



wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 12:06 PM EST

PDB ID : 7LO6
EMDB ID : EMD-23462
Title : Structure of CD4 mimetic BNM-III-170 in complex with BG505 SOSIP.664
HIV-1 Env trimer and 17b Fab
Authors : Jette, C.A.; Bjorkman, P.J.
Deposited on : 2021-02-09
Resolution : 3.90 Å (reported)
Based on initial models : 5F4P, 2NXY, 6U0L

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.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) : 2.31.2

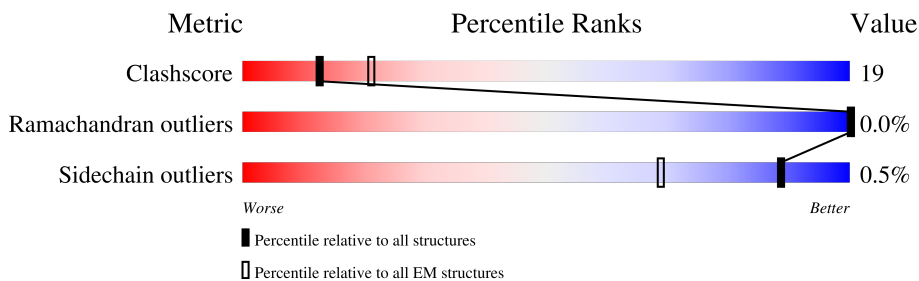
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	479	
1	C	479	
1	E	479	
2	B	153	
2	D	153	
2	F	153	
3	G	214	
3	I	214	

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Mol	Chain	Length	Quality of chain
3	K	214	
4	H	239	
4	J	239	
4	L	239	
5	M	2	
5	O	2	
5	Q	2	
5	R	2	
5	T	2	
5	U	2	
5	V	2	
6	N	5	
7	P	6	
8	S	7	

2 Entry composition i

There are 10 unique types of molecules in this entry. The entry contains 18006 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 BG505 SOSIP.664 gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	363	2840	1790	497	529	24	0	0
1	C	364	2848	1794	499	531	24	0	0
1	E	365	2862	1803	503	532	24	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	332	ASN	THR	engineered mutation	UNP Q2N0S6
A	501	CYS	ALA	engineered mutation	UNP Q2N0S6
A	509	ARG	GLU	engineered mutation	UNP Q2N0S6
A	510	ARG	LYS	engineered mutation	UNP Q2N0S6
A	511	ARG	-	insertion	UNP Q2N0S6
A	512	ARG	-	insertion	UNP Q2N0S6
C	332	ASN	THR	engineered mutation	UNP Q2N0S6
C	501	CYS	ALA	engineered mutation	UNP Q2N0S6
C	509	ARG	GLU	engineered mutation	UNP Q2N0S6
C	510	ARG	LYS	engineered mutation	UNP Q2N0S6
C	511	ARG	-	insertion	UNP Q2N0S6
C	512	ARG	-	insertion	UNP Q2N0S6
E	332	ASN	THR	engineered mutation	UNP Q2N0S6
E	501	CYS	ALA	engineered mutation	UNP Q2N0S6
E	509	ARG	GLU	engineered mutation	UNP Q2N0S6
E	510	ARG	LYS	engineered mutation	UNP Q2N0S6
E	511	ARG	-	insertion	UNP Q2N0S6
E	512	ARG	-	insertion	UNP Q2N0S6

- Molecule 2 is a protein called HIV-1 Envelope Glycoprotein BG505 SOSIP.664 gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	132	Total	C	N	O	S	0	0
			1026	653	180	187	6		
2	D	134	Total	C	N	O	S	0	0
			1049	666	185	192	6		
2	F	120	Total	C	N	O	S	0	0
			960	609	165	180	6		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	559	PRO	ILE	engineered mutation	UNP Q2N0S6
B	605	CYS	THR	engineered mutation	UNP Q2N0S6
D	559	PRO	ILE	engineered mutation	UNP Q2N0S6
D	605	CYS	THR	engineered mutation	UNP Q2N0S6
F	559	PRO	ILE	engineered mutation	UNP Q2N0S6
F	605	CYS	THR	engineered mutation	UNP Q2N0S6

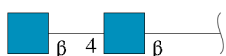
- Molecule 3 is a protein called 17b Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	111	Total	C	N	O	S	0	0
			853	533	149	168	3		
3	I	111	Total	C	N	O	S	0	0
			850	532	149	166	3		
3	K	111	Total	C	N	O	S	0	0
			847	530	146	168	3		

- Molecule 4 is a protein called 17b Fab Heavy Chain.

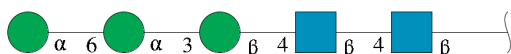
Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	129	Total	C	N	O	S	0	0
			996	627	170	196	3		
4	J	129	Total	C	N	O	S	0	0
			996	627	170	196	3		
4	L	129	Total	C	N	O	S	0	0
			996	627	170	196	3		

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



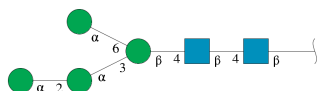
Mol	Chain	Residues	Atoms				AltConf	Trace
5	M	2	Total	C	N	O	0	0
			28	16	2	10		
5	O	2	Total	C	N	O	0	0
			28	16	2	10		
5	Q	2	Total	C	N	O	0	0
			28	16	2	10		
5	R	2	Total	C	N	O	0	0
			28	16	2	10		
5	T	2	Total	C	N	O	0	0
			28	16	2	10		
5	U	2	Total	C	N	O	0	0
			28	16	2	10		
5	V	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is an oligosaccharide called 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.



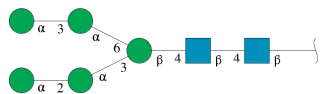
Mol	Chain	Residues	Atoms				AltConf	Trace
6	N	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 7 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.



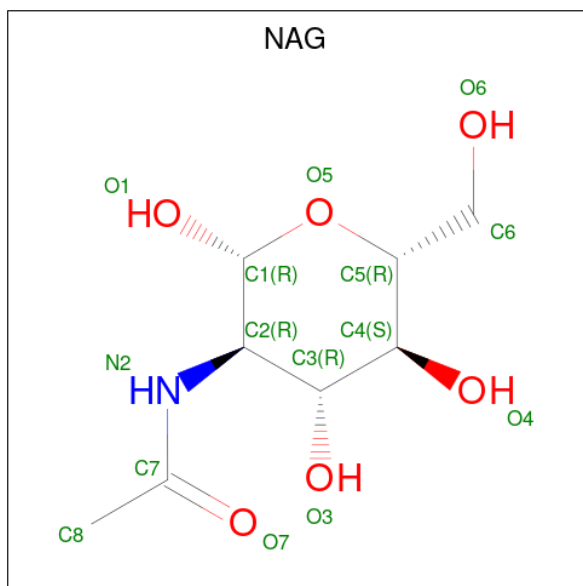
Mol	Chain	Residues	Atoms				AltConf	Trace
7	P	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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
			Total	C	N	O		
8	S	7	83	46	2	35	0	0

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



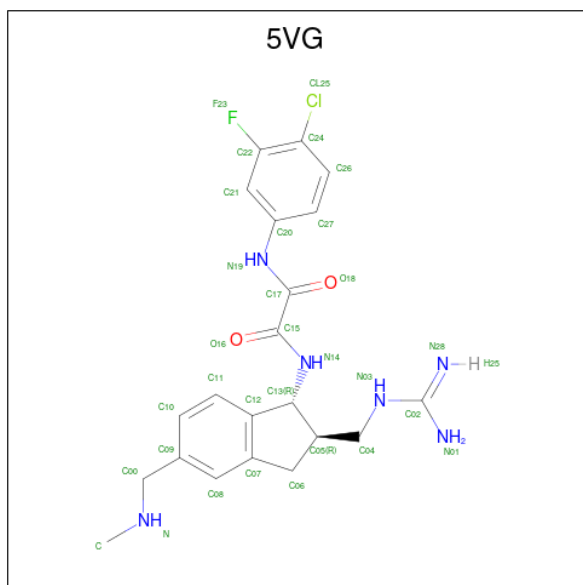
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
9	A	1	112	64	8	40	0
9	A	1	112	64	8	40	0
9	A	1	112	64	8	40	0
9	A	1	112	64	8	40	0
9	A	1	112	64	8	40	0
9	A	1	112	64	8	40	0
9	A	1	112	64	8	40	0
9	A	1	112	64	8	40	0

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
9	C	1	112	64	8	40	0
9	C	1	112	64	8	40	0
9	C	1	112	64	8	40	0
9	C	1	112	64	8	40	0
9	C	1	112	64	8	40	0
9	C	1	112	64	8	40	0
9	C	1	112	64	8	40	0
9	C	1	112	64	8	40	0
9	D	1	14	8	1	5	0
9	E	1	112	64	8	40	0
9	E	1	112	64	8	40	0
9	E	1	112	64	8	40	0
9	E	1	112	64	8	40	0
9	E	1	112	64	8	40	0
9	E	1	112	64	8	40	0
9	E	1	112	64	8	40	0
9	E	1	112	64	8	40	0
9	F	1	28	16	2	10	0
9	F	1	28	16	2	10	0

- Molecule 10 is {N}'-[(1 {R},2 {R})-2-(carbamimidamidomethyl)-5-(methylaminomethyl)-2,3-dihydro-1 {H}-inden-1-yl]- {N}-(4-chloranyl-3-fluoranyl-phenyl)ethanediamide (three-letter code: 5VG) (formula: C₂₁H₂₄ClFN₆O₂) (labeled as "Ligand of Interest" by depositor).



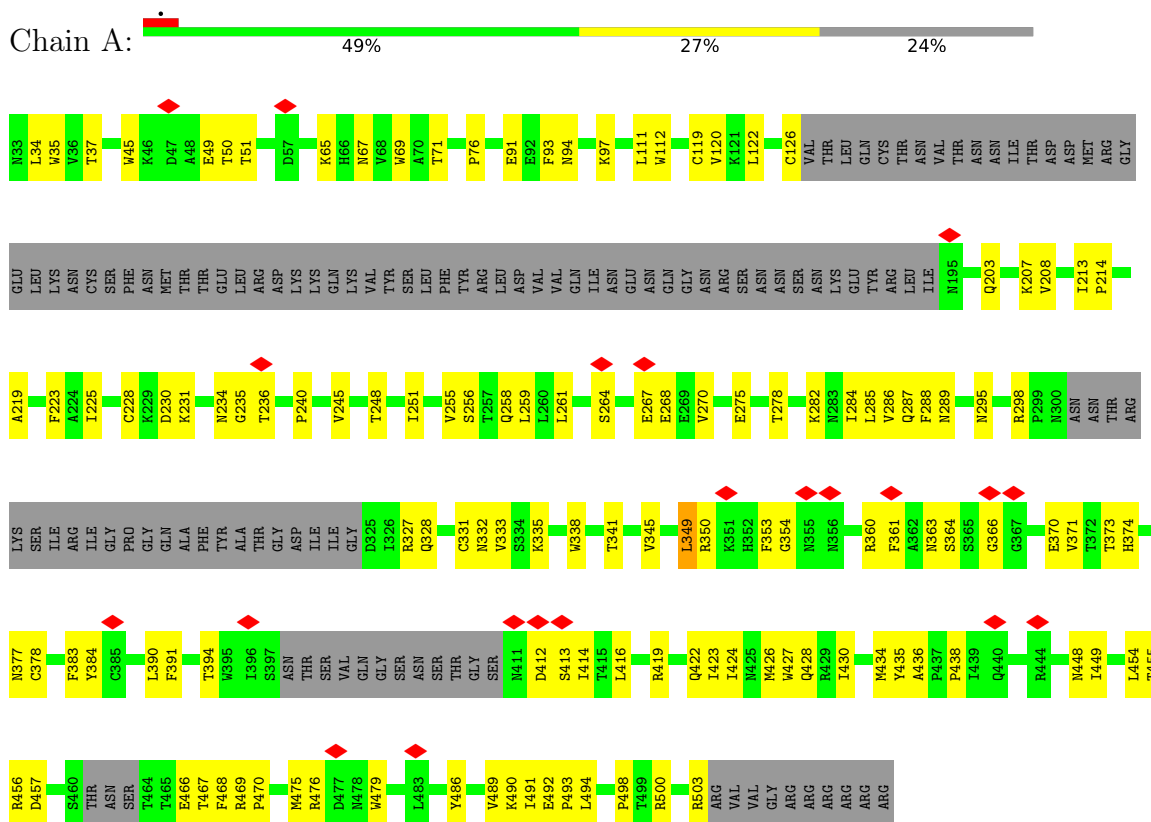
Mol	Chain	Residues	Atoms					AltConf		
			Total	C	Cl	F	N		O	
10	A	1	Total	31	21	1	1	6	2	0
10	C	1	Total	31	21	1	1	6	2	0
10	E	1	Total	31	21	1	1	6	2	0

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.

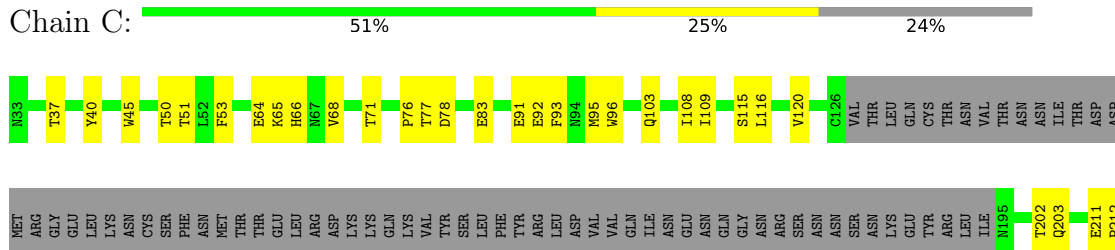
- Molecule 1: Envelope glycoprotein BG505 SOSIP.664 gp120

Chain A:



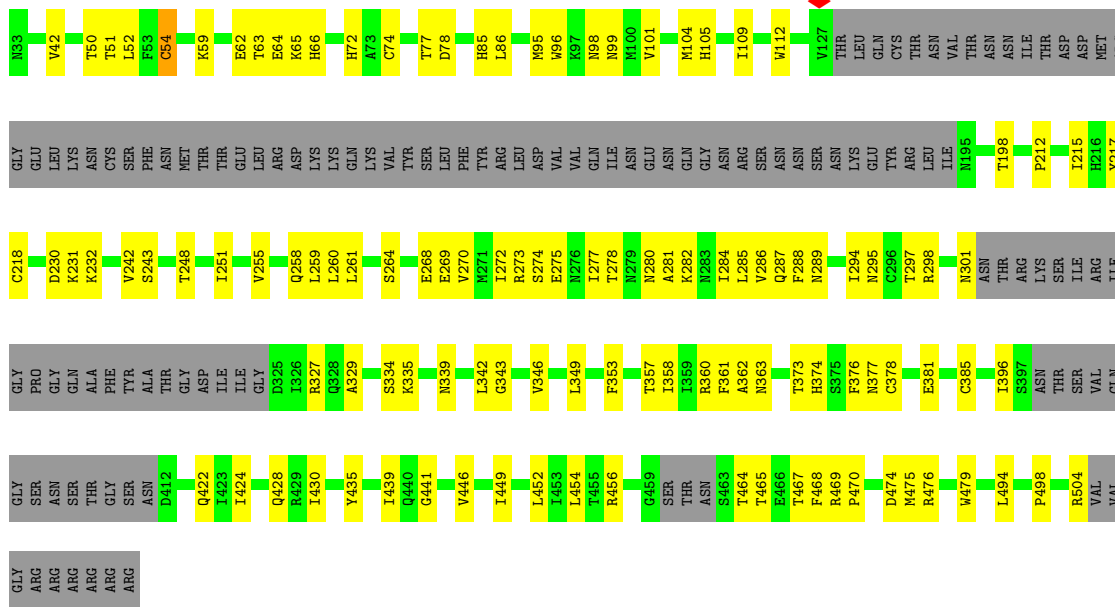
- Molecule 1: Envelope glycoprotein BG505 SOSIP.664 gp120

Chain C:

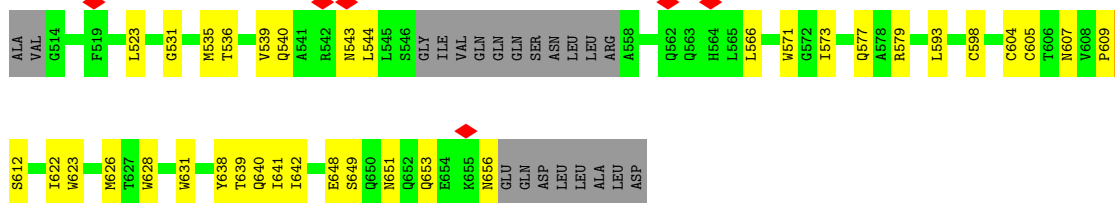




● Molecule 1: Envelope glycoprotein BG505 SOSIP.664 gp120

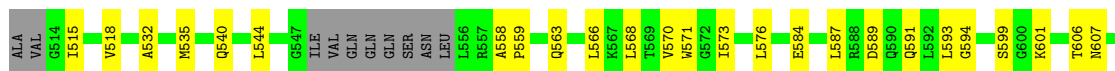


● Molecule 2: HIV-1 Envelope Glycoprotein BG505 SOSIP.664 gp41

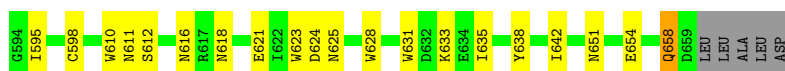
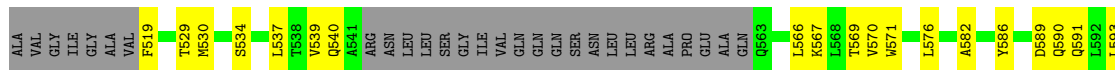


● Molecule 2: HIV-1 Envelope Glycoprotein BG505 SOSIP.664 gp41

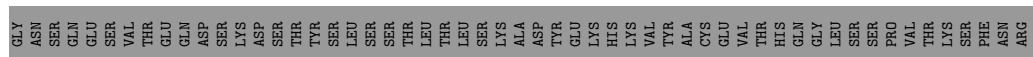
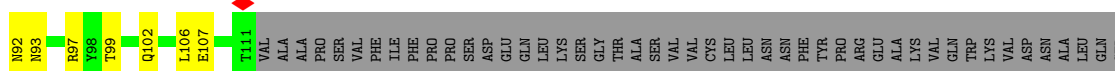
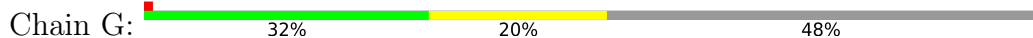




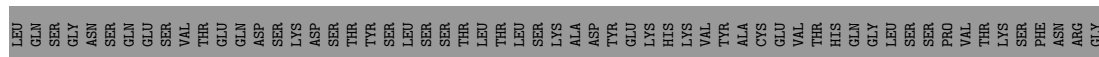
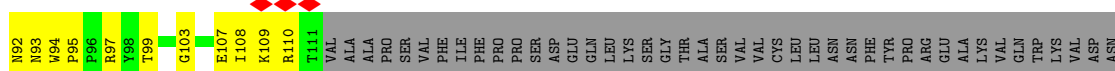
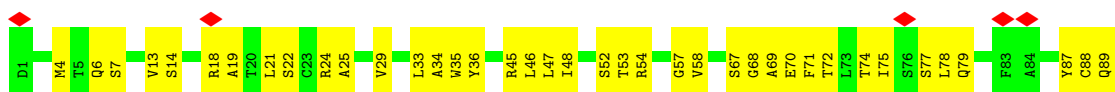
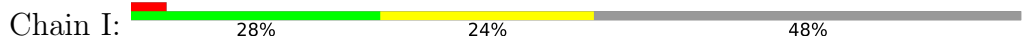
• Molecule 2: HIV-1 Envelope Glycoprotein BG505 SOSIP.664 gp41



• Molecule 3: 17b Fab Light Chain

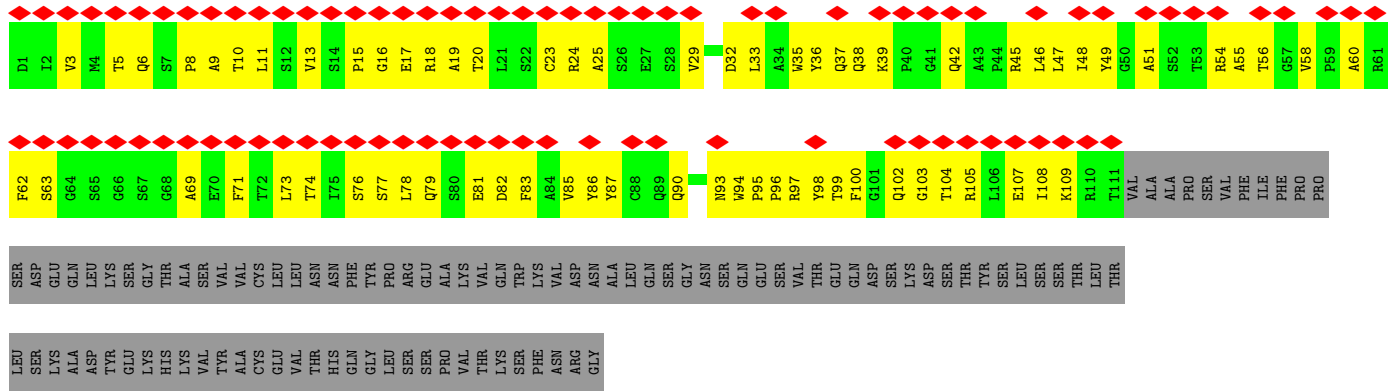


• Molecule 3: 17b Fab Light Chain

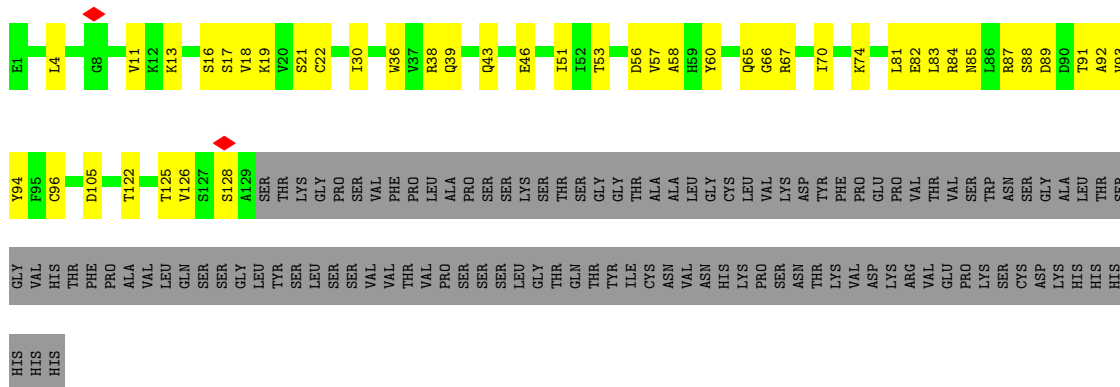
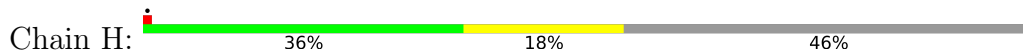


• Molecule 3: 17b Fab Light Chain

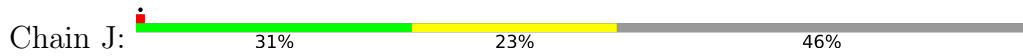




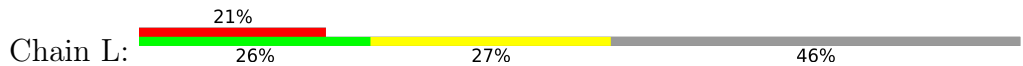
● Molecule 4: 17b Fab Heavy Chain

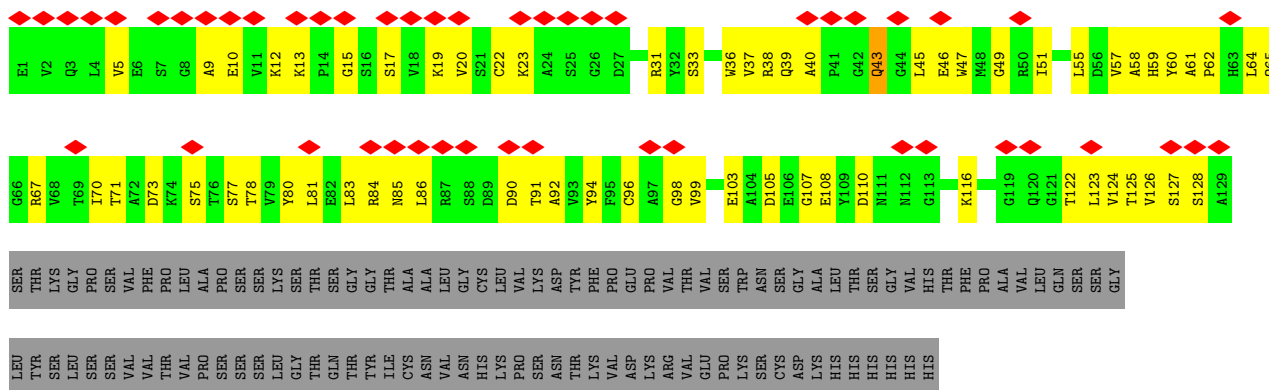


● Molecule 4: 17b Fab Heavy Chain



● Molecule 4: 17b Fab Heavy Chain





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

Chain M: 100%

MAG1
MAG2

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

Chain O: 50%

MAG1
MAG2

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

Chain Q: 50%

MAG1
MAG2

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

Chain R: 50%

MAG1
MAG2

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

Chain T: 50%



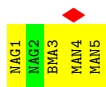
- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



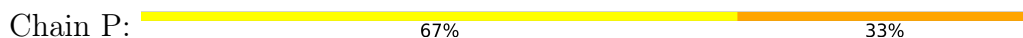
- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



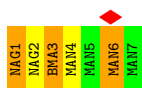
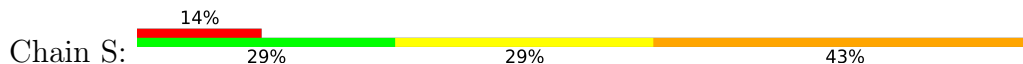
- Molecule 6: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 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



- Molecule 8: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	662861	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	0.079	Depositor
Minimum map value	-0.041	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.013	Depositor
Map size (Å)	282.624, 282.624, 282.624	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.104, 1.104, 1.104	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: BMA, MAN, NAG, 5VG

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	0.41	0/2904	0.52	0/3946
1	C	0.60	0/2912	0.58	1/3957 (0.0%)
1	E	0.74	1/2926 (0.0%)	0.62	1/3976 (0.0%)
2	B	0.45	0/1046	0.50	0/1420
2	D	0.54	0/1069	0.57	0/1450
2	F	0.59	0/979	0.56	0/1327
3	G	0.50	0/873	0.55	0/1187
3	I	0.42	0/870	0.52	0/1183
3	K	0.31	0/867	0.55	0/1180
4	H	0.51	0/1017	0.52	0/1380
4	J	0.48	0/1017	0.53	0/1380
4	L	0.31	0/1017	0.50	0/1380
All	All	0.54	1/17497 (0.0%)	0.56	2/23766 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	54	CYS	CB-SG	-5.21	1.73	1.81

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	116	LEU	C-N-CA	-5.73	107.37	121.70
1	E	54	CYS	CA-CB-SG	5.67	124.22	114.00

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	2840	0	2771	112	0
1	C	2848	0	2776	102	0
1	E	2862	0	2799	94	0
2	B	1026	0	1009	31	0
2	D	1049	0	1034	33	0
2	F	960	0	931	32	0
3	G	853	0	825	34	0
3	I	850	0	823	34	0
3	K	847	0	814	62	0
4	H	996	0	962	35	0
4	J	996	0	962	44	0
4	L	996	0	962	67	0
5	M	28	0	25	0	0
5	O	28	0	25	1	0
5	Q	28	0	25	2	0
5	R	28	0	25	2	0
5	T	28	0	25	1	0
5	U	28	0	25	1	0
5	V	28	0	25	2	0
6	N	61	0	52	3	0
7	P	72	0	61	3	0
8	S	83	0	70	4	0
9	A	112	0	104	7	0
9	C	112	0	104	5	0
9	D	14	0	13	0	0
9	E	112	0	104	4	0
9	F	28	0	26	0	0
10	A	31	0	0	2	0
10	C	31	0	0	1	0
10	E	31	0	0	1	0
All	All	18006	0	17377	662	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 19.

The worst 5 of 662 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:C:259:LEU:HD13	1:C:449:ILE:HD13	1.20	1.10
1:C:259:LEU:HD13	1:C:449:ILE:CD1	1.84	1.08
1:C:259:LEU:HD22	1:C:449:ILE:HG21	1.39	1.00
1:C:218:CYS:HA	1:C:247:CYS:HB3	1.45	0.96
4:J:94:TYR:O	4:J:121:GLY:HA2	1.70	0.92

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	353/479 (74%)	305 (86%)	48 (14%)	0	100	100
1	C	354/479 (74%)	314 (89%)	40 (11%)	0	100	100
1	E	355/479 (74%)	297 (84%)	58 (16%)	0	100	100
2	B	128/153 (84%)	110 (86%)	18 (14%)	0	100	100
2	D	130/153 (85%)	113 (87%)	17 (13%)	0	100	100
2	F	116/153 (76%)	97 (84%)	19 (16%)	0	100	100
3	G	109/214 (51%)	96 (88%)	12 (11%)	1 (1%)	17	54
3	I	109/214 (51%)	101 (93%)	8 (7%)	0	100	100
3	K	109/214 (51%)	92 (84%)	17 (16%)	0	100	100
4	H	127/239 (53%)	120 (94%)	7 (6%)	0	100	100
4	J	127/239 (53%)	111 (87%)	16 (13%)	0	100	100
4	L	127/239 (53%)	111 (87%)	16 (13%)	0	100	100
All	All	2144/3255 (66%)	1867 (87%)	276 (13%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	30	SER

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	321/427 (75%)	319 (99%)	2 (1%)	86	91
1	C	322/427 (75%)	320 (99%)	2 (1%)	86	91
1	E	324/427 (76%)	322 (99%)	2 (1%)	86	91
2	B	107/129 (83%)	105 (98%)	2 (2%)	57	75
2	D	110/129 (85%)	110 (100%)	0	100	100
2	F	103/129 (80%)	102 (99%)	1 (1%)	76	86
3	G	92/184 (50%)	92 (100%)	0	100	100
3	I	91/184 (50%)	91 (100%)	0	100	100
3	K	91/184 (50%)	91 (100%)	0	100	100
4	H	106/203 (52%)	106 (100%)	0	100	100
4	J	106/203 (52%)	106 (100%)	0	100	100
4	L	106/203 (52%)	105 (99%)	1 (1%)	78	87
All	All	1879/2829 (66%)	1869 (100%)	10 (0%)	89	93

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	301	ASN
2	F	658	GLN
4	L	43	GLN
2	B	610	TRP
1	C	203	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	422	GLN
3	G	79	GLN
3	G	6	GLN
3	G	102	GLN
1	C	374	HIS

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](#)

32 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	NAG	M	1	1,5	14,14,15	0.56	0	17,19,21	0.48	0
5	NAG	M	2	5	14,14,15	0.19	0	17,19,21	0.55	0
6	NAG	N	1	6,1	14,14,15	0.28	0	17,19,21	0.65	0
6	NAG	N	2	6	14,14,15	0.29	0	17,19,21	0.87	0
6	BMA	N	3	6	11,11,12	0.52	0	15,15,17	1.34	1 (6%)
6	MAN	N	4	6	11,11,12	0.25	0	15,15,17	0.81	0
6	MAN	N	5	6	11,11,12	0.32	0	15,15,17	0.82	0
5	NAG	O	1	1,5	14,14,15	0.67	1 (7%)	17,19,21	0.49	0
5	NAG	O	2	5	14,14,15	0.28	0	17,19,21	0.38	0
7	NAG	P	1	1,7	14,14,15	0.67	1 (7%)	17,19,21	0.46	0
7	NAG	P	2	7	14,14,15	0.47	0	17,19,21	0.62	0
7	BMA	P	3	7	11,11,12	1.08	1 (9%)	15,15,17	1.07	1 (6%)
7	MAN	P	4	7	11,11,12	1.54	1 (9%)	15,15,17	1.92	4 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	MAN	P	5	7	11,11,12	1.39	1 (9%)	15,15,17	1.14	1 (6%)
7	MAN	P	6	7	11,11,12	0.90	0	15,15,17	1.03	0
5	NAG	Q	1	1,5	14,14,15	0.40	0	17,19,21	1.29	2 (11%)
5	NAG	Q	2	5	14,14,15	0.28	0	17,19,21	0.43	0
5	NAG	R	1	1,5	14,14,15	0.63	1 (7%)	17,19,21	0.60	0
5	NAG	R	2	5	14,14,15	0.21	0	17,19,21	0.69	0
8	NAG	S	1	8,1	14,14,15	0.31	0	17,19,21	1.05	2 (11%)
8	NAG	S	2	8	14,14,15	0.30	0	17,19,21	0.99	1 (5%)
8	BMA	S	3	8	11,11,12	0.39	0	15,15,17	1.37	3 (20%)
8	MAN	S	4	8	11,11,12	0.25	0	15,15,17	1.09	2 (13%)
8	MAN	S	5	8	11,11,12	0.24	0	15,15,17	0.90	0
8	MAN	S	6	8	11,11,12	0.33	0	15,15,17	0.95	1 (6%)
8	MAN	S	7	8	11,11,12	0.24	0	15,15,17	0.93	0
5	NAG	T	1	1,5	14,14,15	0.41	0	17,19,21	0.46	0
5	NAG	T	2	5	14,14,15	0.18	0	17,19,21	0.46	0
5	NAG	U	1	1,5	14,14,15	0.58	1 (7%)	17,19,21	0.62	0
5	NAG	U	2	5	14,14,15	0.25	0	17,19,21	0.37	0
5	NAG	V	1	1,5	14,14,15	0.79	1 (7%)	17,19,21	0.54	0
5	NAG	V	2	5	14,14,15	0.32	0	17,19,21	0.50	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	M	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	M	2	5	-	3/6/23/26	0/1/1/1
6	NAG	N	1	6,1	-	2/6/23/26	0/1/1/1
6	NAG	N	2	6	-	3/6/23/26	0/1/1/1
6	BMA	N	3	6	-	0/2/19/22	0/1/1/1
6	MAN	N	4	6	-	2/2/19/22	0/1/1/1
6	MAN	N	5	6	-	1/2/19/22	0/1/1/1
5	NAG	O	1	1,5	-	4/6/23/26	0/1/1/1
5	NAG	O	2	5	-	3/6/23/26	0/1/1/1
7	NAG	P	1	1,7	-	3/6/23/26	0/1/1/1
7	NAG	P	2	7	-	4/6/23/26	0/1/1/1
7	BMA	P	3	7	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MAN	P	4	7	-	2/2/19/22	0/1/1/1
7	MAN	P	5	7	-	2/2/19/22	0/1/1/1
7	MAN	P	6	7	-	1/2/19/22	0/1/1/1
5	NAG	Q	1	1,5	-	5/6/23/26	0/1/1/1
5	NAG	Q	2	5	-	2/6/23/26	0/1/1/1
5	NAG	R	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	R	2	5	-	3/6/23/26	0/1/1/1
8	NAG	S	1	8,1	-	3/6/23/26	0/1/1/1
8	NAG	S	2	8	-	0/6/23/26	0/1/1/1
8	BMA	S	3	8	-	0/2/19/22	0/1/1/1
8	MAN	S	4	8	-	2/2/19/22	0/1/1/1
8	MAN	S	5	8	-	0/2/19/22	0/1/1/1
8	MAN	S	6	8	-	0/2/19/22	0/1/1/1
8	MAN	S	7	8	-	1/2/19/22	0/1/1/1
5	NAG	T	1	1,5	-	3/6/23/26	0/1/1/1
5	NAG	T	2	5	-	2/6/23/26	0/1/1/1
5	NAG	U	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	U	2	5	-	2/6/23/26	0/1/1/1
5	NAG	V	1	1,5	-	3/6/23/26	0/1/1/1
5	NAG	V	2	5	-	3/6/23/26	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	P	4	MAN	C2-C3	-4.02	1.46	1.52
7	P	5	MAN	O5-C1	-3.63	1.37	1.43
5	V	1	NAG	O5-C1	-2.78	1.39	1.43
5	O	1	NAG	O5-C1	-2.27	1.40	1.43
7	P	3	BMA	O5-C1	-2.20	1.40	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	P	4	MAN	O2-C2-C3	-4.84	100.44	110.14
5	Q	1	NAG	C2-N2-C7	4.18	128.85	122.90
7	P	4	MAN	C1-O5-C5	3.81	117.36	112.19
7	P	5	MAN	O2-C2-C3	-3.23	103.67	110.14
7	P	4	MAN	C2-C3-C4	-2.89	105.89	110.89

There are no chirality outliers.

5 of 67 torsion outliers are listed below:

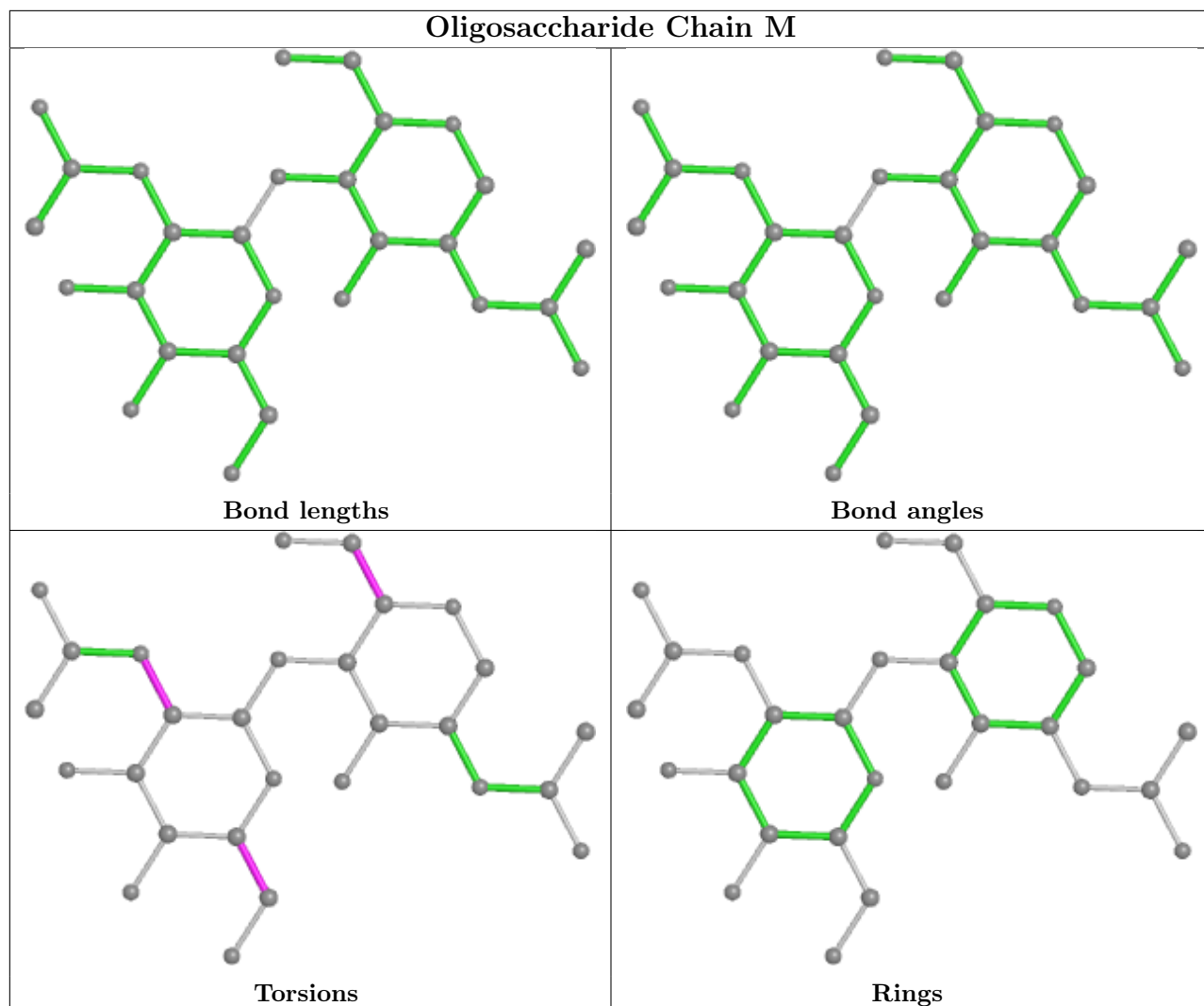
Mol	Chain	Res	Type	Atoms
6	N	2	NAG	C3-C2-N2-C7
6	N	2	NAG	C8-C7-N2-C2
6	N	2	NAG	O7-C7-N2-C2
8	S	1	NAG	C3-C2-N2-C7
5	M	2	NAG	C4-C5-C6-O6

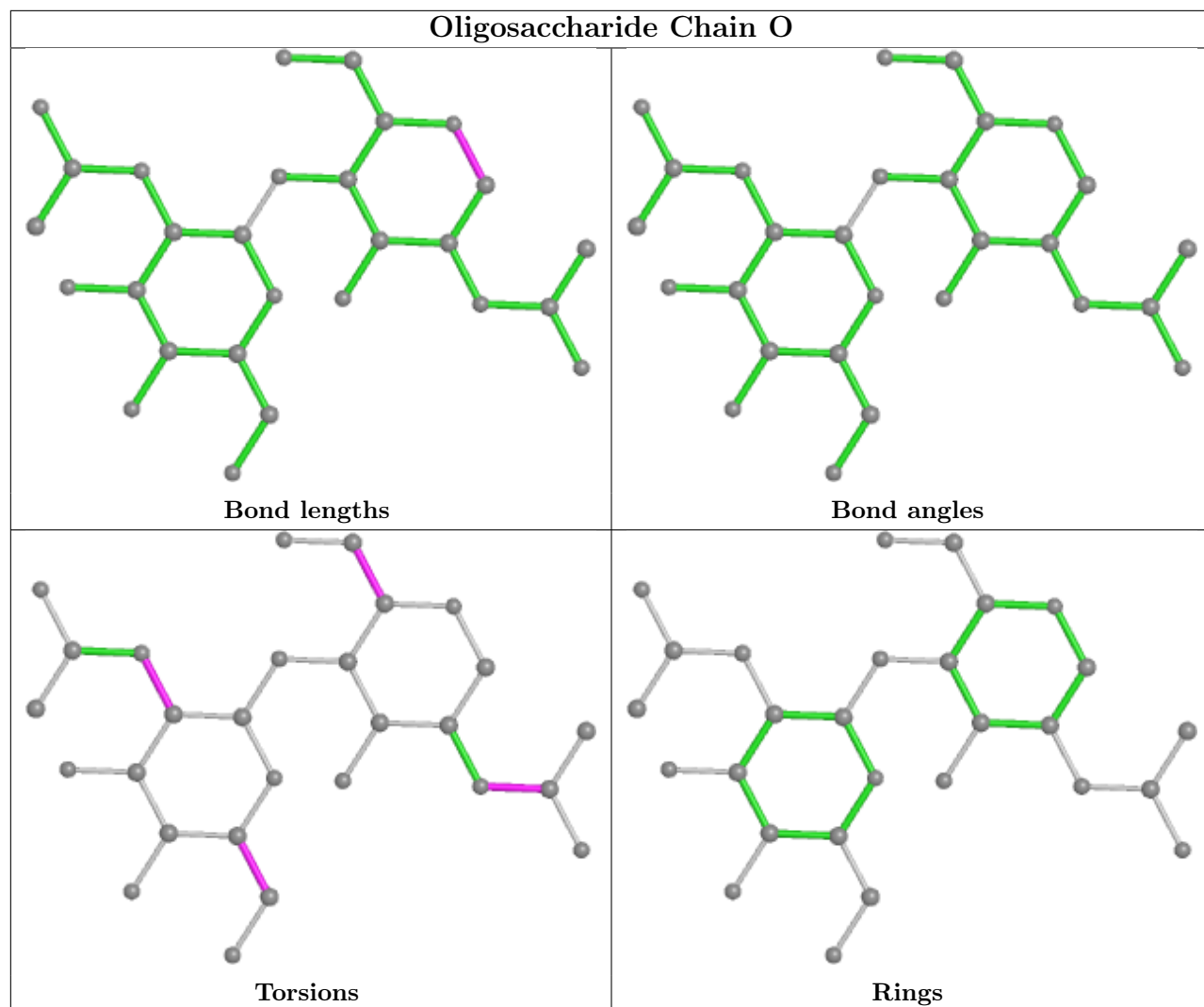
There are no ring outliers.

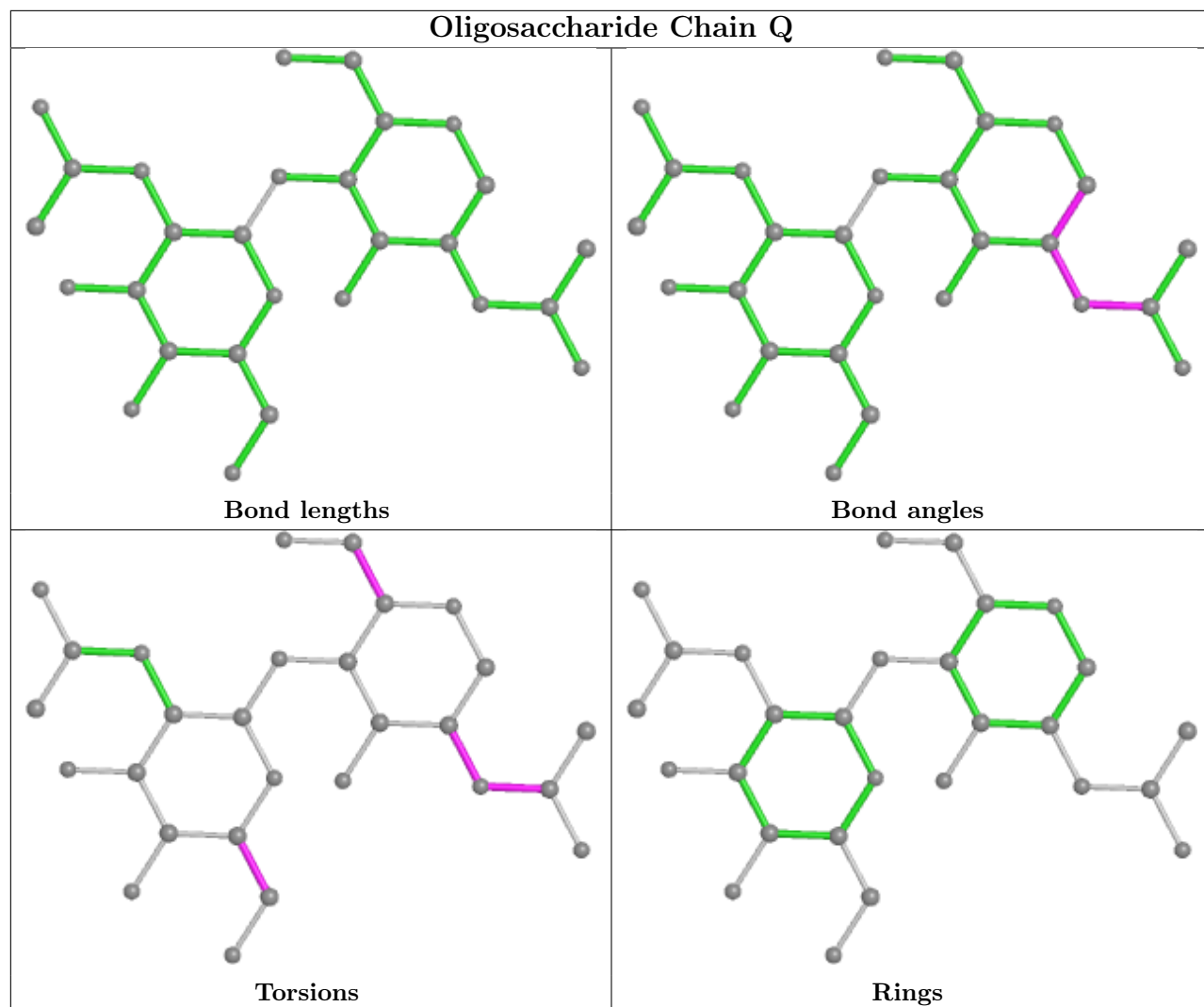
17 monomers are involved in 19 short contacts:

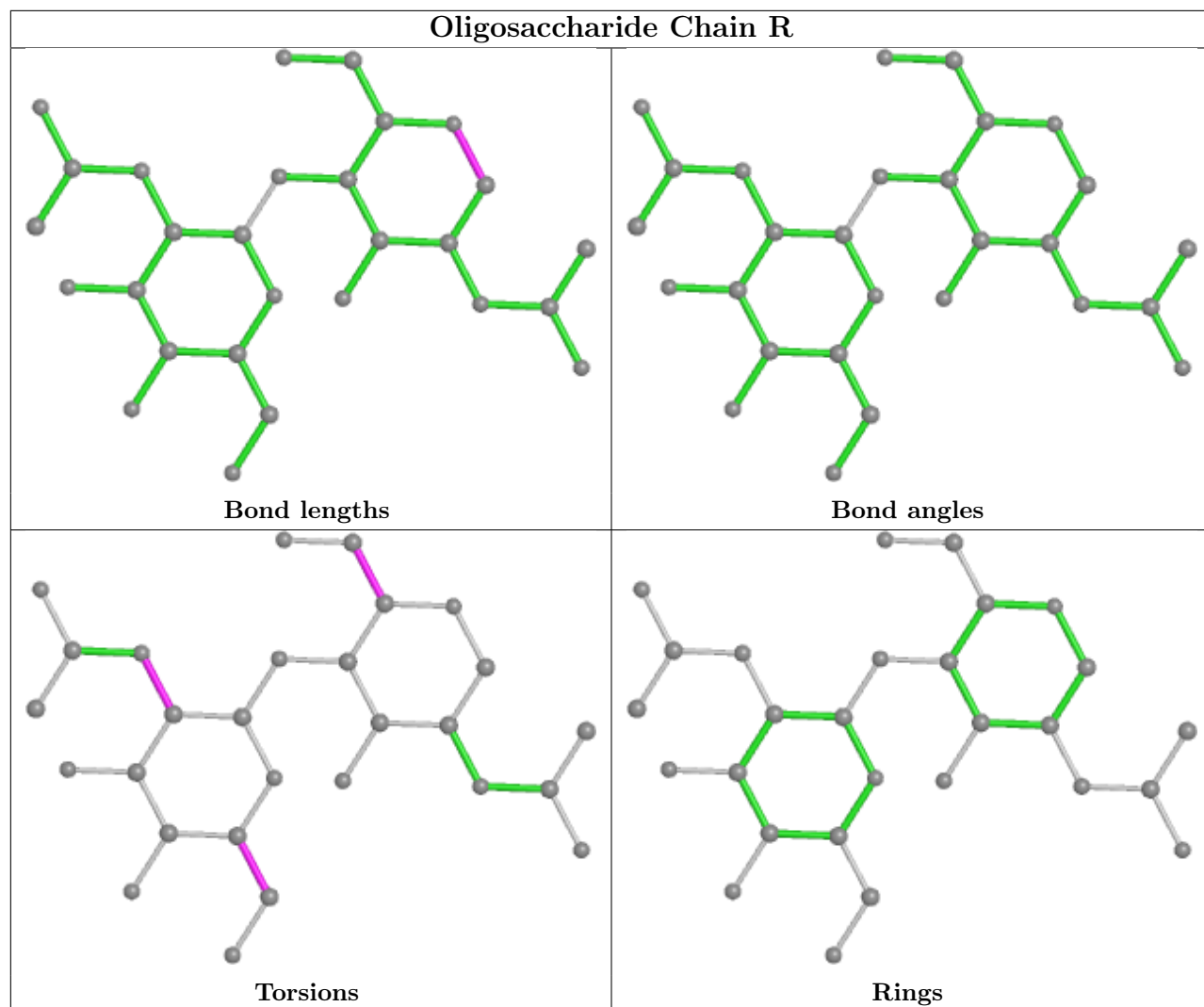
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	V	1	NAG	2	0
7	P	1	NAG	1	0
5	U	1	NAG	1	0
5	O	1	NAG	1	0
6	N	1	NAG	2	0
5	R	1	NAG	1	0
5	R	2	NAG	1	0
6	N	4	MAN	1	0
7	P	6	MAN	1	0
8	S	6	MAN	1	0
7	P	2	NAG	1	0
8	S	3	BMA	1	0
7	P	3	BMA	1	0
8	S	1	NAG	3	0
5	Q	1	NAG	2	0
5	T	1	NAG	1	0
6	N	5	MAN	1	0

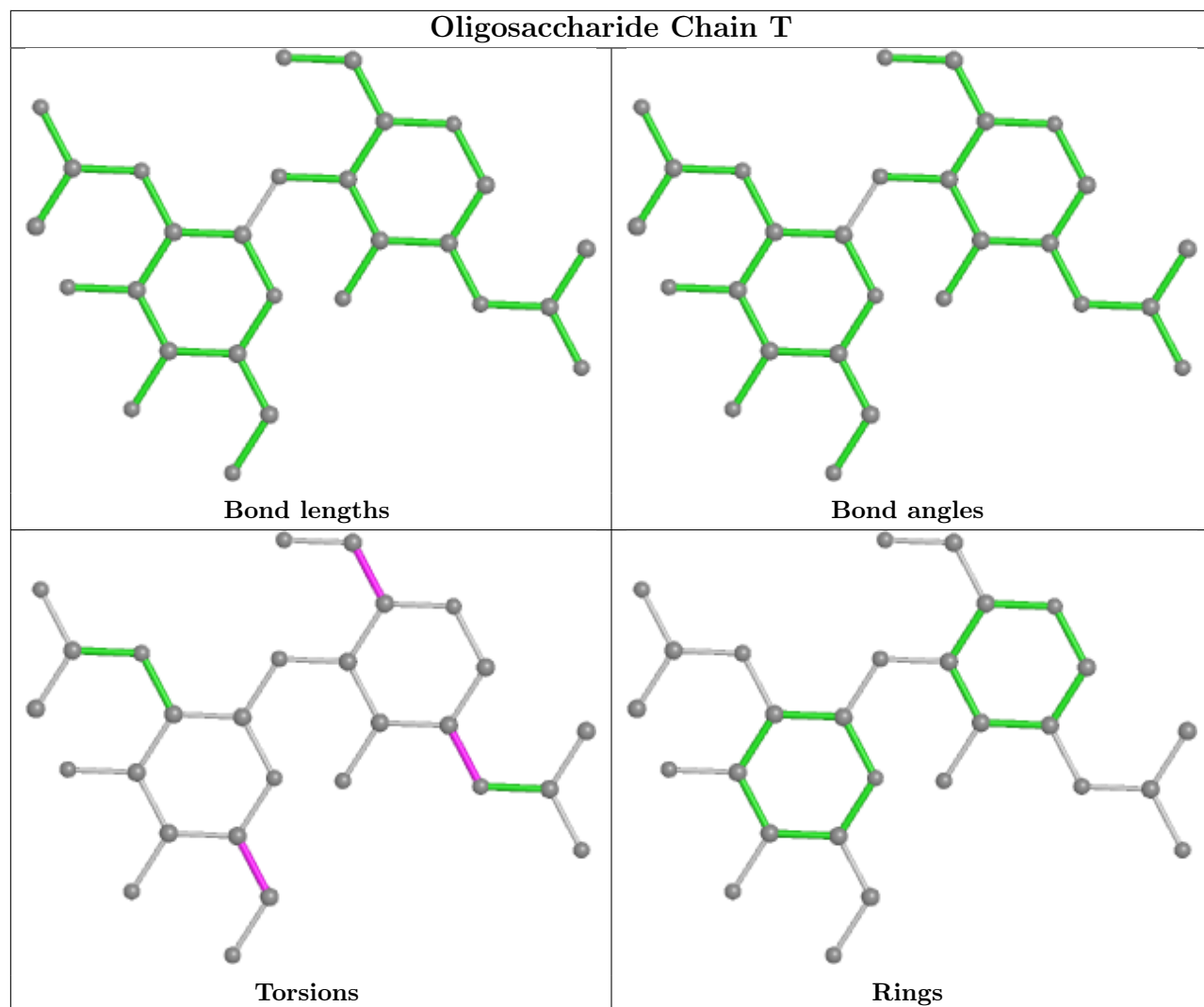
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

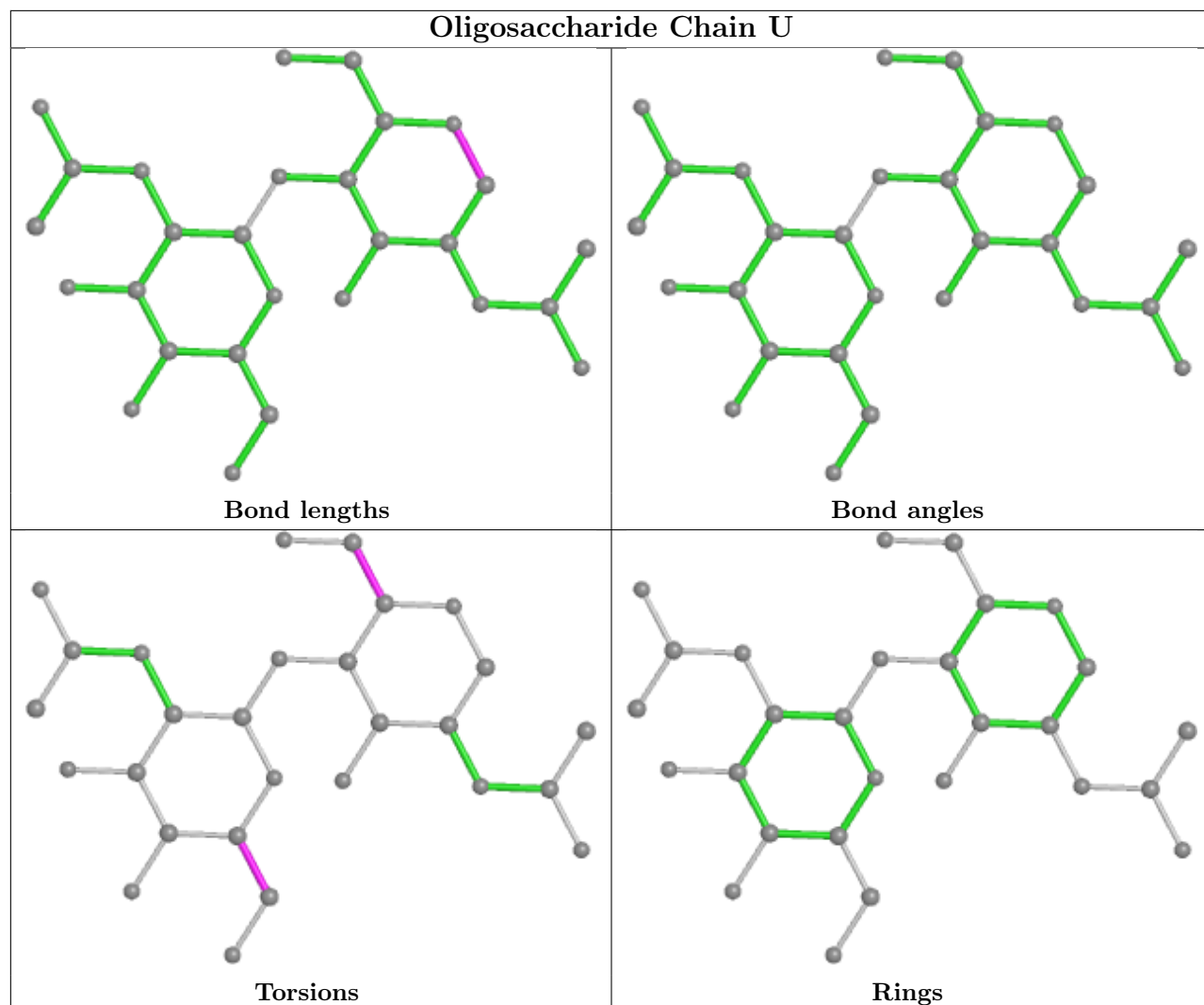


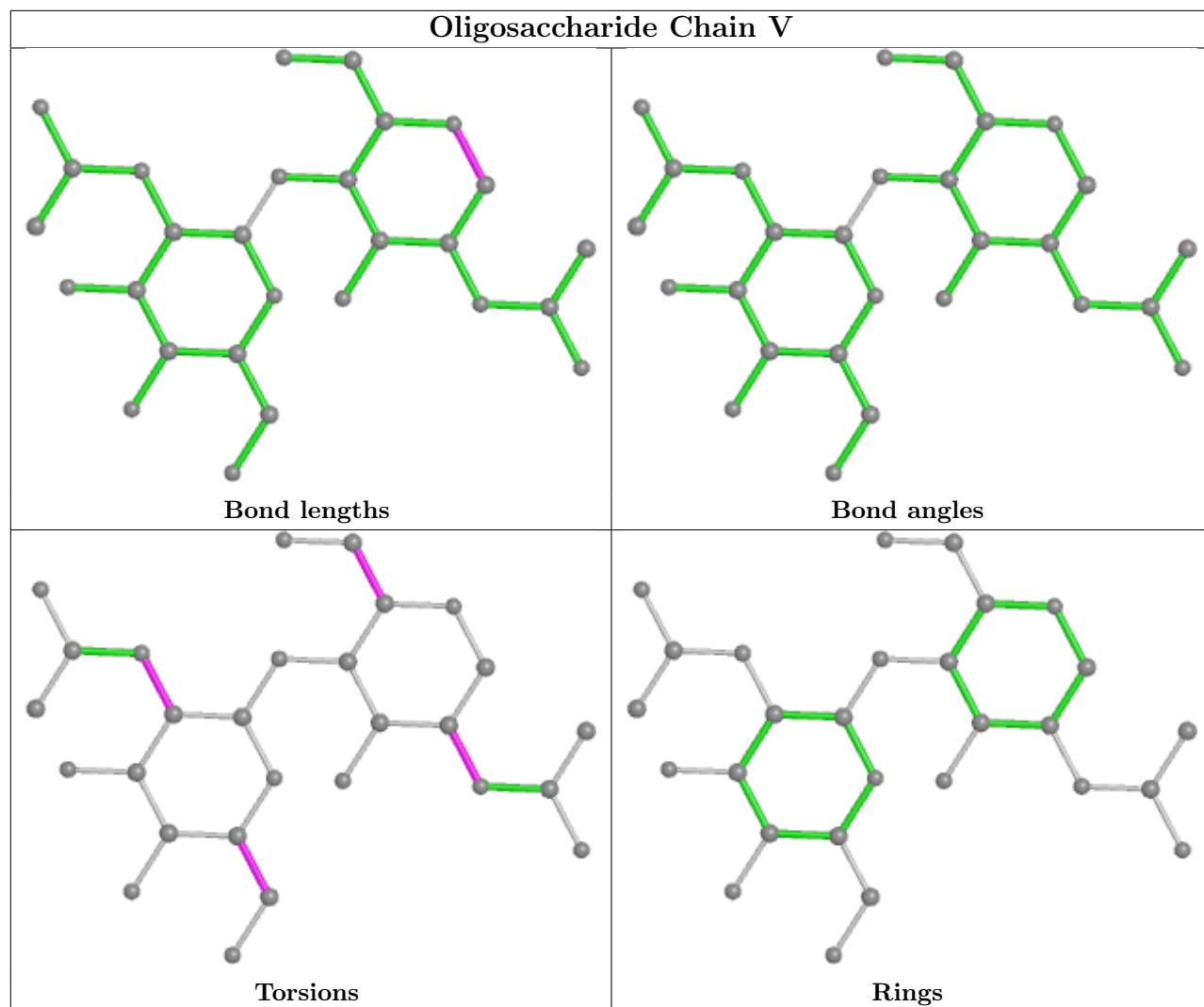


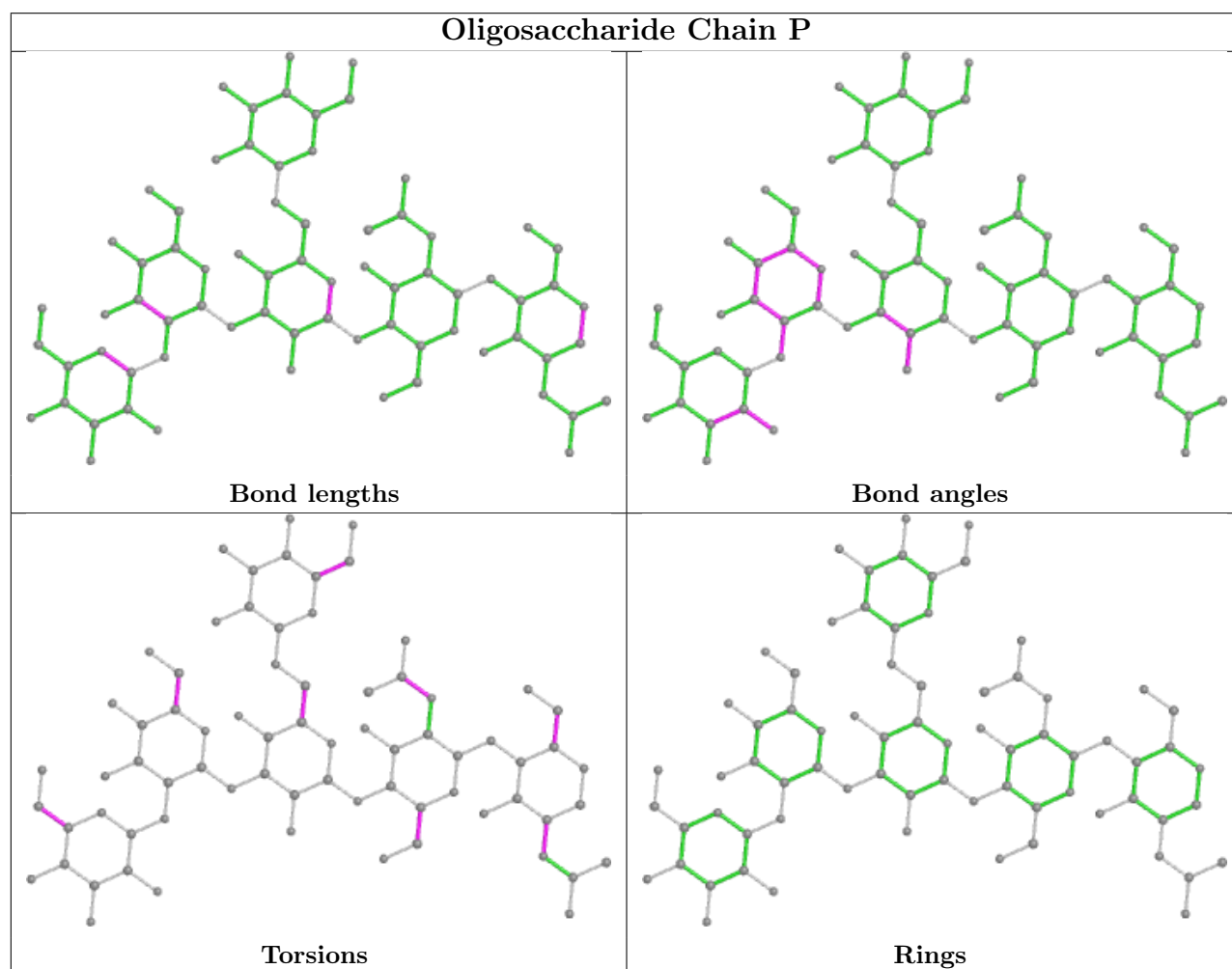
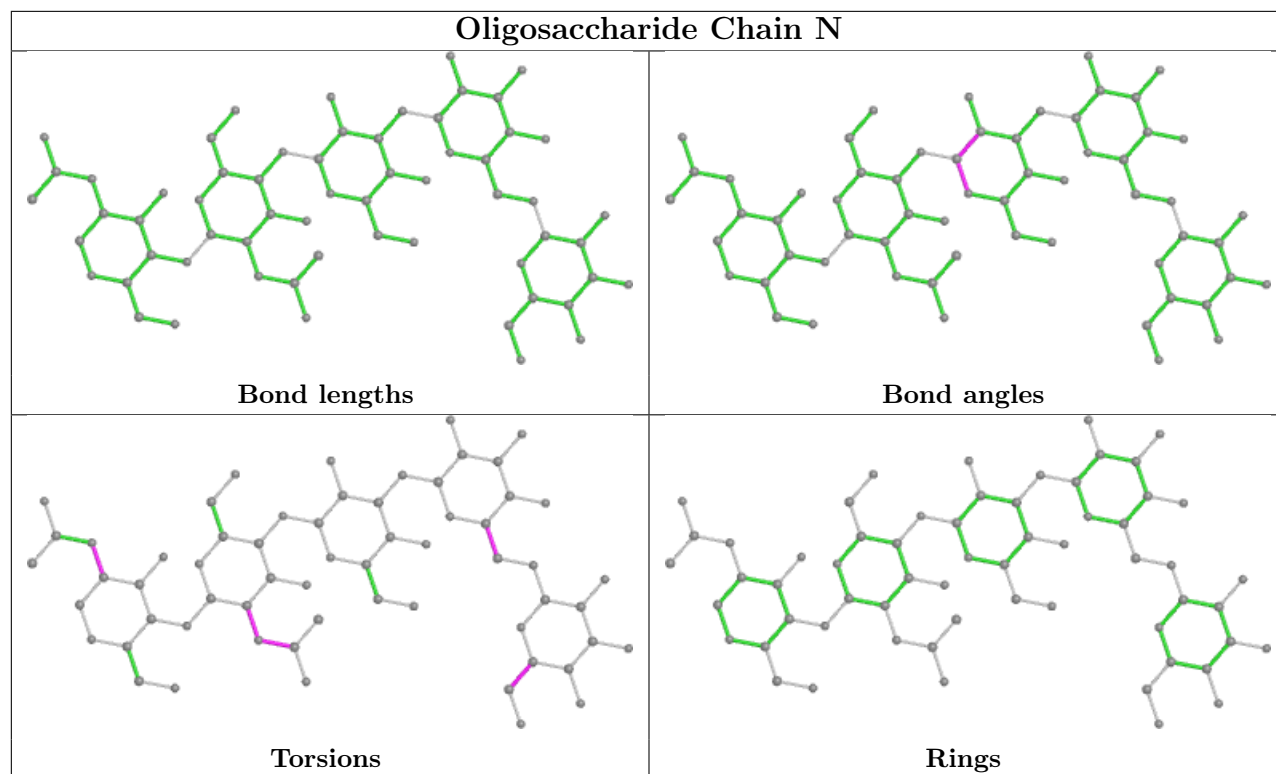


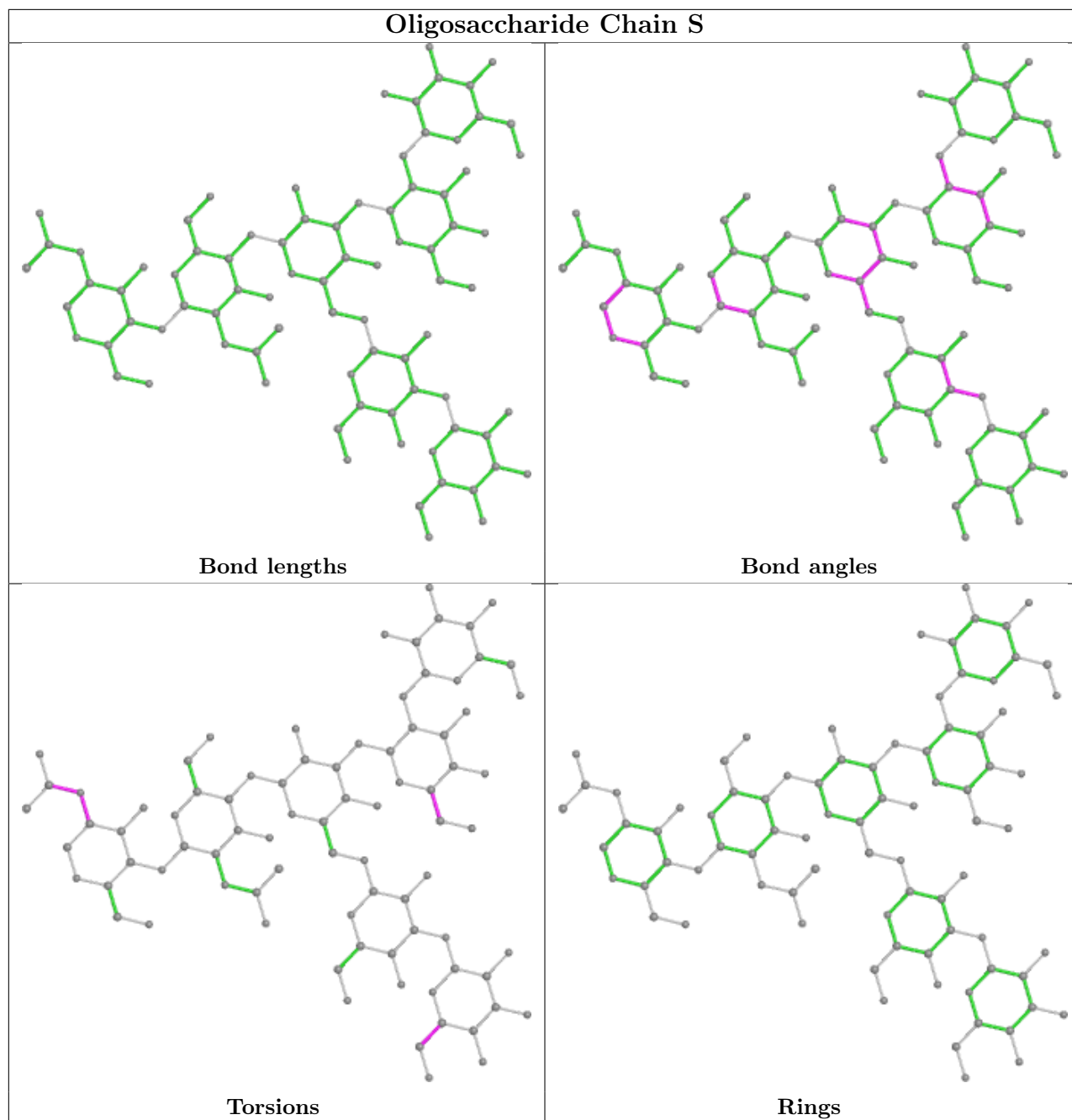












5.6 Ligand geometry [i](#)

30 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
9	NAG	E	603	1	14,14,15	0.32	0	17,19,21	0.48	0
9	NAG	C	602	1	14,14,15	0.90	1 (7%)	17,19,21	0.97	1 (5%)
9	NAG	E	602	1	14,14,15	0.27	0	17,19,21	0.37	0
9	NAG	A	603	1	14,14,15	0.74	1 (7%)	17,19,21	0.63	0
9	NAG	C	606	1	14,14,15	0.26	0	17,19,21	0.62	0
10	5VG	A	609	-	33,33,33	2.34	11 (33%)	40,46,46	1.98	10 (25%)
9	NAG	A	601	1	14,14,15	0.26	0	17,19,21	0.51	0
9	NAG	E	606	1	14,14,15	0.24	0	17,19,21	0.51	0
9	NAG	C	604	1	14,14,15	0.32	0	17,19,21	1.26	1 (5%)
9	NAG	D	701	2	14,14,15	0.24	0	17,19,21	0.36	0
9	NAG	C	601	1	14,14,15	0.16	0	17,19,21	0.66	1 (5%)
9	NAG	E	604	1	14,14,15	0.41	0	17,19,21	1.55	3 (17%)
9	NAG	A	608	1	14,14,15	0.20	0	17,19,21	0.49	0
10	5VG	E	609	-	33,33,33	2.37	12 (36%)	40,46,46	2.07	14 (35%)
9	NAG	A	604	1	14,14,15	0.26	0	17,19,21	0.41	0
9	NAG	E	605	1	14,14,15	0.27	0	17,19,21	0.46	0
9	NAG	E	601	1	14,14,15	0.37	0	17,19,21	0.58	0
9	NAG	A	602	1	14,14,15	0.50	0	17,19,21	1.21	1 (5%)
9	NAG	E	608	1	14,14,15	0.27	0	17,19,21	0.49	0
9	NAG	C	603	1	14,14,15	0.17	0	17,19,21	0.43	0
9	NAG	C	605	1	14,14,15	0.22	0	17,19,21	0.41	0
9	NAG	A	605	1	14,14,15	0.33	0	17,19,21	1.25	1 (5%)
9	NAG	F	702	2	14,14,15	0.31	0	17,19,21	0.38	0
9	NAG	A	607	1	14,14,15	0.26	0	17,19,21	0.57	0
10	5VG	C	609	-	33,33,33	2.34	11 (33%)	40,46,46	1.84	10 (25%)
9	NAG	C	608	1	14,14,15	0.29	0	17,19,21	0.81	0
9	NAG	F	701	2	14,14,15	0.29	0	17,19,21	0.83	1 (5%)
9	NAG	C	607	1	14,14,15	0.27	0	17,19,21	0.48	0
9	NAG	E	607	1	14,14,15	0.45	0	17,19,21	0.45	0
9	NAG	A	606	1	14,14,15	0.21	0	17,19,21	0.44	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
9	NAG	E	603	1	-	2/6/23/26	0/1/1/1
9	NAG	C	602	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	E	602	1	-	3/6/23/26	0/1/1/1
9	NAG	A	603	1	-	1/6/23/26	0/1/1/1
9	NAG	C	606	1	-	0/6/23/26	0/1/1/1
10	5VG	A	609	-	-	2/19/32/32	0/3/3/3
9	NAG	A	601	1	-	4/6/23/26	0/1/1/1
9	NAG	E	606	1	-	2/6/23/26	0/1/1/1
9	NAG	C	604	1	-	5/6/23/26	0/1/1/1
9	NAG	D	701	2	-	3/6/23/26	0/1/1/1
9	NAG	C	601	1	-	0/6/23/26	0/1/1/1
9	NAG	E	604	1	-	3/6/23/26	0/1/1/1
9	NAG	A	608	1	-	4/6/23/26	0/1/1/1
10	5VG	E	609	-	-	2/19/32/32	0/3/3/3
9	NAG	A	604	1	-	1/6/23/26	0/1/1/1
9	NAG	E	605	1	-	2/6/23/26	0/1/1/1
9	NAG	E	601	1	-	0/6/23/26	0/1/1/1
9	NAG	A	602	1	-	3/6/23/26	0/1/1/1
9	NAG	E	608	1	-	3/6/23/26	0/1/1/1
9	NAG	C	603	1	-	2/6/23/26	0/1/1/1
9	NAG	C	605	1	-	2/6/23/26	0/1/1/1
9	NAG	A	605	1	-	5/6/23/26	0/1/1/1
9	NAG	F	702	2	-	1/6/23/26	0/1/1/1
9	NAG	A	607	1	-	3/6/23/26	0/1/1/1
10	5VG	C	609	-	-	2/19/32/32	0/3/3/3
9	NAG	C	608	1	-	4/6/23/26	0/1/1/1
9	NAG	F	701	2	-	0/6/23/26	0/1/1/1
9	NAG	C	607	1	-	3/6/23/26	0/1/1/1
9	NAG	E	607	1	-	3/6/23/26	0/1/1/1
9	NAG	A	606	1	-	2/6/23/26	0/1/1/1

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	609	5VG	C02-N03	6.06	1.45	1.33
10	E	609	5VG	C05-C13	-5.55	1.47	1.54
10	C	609	5VG	C05-C13	-5.32	1.47	1.54
10	C	609	5VG	C02-N03	5.24	1.43	1.33
10	C	609	5VG	C15-N14	5.19	1.44	1.34

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	E	609	5VG	C05-C04-N03	-6.16	101.87	112.11
10	A	609	5VG	C12-C13-N14	-5.96	105.05	114.61
10	A	609	5VG	C15-C17-N19	5.47	120.95	112.31
10	C	609	5VG	C05-C04-N03	-4.98	103.85	112.11
10	E	609	5VG	C15-C17-N19	4.85	119.98	112.31

There are no chirality outliers.

5 of 69 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	C	608	NAG	C3-C2-N2-C7
9	C	608	NAG	C8-C7-N2-C2
9	C	608	NAG	O7-C7-N2-C2
10	A	609	5VG	N03-C04-C05-C13
10	A	609	5VG	N03-C04-C05-C06

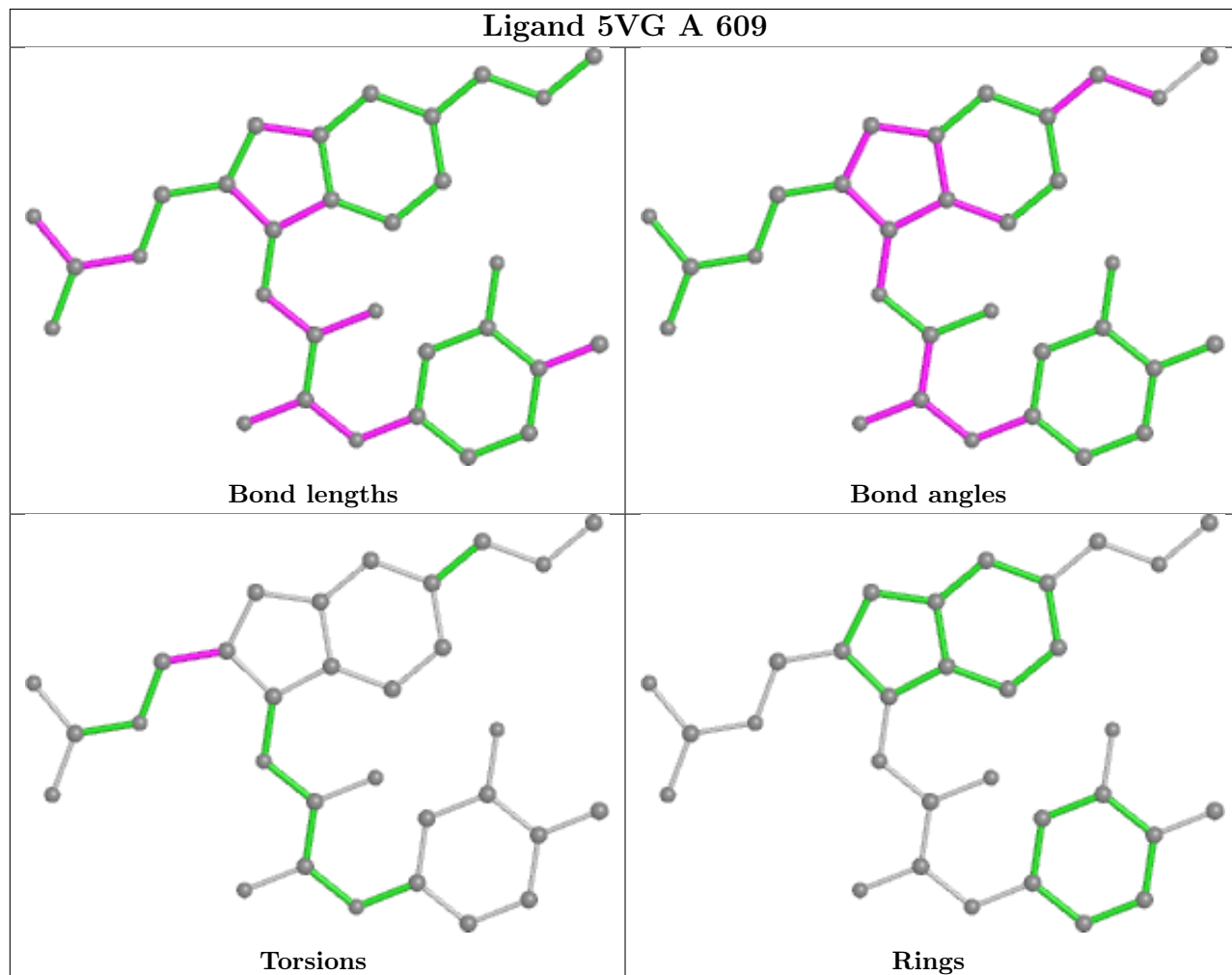
There are no ring outliers.

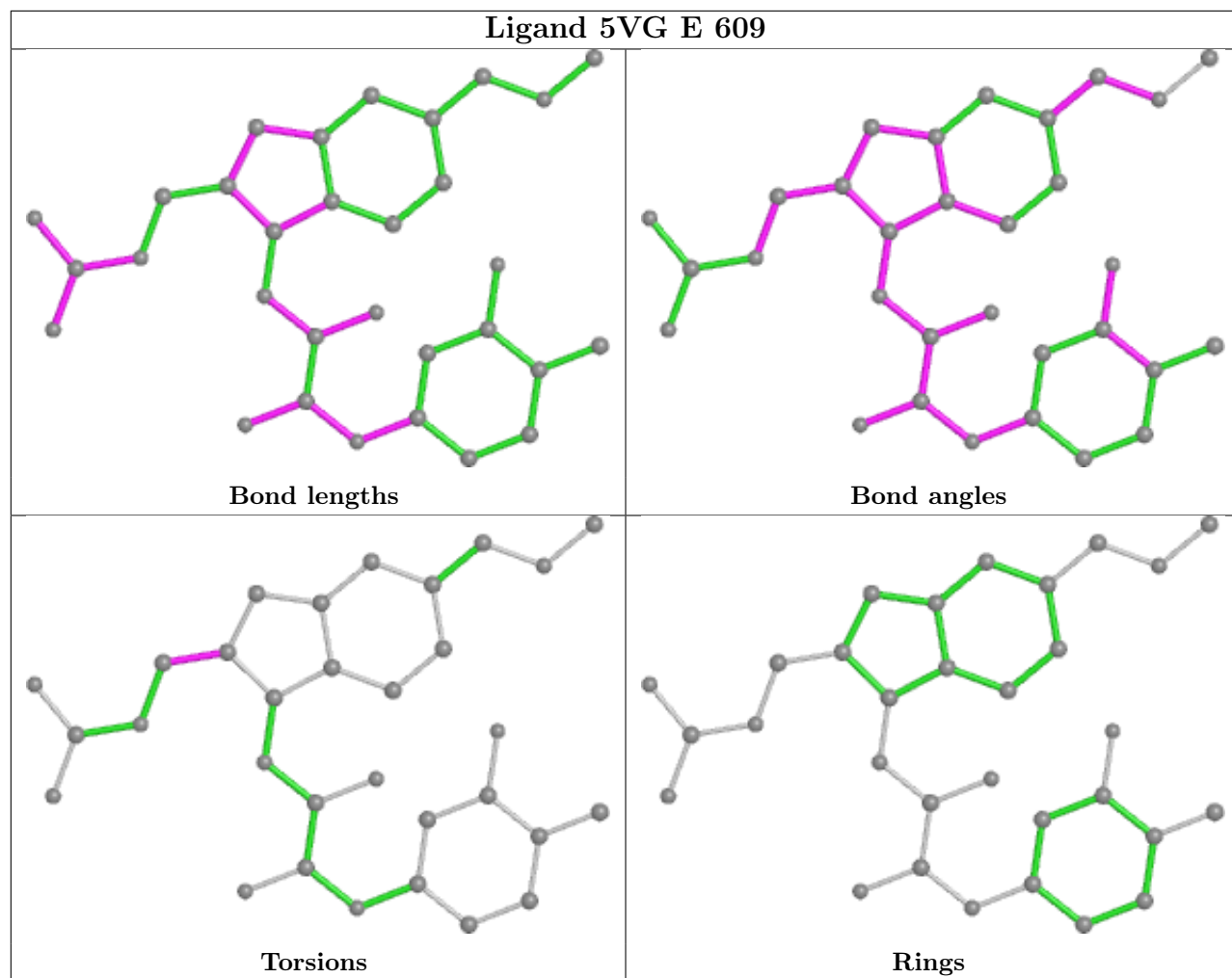
15 monomers are involved in 20 short contacts:

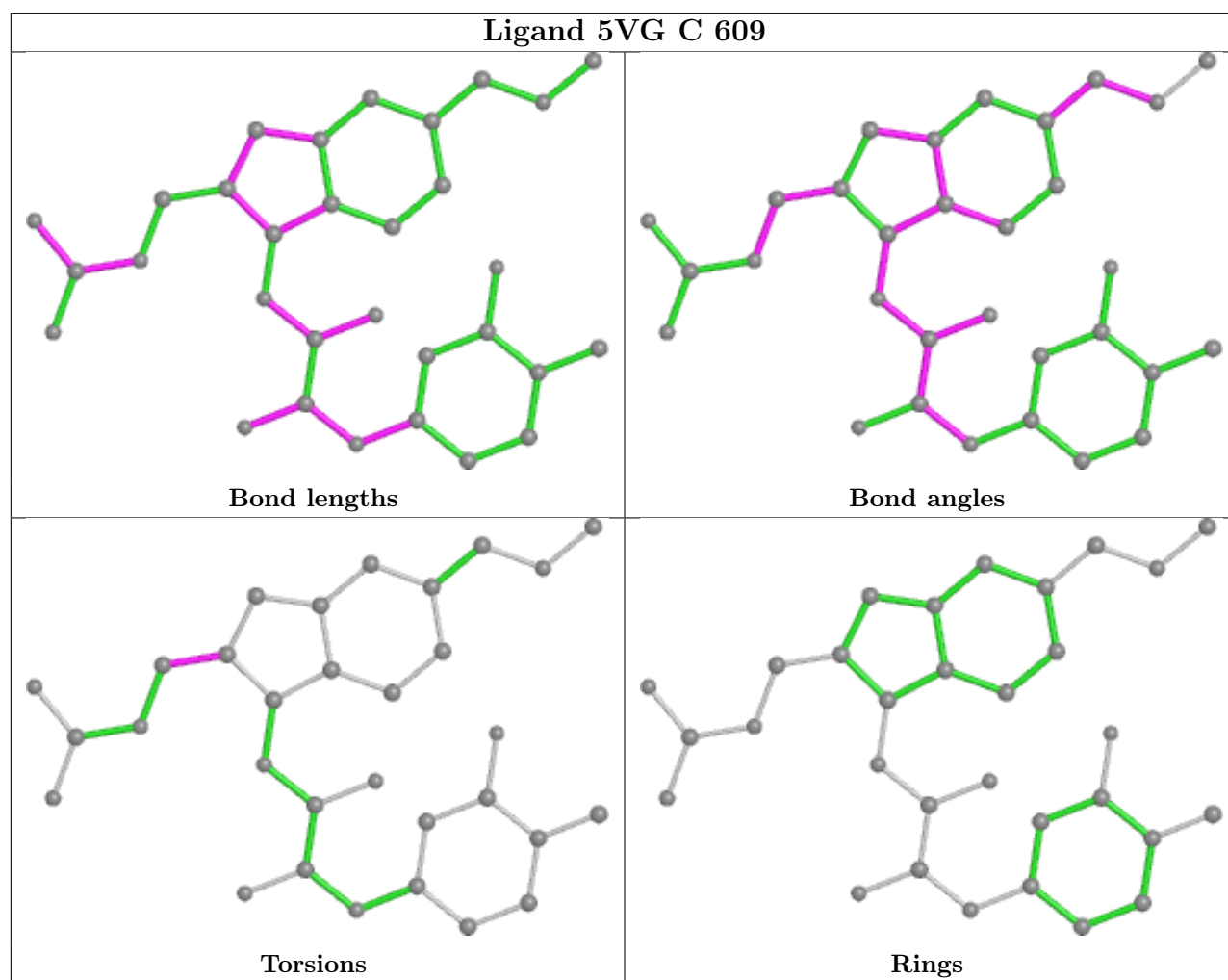
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	603	NAG	1	0
9	C	606	NAG	2	0
10	A	609	5VG	2	0
9	E	606	NAG	2	0
9	C	604	NAG	1	0
9	E	604	NAG	1	0
9	A	608	NAG	1	0
10	E	609	5VG	1	0
9	A	602	NAG	2	0
9	E	608	NAG	1	0
9	A	605	NAG	1	0
9	A	607	NAG	1	0
10	C	609	5VG	1	0
9	C	608	NAG	2	0
9	A	606	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for 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 [i](#)

There are no chain breaks in this entry.

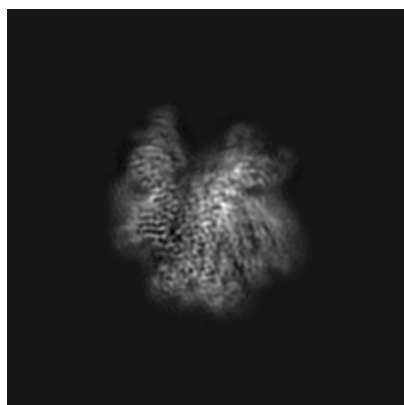
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23462. These allow visual inspection of the internal detail of the map and identification of artifacts.

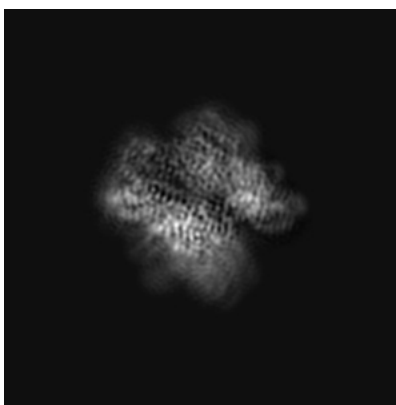
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

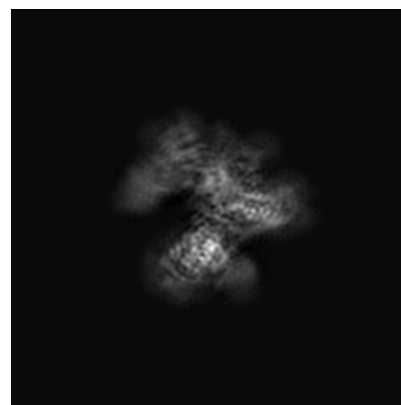
6.1.1 Primary map



X



Y

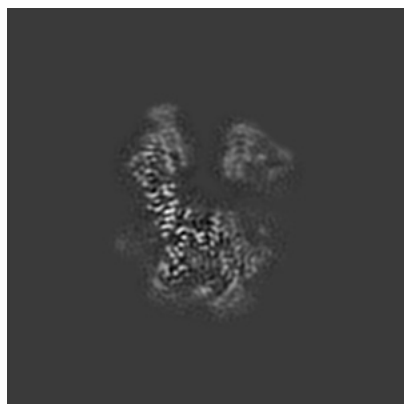


Z

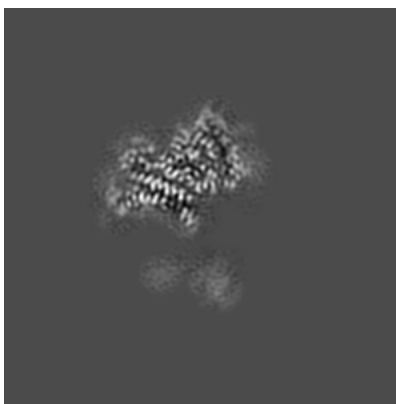
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

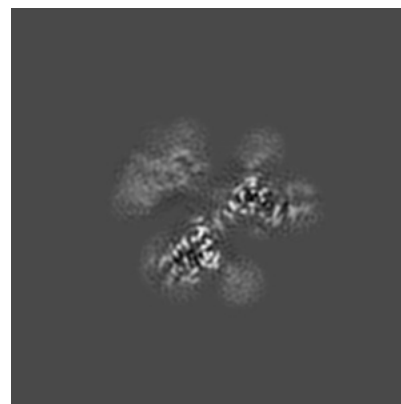
6.2.1 Primary map



X Index: 128



Y Index: 128

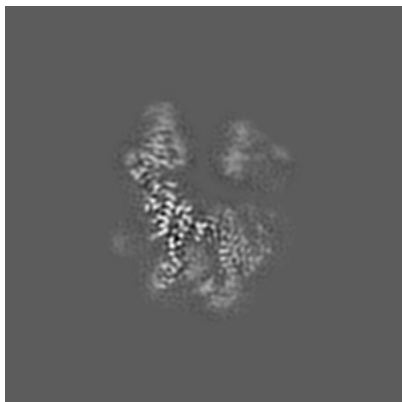


Z Index: 128

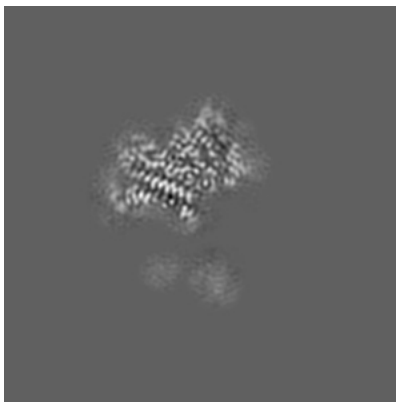
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

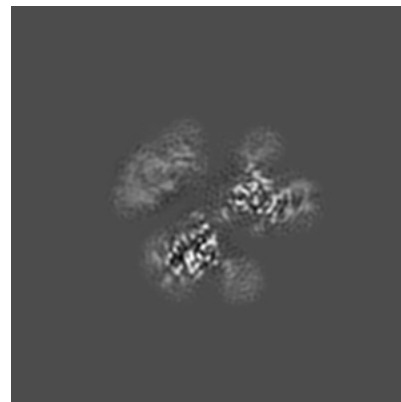
6.3.1 Primary map



X Index: 126



Y Index: 127

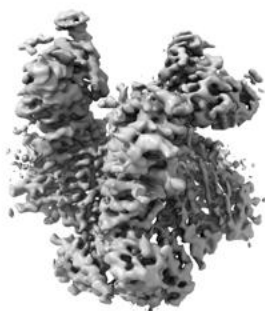


Z Index: 130

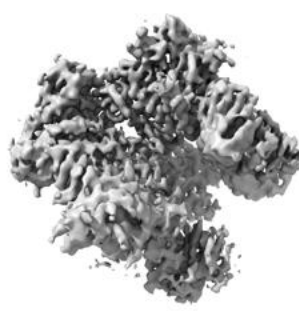
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.013. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

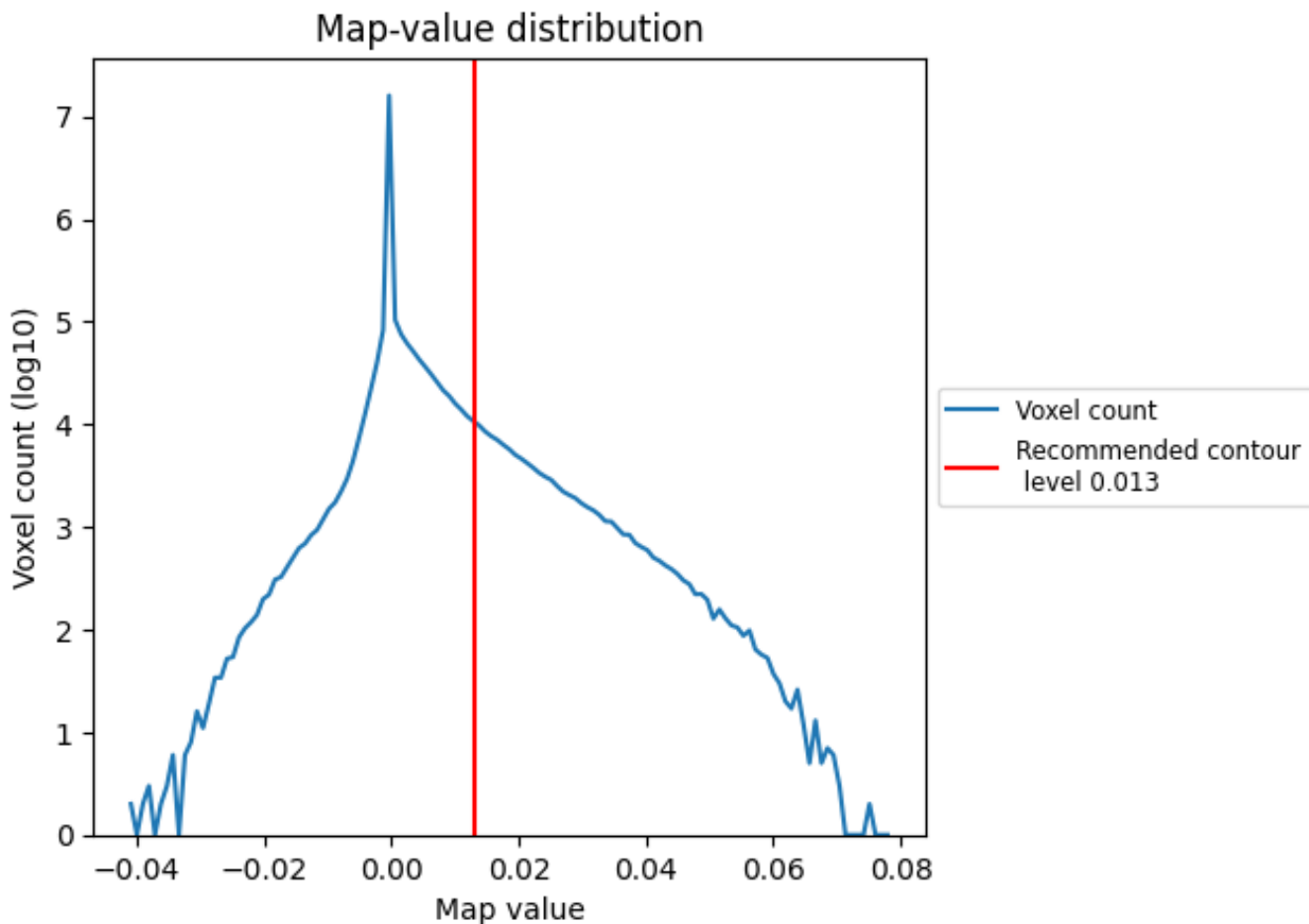
6.5 Mask visualisation

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

7 Map analysis [i](#)

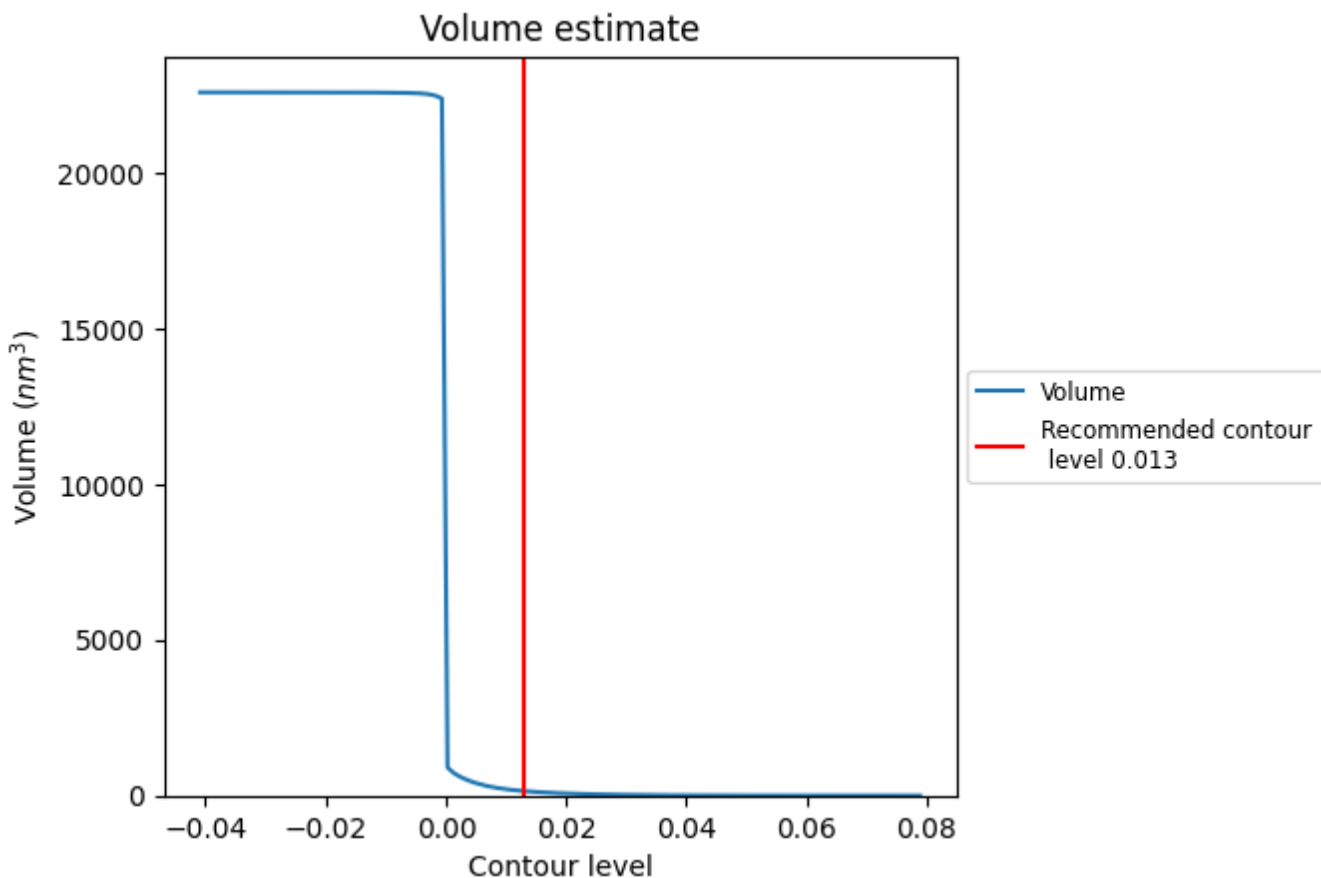
This section contains the results of statistical analysis of the map.

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.

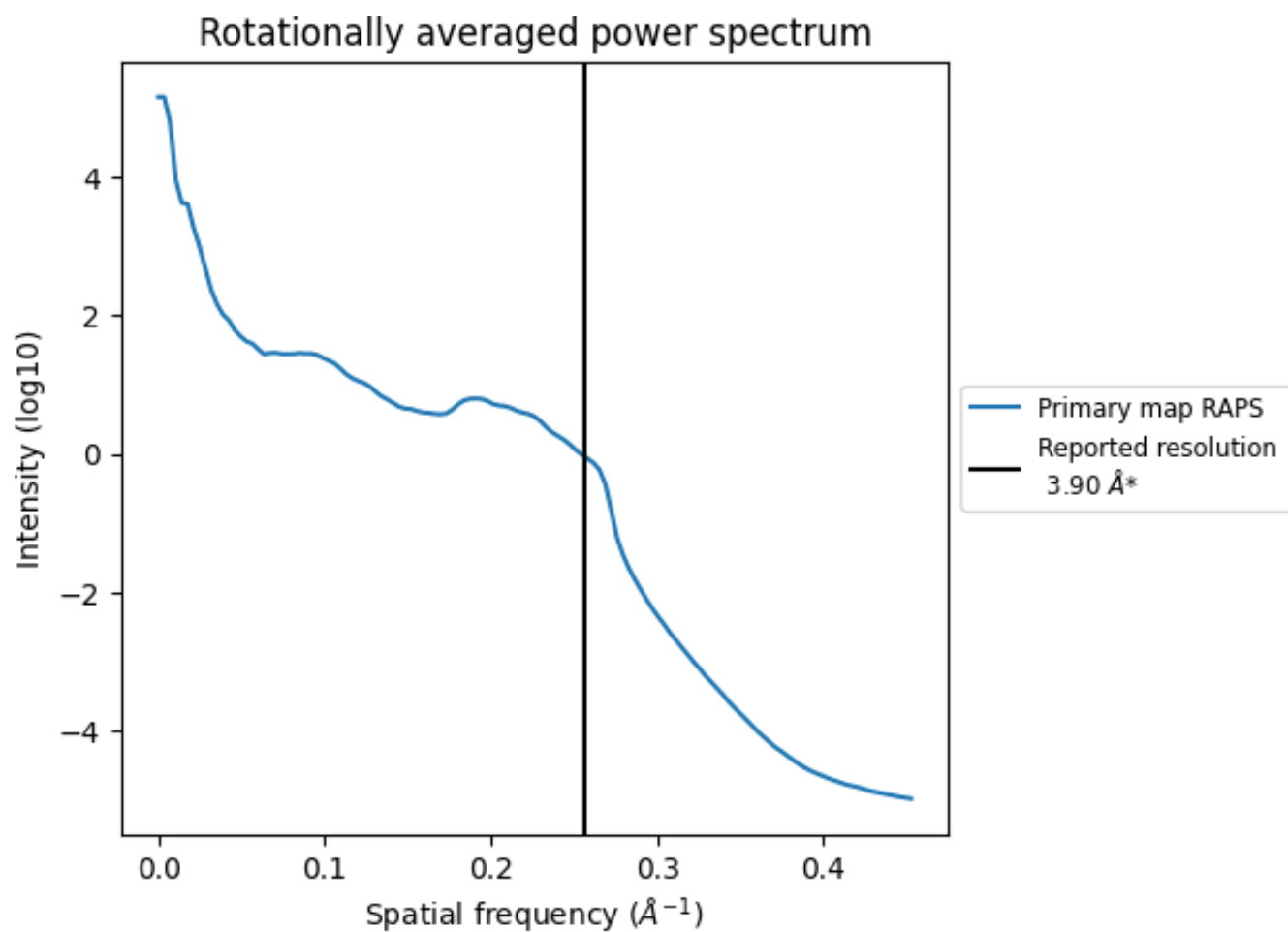
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 144 nm³; this corresponds to an approximate mass of 130 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.256\AA^{-1}

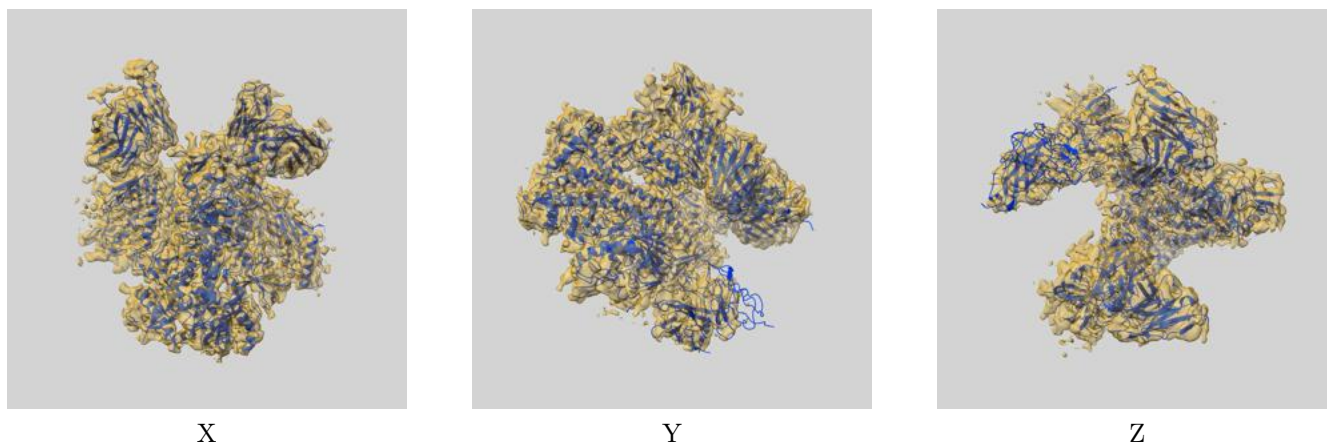
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

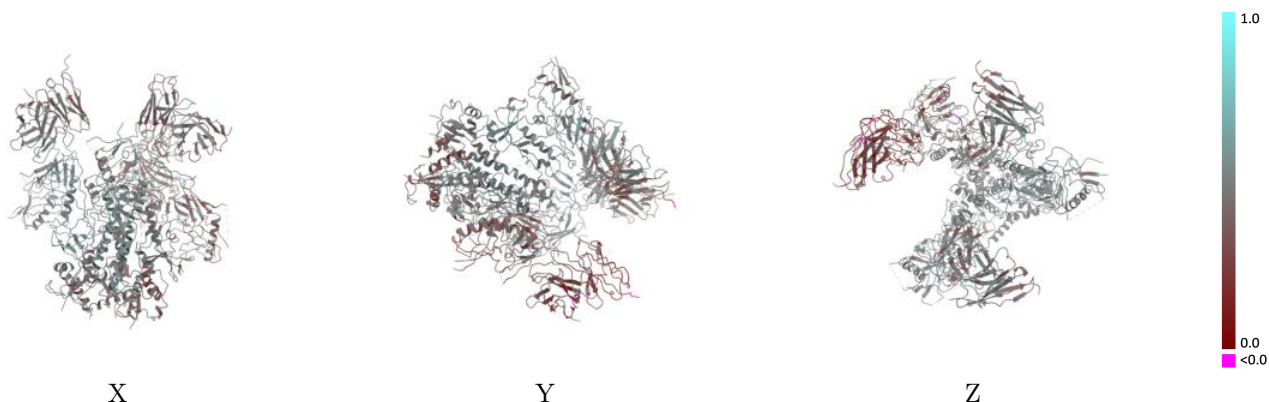
This section contains information regarding the fit between EMDB map EMD-23462 and PDB model 7LO6. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



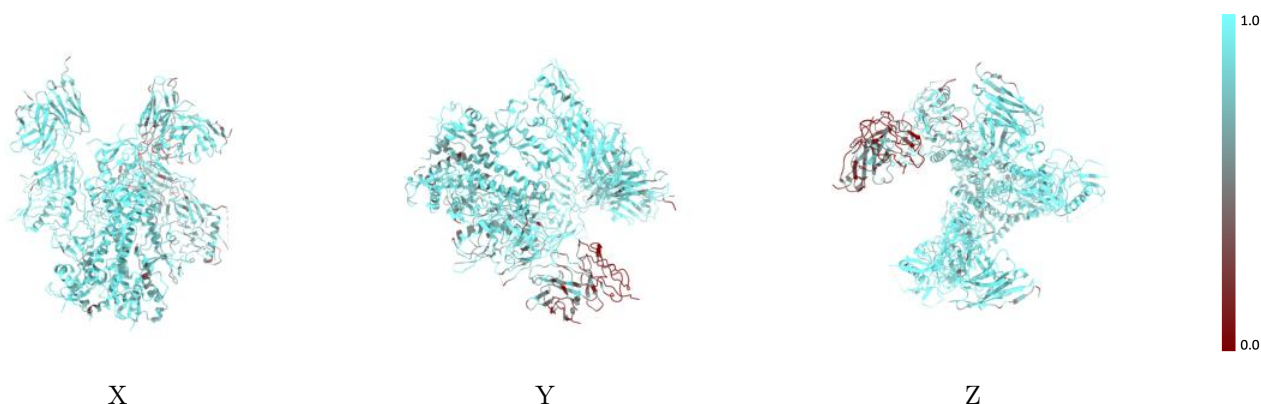
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



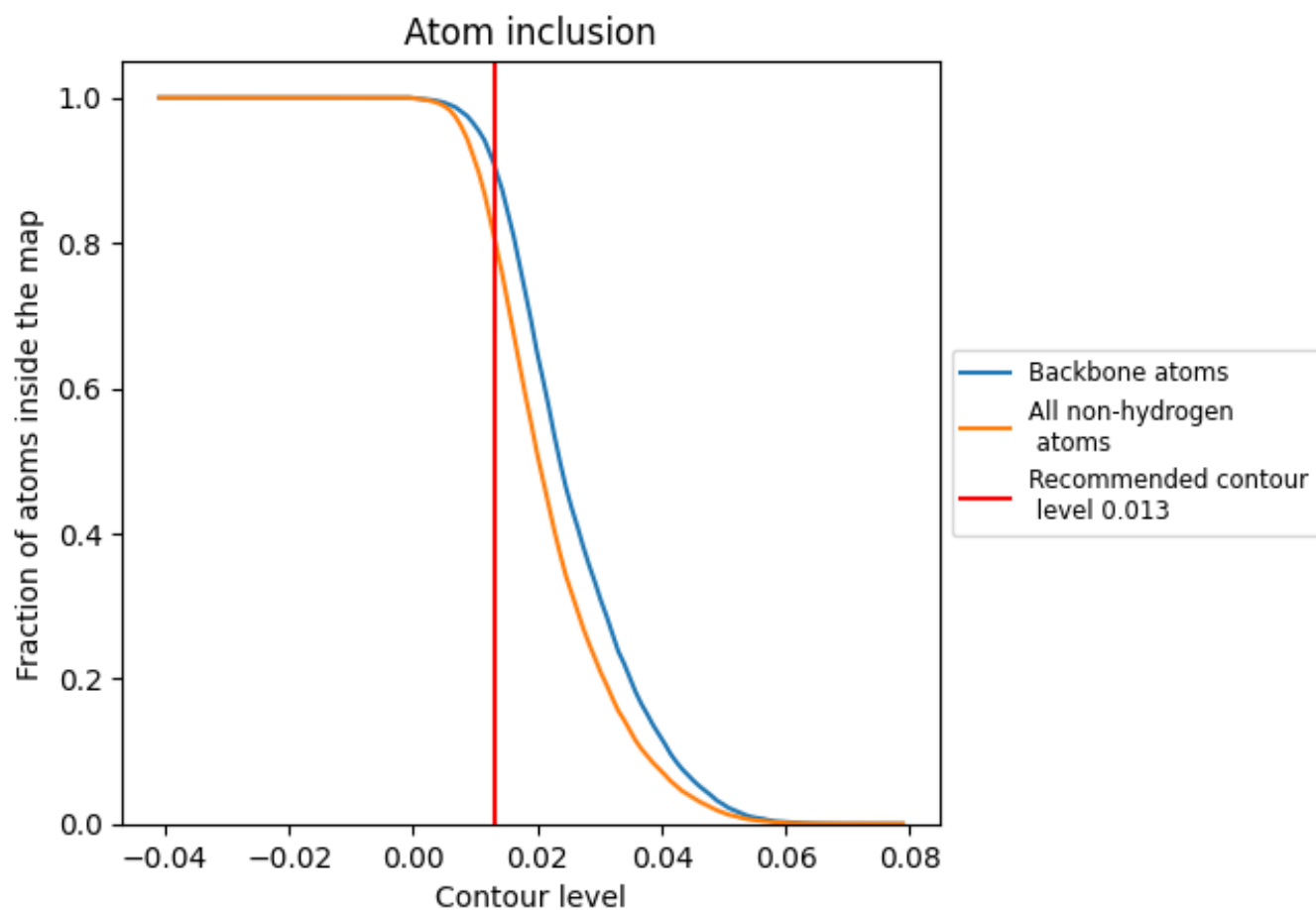
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.013).















































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 81% 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 (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8099	 0.4560
A	 0.7679	 0.4270
B	 0.8101	 0.4450
C	 0.9080	 0.5120
D	 0.8761	 0.4790
E	 0.9277	 0.5220
F	 0.8804	 0.4860
G	 0.8480	 0.4350
H	 0.8769	 0.4720
I	 0.7930	 0.4330
J	 0.8513	 0.4590
K	 0.2242	 0.2570
L	 0.5087	 0.3130
M	 0.8214	 0.4170
N	 0.7377	 0.4490
O	 0.5357	 0.4520
P	 0.9306	 0.5460
Q	 0.7500	 0.4630
R	 0.9286	 0.4770
S	 0.8313	 0.4650
T	 0.9643	 0.4820
U	 0.5357	 0.4490
V	 0.9643	 0.4650

