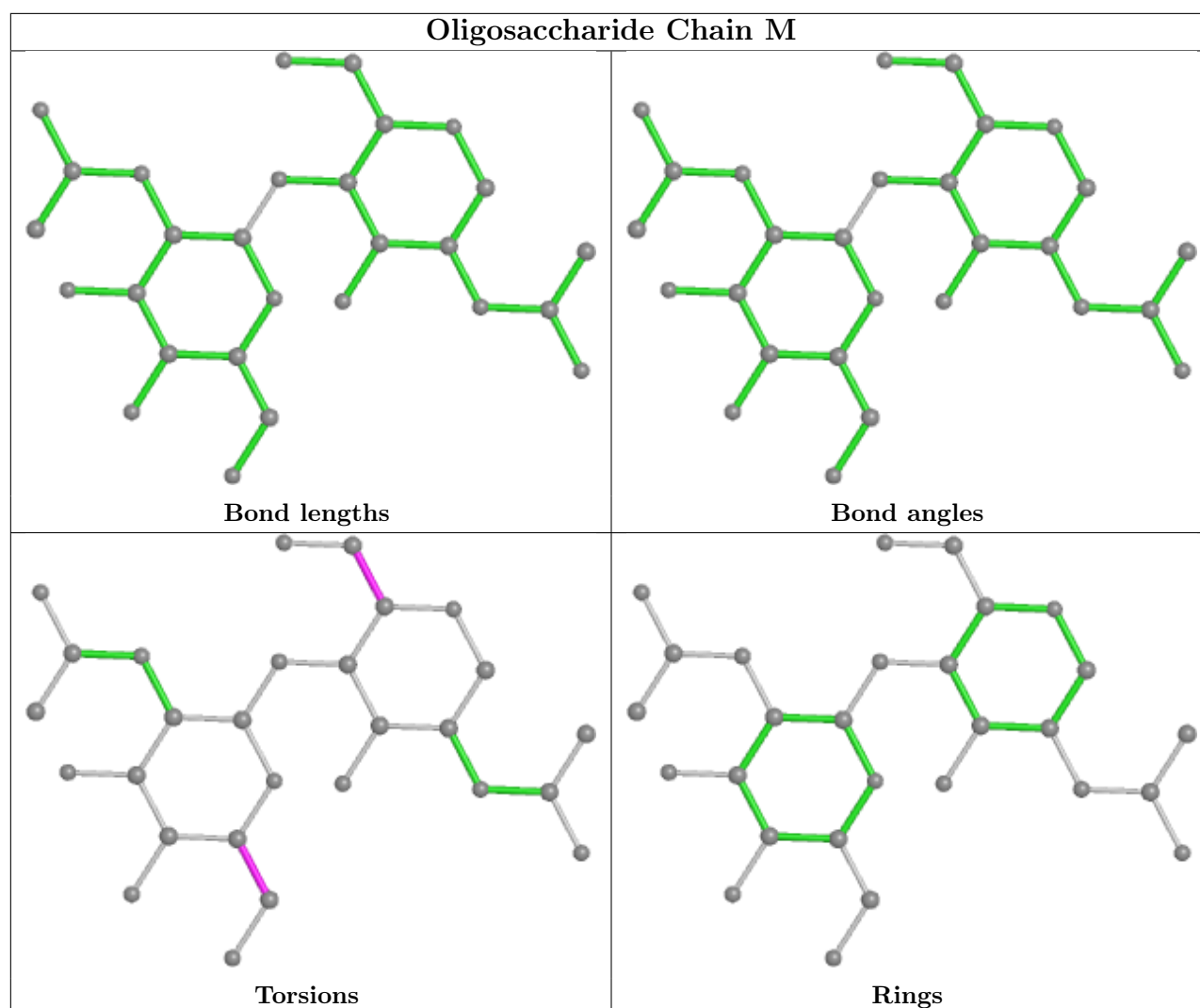












5.6 Ligand geometry [i](#)

24 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	A	1306	1	14,14,15	0.22	0	17,19,21	0.39	0
5	NAG	C	1302	1	14,14,15	0.23	0	17,19,21	0.45	0
5	NAG	C	1305	1	14,14,15	0.25	0	17,19,21	0.42	0
5	NAG	C	1307	1	14,14,15	0.24	0	17,19,21	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	C	1303	1	14,14,15	0.26	0	17,19,21	0.37	0
5	NAG	A	1304	1	14,14,15	0.26	0	17,19,21	0.41	0
5	NAG	B	1307	1	14,14,15	0.25	0	17,19,21	0.33	0
5	NAG	A	1307	1	14,14,15	0.25	0	17,19,21	0.34	0
5	NAG	C	1306	1	14,14,15	0.23	0	17,19,21	0.40	0
5	NAG	B	1306	1	14,14,15	0.21	0	17,19,21	0.40	0
5	NAG	A	1308	1	14,14,15	0.23	0	17,19,21	0.39	0
5	NAG	B	1304	1	14,14,15	0.25	0	17,19,21	0.41	0
5	NAG	B	1301	1	14,14,15	0.23	0	17,19,21	0.45	0
5	NAG	C	1304	1	14,14,15	0.25	0	17,19,21	0.41	0
5	NAG	C	1301	1	14,14,15	0.25	0	17,19,21	0.47	0
5	NAG	A	1305	1	14,14,15	0.24	0	17,19,21	0.42	0
5	NAG	B	1305	1	14,14,15	0.24	0	17,19,21	0.42	0
5	NAG	A	1302	1	14,14,15	0.24	0	17,19,21	0.44	0
5	NAG	B	1303	1	14,14,15	0.28	0	17,19,21	0.37	0
5	NAG	C	1308	1	14,14,15	0.23	0	17,19,21	0.40	0
5	NAG	B	1302	1	14,14,15	0.25	0	17,19,21	0.43	0
5	NAG	A	1303	1	14,14,15	0.28	0	17,19,21	0.36	0
5	NAG	A	1301	1	14,14,15	0.24	0	17,19,21	0.45	0
5	NAG	B	1308	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	A	1306	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1302	1	-	4/6/23/26	0/1/1/1
5	NAG	C	1305	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1307	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1303	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1304	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1307	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1307	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1306	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1306	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1308	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1304	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1301	1	-	4/6/23/26	0/1/1/1
5	NAG	C	1304	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	C	1301	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1305	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1305	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1302	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1303	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1308	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1302	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1303	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1301	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1308	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.

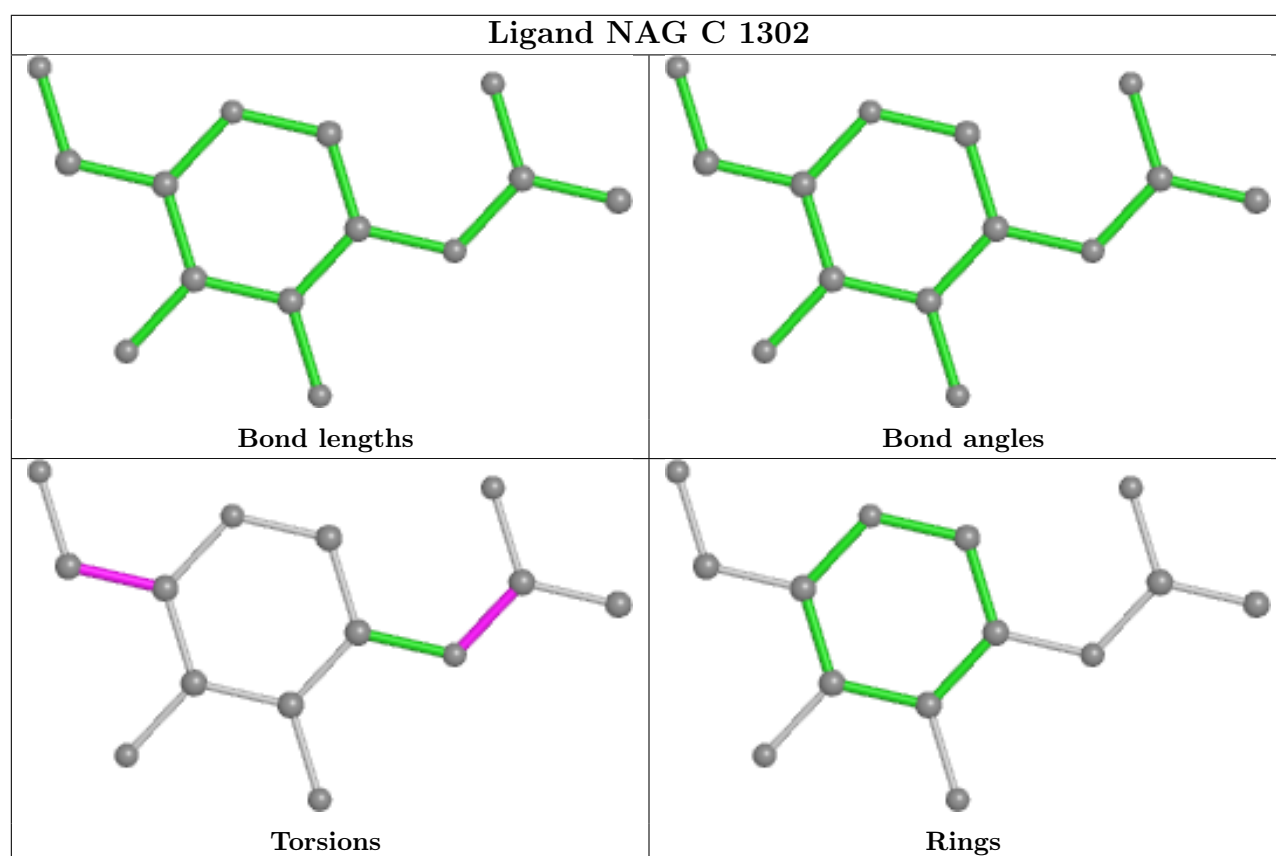
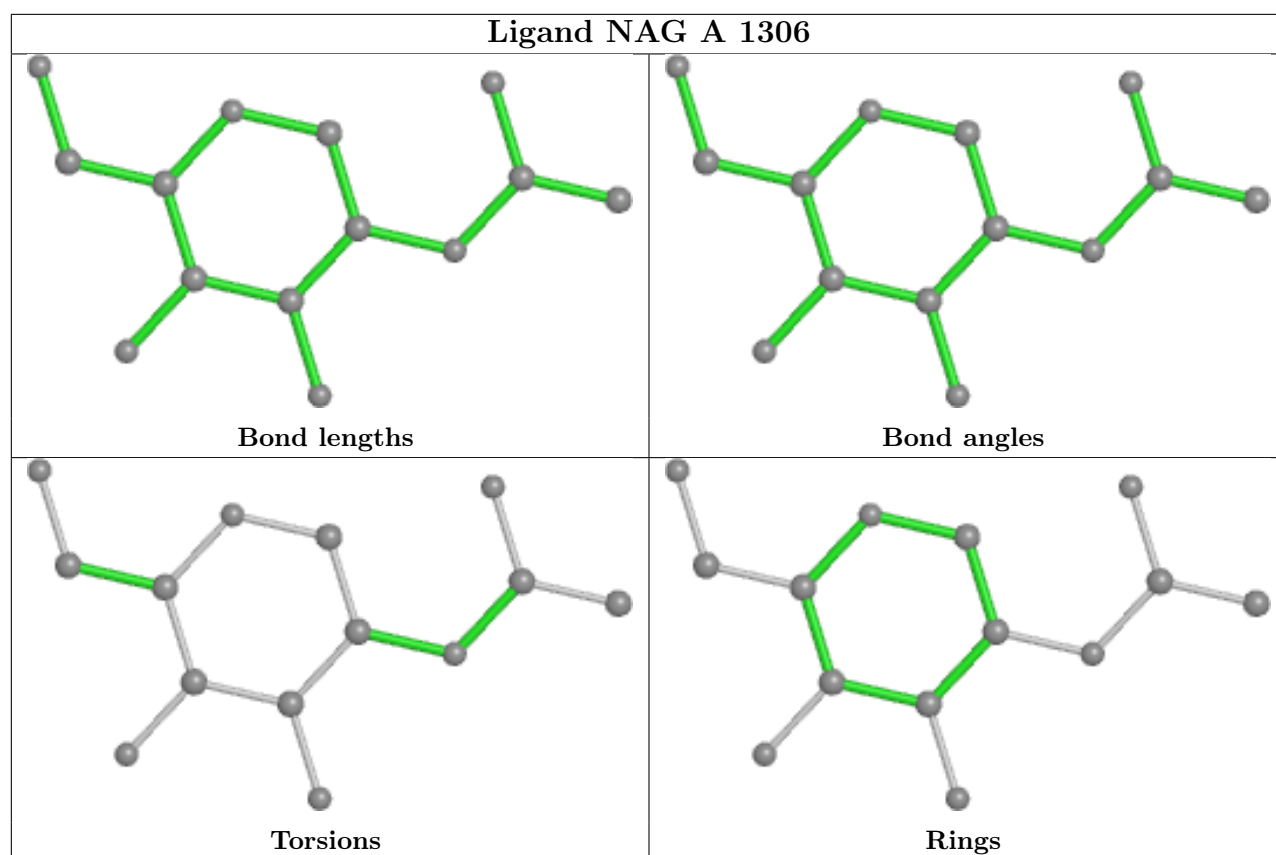
5 of 43 torsion outliers are listed below:

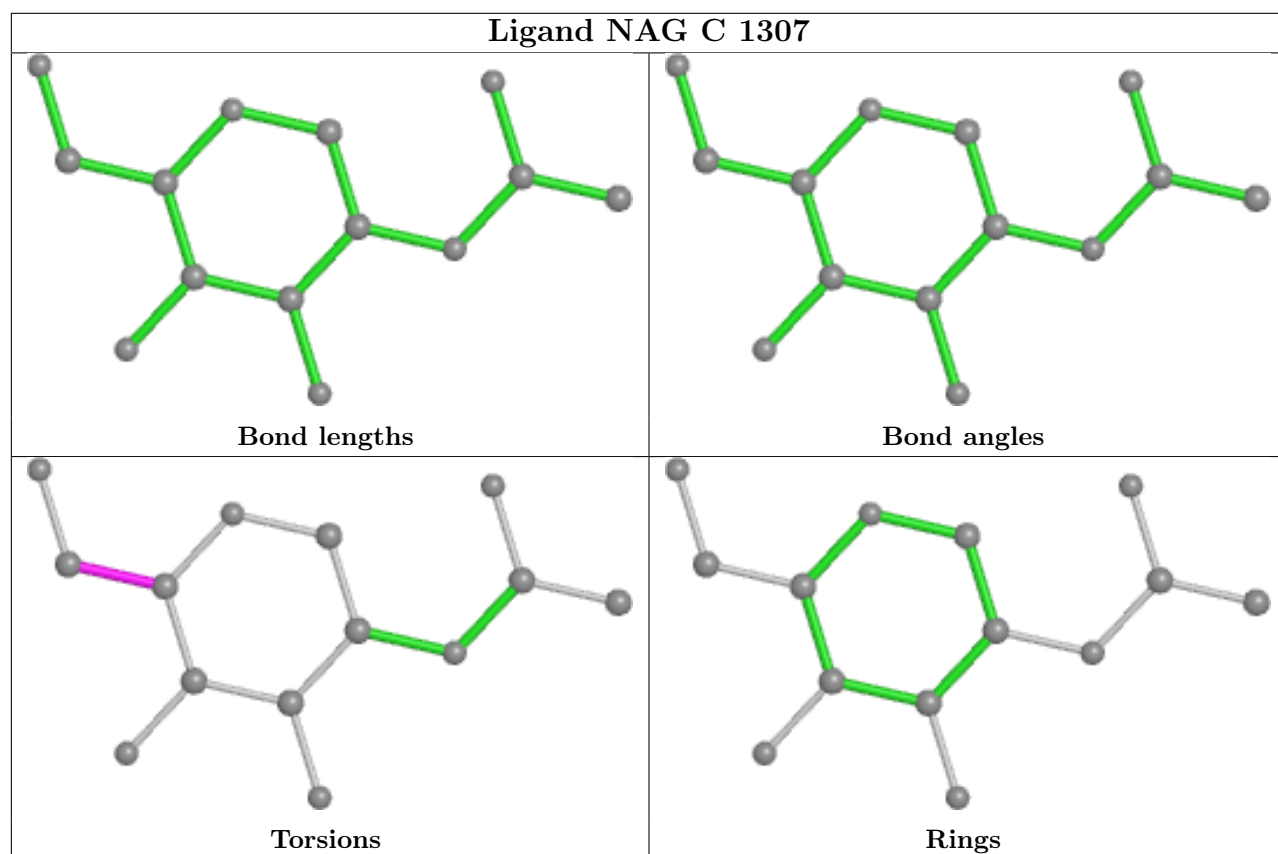
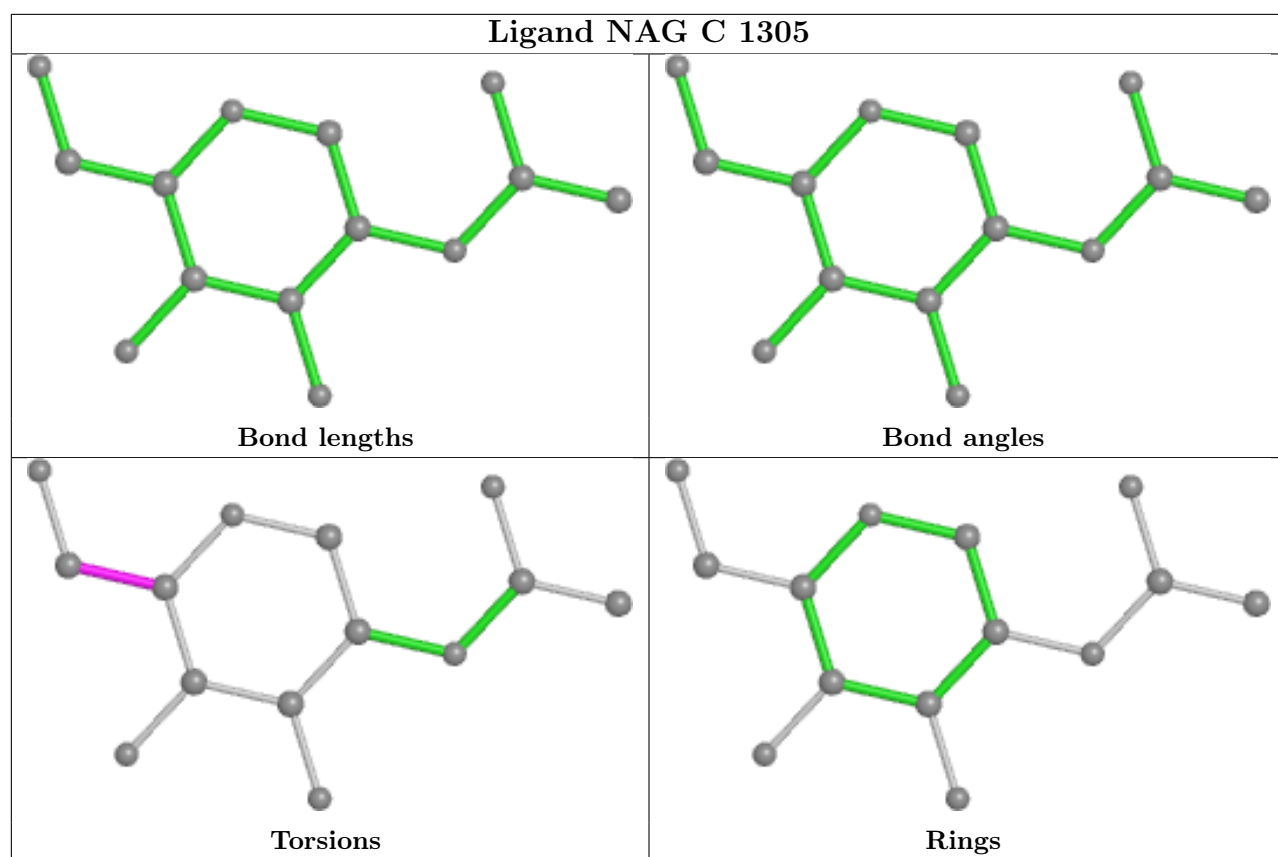
Mol	Chain	Res	Type	Atoms
5	A	1302	NAG	O5-C5-C6-O6
5	A	1305	NAG	O5-C5-C6-O6
5	B	1301	NAG	O5-C5-C6-O6
5	B	1305	NAG	O5-C5-C6-O6
5	C	1302	NAG	O5-C5-C6-O6

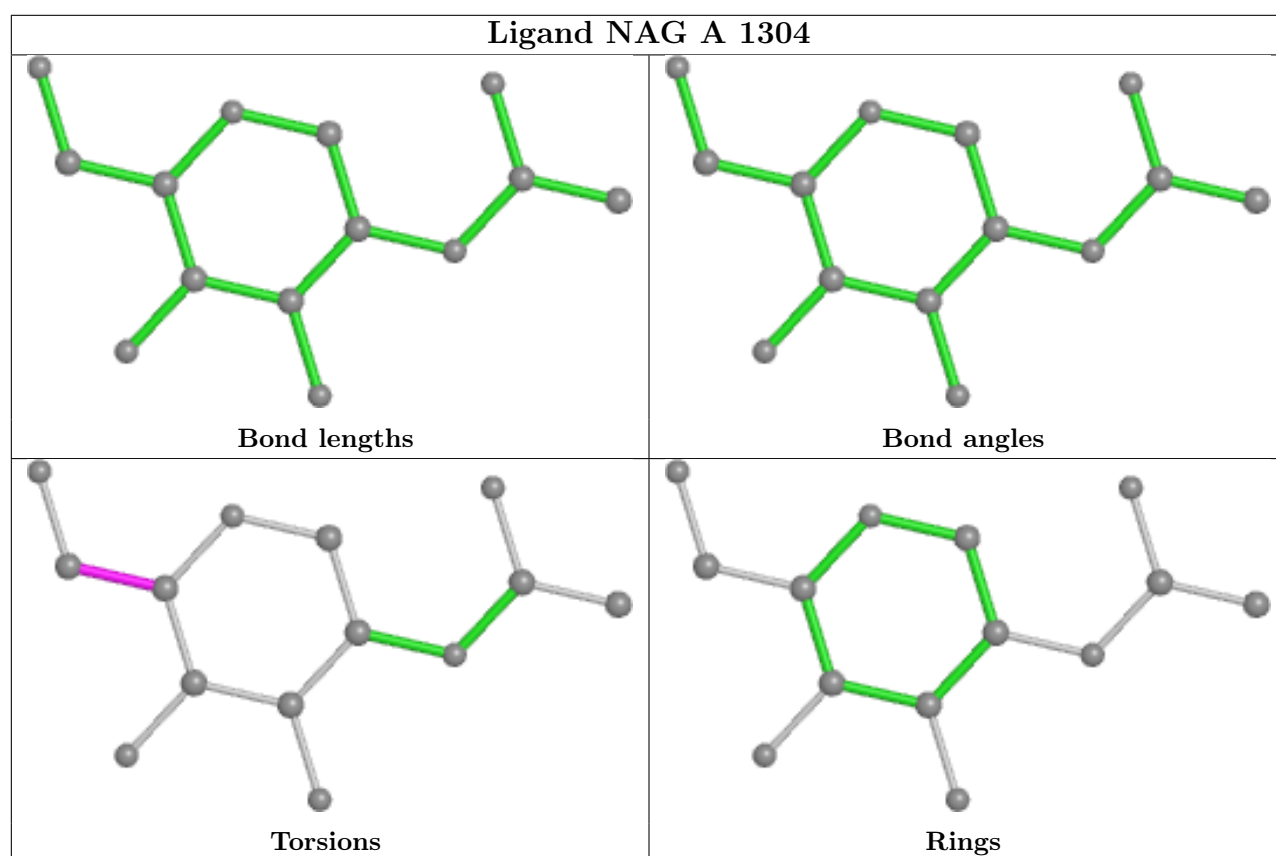
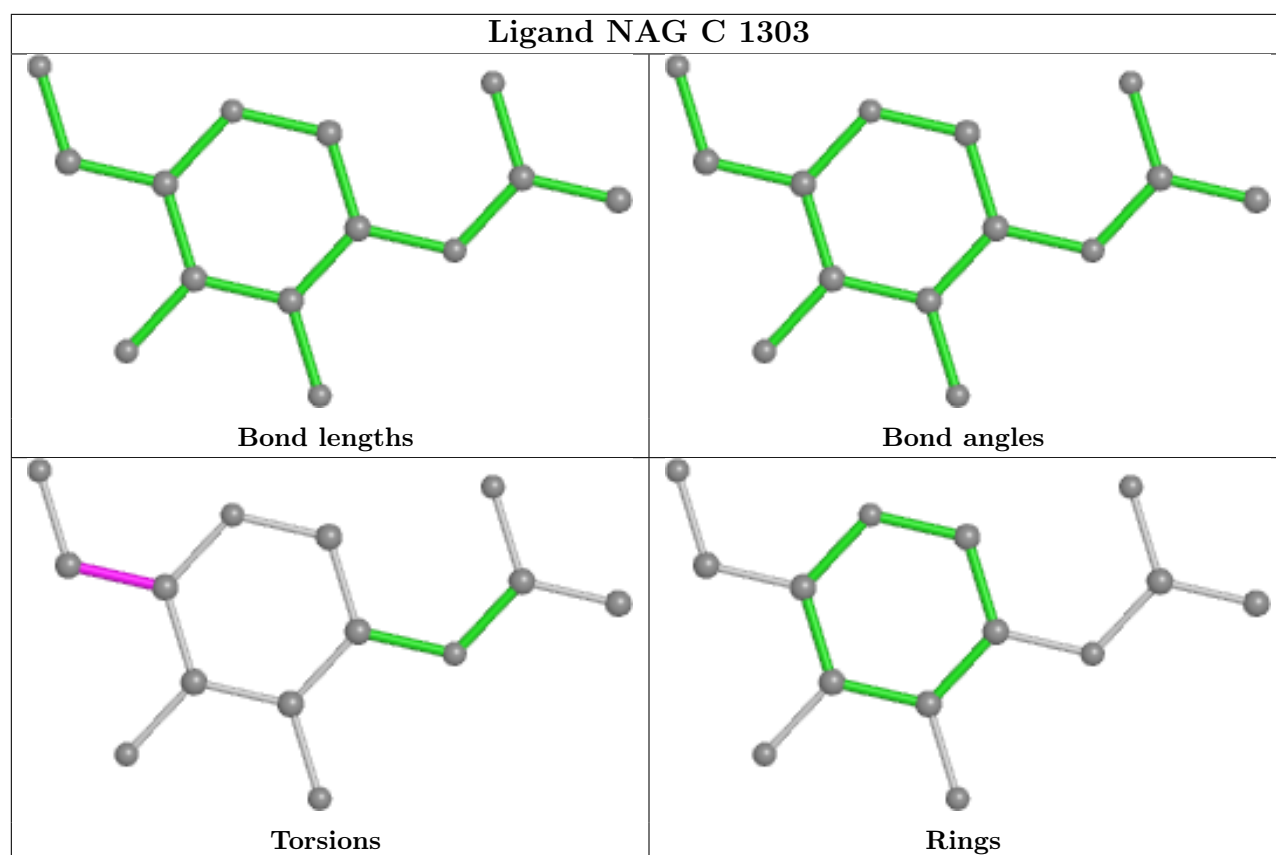
There are no ring outliers.

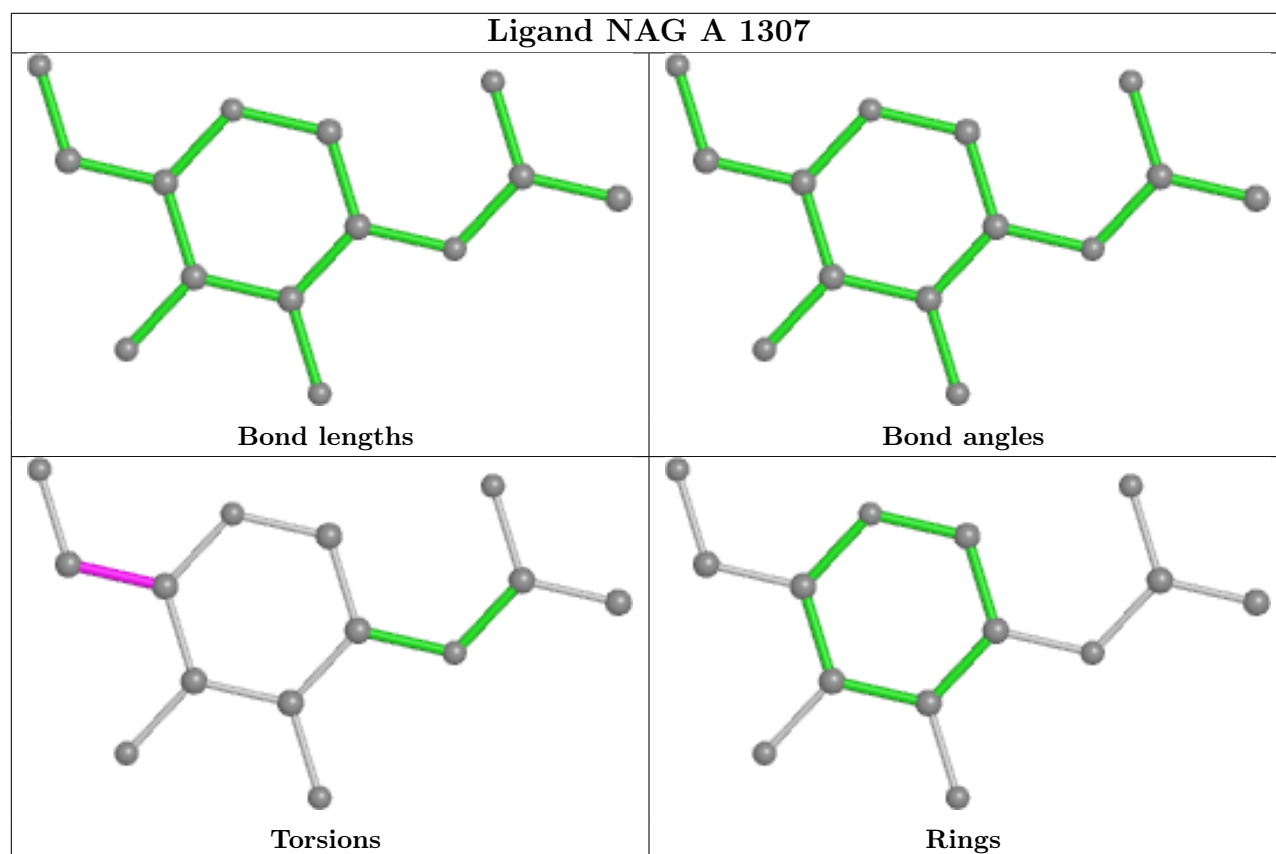
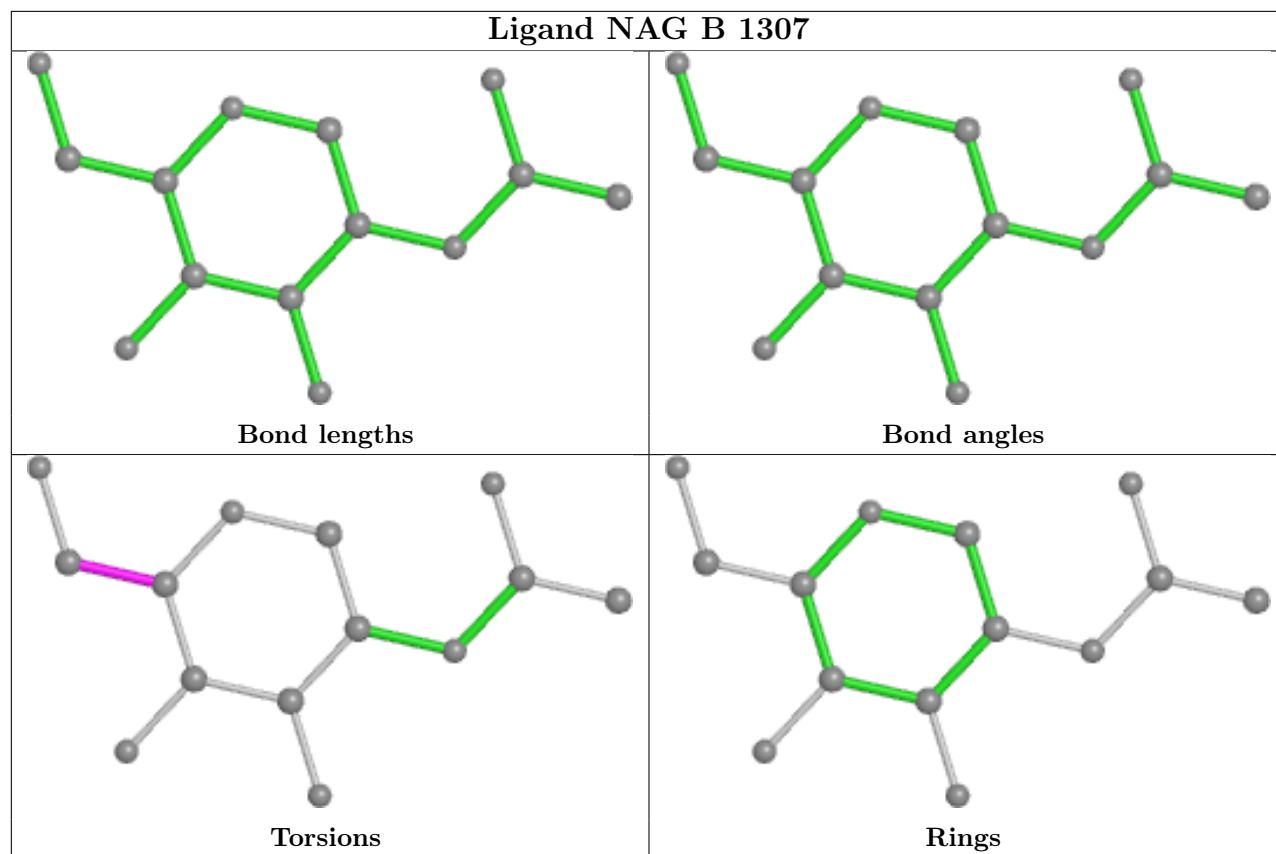
No monomer is involved in short contacts.

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

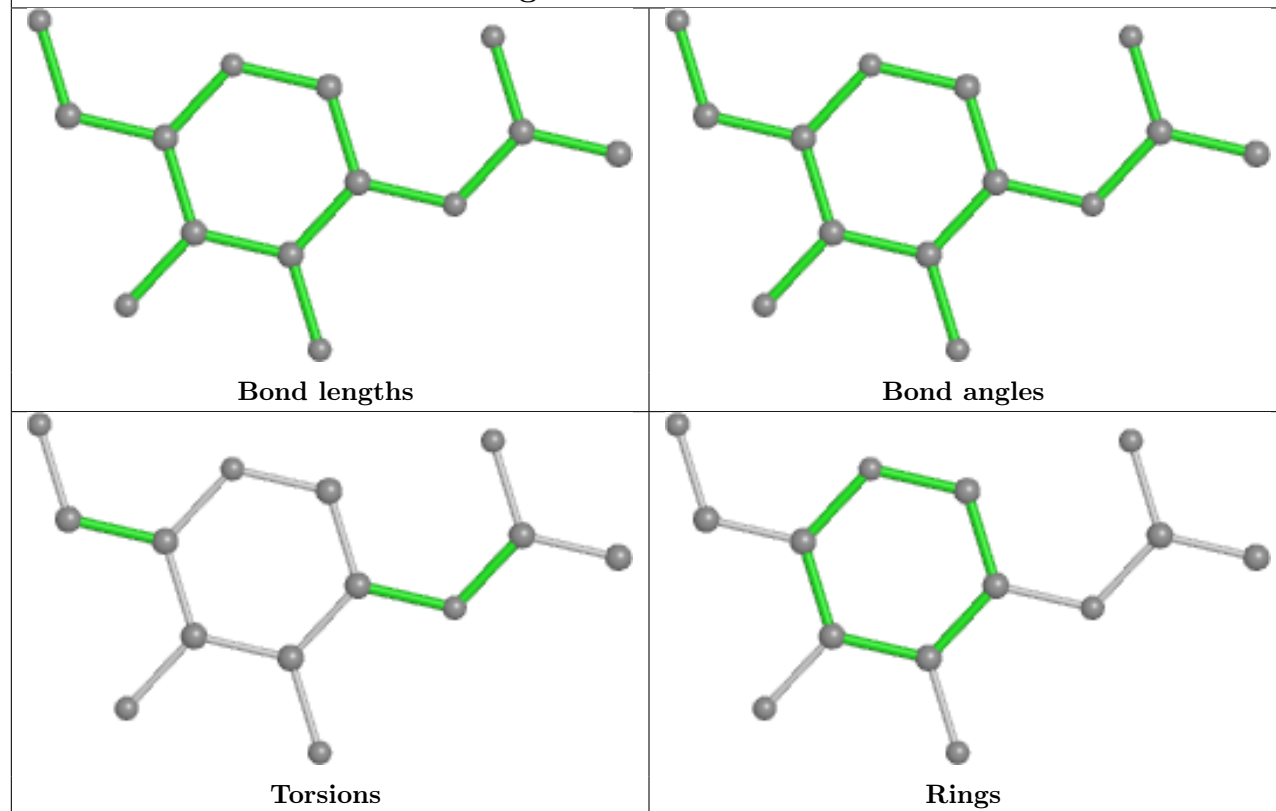




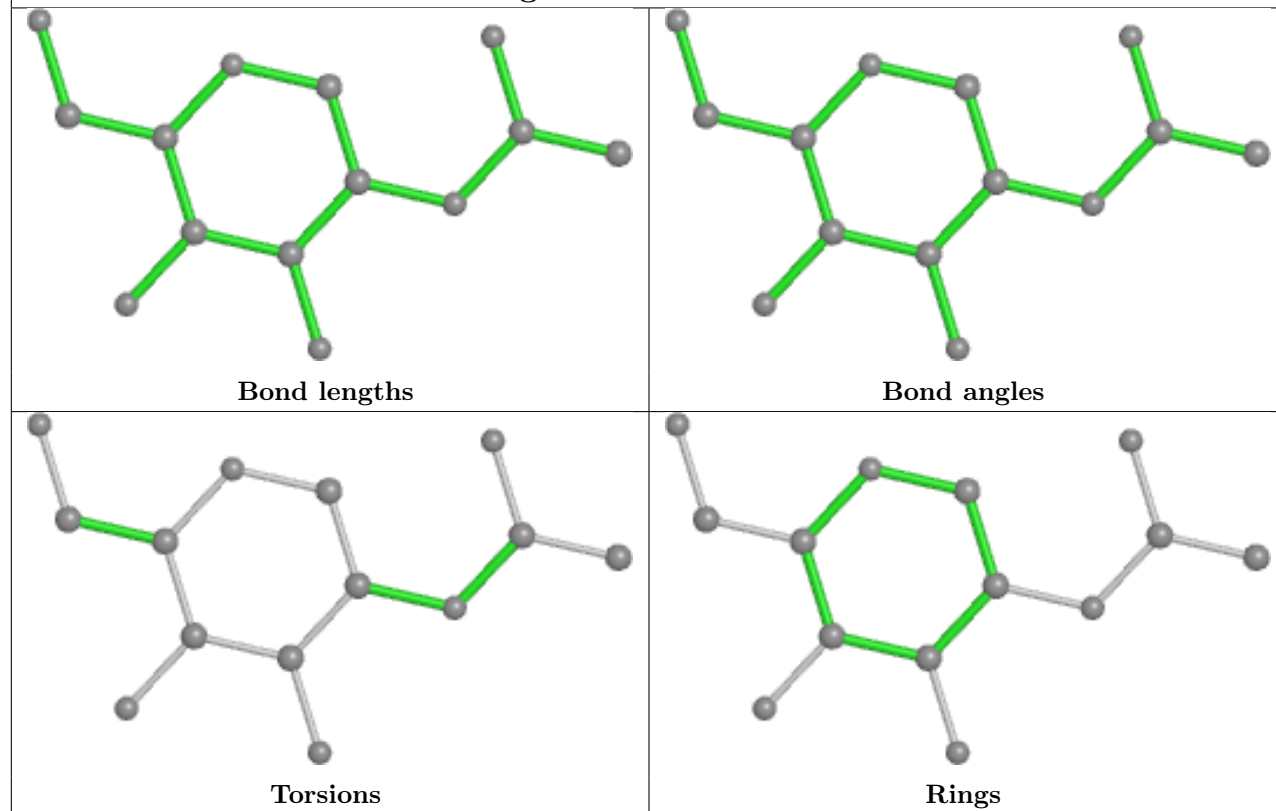


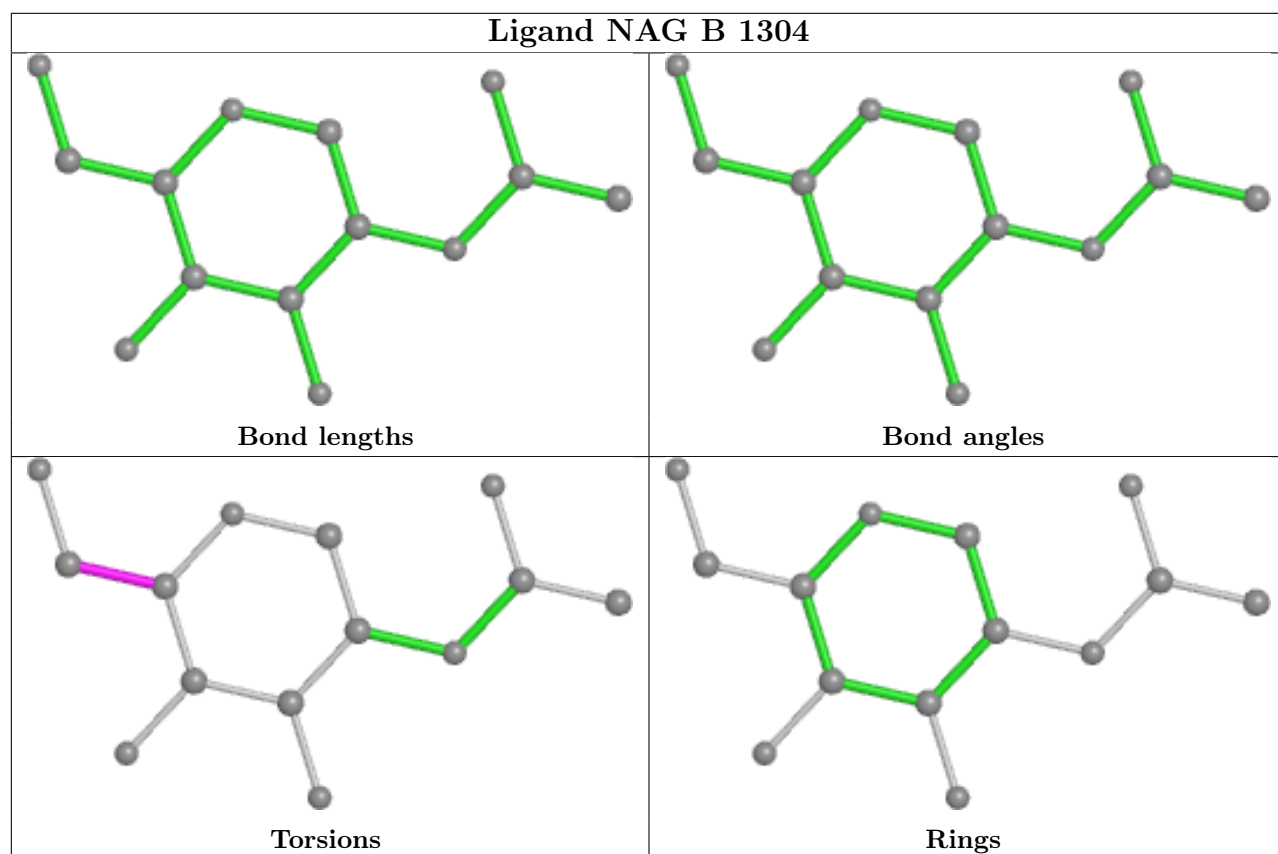
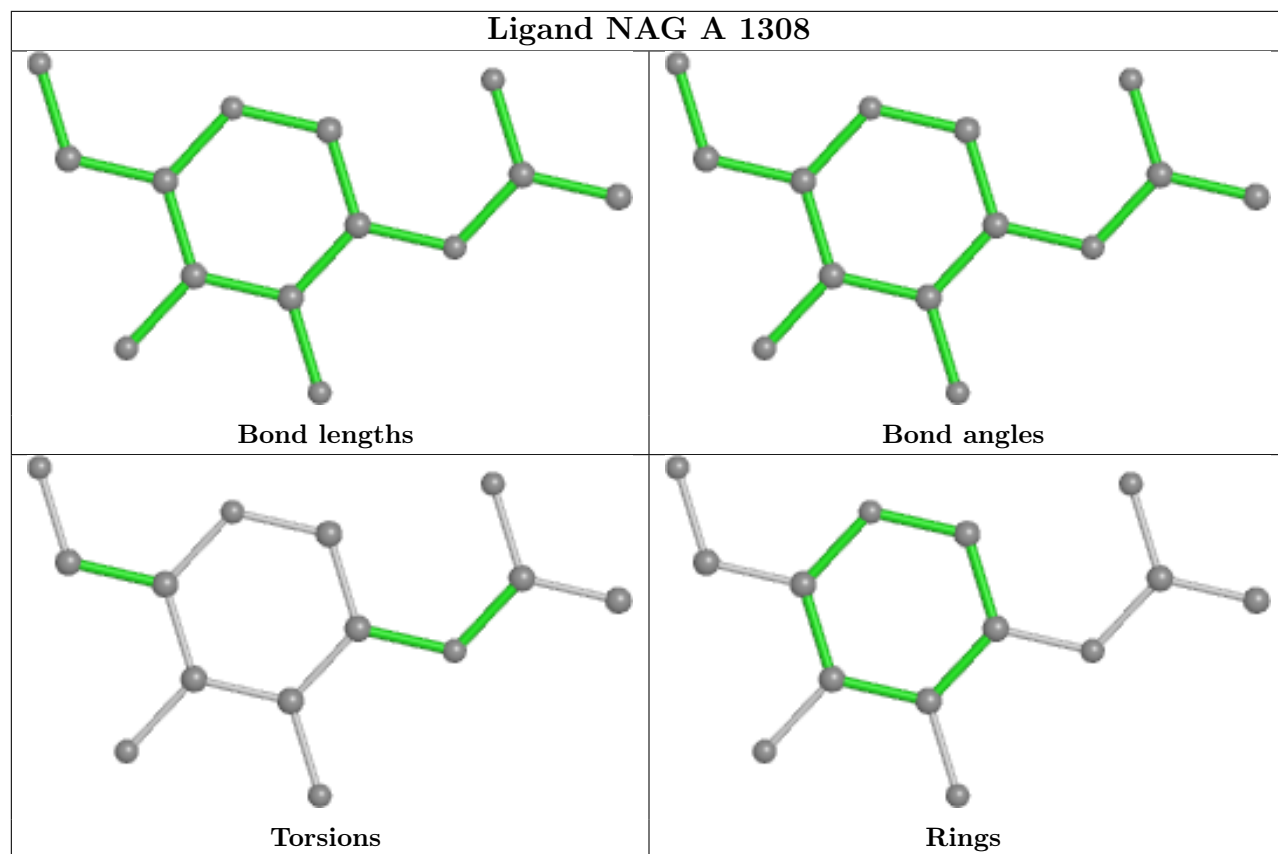


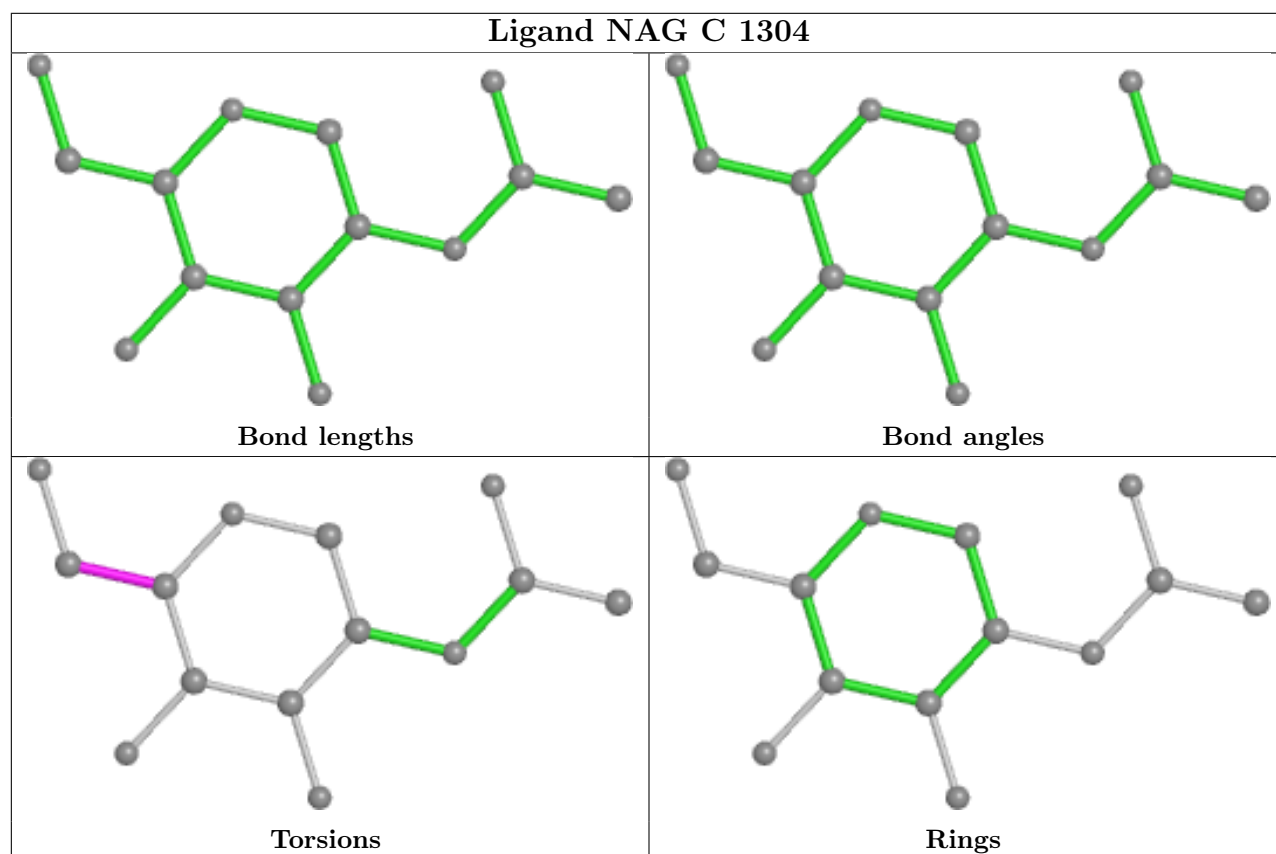
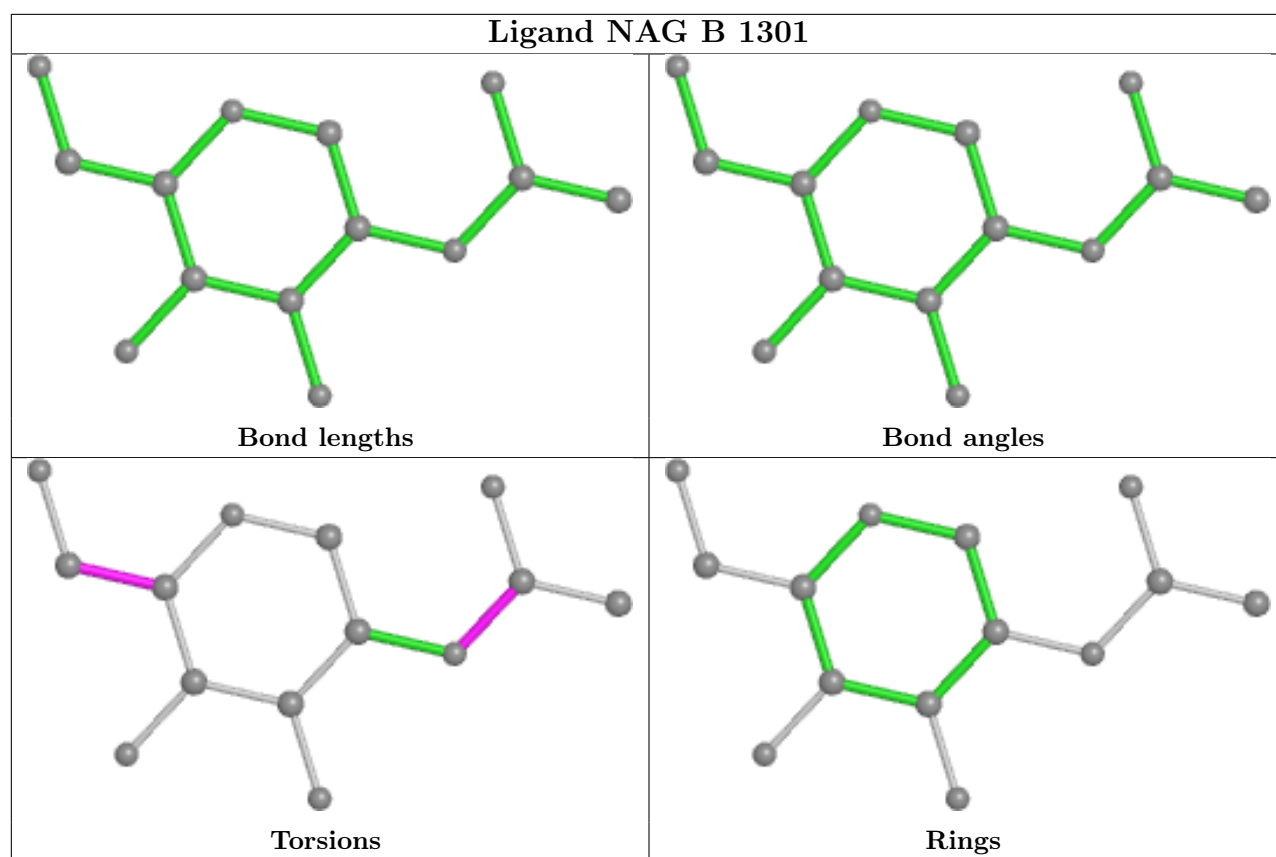
Ligand NAG C 1306



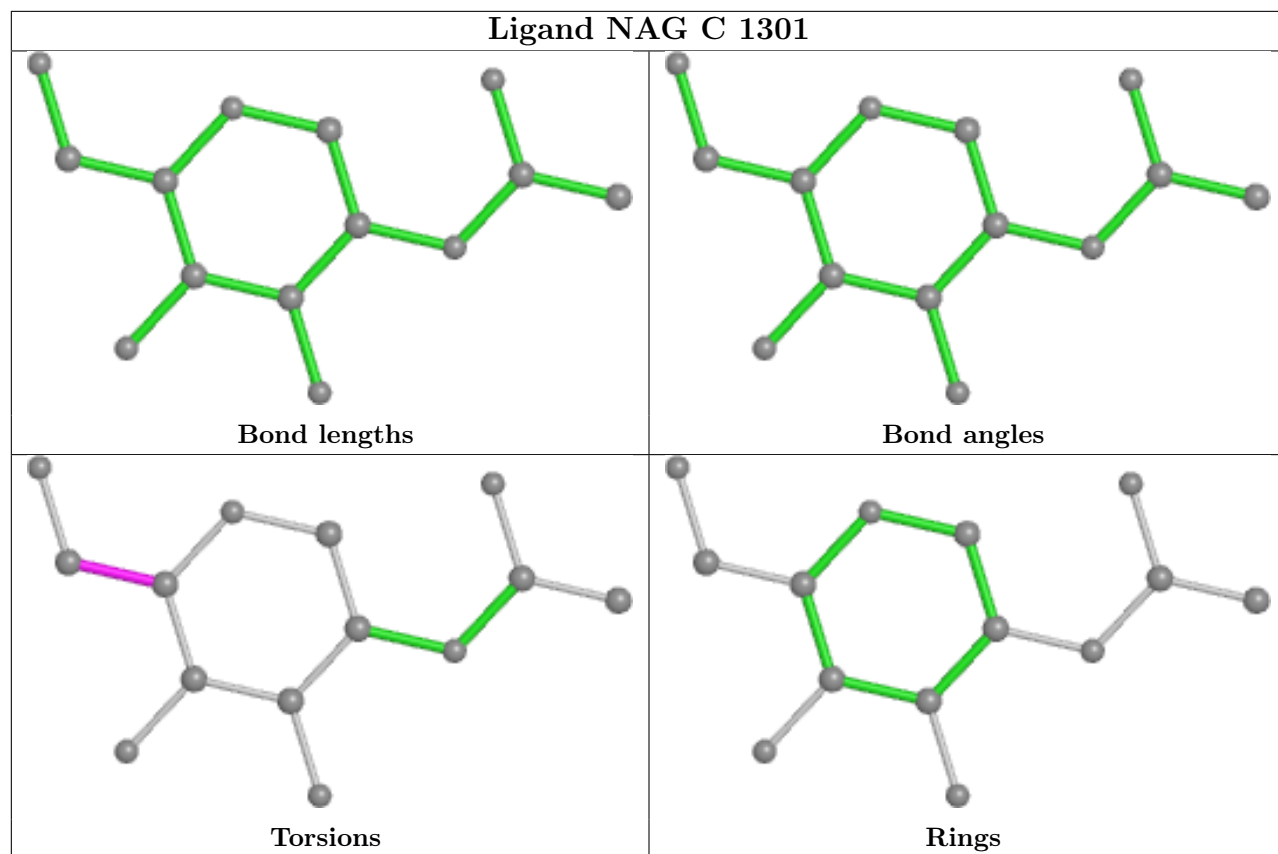
Ligand NAG B 1306



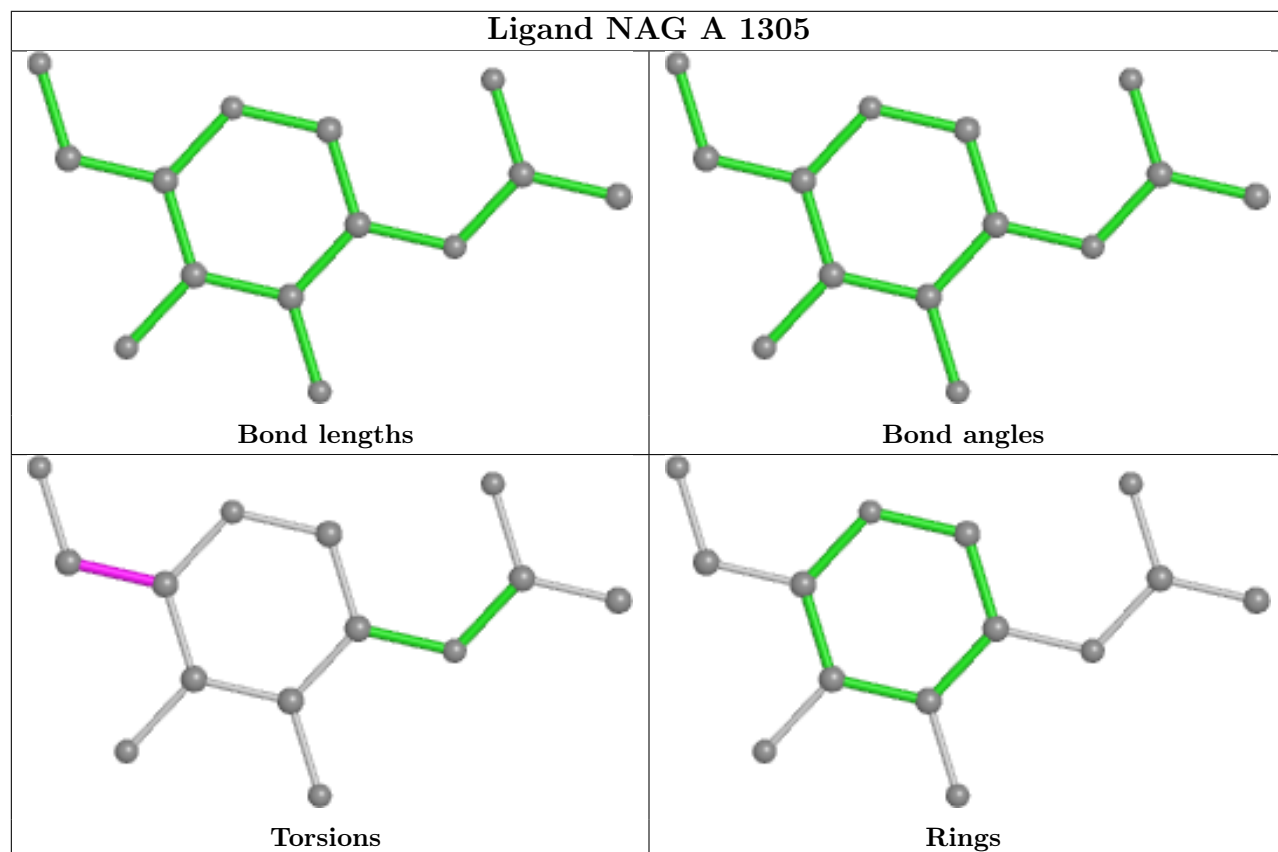


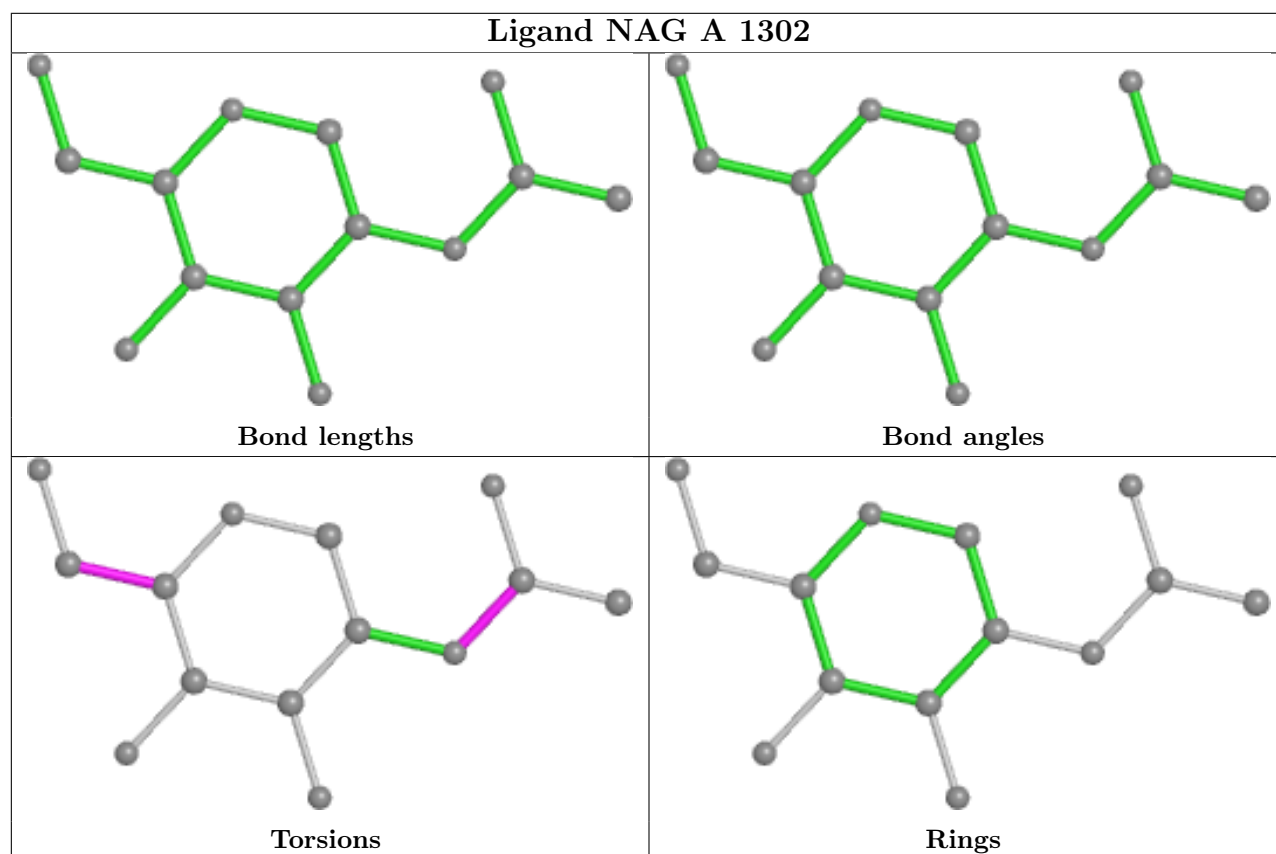
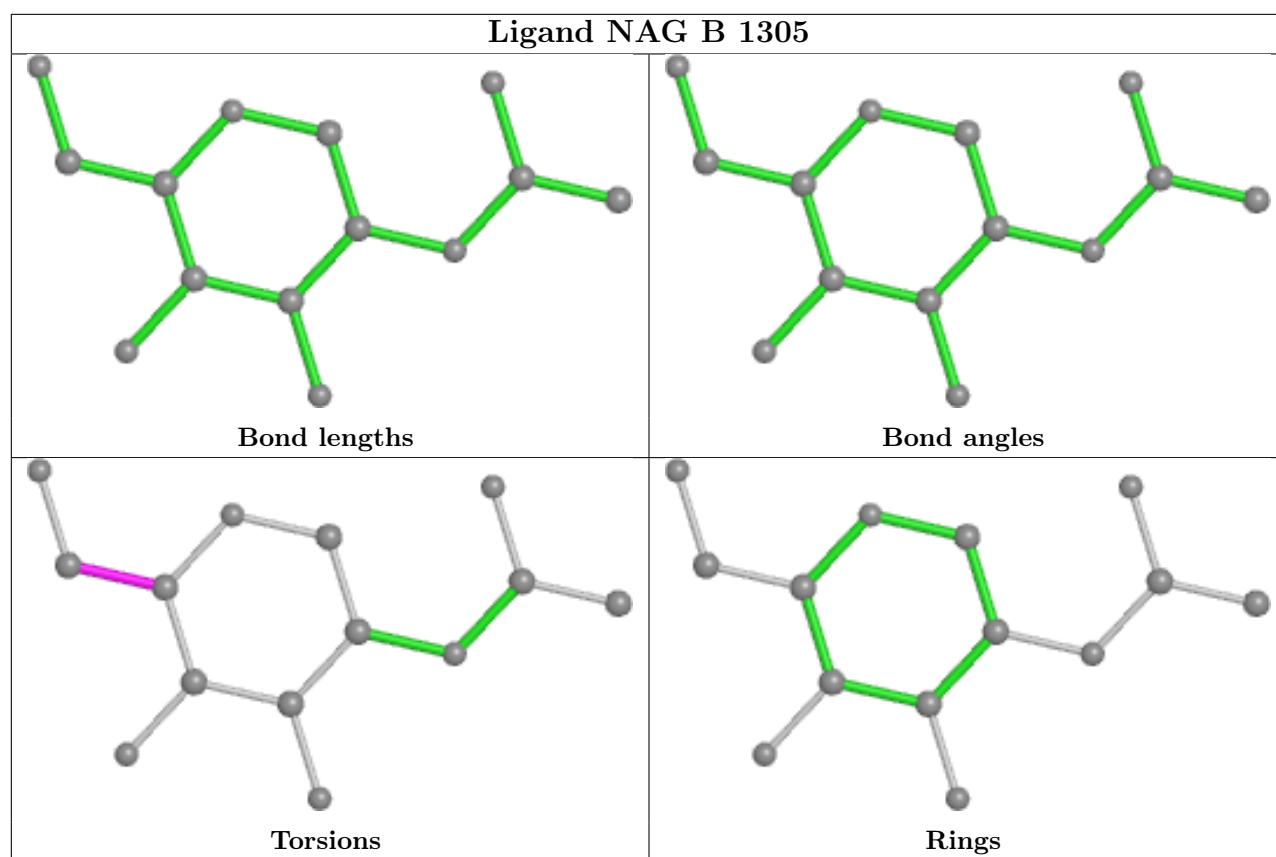


Ligand NAG C 1301

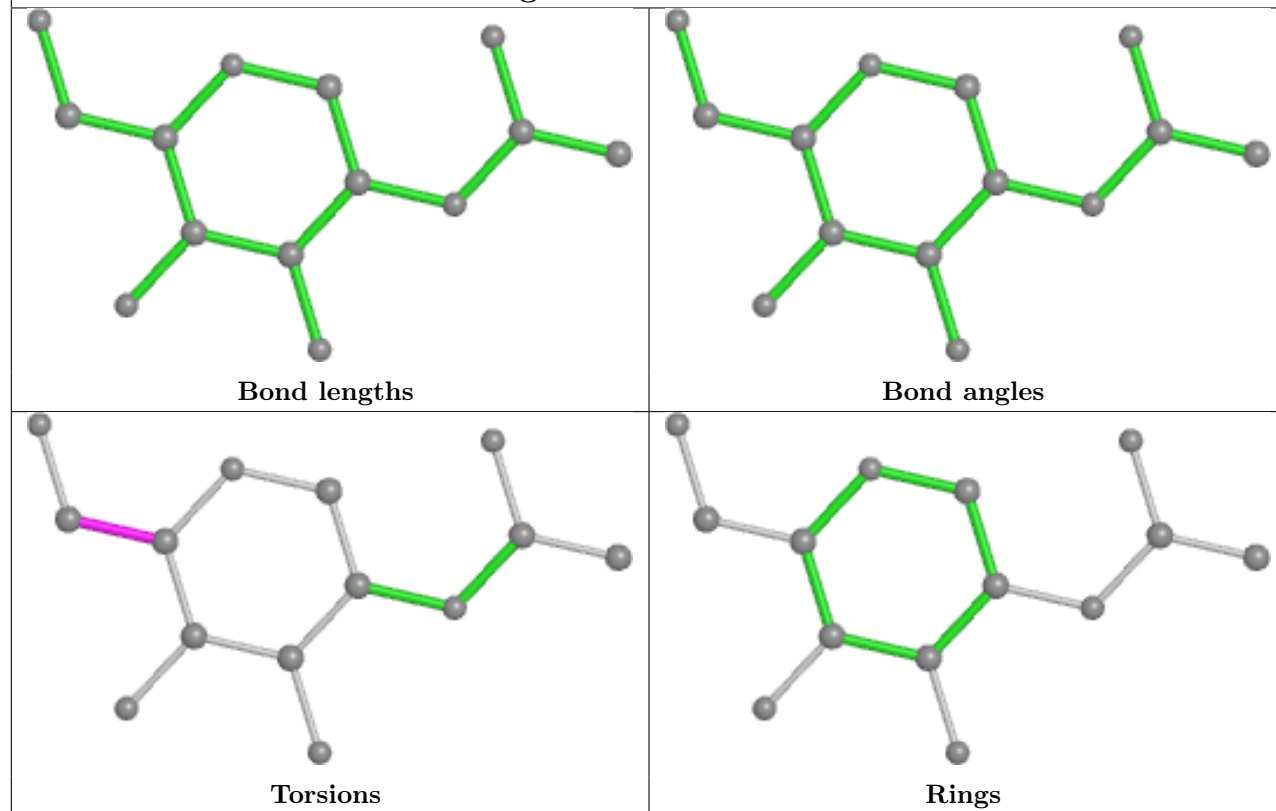


Ligand NAG A 1305

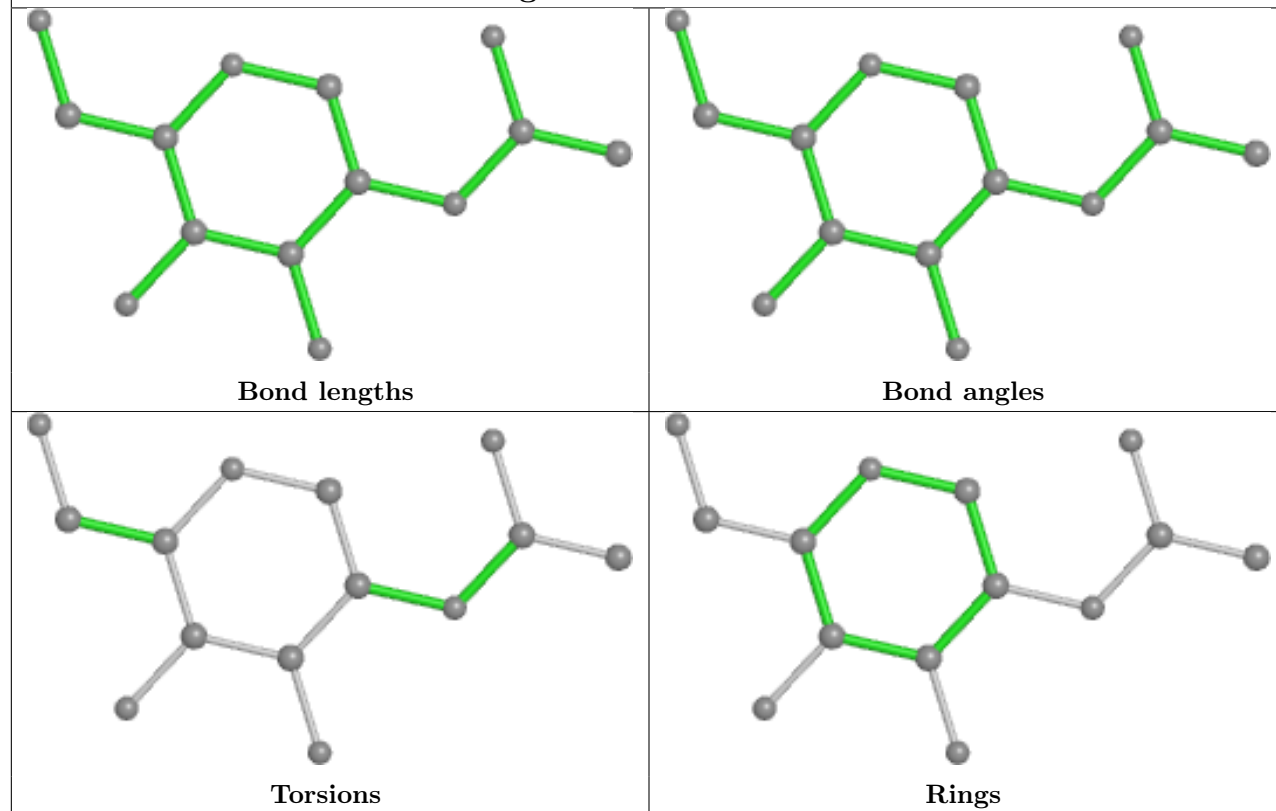


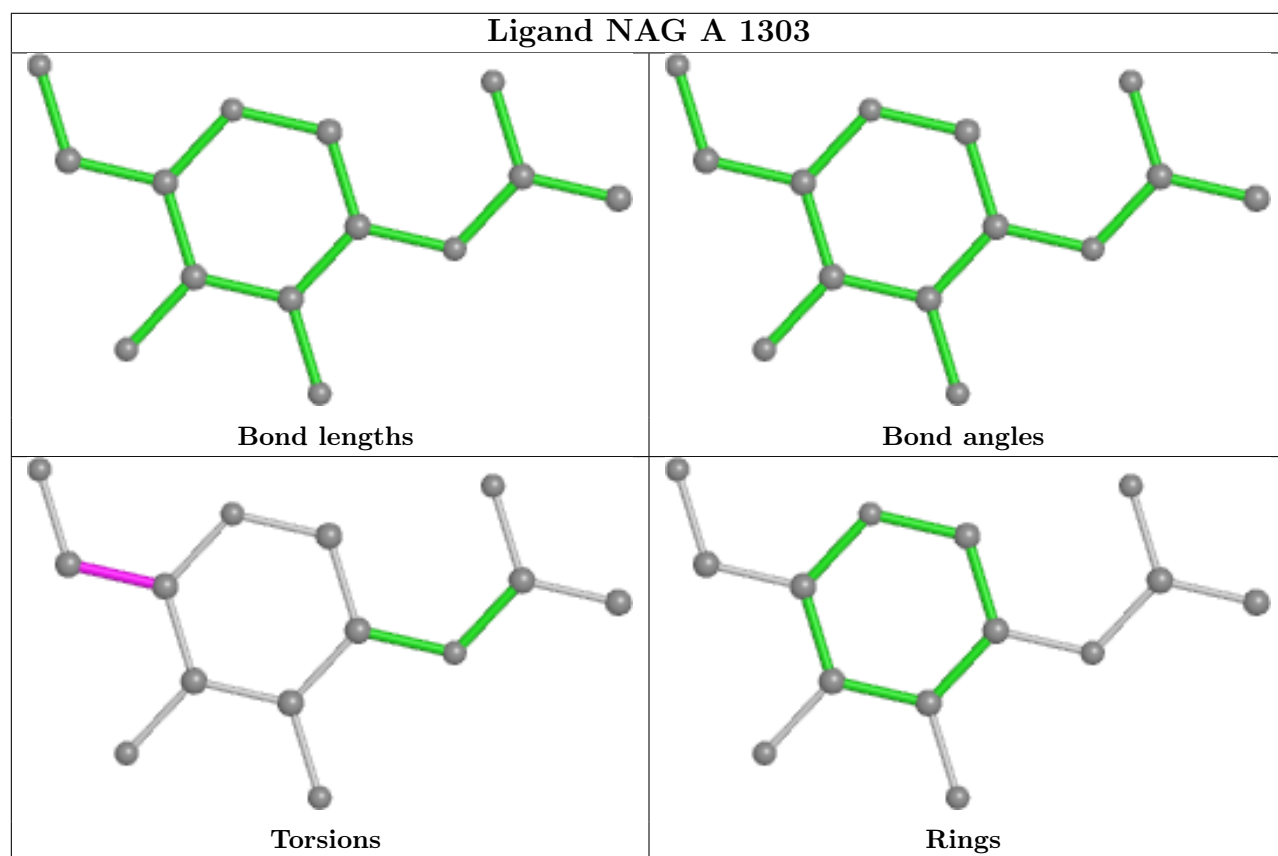
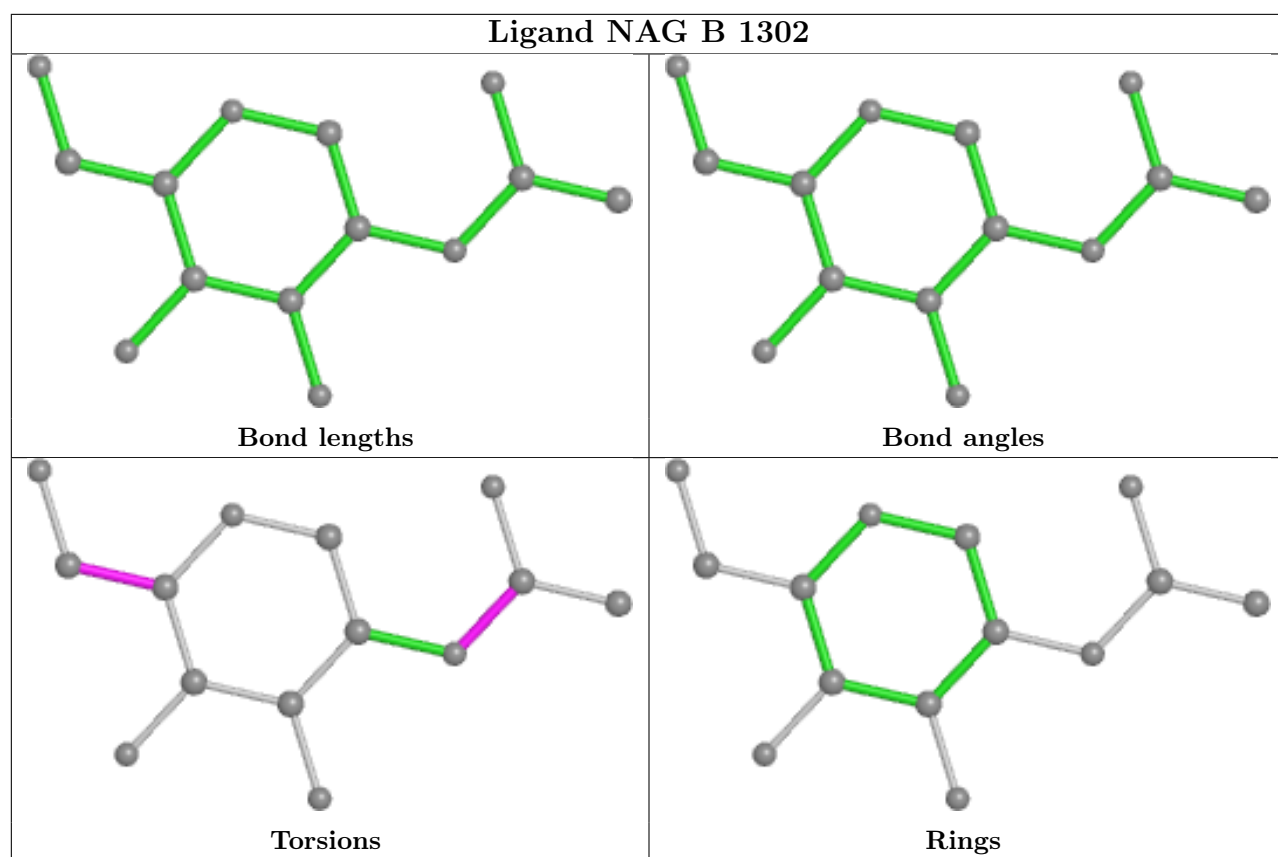


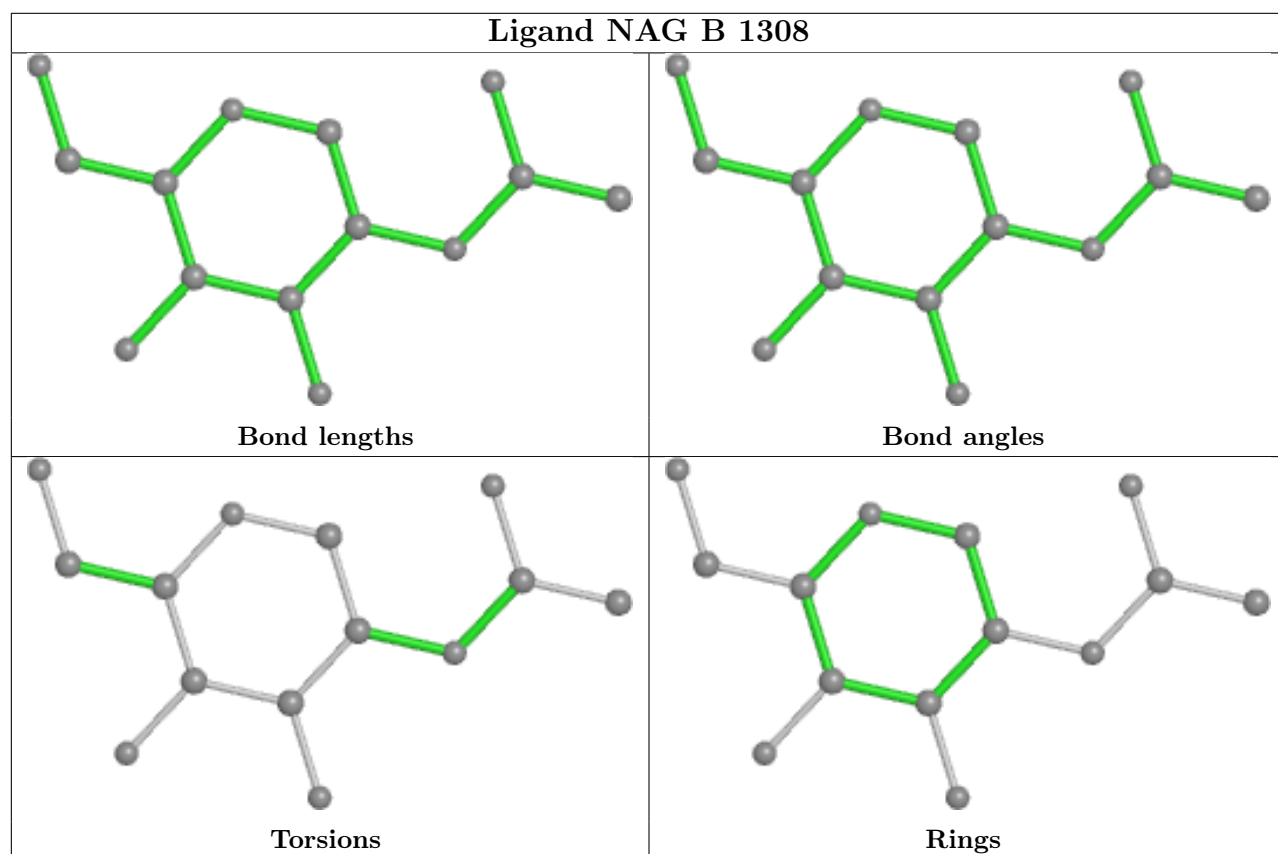
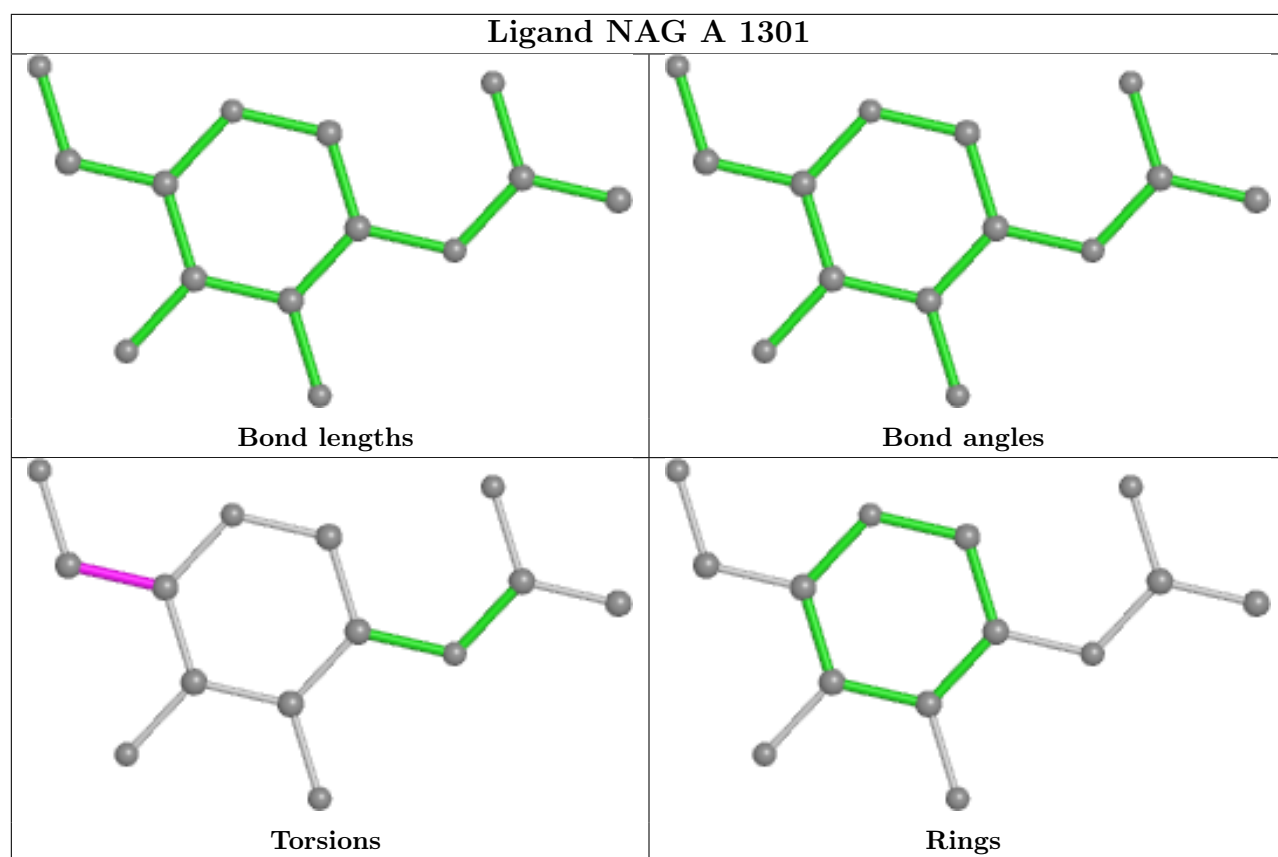
Ligand NAG B 1303



Ligand NAG C 1308







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.

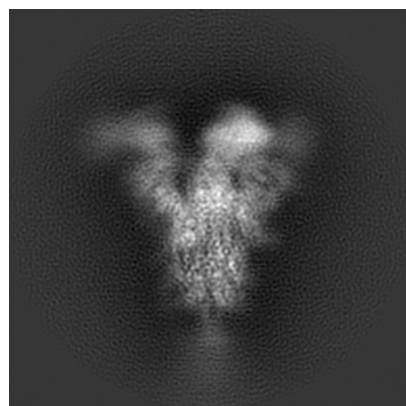
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33766. These allow visual inspection of the internal detail of the map and identification of artifacts.

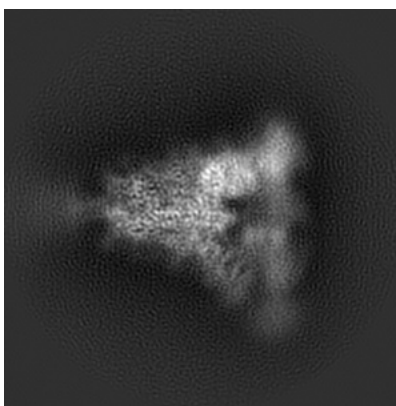
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

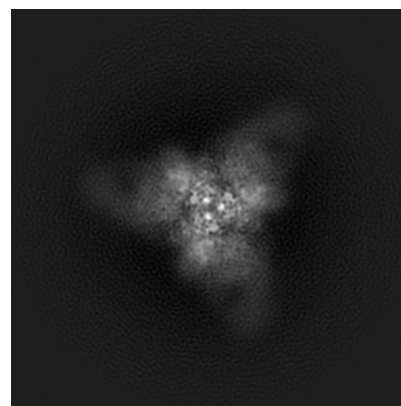
6.1.1 Primary map



X

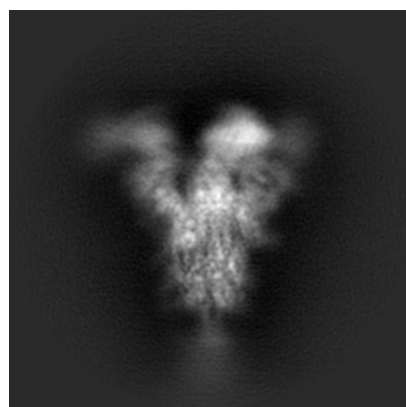


Y

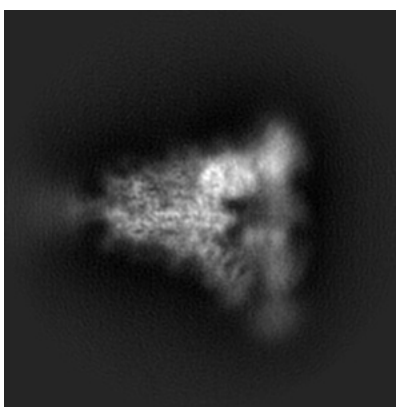


Z

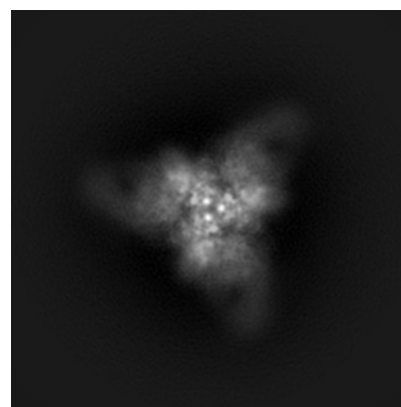
6.1.2 Raw map



X



Y

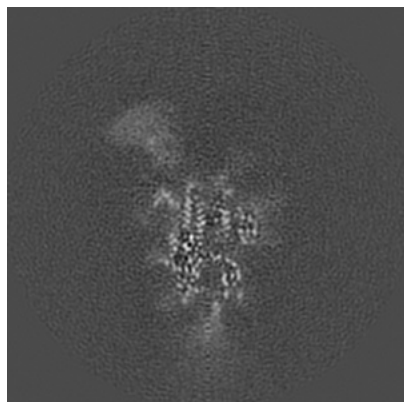


Z

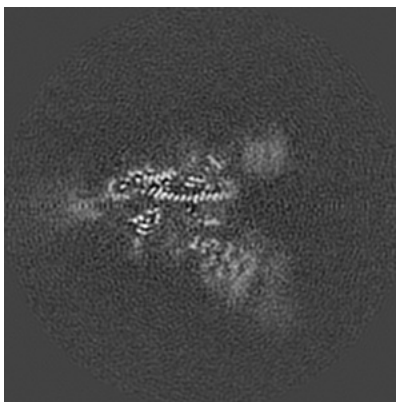
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

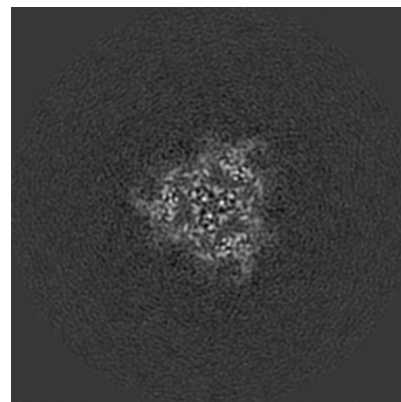
6.2.1 Primary map



X Index: 96

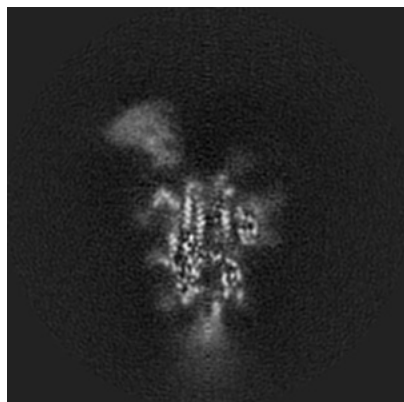


Y Index: 96

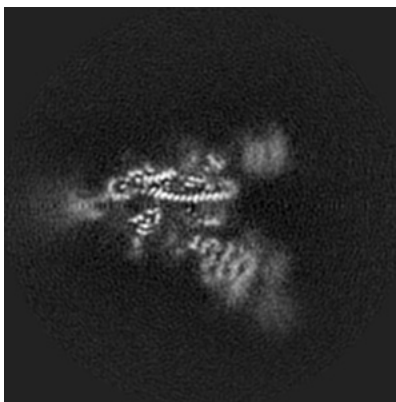


Z Index: 96

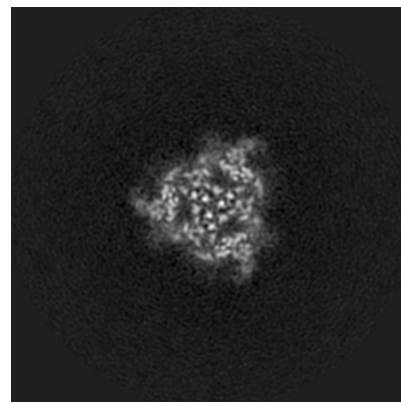
6.2.2 Raw map



X Index: 96



Y Index: 96

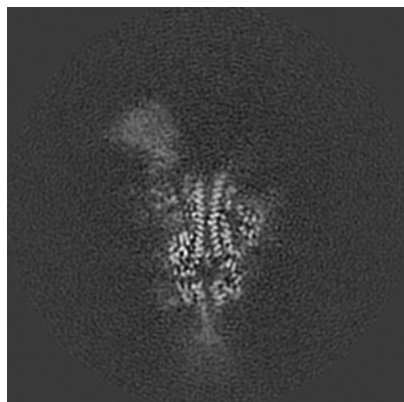


Z Index: 96

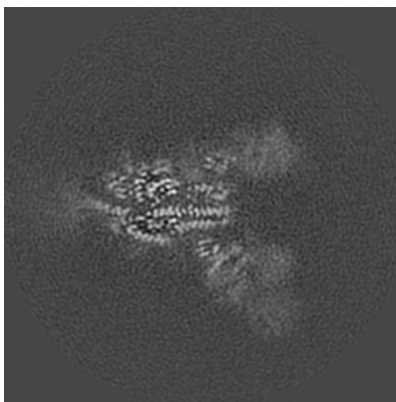
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

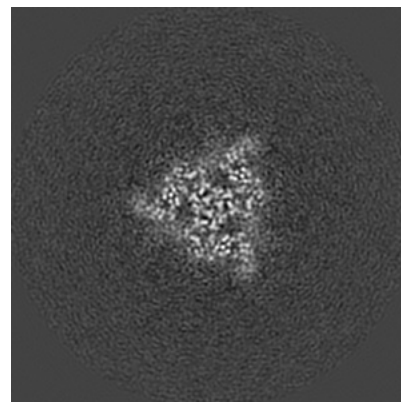
6.3.1 Primary map



X Index: 94

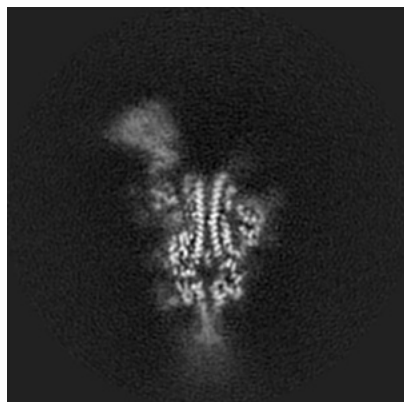


Y Index: 100

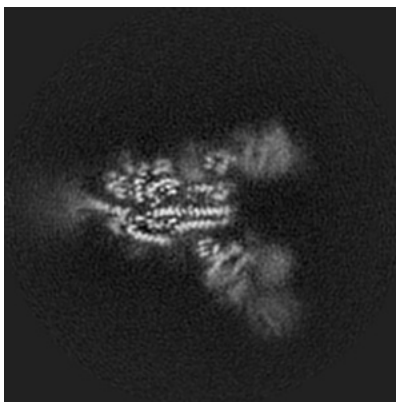


Z Index: 97

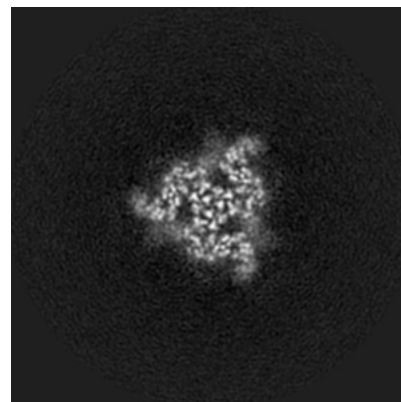
6.3.2 Raw map



X Index: 94



Y Index: 100

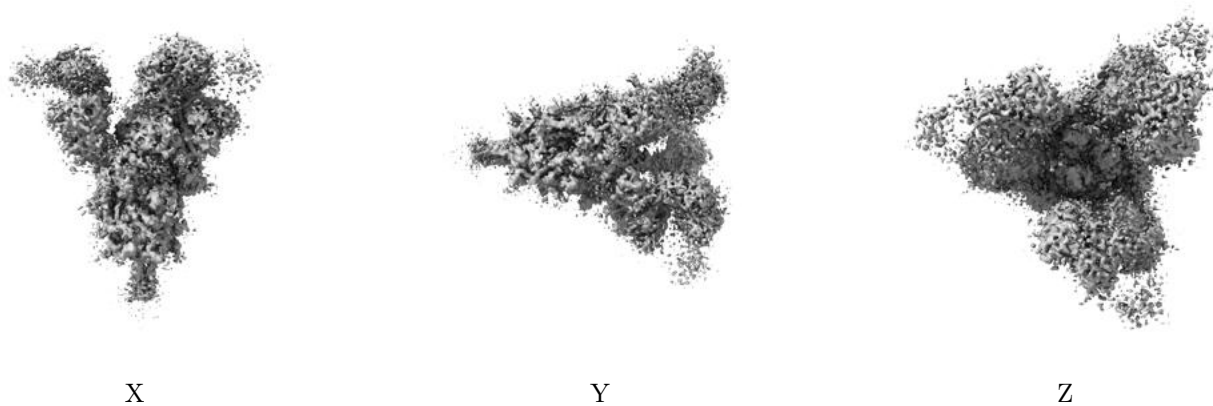


Z Index: 97

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

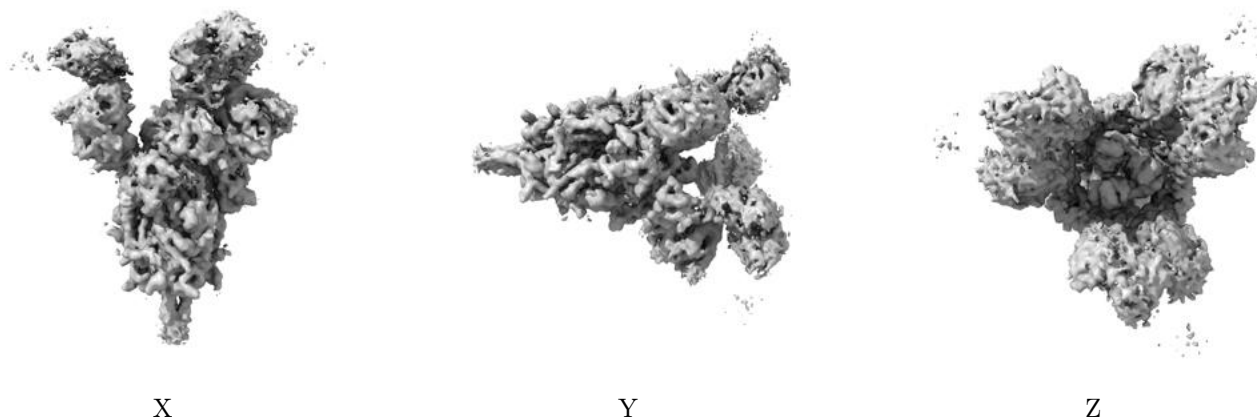
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. 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



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.

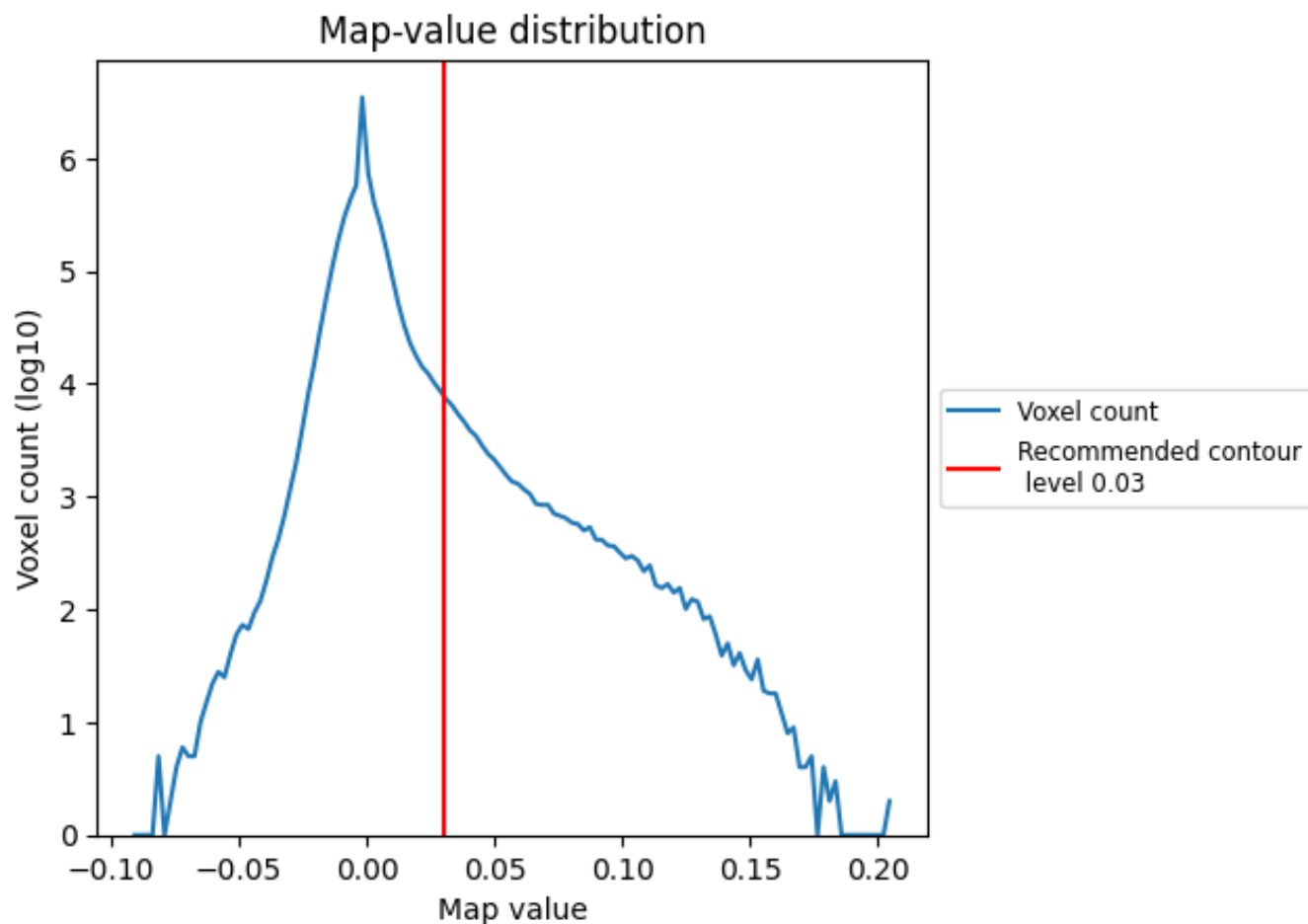
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

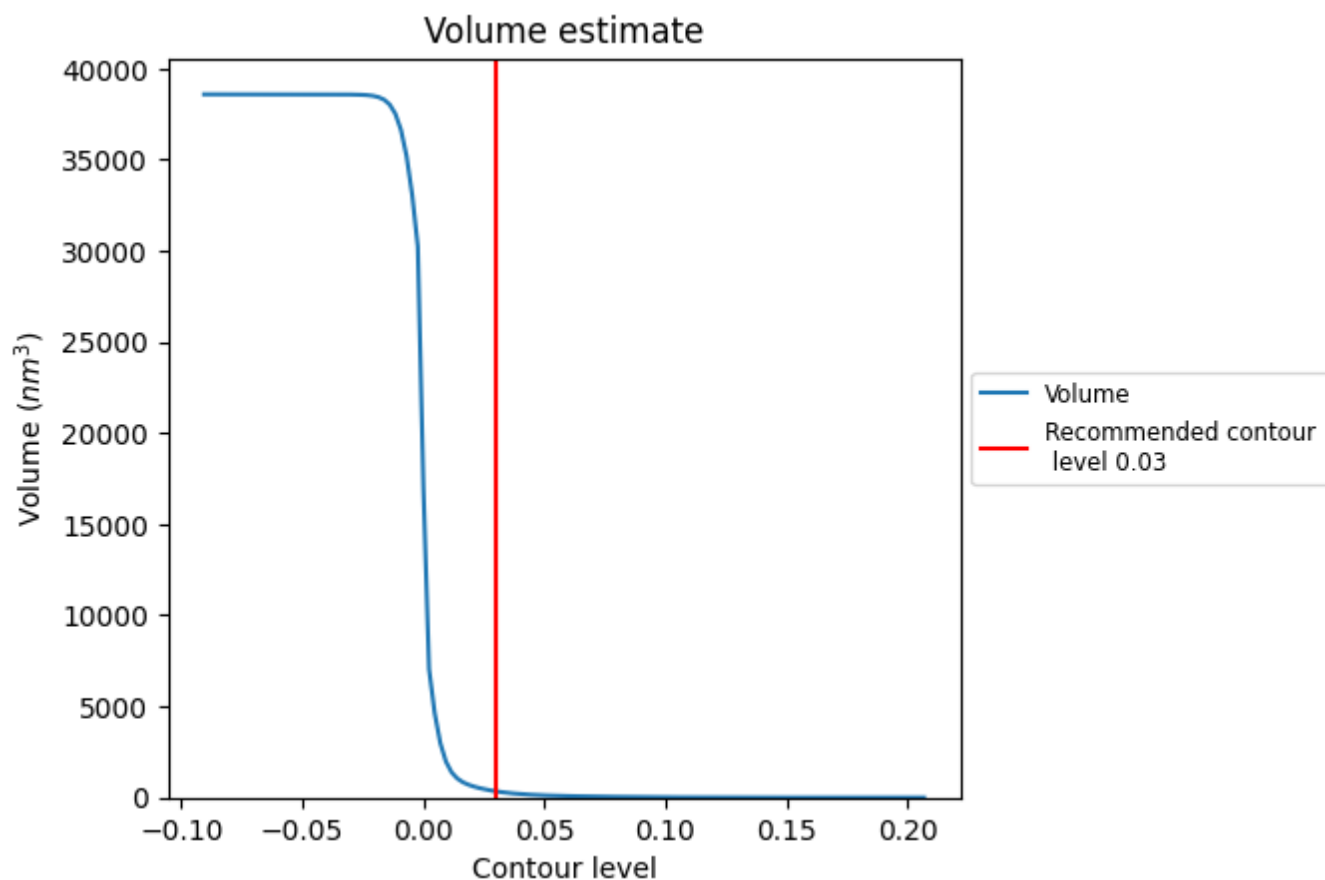
This section contains the results of statistical analysis of the map.

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.

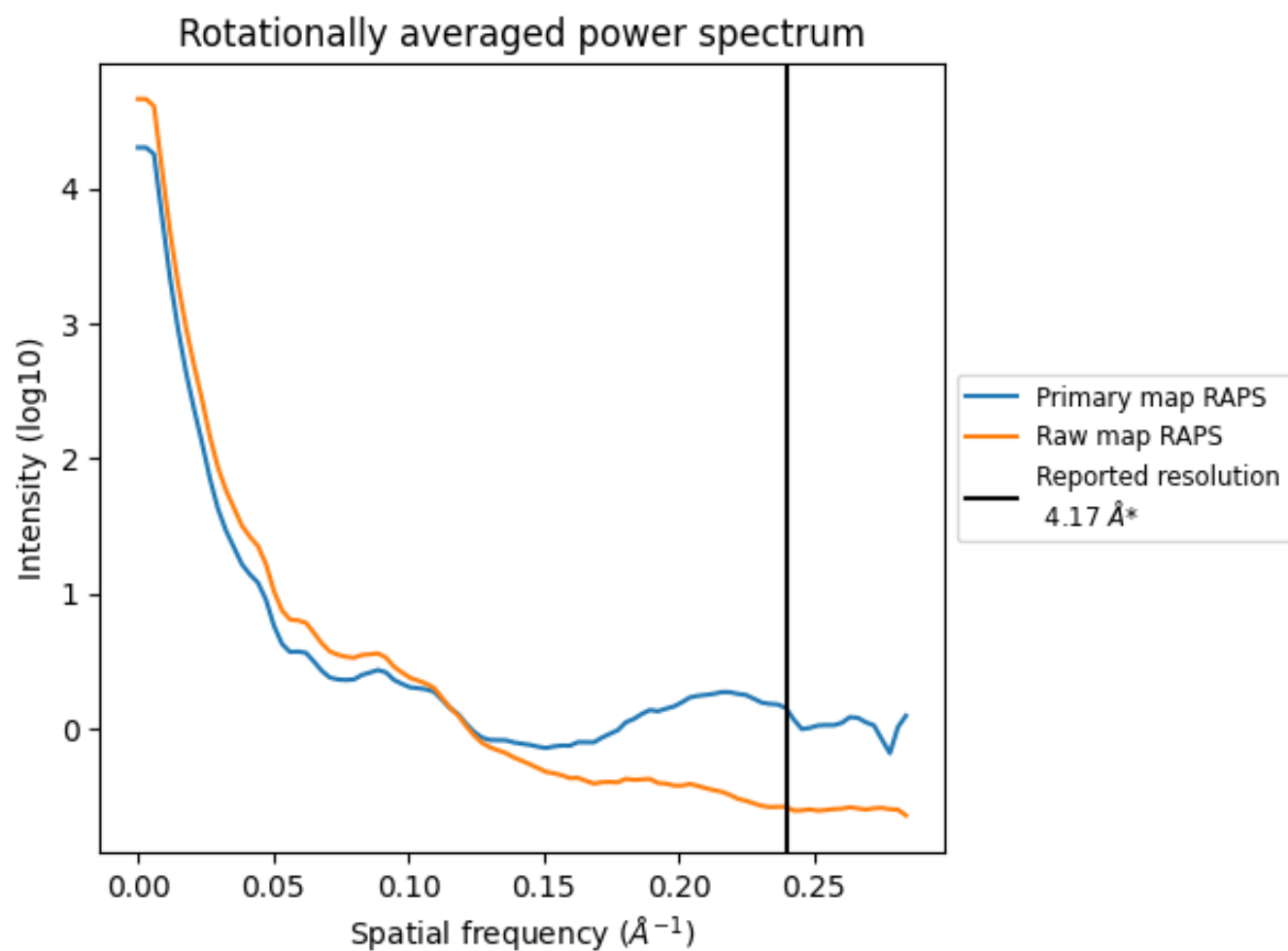
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 342 nm³; this corresponds to an approximate mass of 309 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 ⓘ

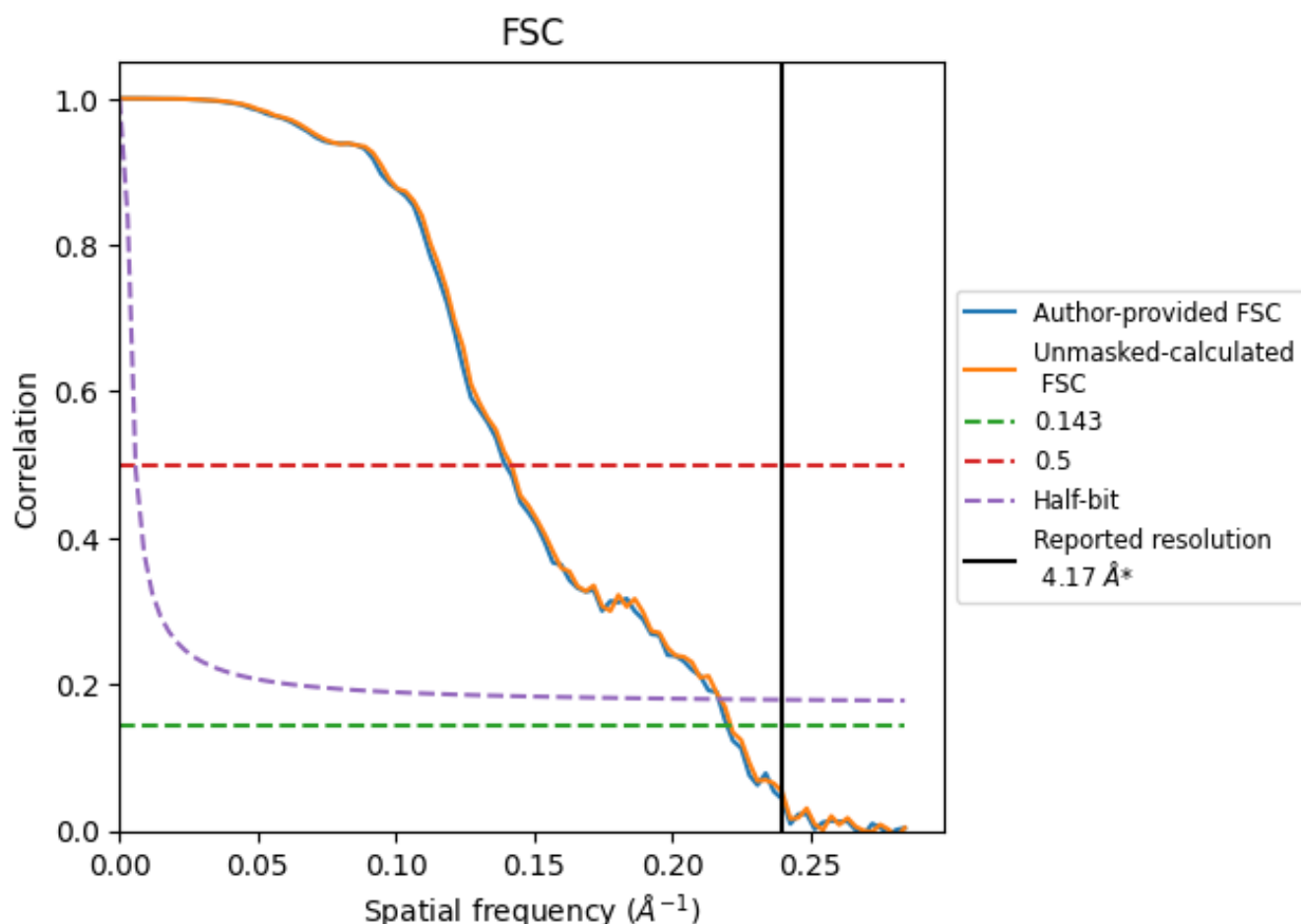


*Reported resolution corresponds to spatial frequency of 0.240 Å⁻¹

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 0.240 Å⁻¹

8.2 Resolution estimates [i](#)

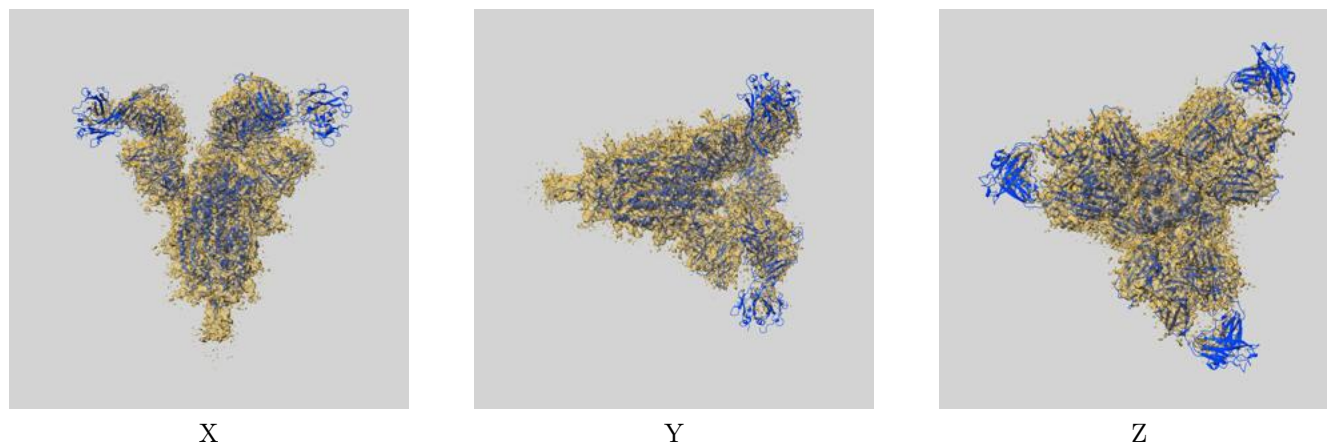
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.17	-	-
Author-provided FSC curve	4.55	7.16	4.61
Unmasked-calculated*	4.52	7.06	4.60

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

9 Map-model fit [i](#)

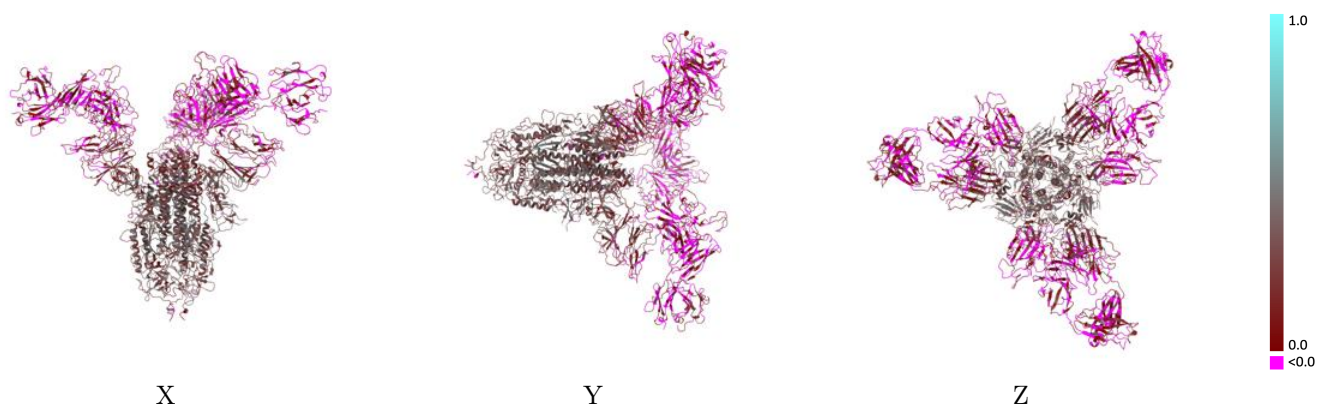
This section contains information regarding the fit between EMDB map EMD-33766 and PDB model 7YE9. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.03 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](#)



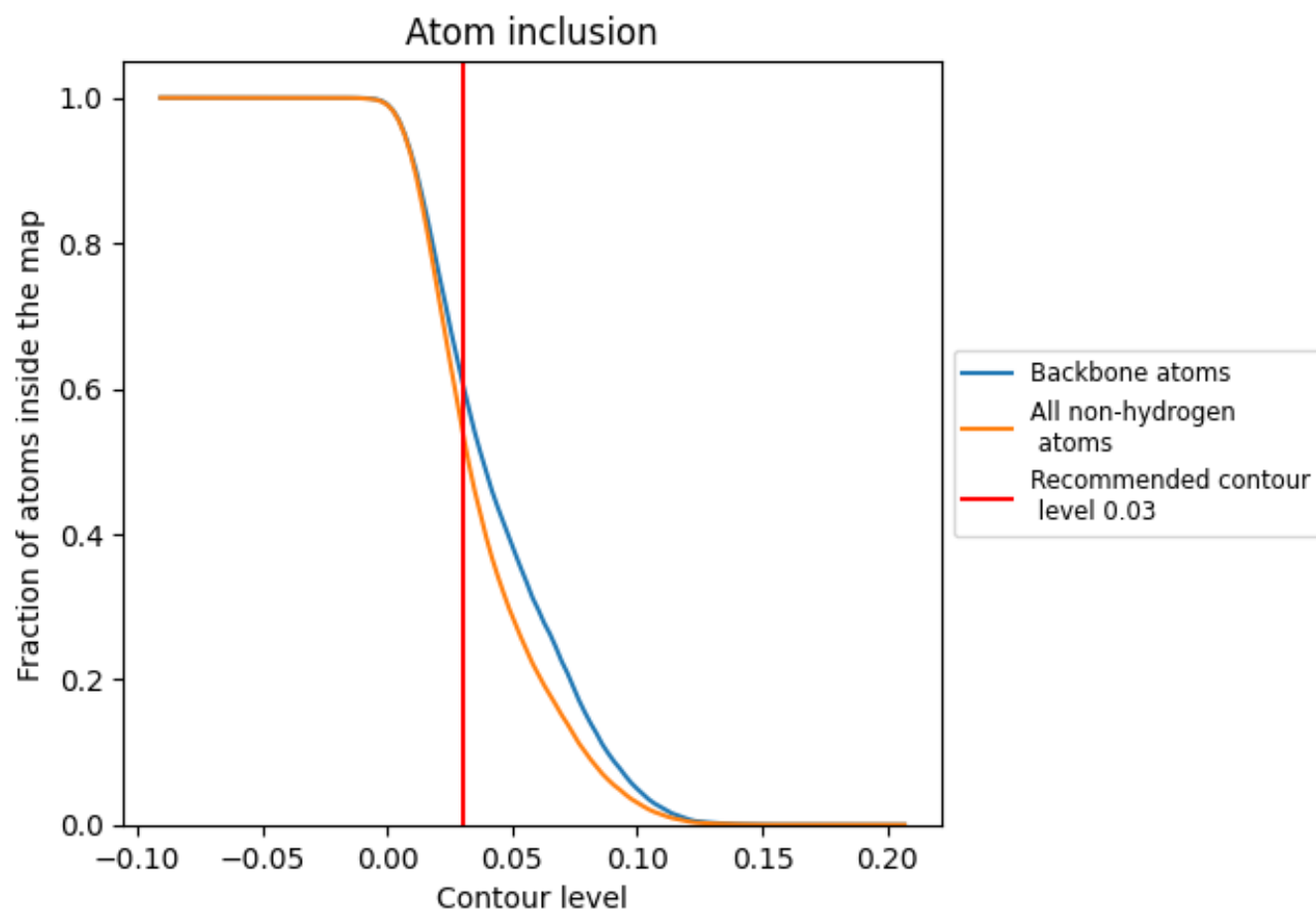
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 54% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5441	<div></div> 0.1700
A	<div></div> 0.6863	<div></div> 0.2230
B	<div></div> 0.6899	<div></div> 0.2200
C	<div></div> 0.6911	<div></div> 0.2230
D	<div></div> 0.6786	<div></div> 0.2690
E	<div></div> 0.6071	<div></div> 0.2190
F	<div></div> 0.7857	<div></div> 0.3110
G	<div></div> 0.1655	<div></div> 0.0130
H	<div></div> 0.1741	<div></div> 0.0280
I	<div></div> 0.1484	<div></div> 0.0310
J	<div></div> 0.5357	<div></div> 0.2070
K	<div></div> 0.7857	<div></div> 0.3030
L	<div></div> 0.1478	<div></div> 0.0370
M	<div></div> 0.5357	<div></div> 0.2160
N	<div></div> 0.1869	<div></div> 0.0360
O	<div></div> 0.1445	<div></div> 0.0410

