



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 07:40 AM UTC

PDB ID : 7L02 / pdb_00007l02
EMDB ID : EMD-23094
Title : Cryo-EM structure of SARS-CoV-2 2P S ectodomain bound to one copy of domain-swapped antibody 2G12
Authors : Manne, K.; Henderson, R.; Acharya, P.
Deposited on : 2020-12-10
Resolution : 3.20 Å(reported)
Based on initial model : 6VXX

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

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

A user guide is available at

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

The 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:

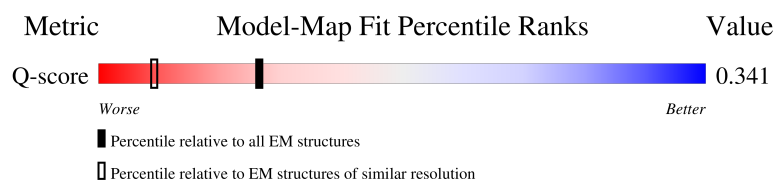
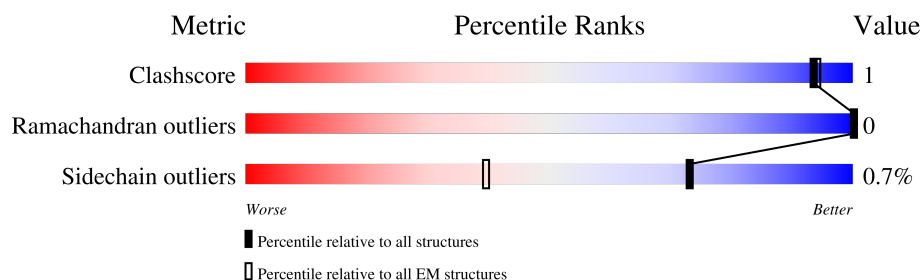
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.20 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.



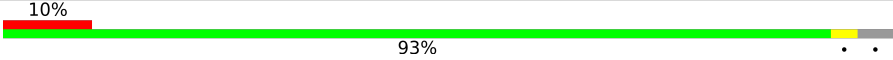
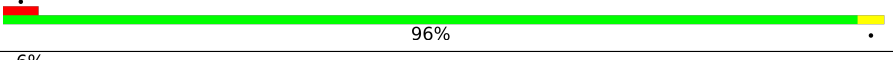
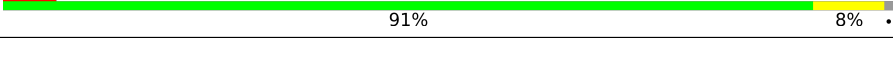
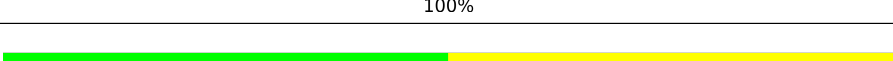
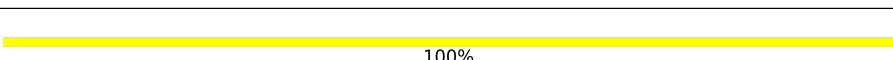
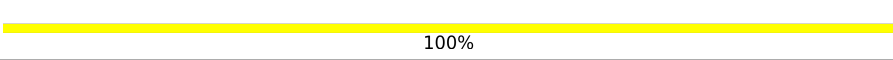
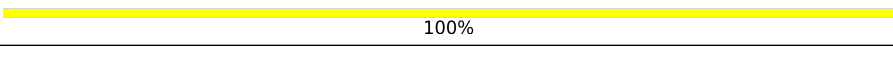
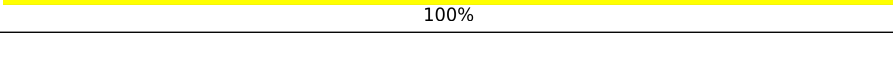
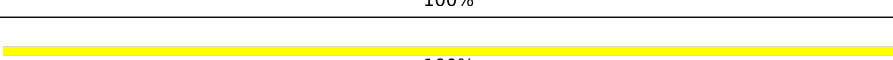
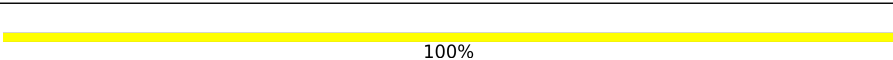
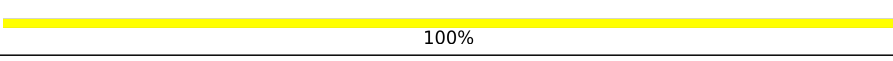
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	1121	
1	B	1121	
1	C	1121	
2	H	226	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	M	226	
3	K	213	
3	L	213	
4	D	2	
4	G	2	
4	I	2	
4	J	2	
4	N	2	
4	O	2	
4	P	2	
4	Q	2	
4	R	2	
4	S	2	
5	E	5	
6	F	8	
7	T	5	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 44358 atoms, of which 14089 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	972	Total	C	H	N	O	S	0	0
			15044	4861	7440	1262	1448	33		
1	B	972	Total	C	N	O	S		0	0
			7604	4861	1262	1448	33			
1	C	972	Total	C	N	O	S		0	0
			7604	4861	1262	1448	33			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	986	PRO	LYS	conflict	UNP P0DTC2
A	987	PRO	VAL	conflict	UNP P0DTC2
B	986	PRO	LYS	conflict	UNP P0DTC2
B	987	PRO	VAL	conflict	UNP P0DTC2
C	986	PRO	LYS	conflict	UNP P0DTC2
C	987	PRO	VAL	conflict	UNP P0DTC2

- Molecule 2 is a protein called 2G12 heavy chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	H	218	Total	C	H	N	O	S	0	0
			3251	1032	1614	279	319	7		
2	M	218	Total	C	H	N	O	S	0	0
			3247	1032	1610	279	319	7		

- Molecule 3 is a protein called 2G12 light chain.

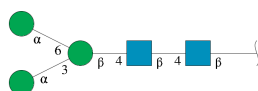
Mol	Chain	Residues	Atoms						AltConf	Trace
3	K	213	Total	C	H	N	O	S	0	0
			3230	1027	1595	274	329	5		
3	L	211	Total	C	H	N	O	S	0	0
			3200	1018	1582	272	323	5		

- 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	H	N	O	0	0
			54	16	26	2	10		
4	G	2	Total	C	N	O		0	0
			28	16	2	10			
4	I	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	N	2	Total	C	N	O		0	0
			28	16	2	10			
4	O	2	Total	C	N	O		0	0
			28	16	2	10			
4	P	2	Total	C	N	O		0	0
			28	16	2	10			
4	Q	2	Total	C	N	O		0	0
			28	16	2	10			
4	R	2	Total	C	N	O		0	0
			28	16	2	10			
4	S	2	Total	C	N	O		0	0
			28	16	2	10			

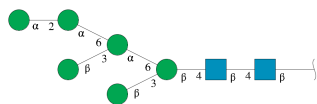
- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	5	Total	C	H	N	O	0	0
			118	34	57	2	25		

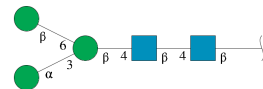
- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[beta-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)-[beta-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a

cetamido-2-deoxy-beta-D-glucopyranose.



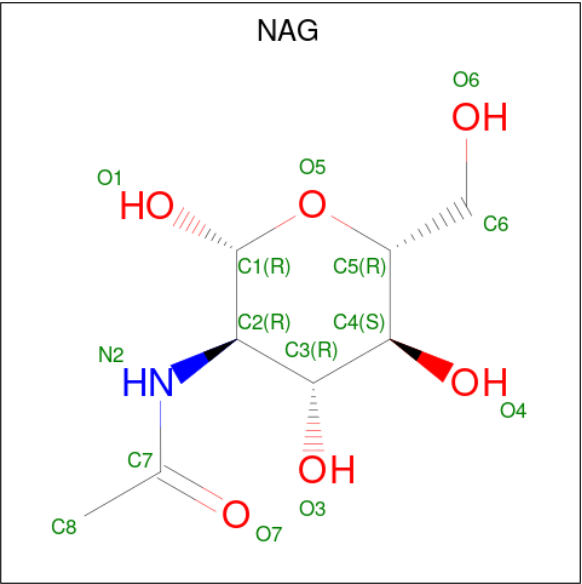
Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	8	Total	C	H	N	O	0	0
			181	52	87	2	40		

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[beta-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	T	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms					AltConf
8	A	1	Total	C	H	N	O	0
			27	8	13	1	5	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf
8	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
8	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
8	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
8	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
8	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
8	A	1	Total	C	N	O		0
			14	8	1	5		
8	A	1	Total	C	N	O		0
			14	8	1	5		
8	A	1	Total	C	N	O		0
			14	8	1	5		
8	A	1	Total	C	N	O		0
			14	8	1	5		
8	B	1	Total	C	N	O		0
			14	8	1	5		
8	B	1	Total	C	N	O		0
			14	8	1	5		
8	B	1	Total	C	N	O		0
			14	8	1	5		
8	B	1	Total	C	N	O		0
			14	8	1	5		
8	B	1	Total	C	N	O		0
			14	8	1	5		
8	B	1	Total	C	N	O		0
			14	8	1	5		
8	B	1	Total	C	N	O		0
			14	8	1	5		
8	B	1	Total	C	N	O		0
			14	8	1	5		
8	B	1	Total	C	N	O		0
			14	8	1	5		
8	C	1	Total	C	N	O		0
			14	8	1	5		

Continued on next page...

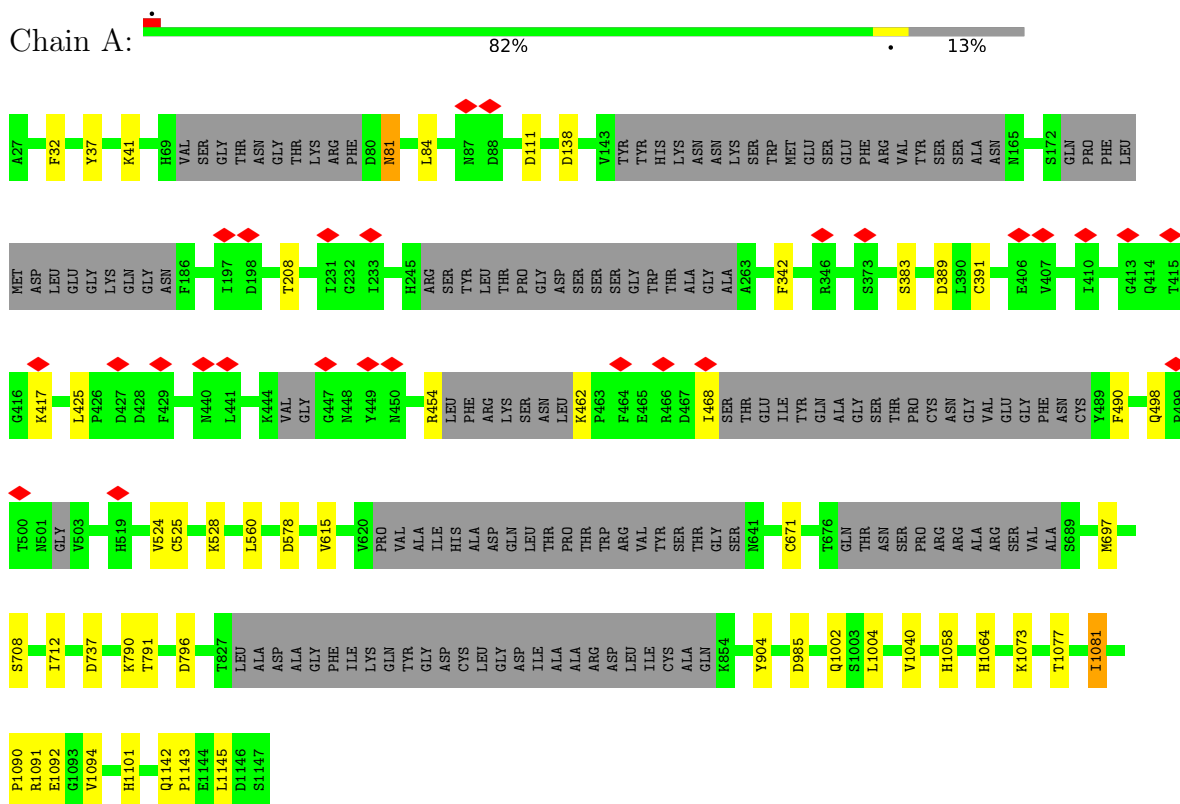
Continued from previous page...

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

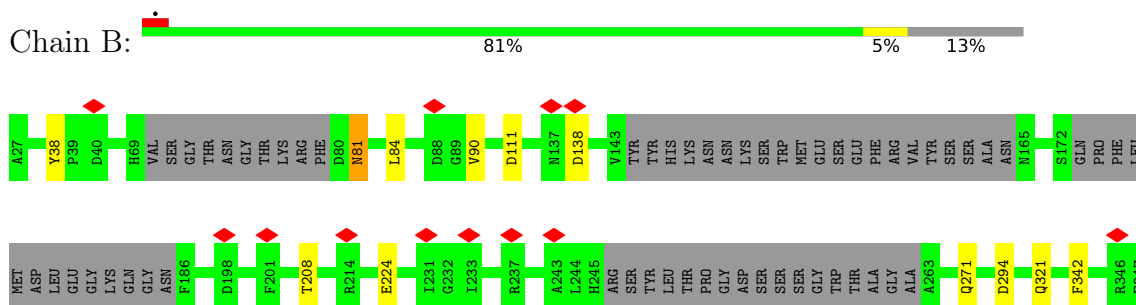
3 Residue-property plots

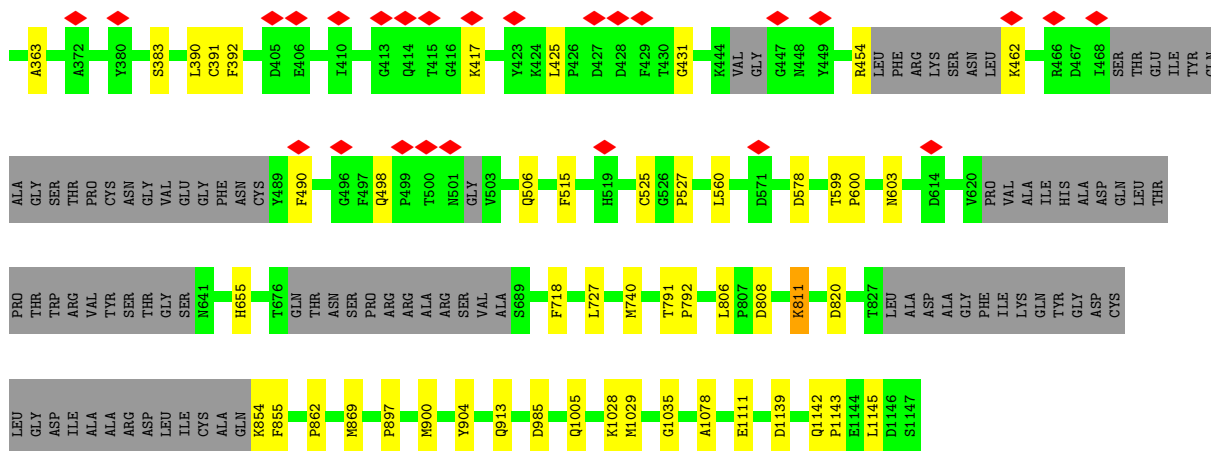
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Spike glycoprotein

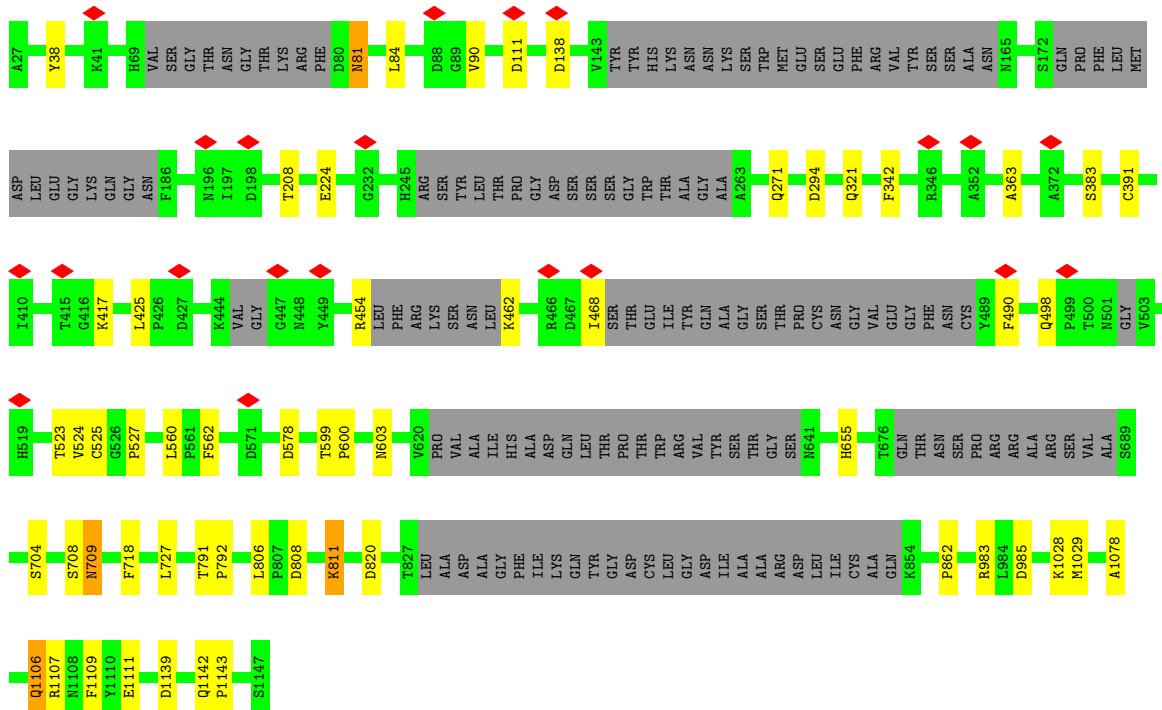
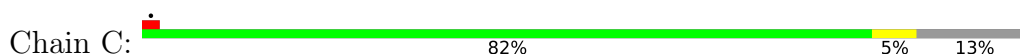


• Molecule 1: Spike glycoprotein

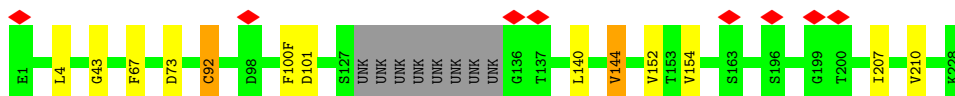




- Molecule 1: Spike glycoprotein

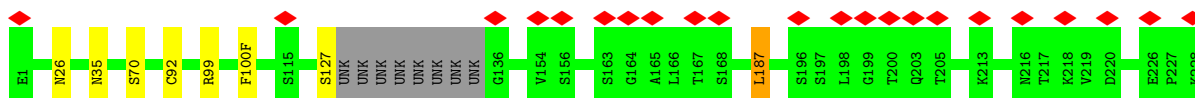


- Molecule 2: 2G12 heavy chain

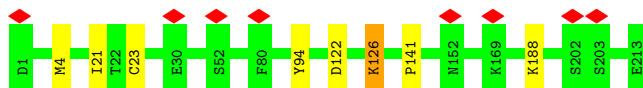


- Molecule 2: 2G12 heavy chain

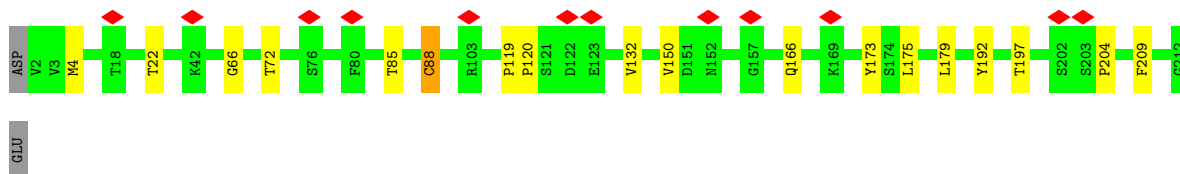
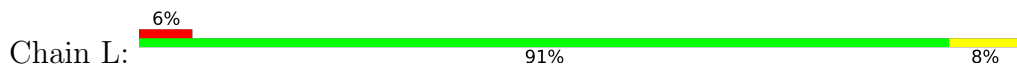




- Molecule 3: 2G12 light chain



- Molecule 3: 2G12 light chain



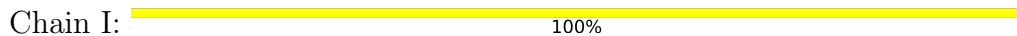
- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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



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



MAG1
MAG2

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

Chain N:  100%MAG1
MAG2

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

Chain O:  100%MAG1
MAG2

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

Chain P:  100%MAG1
MAG2

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

Chain Q:  100%MAG1
MAG2

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

Chain R:  100%MAG1
MAG2

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

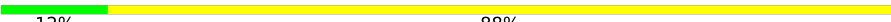
Chain S:  100%MAG1
MAG2

- Molecule 5: 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

Chain E:  40% 60%

MAG1	MAG2	EMA3	MAN4	MAN5
------	------	------	------	------

- Molecule 6: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[beta-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)-[beta-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

Chain F:  12% 88%

MAG1	MAG2	EMA3	MAN4	MAN5	MAN6	EMA7	EMA8
------	------	------	------	------	------	------	------

- Molecule 7: alpha-D-mannopyranose-(1-3)-[beta-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

Chain T:  80% 20%

MAG1	MAG2	EMA3	MAN4	EMA5
------	------	------	------	------

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	107551	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 ($e^-/\text{\AA}^2$)	66.43	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	1.793	Depositor
Minimum map value	-0.812	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.184	Depositor
Map size (Å)	338.56, 338.56, 338.56	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.058, 1.058, 1.058	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, MAN, BMA

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	0.80	4/7772 (0.1%)	1.23	34/10572 (0.3%)
1	B	0.81	1/7772 (0.0%)	1.03	60/10572 (0.6%)
1	C	0.81	2/7772 (0.0%)	1.03	59/10572 (0.6%)
2	H	0.81	1/1675 (0.1%)	1.30	7/2281 (0.3%)
2	M	0.70	0/1675	1.13	3/2281 (0.1%)
3	K	0.71	0/1671	1.23	5/2269 (0.2%)
3	L	0.76	0/1654	1.02	2/2246 (0.1%)
All	All	0.80	8/29991 (0.0%)	1.12	170/40793 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
3	K	0	1
All	All	0	2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1081	ILE	C-O	-7.24	1.16	1.24
1	A	454	ARG	NE-CZ	5.72	1.39	1.33
2	H	144	VAL	C-O	-5.66	1.17	1.24
1	B	454	ARG	NE-CZ	5.59	1.39	1.33
1	C	454	ARG	NE-CZ	5.50	1.39	1.33
1	A	737	ASP	CG-OD2	-5.32	1.15	1.25
1	A	468	ILE	CB-CG1	5.09	1.63	1.53
1	C	468	ILE	CB-CG1	5.03	1.63	1.53

All (170) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	708	SER	CA-C-N	13.51	139.74	120.28
1	A	708	SER	C-N-CA	13.51	139.74	120.28
1	A	490	PHE	CA-C-N	7.36	127.52	119.87
1	A	490	PHE	C-N-CA	7.36	127.52	119.87
1	C	808	ASP	CA-C-N	7.33	127.03	119.56
1	C	808	ASP	C-N-CA	7.33	127.03	119.56
1	B	490	PHE	CA-C-N	7.32	127.49	119.87
1	B	490	PHE	C-N-CA	7.32	127.49	119.87
1	C	490	PHE	CA-C-N	7.32	127.48	119.87
1	C	490	PHE	C-N-CA	7.32	127.48	119.87
1	B	808	ASP	CA-C-N	7.27	126.98	119.56
1	B	808	ASP	C-N-CA	7.27	126.98	119.56
1	C	792	PRO	CA-C-N	7.21	126.91	119.56
1	C	792	PRO	C-N-CA	7.21	126.91	119.56
1	B	792	PRO	CA-C-N	7.13	126.83	119.56
1	B	792	PRO	C-N-CA	7.13	126.83	119.56
1	A	708	SER	CA-C-O	-7.08	113.07	120.99
1	C	1139	ASP	CA-C-N	7.01	126.71	119.56
1	C	1139	ASP	C-N-CA	7.01	126.71	119.56
1	B	1139	ASP	CA-C-N	6.94	126.64	119.56
1	B	1139	ASP	C-N-CA	6.94	126.64	119.56
1	C	383	SER	CA-C-N	6.90	126.59	119.56
1	C	383	SER	C-N-CA	6.90	126.59	119.56
1	A	383	SER	CA-C-N	6.86	126.56	119.56
1	A	383	SER	C-N-CA	6.86	126.56	119.56
1	C	578	ASP	CA-C-N	6.85	126.47	119.56
1	C	578	ASP	C-N-CA	6.85	126.47	119.56
1	B	811	LYS	CA-C-N	6.83	126.53	119.56
1	B	811	LYS	C-N-CA	6.83	126.53	119.56
1	C	811	LYS	CA-C-N	6.83	126.52	119.56
1	C	811	LYS	C-N-CA	6.83	126.52	119.56
1	B	383	SER	CA-C-N	6.82	126.51	119.56
1	B	383	SER	C-N-CA	6.82	126.51	119.56
1	A	578	ASP	CA-C-N	6.80	126.43	119.56
1	A	578	ASP	C-N-CA	6.80	126.43	119.56
1	B	578	ASP	CA-C-N	6.78	126.41	119.56
1	B	578	ASP	C-N-CA	6.78	126.41	119.56
1	A	498	GLN	CA-C-N	6.64	126.34	119.56
1	A	498	GLN	C-N-CA	6.64	126.34	119.56
1	C	81	ASN	CA-C-N	6.61	126.56	120.21
1	C	81	ASN	C-N-CA	6.61	126.56	120.21
2	H	144	VAL	CA-C-O	-6.61	113.49	120.57

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	862	PRO	CA-C-N	6.59	126.51	119.85
1	B	862	PRO	C-N-CA	6.59	126.51	119.85
3	K	141	PRO	CA-C-N	6.59	129.77	120.28
3	K	141	PRO	C-N-CA	6.59	129.77	120.28
1	B	81	ASN	CA-C-N	6.57	126.52	120.21
1	B	81	ASN	C-N-CA	6.57	126.52	120.21
1	B	498	GLN	CA-C-N	6.57	126.26	119.56
1	B	498	GLN	C-N-CA	6.57	126.26	119.56
1	C	862	PRO	CA-C-N	6.57	126.48	119.85
1	C	862	PRO	C-N-CA	6.57	126.48	119.85
1	A	81	ASN	CA-C-N	6.54	126.49	120.21
1	A	81	ASN	C-N-CA	6.54	126.49	120.21
1	C	498	GLN	CA-C-N	6.52	126.21	119.56
1	C	498	GLN	C-N-CA	6.52	126.21	119.56
1	C	806	LEU	CA-C-N	6.40	126.35	119.76
1	C	806	LEU	C-N-CA	6.40	126.35	119.76
1	B	1078	ALA	CA-C-N	6.37	126.00	119.56
1	B	1078	ALA	C-N-CA	6.37	126.00	119.56
1	B	806	LEU	CA-C-N	6.37	126.32	119.76
1	B	806	LEU	C-N-CA	6.37	126.32	119.76
1	C	1078	ALA	CA-C-N	6.23	125.85	119.56
1	C	1078	ALA	C-N-CA	6.23	125.85	119.56
3	L	66	GLY	CA-C-O	-6.21	118.18	122.22
2	H	100(F)	PHE	CA-CB-CG	6.14	119.94	113.80
1	C	138	ASP	CA-C-N	6.09	126.41	119.83
1	C	138	ASP	C-N-CA	6.09	126.41	119.83
2	M	99	ARG	NE-CZ-NH2	6.06	124.66	119.20
1	B	38	TYR	CA-C-N	6.06	125.68	119.56
1	B	38	TYR	C-N-CA	6.06	125.68	119.56
1	B	138	ASP	CA-C-N	6.06	126.37	119.83
1	B	138	ASP	C-N-CA	6.06	126.37	119.83
1	A	138	ASP	CA-C-N	6.05	126.36	119.83
1	A	138	ASP	C-N-CA	6.05	126.36	119.83
1	C	38	TYR	CA-C-N	5.95	125.56	119.56
1	C	38	TYR	C-N-CA	5.95	125.56	119.56
1	C	224	GLU	CA-C-N	5.94	125.70	119.76
1	C	224	GLU	C-N-CA	5.94	125.70	119.76
1	B	224	GLU	CA-C-N	5.94	125.70	119.76
1	B	224	GLU	C-N-CA	5.94	125.70	119.76
1	C	321	GLN	CA-C-N	5.92	125.83	119.85
1	C	321	GLN	C-N-CA	5.92	125.83	119.85
1	B	321	GLN	CA-C-N	5.89	125.80	119.85

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	321	GLN	C-N-CA	5.89	125.80	119.85
3	K	21	ILE	CA-C-O	-5.88	115.49	121.67
1	C	727	LEU	CA-C-N	5.75	125.68	119.76
1	C	727	LEU	C-N-CA	5.75	125.68	119.76
1	B	727	LEU	CA-C-N	5.73	125.66	119.76
1	B	727	LEU	C-N-CA	5.73	125.66	119.76
1	A	796	ASP	CA-CB-CG	5.70	118.30	112.60
1	A	1064	HIS	CB-CG-CD2	-5.64	123.86	131.20
1	B	90	VAL	N-CA-C	5.64	116.25	108.12
1	B	985	ASP	CA-C-N	5.62	126.17	120.38
1	B	985	ASP	C-N-CA	5.62	126.17	120.38
1	C	985	ASP	CA-C-N	5.59	126.14	120.38
1	C	985	ASP	C-N-CA	5.59	126.14	120.38
1	A	985	ASP	CA-C-N	5.57	126.12	120.38
1	A	985	ASP	C-N-CA	5.57	126.12	120.38
1	C	90	VAL	N-CA-C	5.57	116.14	108.12
2	H	207	ILE	CA-C-O	-5.54	115.41	121.28
1	C	791	THR	CA-C-N	5.52	126.06	120.38
1	C	791	THR	C-N-CA	5.52	126.06	120.38
1	B	791	THR	CA-C-N	5.48	126.03	120.38
1	B	791	THR	C-N-CA	5.48	126.03	120.38
1	C	294	ASP	CA-C-N	5.45	125.80	119.47
1	C	294	ASP	C-N-CA	5.45	125.80	119.47
1	B	294	ASP	CA-C-N	5.41	125.74	119.47
1	B	294	ASP	C-N-CA	5.41	125.74	119.47
3	K	122	ASP	CA-C-N	5.37	127.47	120.28
3	K	122	ASP	C-N-CA	5.37	127.47	120.28
1	B	1111	GLU	CA-C-N	5.37	125.12	119.76
1	B	1111	GLU	C-N-CA	5.37	125.12	119.76
1	C	1111	GLU	CA-C-N	5.35	125.11	119.76
1	C	1111	GLU	C-N-CA	5.35	125.11	119.76
1	C	599	THR	CA-C-N	5.33	125.31	120.03
1	C	599	THR	C-N-CA	5.33	125.31	120.03
1	A	32	PHE	CA-C-N	5.29	130.85	122.60
1	A	32	PHE	C-N-CA	5.29	130.85	122.60
1	A	84	LEU	CA-C-N	5.29	125.23	119.78
1	A	84	LEU	C-N-CA	5.29	125.23	119.78
1	B	84	LEU	CA-C-N	5.28	125.22	119.78
1	B	84	LEU	C-N-CA	5.28	125.22	119.78
2	H	67	PHE	CA-CB-CG	5.27	119.07	113.80
1	C	523	THR	N-CA-C	-5.26	107.41	113.88
1	B	600	PRO	N-CA-C	-5.24	103.55	111.41

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	462	LYS	CA-C-N	5.24	125.48	119.83
1	B	462	LYS	C-N-CA	5.24	125.48	119.83
1	B	599	THR	CA-C-N	5.23	125.20	120.03
1	B	599	THR	C-N-CA	5.23	125.20	120.03
1	C	462	LYS	CA-C-N	5.22	125.47	119.83
1	C	462	LYS	C-N-CA	5.22	125.47	119.83
2	H	43	GLY	CA-C-N	5.22	125.87	120.60
2	H	43	GLY	C-N-CA	5.22	125.87	120.60
1	C	600	PRO	N-CA-C	-5.22	103.58	111.41
2	H	101	ASP	CA-CB-CG	5.22	117.82	112.60
1	B	208	THR	CA-C-N	5.21	124.97	119.76
1	B	208	THR	C-N-CA	5.21	124.97	119.76
1	B	560	LEU	CA-C-N	5.21	126.35	119.84
1	B	560	LEU	C-N-CA	5.21	126.35	119.84
1	C	560	LEU	CA-C-N	5.21	126.35	119.84
1	C	560	LEU	C-N-CA	5.21	126.35	119.84
1	C	84	LEU	CA-C-N	5.19	125.13	119.78
1	C	84	LEU	C-N-CA	5.19	125.13	119.78
1	A	462	LYS	CA-C-N	5.18	125.43	119.83
1	A	462	LYS	C-N-CA	5.18	125.43	119.83
1	A	560	LEU	CA-C-N	5.13	126.26	119.84
1	A	560	LEU	C-N-CA	5.13	126.26	119.84
1	C	208	THR	CA-C-N	5.13	124.89	119.76
1	C	208	THR	C-N-CA	5.13	124.89	119.76
2	M	100(F)	PHE	CA-CB-CG	5.10	118.90	113.80
1	A	1058	HIS	CB-CG-CD2	-5.10	124.58	131.20
1	C	425	LEU	CA-C-N	5.09	125.03	119.78
1	C	425	LEU	C-N-CA	5.09	125.03	119.78
1	A	1091	ARG	N-CA-C	-5.09	105.63	111.07
3	L	88	CYS	CA-C-O	-5.07	116.03	121.56
1	B	271	GLN	CA-C-N	5.06	126.16	119.84
1	B	271	GLN	C-N-CA	5.06	126.16	119.84
1	C	271	GLN	CA-C-N	5.05	126.16	119.84
1	C	271	GLN	C-N-CA	5.05	126.16	119.84
1	A	208	THR	CA-C-N	5.05	124.81	119.76
1	A	208	THR	C-N-CA	5.05	124.81	119.76
1	A	425	LEU	CA-C-N	5.04	124.98	119.78
1	A	425	LEU	C-N-CA	5.04	124.98	119.78
2	M	26	ASN	CA-CB-CG	5.04	117.64	112.60
1	A	1073	LYS	CA-C-O	-5.03	115.55	121.44
1	B	506	GLN	CA-C-N	5.02	124.78	119.76
1	B	506	GLN	C-N-CA	5.02	124.78	119.76

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	425	LEU	CA-C-N	5.01	124.94	119.78
1	B	425	LEU	C-N-CA	5.01	124.94	119.78

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	37	TYR	Sidechain
3	K	94	TYR	Sidechain

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	7604	7440	7414	26	0
1	B	7604	0	7415	26	0
1	C	7604	0	7415	19	0
2	H	1637	1614	1609	3	0
2	M	1637	1610	1609	4	0
3	K	1635	1595	1593	3	0
3	L	1618	1582	1580	10	0
4	D	28	26	25	0	0
4	G	28	0	25	1	0
4	I	28	0	25	0	0
4	J	28	0	25	0	0
4	N	28	0	25	0	0
4	O	28	0	25	0	0
4	P	28	0	25	0	0
4	Q	28	0	25	0	0
4	R	28	0	25	0	0
4	S	28	0	25	0	0
5	E	61	57	52	0	0
6	F	94	87	79	0	0
7	T	61	0	52	0	0
8	A	140	78	130	2	0
8	B	154	0	143	2	0
8	C	140	0	130	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	30269	14089	29471	77	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (77) 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:391:CYS:HB2	1:B:525:CYS:HA	1.43	0.99
1:C:391:CYS:HB2	1:C:525:CYS:HA	1.59	0.81
1:C:391:CYS:CB	1:C:525:CYS:HA	2.12	0.79
2:M:187:LEU:C	2:M:187:LEU:HD12	2.15	0.71
1:A:790:LYS:HE3	1:C:704:SER:HB3	1.75	0.67
1:A:391:CYS:HB2	1:A:524:VAL:O	1.97	0.63
1:A:1094:VAL:HG13	1:B:900:MET:HE1	1.79	0.63
3:K:188:LYS:HA	3:K:188:LYS:HE2	1.79	0.63
1:A:391:CYS:CB	1:A:525:CYS:HA	2.29	0.62
1:A:391:CYS:HB2	1:A:525:CYS:HA	1.83	0.61
1:B:391:CYS:CB	1:B:525:CYS:HA	2.26	0.60
1:C:363:ALA:O	1:C:527:PRO:HD3	2.03	0.59
1:A:1090:PRO:O	1:B:913:GLN:NE2	2.39	0.54
1:B:740:MET:HE2	1:B:855:PHE:O	2.08	0.54
1:B:811:LYS:NZ	1:B:820:ASP:OD2	2.41	0.54
1:C:811:LYS:NZ	1:C:820:ASP:OD2	2.41	0.53
1:A:712:ILE:HD13	1:A:1094:VAL:HG11	1.90	0.53
3:L:166:GLN:HG3	3:L:173:TYR:CZ	2.43	0.53
3:L:4:MET:HE3	3:L:88:CYS:SG	2.49	0.53
1:C:1106:GLN:HG3	1:C:1109:PHE:O	2.09	0.53
1:C:391:CYS:HB2	1:C:524:VAL:O	2.07	0.52
2:M:187:LEU:C	2:M:187:LEU:CD1	2.84	0.51
3:L:132:VAL:CG2	3:L:179:LEU:HB3	2.41	0.50
1:A:904:TYR:CZ	1:C:1107:ARG:HD3	2.47	0.50
1:A:1094:VAL:HG22	1:B:904:TYR:OH	2.11	0.49
2:H:4:LEU:HD23	2:H:92:CYS:SG	2.52	0.49
1:B:390:LEU:HD22	1:C:983:ARG:HG2	1.94	0.49
1:A:391:CYS:HB3	1:A:525:CYS:HA	1.94	0.49
1:A:1094:VAL:HG13	1:B:900:MET:CE	2.43	0.49
1:B:431:GLY:HA2	1:B:515:PHE:CD1	2.48	0.49
2:M:187:LEU:HD12	2:M:187:LEU:O	2.12	0.49
1:A:1077:THR:CG2	1:B:897:PRO:HG2	2.42	0.48
1:C:391:CYS:HB3	1:C:525:CYS:HA	1.93	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1002:GLN:HE21	1:B:1005:GLN:HE22	1.62	0.47
1:B:342:PHE:HB2	8:B:1203:NAG:H82	1.96	0.47
3:L:4:MET:CE	3:L:88:CYS:SG	3.03	0.47
1:A:342:PHE:HB2	8:A:1304:NAG:H82	1.96	0.47
1:A:697:MET:HG2	1:B:869:MET:HE1	1.96	0.46
1:B:655:HIS:O	8:B:1206:NAG:H81	2.16	0.46
2:H:154:VAL:HG22	2:H:210:VAL:HG22	1.96	0.46
3:K:4:MET:HB3	3:K:23:CYS:SG	2.55	0.46
1:A:389:ASP:OD1	1:A:528:LYS:NZ	2.39	0.46
1:C:342:PHE:HB2	8:C:1208:NAG:H82	1.96	0.46
1:C:655:HIS:O	8:C:1201:NAG:H81	2.15	0.46
2:H:144:VAL:HG11	2:H:152:VAL:HG11	1.98	0.46
1:C:81:ASN:OD1	1:C:81:ASN:N	2.49	0.45
1:A:81:ASN:OD1	1:A:81:ASN:N	2.49	0.45
1:B:854:LYS:HE2	1:B:855:PHE:CE1	2.51	0.45
1:B:81:ASN:OD1	1:B:81:ASN:N	2.49	0.45
3:L:197:THR:HG22	3:L:204:PRO:HB3	1.99	0.45
1:A:1002:GLN:HE21	1:B:1005:GLN:NE2	2.16	0.44
3:K:126:LYS:HA	3:K:126:LYS:CE	2.48	0.44
1:C:709:ASN:N	1:C:709:ASN:OD1	2.50	0.44
1:C:111:ASP:N	1:C:111:ASP:OD1	2.49	0.44
3:L:22:THR:HG22	3:L:72:THR:HG22	1.99	0.44
3:L:120:PRO:HD3	3:L:132:VAL:HG12	2.00	0.43
1:A:1040:VAL:HG21	1:B:1035:GLY:HA3	2.00	0.43
1:C:718:PHE:CD1	1:C:718:PHE:C	2.97	0.43
1:A:111:ASP:N	1:A:111:ASP:OD1	2.48	0.43
1:A:671:CYS:SG	1:A:697:MET:HB3	2.58	0.43
1:B:1028:LYS:O	1:B:1029:MET:C	2.59	0.43
2:M:92:CYS:O	2:M:92:CYS:SG	2.77	0.43
1:C:1142:GLN:N	1:C:1143:PRO:HD2	2.34	0.42
1:A:1077:THR:HG23	1:B:897:PRO:HG2	2.00	0.42
8:A:1310:NAG:H82	8:A:1310:NAG:H3	2.01	0.42
1:B:1142:GLN:N	1:B:1143:PRO:HD2	2.34	0.42
1:B:718:PHE:CD1	1:B:718:PHE:C	2.97	0.42
1:B:363:ALA:O	1:B:527:PRO:HD3	2.20	0.42
1:A:1142:GLN:N	1:A:1143:PRO:HD2	2.35	0.42
3:L:150:VAL:HG22	3:L:192:TYR:CD2	2.55	0.41
1:A:1101:HIS:ND1	4:G:1:NAG:H5	2.35	0.41
3:L:119:PRO:HB3	3:L:209:PHE:CE1	2.55	0.41
1:A:41:LYS:HG2	1:C:562:PHE:HD1	1.86	0.41
1:A:1145:LEU:HD21	1:B:1145:LEU:HD12	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:175:LEU:C	3:L:175:LEU:HD23	2.45	0.41
1:B:111:ASP:N	1:B:111:ASP:OD1	2.48	0.40
1:C:1028:LYS:O	1:C:1029:MET:C	2.60	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	948/1121 (85%)	906 (96%)	42 (4%)	0	100	100
1	B	948/1121 (85%)	924 (98%)	24 (2%)	0	100	100
1	C	948/1121 (85%)	923 (97%)	25 (3%)	0	100	100
2	H	214/226 (95%)	204 (95%)	10 (5%)	0	100	100
2	M	214/226 (95%)	206 (96%)	8 (4%)	0	100	100
3	K	211/213 (99%)	204 (97%)	7 (3%)	0	100	100
3	L	209/213 (98%)	203 (97%)	6 (3%)	0	100	100
All	All	3692/4241 (87%)	3570 (97%)	122 (3%)	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	852/972 (88%)	846 (99%)	6 (1%)	76	83
1	B	852/972 (88%)	849 (100%)	3 (0%)	84	86
1	C	852/972 (88%)	847 (99%)	5 (1%)	78	84
2	H	184/184 (100%)	181 (98%)	3 (2%)	55	75
2	M	184/184 (100%)	180 (98%)	4 (2%)	45	71
3	K	184/184 (100%)	183 (100%)	1 (0%)	81	85
3	L	182/184 (99%)	181 (100%)	1 (0%)	81	85
All	All	3290/3652 (90%)	3267 (99%)	23 (1%)	73	83

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	417	LYS
1	A	615	VAL
1	A	791	THR
1	A	1004	LEU
1	A	1081	ILE
1	A	1092	GLU
1	B	392	PHE
1	B	417	LYS
1	B	603	ASN
1	C	417	LYS
1	C	603	ASN
1	C	708	SER
1	C	709	ASN
1	C	1106	GLN
2	H	73	ASP
2	H	92	CYS
2	H	140	LEU
3	K	126	LYS
3	L	85	THR
2	M	35	ASN
2	M	70	SER
2	M	127	SER
2	M	187	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	317	ASN
1	A	321	GLN
1	A	603	ASN
1	A	779	GLN
1	A	804	GLN
1	A	935	GLN
1	A	954	GLN
1	A	1002	GLN
1	B	125	ASN
1	B	388	ASN
1	B	1010	GLN
1	B	1071	GLN
1	B	1088	HIS
1	C	125	ASN
1	C	388	ASN
1	C	913	GLN
1	C	1010	GLN
1	C	1071	GLN
1	C	1088	HIS
2	H	32	HIS
3	K	137	ASN
3	K	138	ASN
3	K	147	GLN
3	K	160	GLN
3	L	37	GLN
3	L	147	GLN
3	L	160	GLN
3	L	210	ASN
2	M	35	ASN
2	M	203	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 ⓘ

38 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	14,14,15	1.52	2 (14%)	17,19,21	0.71	0
4	NAG	D	2	4	14,14,15	1.51	2 (14%)	17,19,21	0.63	0
5	NAG	E	1	1,5	14,14,15	0.99	0	17,19,21	0.67	0
5	NAG	E	2	5	14,14,15	0.97	0	17,19,21	0.77	0
5	BMA	E	3	5	11,11,12	1.03	1 (9%)	15,15,17	0.87	0
5	MAN	E	4	5	11,11,12	1.14	1 (9%)	15,15,17	1.48	2 (13%)
5	MAN	E	5	5	11,11,12	1.29	2 (18%)	15,15,17	0.69	0
6	NAG	F	1	1,6	14,14,15	1.07	1 (7%)	17,19,21	0.75	0
6	NAG	F	2	6	14,14,15	1.02	0	17,19,21	1.00	0
6	BMA	F	3	6	11,11,12	1.18	2 (18%)	15,15,17	1.23	1 (6%)
6	MAN	F	4	6	11,11,12	1.33	2 (18%)	15,15,17	1.22	2 (13%)
6	MAN	F	5	6	11,11,12	1.17	2 (18%)	15,15,17	0.90	1 (6%)
6	MAN	F	6	6	11,11,12	1.26	2 (18%)	15,15,17	1.12	1 (6%)
6	BMA	F	7	6	11,11,12	1.03	1 (9%)	15,15,17	0.81	0
6	BMA	F	8	6	11,11,12	1.28	2 (18%)	15,15,17	1.00	1 (6%)
4	NAG	G	1	4,1	14,14,15	0.26	0	17,19,21	0.98	0
4	NAG	G	2	4	14,14,15	0.25	0	17,19,21	0.59	0
4	NAG	I	1	4,1	14,14,15	1.47	2 (14%)	17,19,21	0.71	0
4	NAG	I	2	4	14,14,15	1.48	2 (14%)	17,19,21	0.65	0
4	NAG	J	1	4,1	14,14,15	1.50	2 (14%)	17,19,21	0.75	0
4	NAG	J	2	4	14,14,15	1.50	2 (14%)	17,19,21	0.59	0
4	NAG	N	1	4,1	14,14,15	1.58	2 (14%)	17,19,21	0.79	0
4	NAG	N	2	4	14,14,15	1.36	2 (14%)	17,19,21	0.62	0
4	NAG	O	1	4,1	14,14,15	1.54	2 (14%)	17,19,21	0.70	0
4	NAG	O	2	4	14,14,15	1.51	2 (14%)	17,19,21	0.64	0
4	NAG	P	1	4,1	14,14,15	1.45	2 (14%)	17,19,21	0.71	0
4	NAG	P	2	4	14,14,15	1.47	2 (14%)	17,19,21	0.62	0
4	NAG	Q	1	4,1	14,14,15	1.50	2 (14%)	17,19,21	0.73	0
4	NAG	Q	2	4	14,14,15	1.50	2 (14%)	17,19,21	0.59	0
4	NAG	R	1	4,1	14,14,15	1.57	2 (14%)	17,19,21	0.80	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	R	2	4	14,14,15	1.36	2 (14%)	17,19,21	0.62	0
4	NAG	S	1	4,1	14,14,15	1.53	2 (14%)	17,19,21	0.71	0
4	NAG	S	2	4	14,14,15	1.53	2 (14%)	17,19,21	0.64	0
7	NAG	T	1	7,1	14,14,15	0.29	0	17,19,21	0.53	0
7	NAG	T	2	7	14,14,15	0.30	0	17,19,21	0.66	0
7	BMA	T	3	7	11,11,12	0.32	0	15,15,17	0.84	1 (6%)
7	MAN	T	4	7	11,11,12	0.23	0	15,15,17	0.82	0
7	BMA	T	5	7	11,11,12	0.23	0	15,15,17	0.77	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	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1
5	NAG	E	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	E	2	5	-	0/6/23/26	0/1/1/1
5	BMA	E	3	5	-	0/2/19/22	0/1/1/1
5	MAN	E	4	5	-	2/2/19/22	0/1/1/1
5	MAN	E	5	5	-	0/2/19/22	0/1/1/1
6	NAG	F	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	F	2	6	-	1/6/23/26	0/1/1/1
6	BMA	F	3	6	-	0/2/19/22	0/1/1/1
6	MAN	F	4	6	-	0/2/19/22	0/1/1/1
6	MAN	F	5	6	-	0/2/19/22	0/1/1/1
6	MAN	F	6	6	-	0/2/19/22	0/1/1/1
6	BMA	F	7	6	-	0/2/19/22	0/1/1/1
6	BMA	F	8	6	-	0/2/19/22	0/1/1/1
4	NAG	G	1	4,1	-	3/6/23/26	0/1/1/1
4	NAG	G	2	4	-	3/6/23/26	0/1/1/1
4	NAG	I	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	0/6/23/26	0/1/1/1
4	NAG	J	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	0/6/23/26	0/1/1/1
4	NAG	N	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	0/6/23/26	0/1/1/1
4	NAG	O	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	O	2	4	-	0/6/23/26	0/1/1/1
4	NAG	P	1	4,1	-	0/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

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

All (52) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	R	1	NAG	C1-C2	4.15	1.58	1.52
4	Q	1	NAG	C1-C2	4.15	1.58	1.52
4	N	1	NAG	C1-C2	4.14	1.58	1.52
4	O	1	NAG	C1-C2	4.13	1.58	1.52
4	D	1	NAG	C1-C2	4.10	1.57	1.52
4	J	1	NAG	C1-C2	4.10	1.57	1.52
4	S	2	NAG	C1-C2	4.07	1.57	1.52
4	I	1	NAG	C1-C2	4.06	1.57	1.52
4	S	1	NAG	C1-C2	4.05	1.57	1.52
4	P	1	NAG	C1-C2	4.03	1.57	1.52
4	I	2	NAG	C1-C2	4.00	1.57	1.52
4	P	2	NAG	C1-C2	3.98	1.57	1.52
4	Q	2	NAG	C1-C2	3.95	1.57	1.52
4	J	2	NAG	C1-C2	3.93	1.57	1.52
4	O	2	NAG	C1-C2	3.93	1.57	1.52
4	D	2	NAG	C1-C2	3.91	1.57	1.52
4	R	2	NAG	C1-C2	3.14	1.56	1.52
4	N	2	NAG	C1-C2	3.07	1.56	1.52
6	F	8	BMA	O5-C5	2.95	1.49	1.43
6	F	6	MAN	O5-C5	2.93	1.49	1.43
5	E	5	MAN	O5-C5	2.76	1.48	1.43
4	N	2	NAG	O5-C5	2.65	1.48	1.43
4	N	1	NAG	O5-C5	2.64	1.48	1.43
5	E	4	MAN	O5-C5	2.62	1.48	1.43
4	R	1	NAG	O5-C5	2.58	1.48	1.43
4	R	2	NAG	O5-C5	2.57	1.48	1.43

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	4	MAN	O3-C3	2.55	1.49	1.43
4	D	2	NAG	O5-C5	2.55	1.48	1.43
4	J	2	NAG	O5-C5	2.54	1.48	1.43
4	Q	2	NAG	O5-C5	2.53	1.48	1.43
6	F	6	MAN	O5-C1	2.51	1.47	1.43
4	O	2	NAG	O5-C5	2.50	1.48	1.43
4	S	2	NAG	O5-C5	2.47	1.48	1.43
6	F	3	BMA	O3-C3	2.39	1.48	1.43
4	P	2	NAG	O5-C5	2.38	1.48	1.43
6	F	7	BMA	O5-C5	2.36	1.48	1.43
4	I	2	NAG	O5-C5	2.36	1.48	1.43
6	F	5	MAN	O5-C5	2.32	1.47	1.43
4	O	1	NAG	O5-C5	2.29	1.47	1.43
6	F	4	MAN	O5-C5	2.26	1.47	1.43
4	D	1	NAG	O5-C5	2.26	1.47	1.43
4	S	1	NAG	O5-C5	2.25	1.47	1.43
6	F	8	BMA	O5-C1	2.21	1.47	1.43
6	F	1	NAG	O5-C5	2.21	1.47	1.43
4	P	1	NAG	O5-C5	2.13	1.47	1.43
6	F	5	MAN	O5-C1	2.13	1.47	1.43
4	J	1	NAG	O5-C5	2.09	1.47	1.43
4	I	1	NAG	O5-C5	2.07	1.47	1.43
5	E	3	BMA	O5-C5	2.06	1.47	1.43
4	Q	1	NAG	O5-C5	2.04	1.47	1.43
6	F	3	BMA	O5-C5	2.02	1.47	1.43
5	E	5	MAN	O5-C1	2.01	1.47	1.43

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	4	MAN	C1-O5-C5	4.68	118.46	112.19
6	F	3	BMA	C1-O5-C5	4.39	118.08	112.19
6	F	6	MAN	C1-O5-C5	3.32	116.63	112.19
6	F	8	BMA	C1-O5-C5	2.85	116.00	112.19
6	F	4	MAN	C1-C2-C3	2.73	113.62	109.64
6	F	5	MAN	C1-O5-C5	2.67	115.77	112.19
5	E	4	MAN	O3-C3-C2	-2.66	104.63	110.05
7	T	3	BMA	C2-C3-C4	-2.06	107.23	110.86
6	F	4	MAN	C1-O5-C5	2.05	114.93	112.19

There are no chirality outliers.

All (21) torsion outliers are listed below:

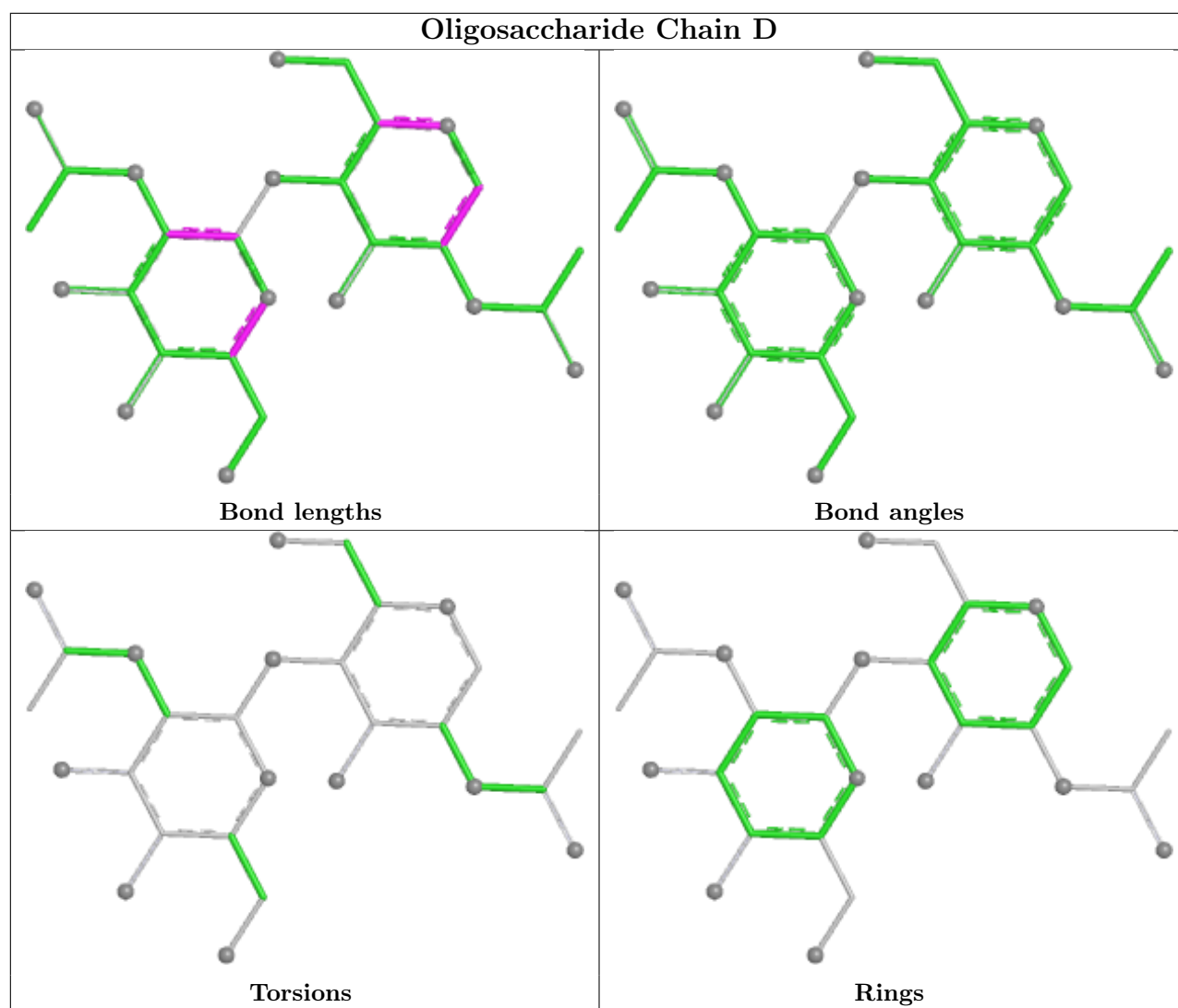
Mol	Chain	Res	Type	Atoms
4	G	1	NAG	C8-C7-N2-C2
4	G	1	NAG	O7-C7-N2-C2
4	G	2	NAG	C1-C2-N2-C7
4	G	2	NAG	C8-C7-N2-C2
4	G	2	NAG	O7-C7-N2-C2
7	T	1	NAG	O7-C7-N2-C2
7	T	2	NAG	C8-C7-N2-C2
7	T	2	NAG	O7-C7-N2-C2
7	T	1	NAG	C8-C7-N2-C2
7	T	3	BMA	O5-C5-C6-O6
7	T	3	BMA	C4-C5-C6-O6
7	T	4	MAN	O5-C5-C6-O6
7	T	1	NAG	C4-C5-C6-O6
5	E	4	MAN	C4-C5-C6-O6
7	T	1	NAG	O5-C5-C6-O6
5	E	4	MAN	O5-C5-C6-O6
4	G	1	NAG	C3-C2-N2-C7
6	F	1	NAG	C1-C2-N2-C7
6	F	2	NAG	C1-C2-N2-C7
7	T	2	NAG	C4-C5-C6-O6
7	T	2	NAG	O5-C5-C6-O6

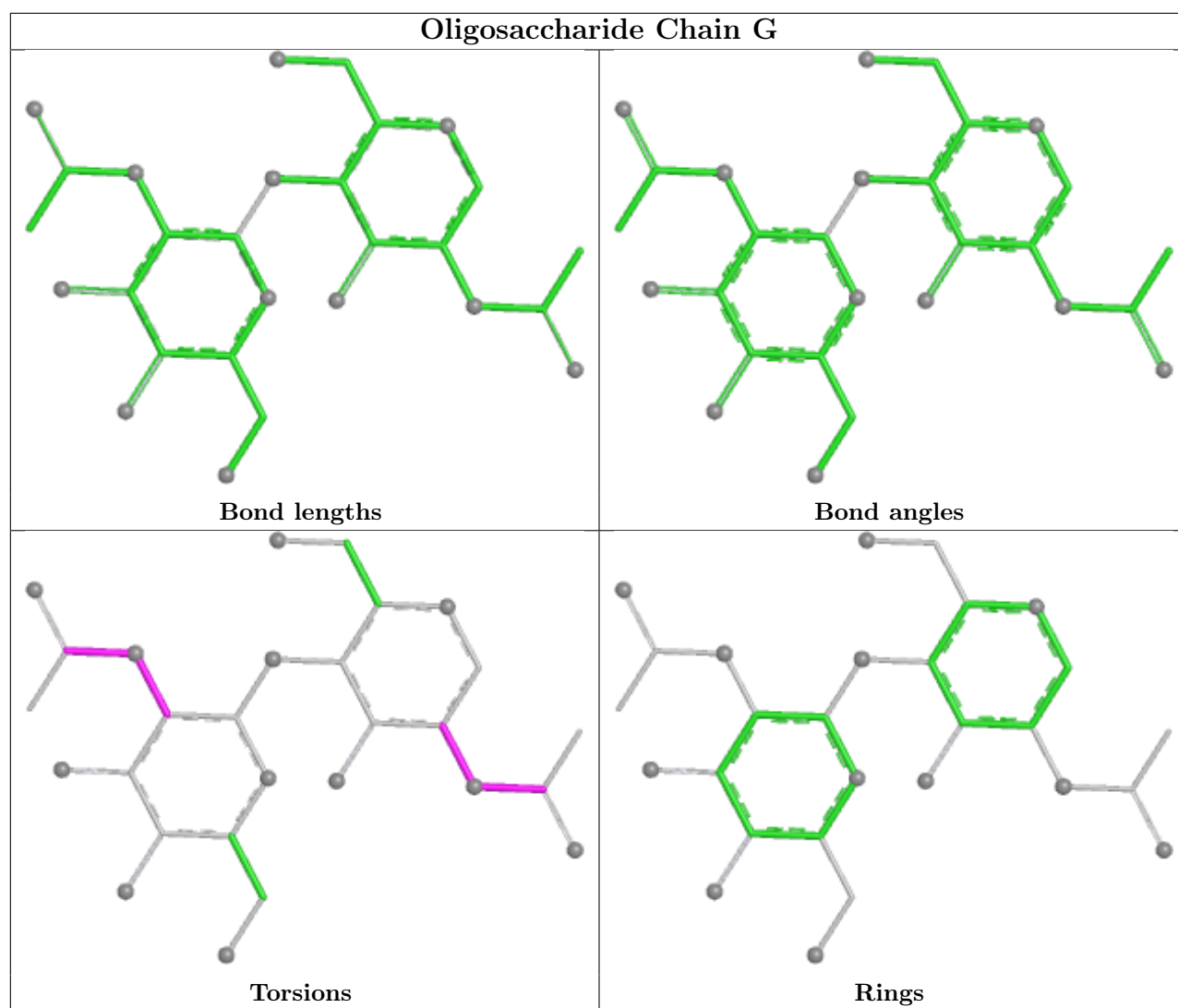
There are no ring outliers.

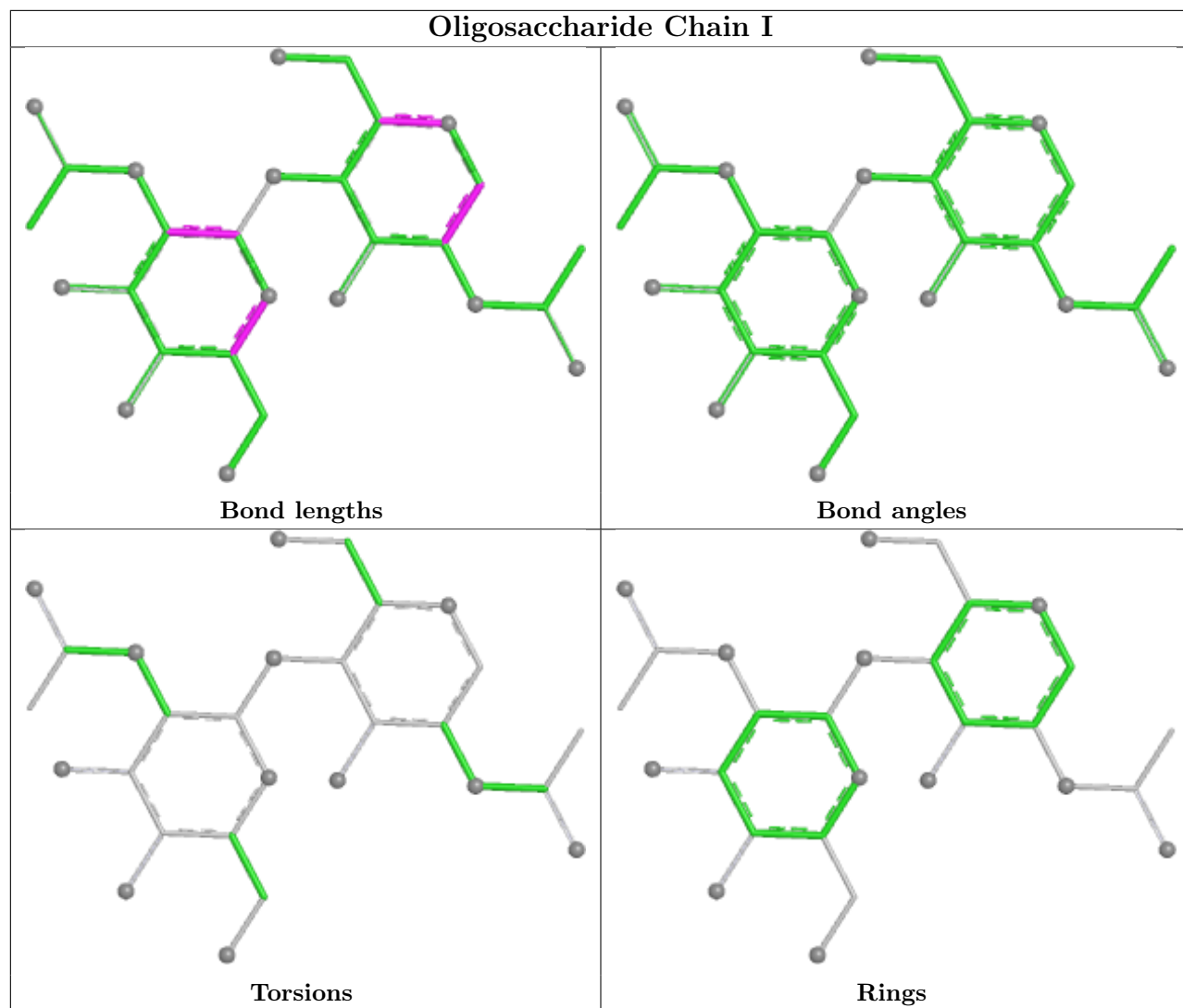
1 monomer is involved in 1 short contact:

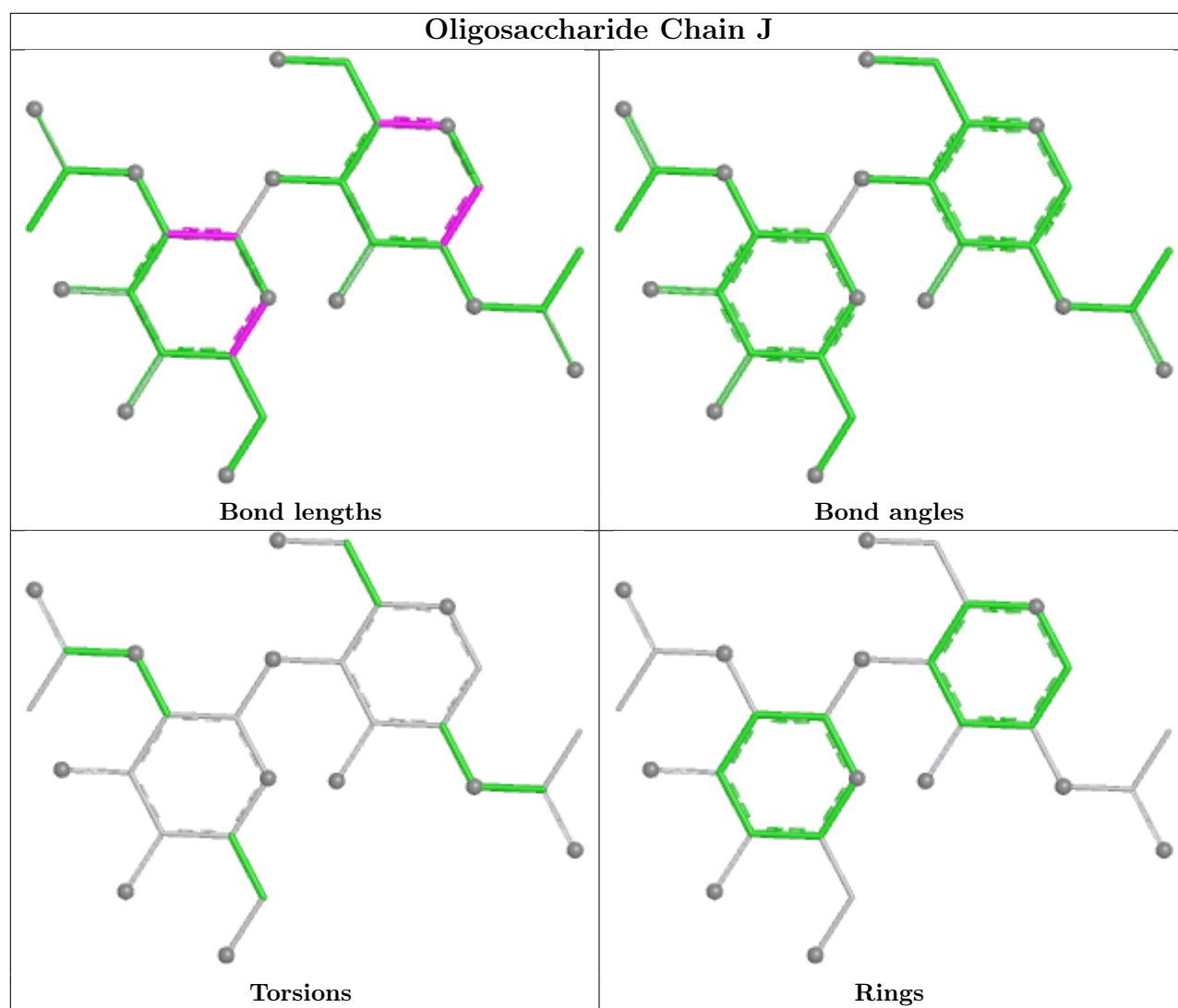
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	1	NAG	1	0

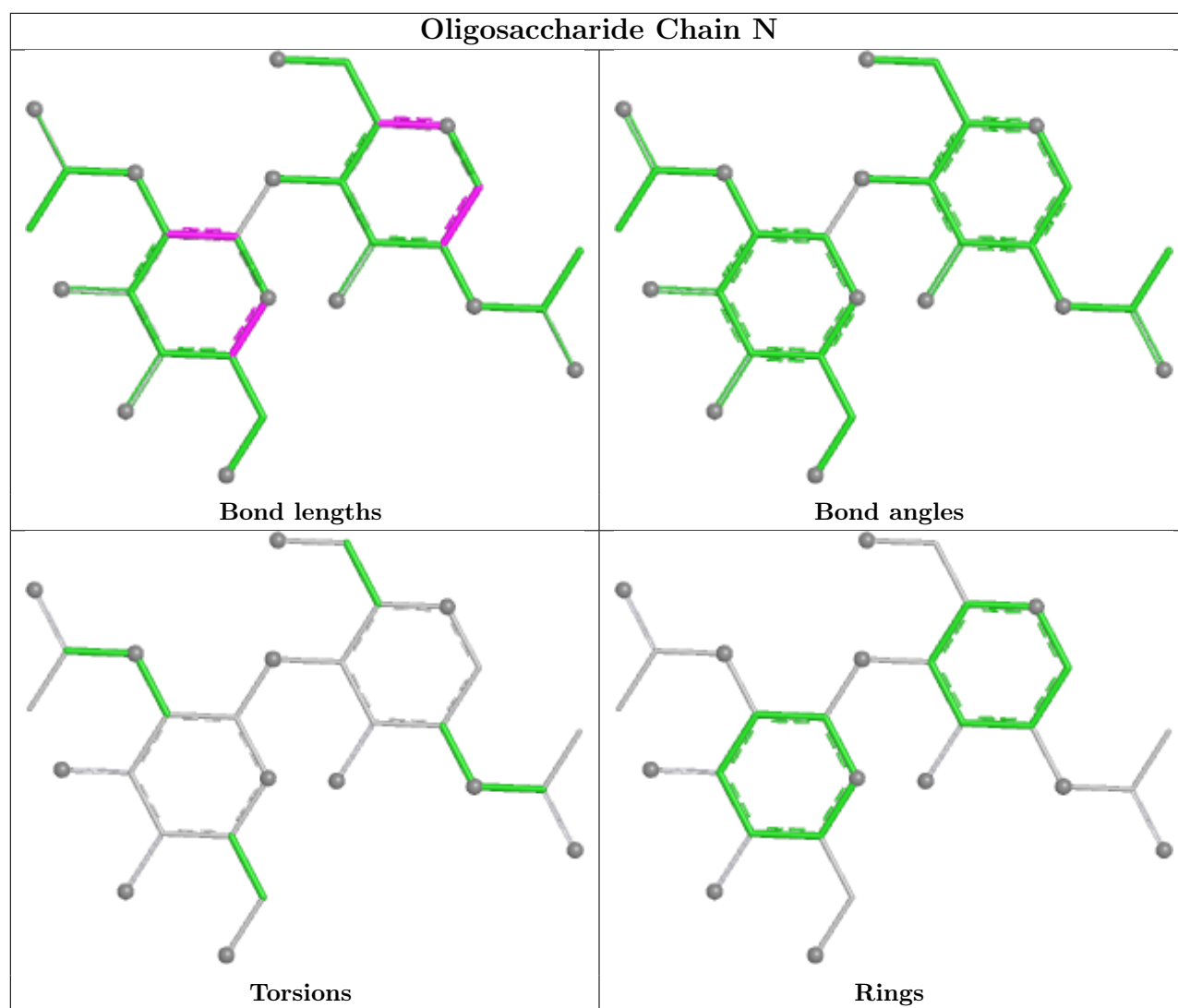
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

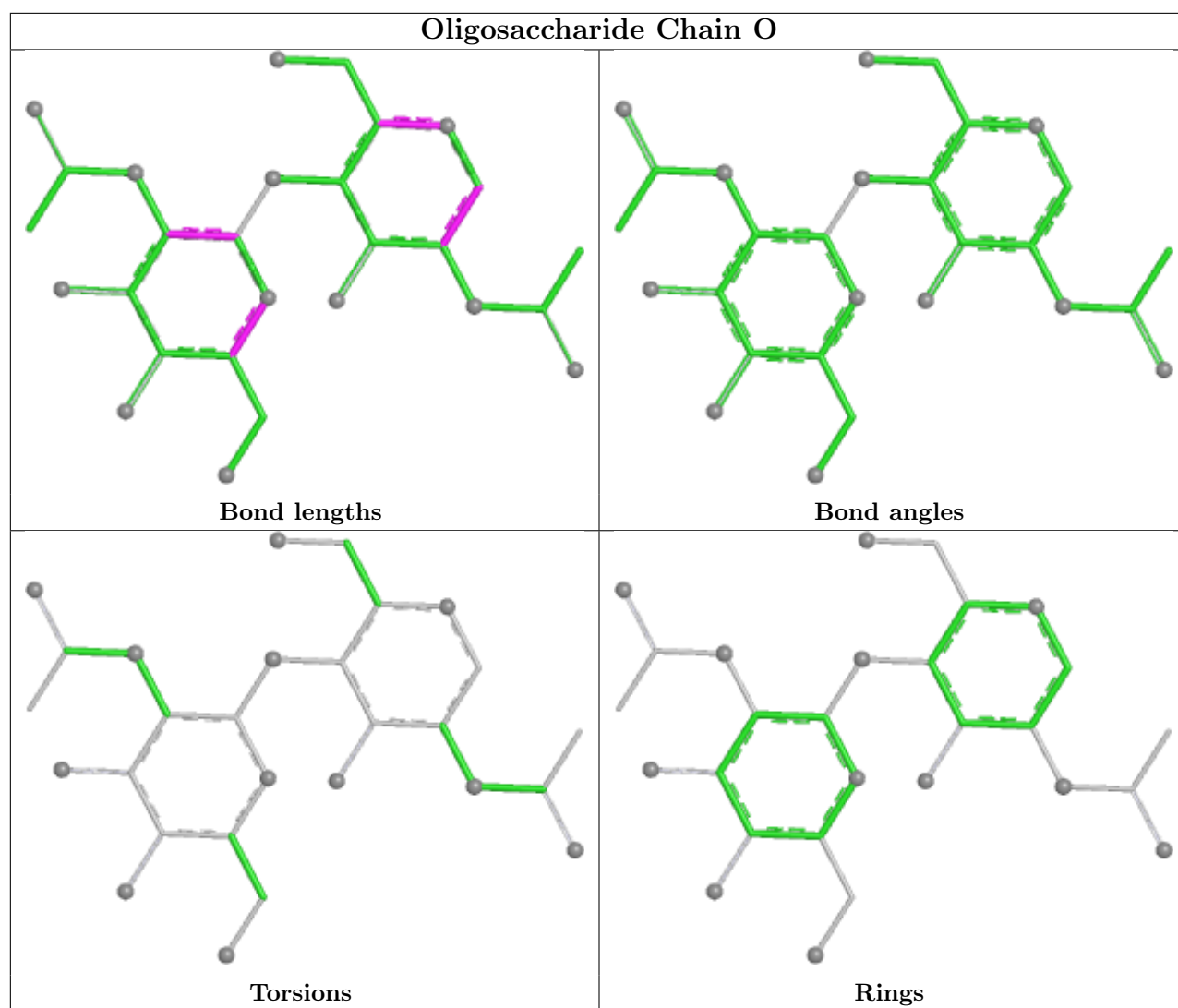


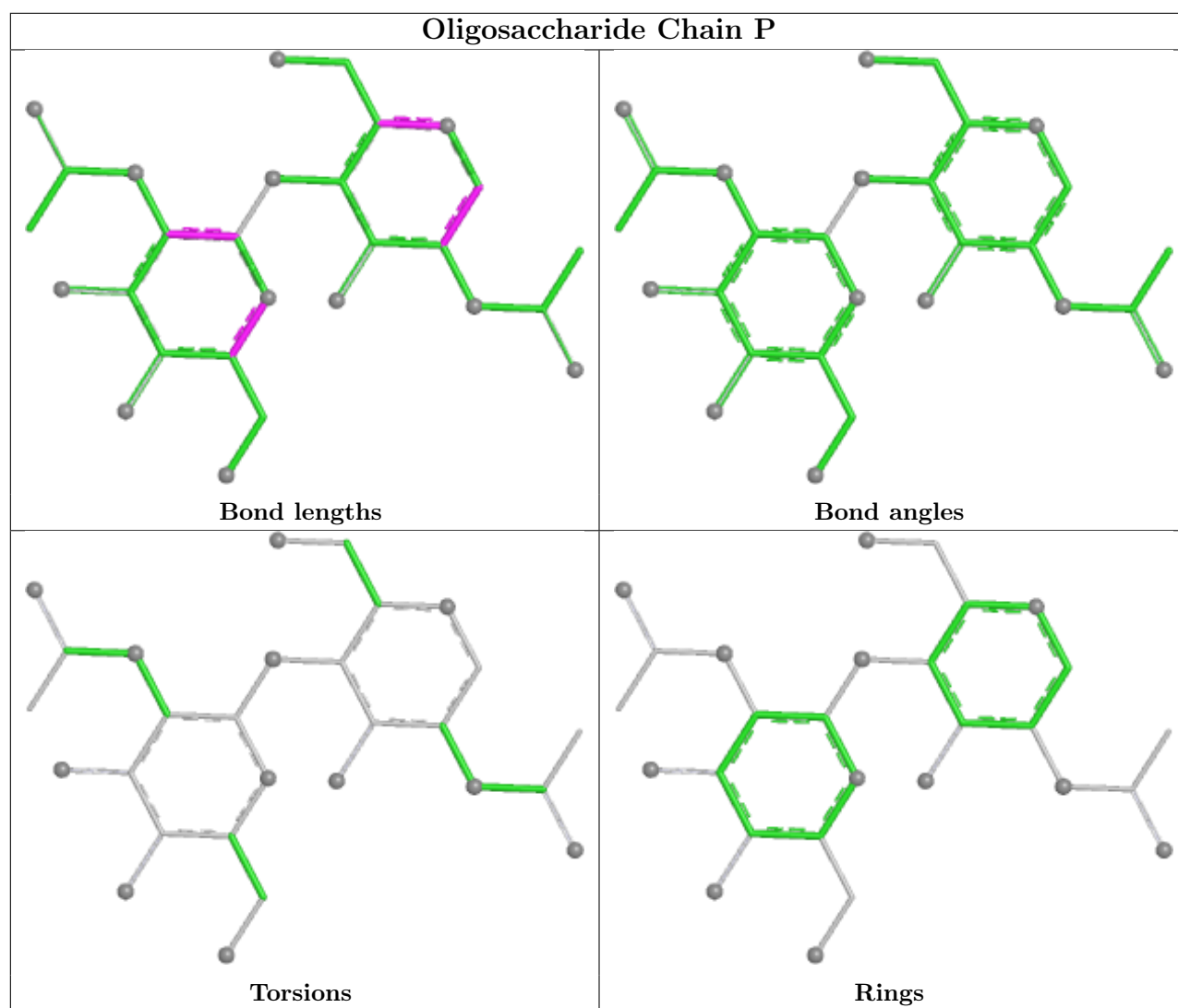


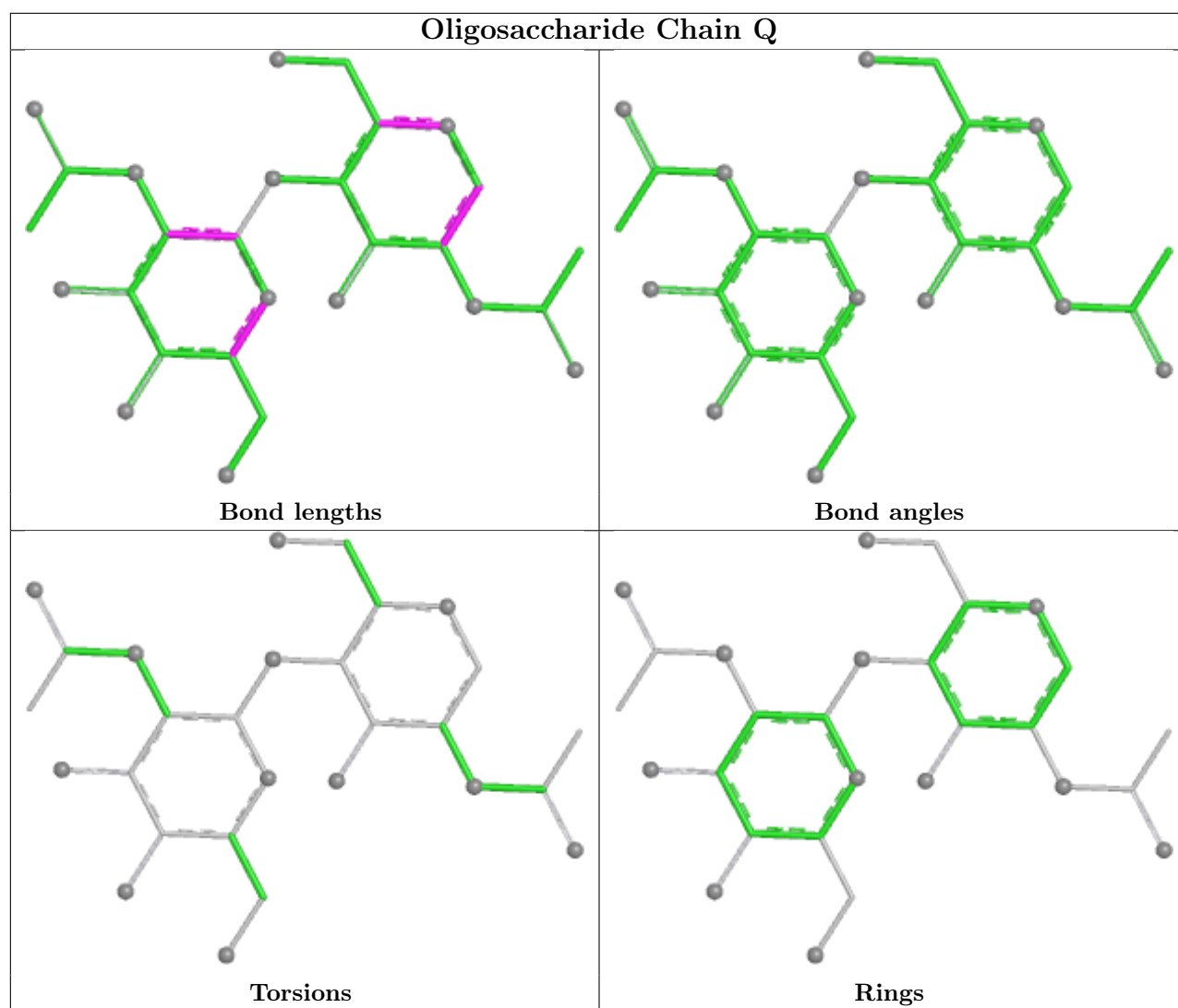


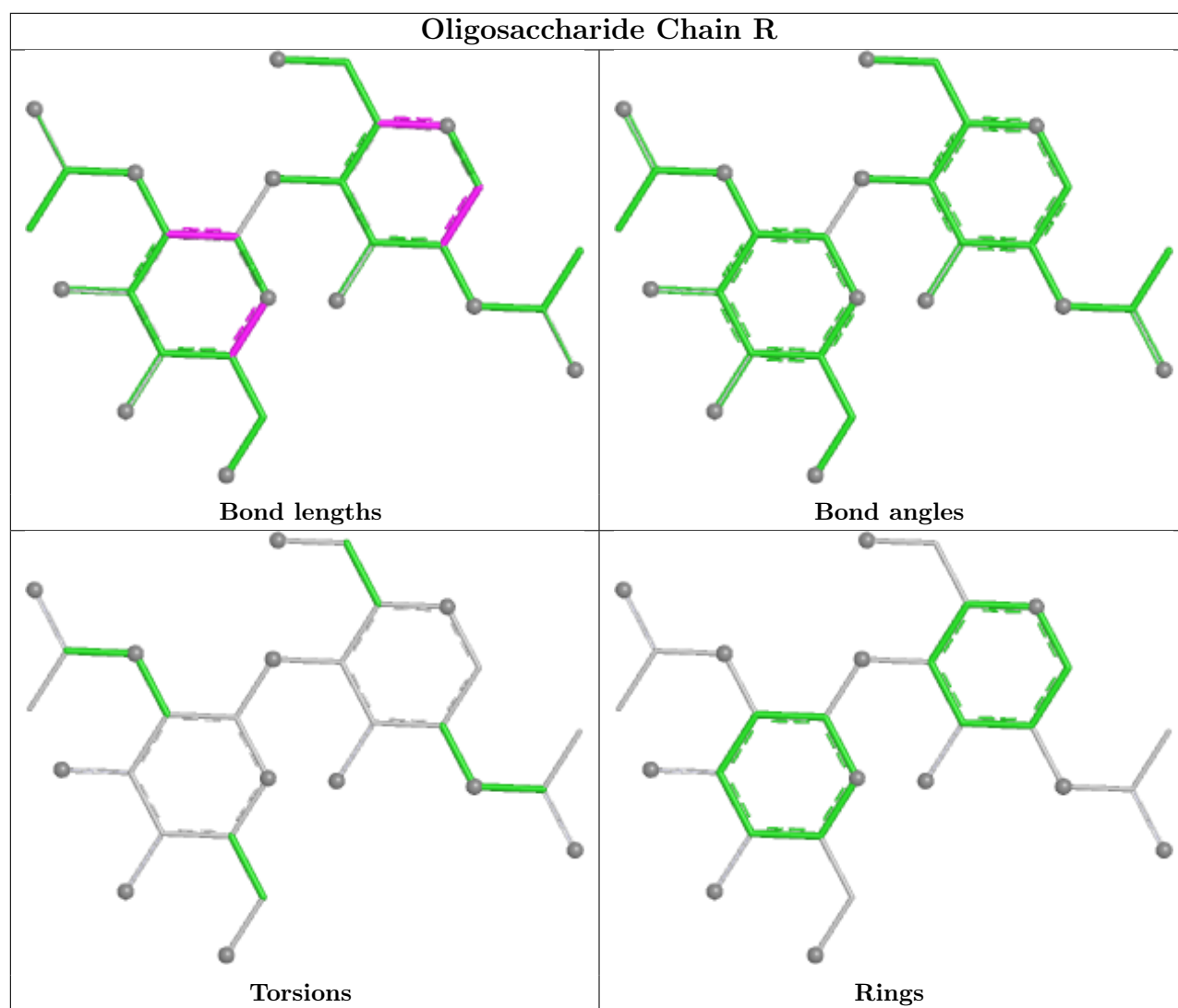


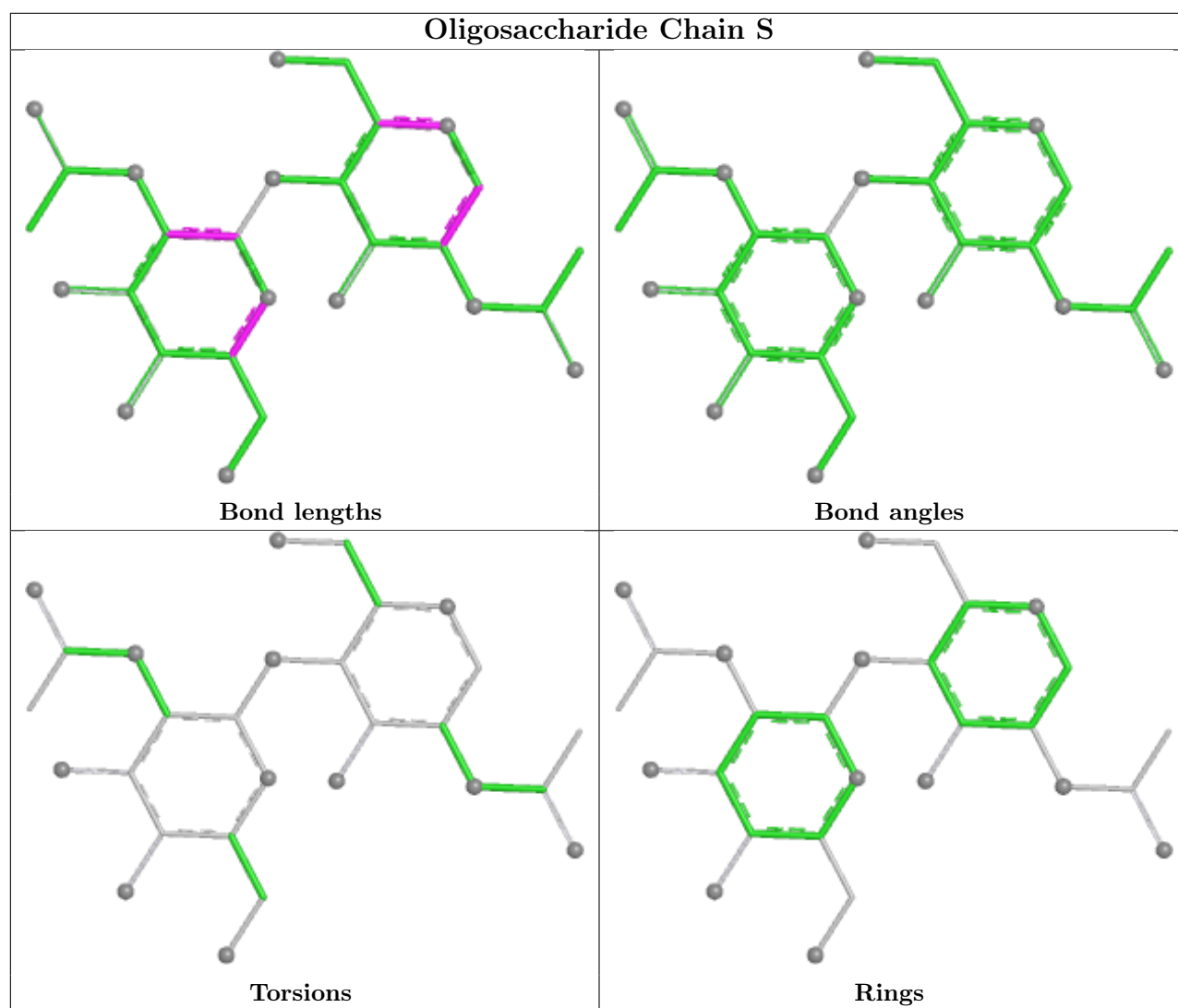


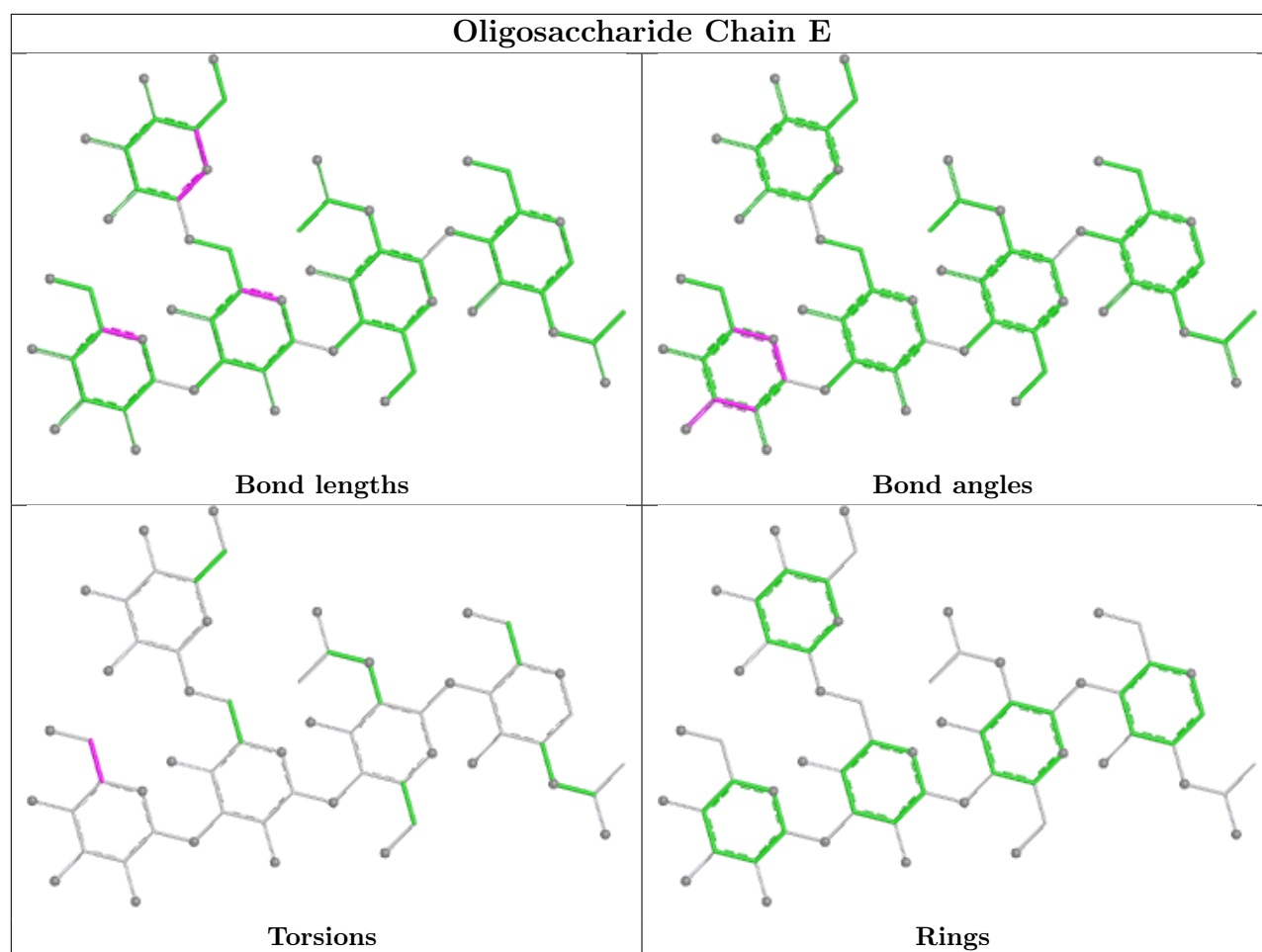


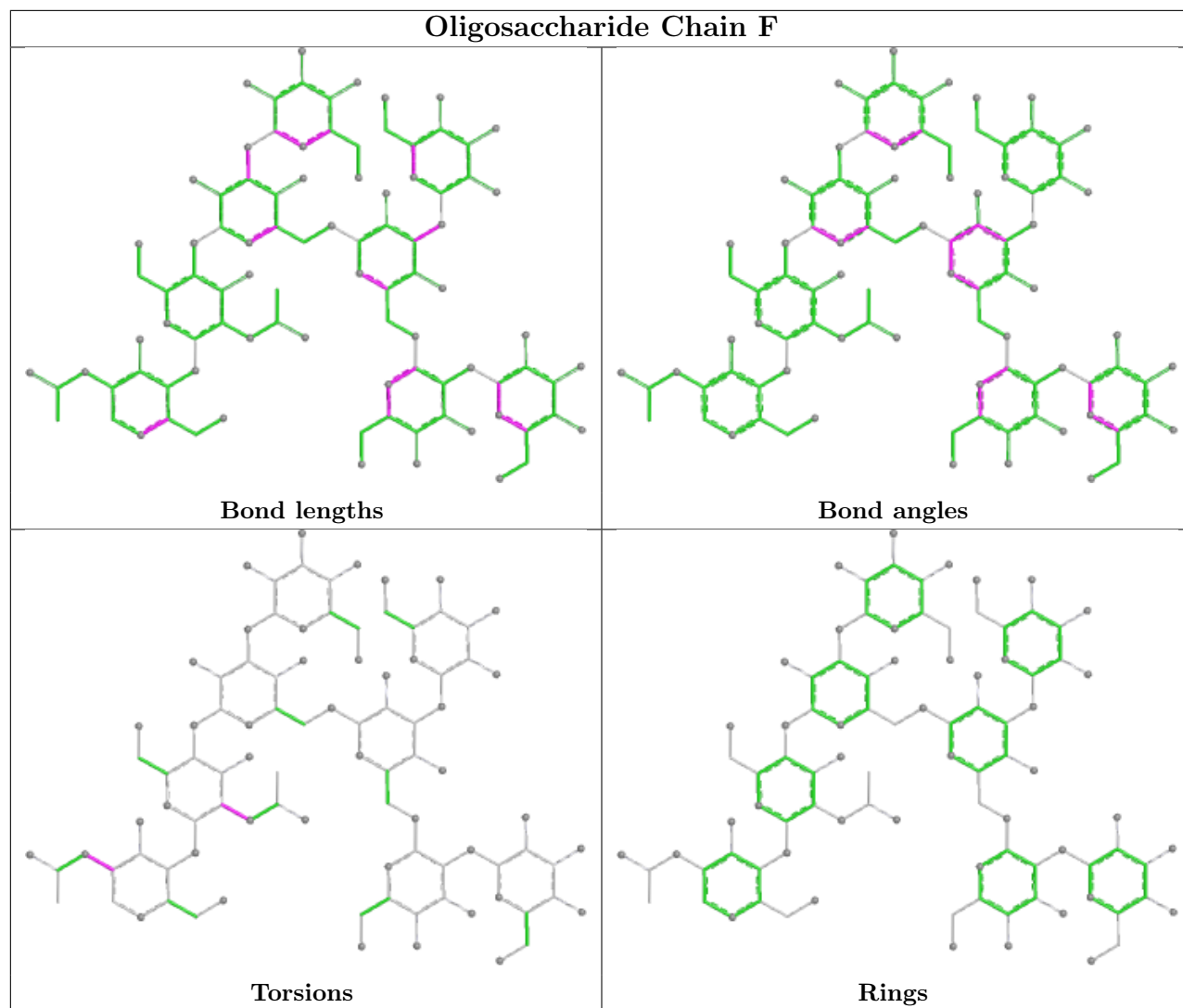


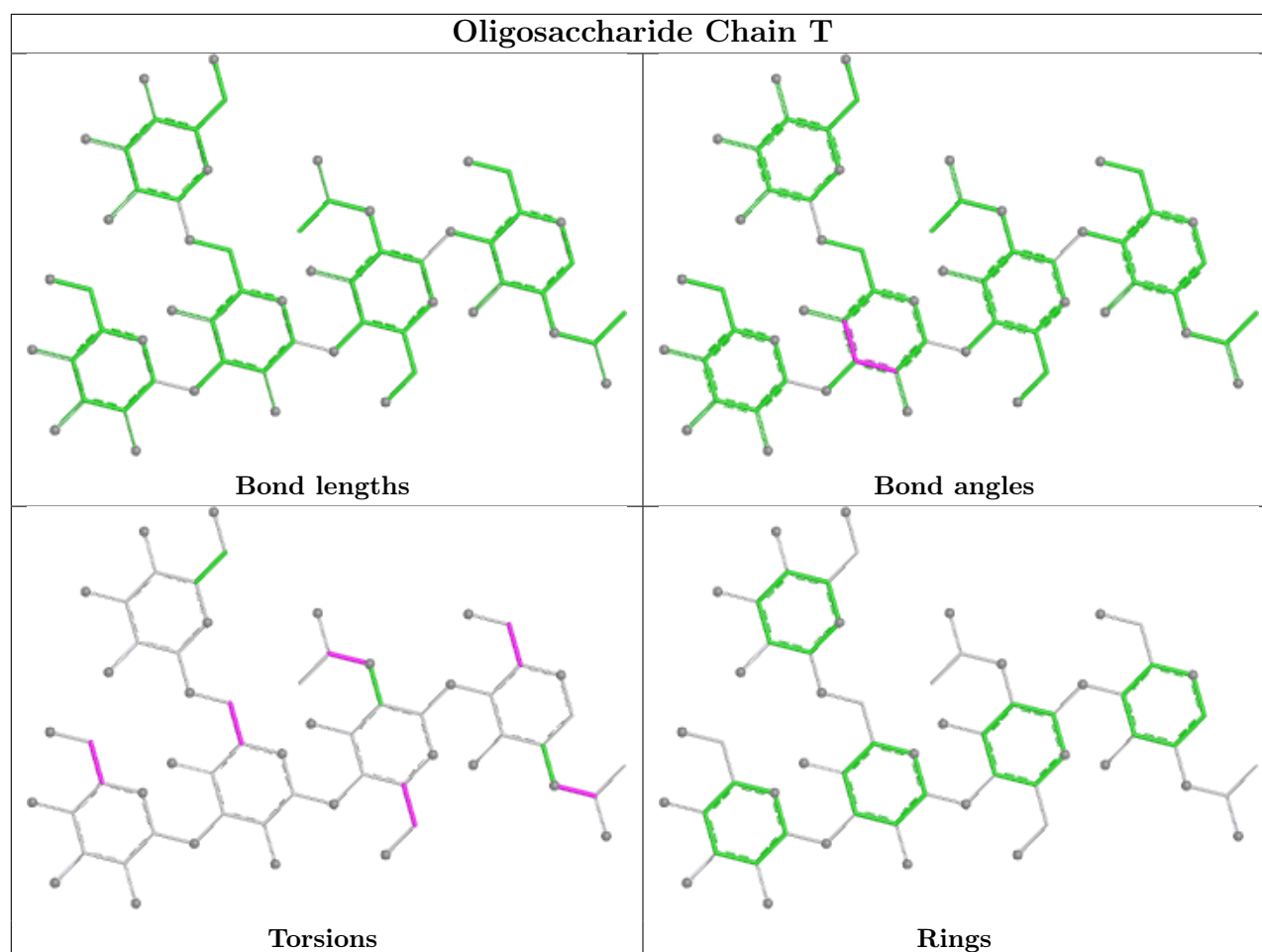












5.6 Ligand geometry [i](#)

31 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	$\# Z > 2$
8	NAG	B	1204	1	14,14,15	1.61	2 (14%)	17,19,21	0.63	0
8	NAG	B	1202	1	14,14,15	1.65	2 (14%)	17,19,21	0.70	0
8	NAG	C	1208	1	14,14,15	1.61	2 (14%)	17,19,21	0.74	0
8	NAG	B	1211	1	14,14,15	1.70	3 (21%)	17,19,21	1.50	2 (11%)
8	NAG	C	1201	1	14,14,15	1.64	2 (14%)	17,19,21	0.77	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	NAG	C	1207	1	14,14,15	1.65	2 (14%)	17,19,21	0.69	0
8	NAG	A	1304	1	14,14,15	1.60	2 (14%)	17,19,21	0.74	0
8	NAG	C	1206	1	14,14,15	1.60	2 (14%)	17,19,21	0.75	0
8	NAG	B	1203	1	14,14,15	1.59	2 (14%)	17,19,21	0.73	0
8	NAG	A	1306	1	14,14,15	1.68	2 (14%)	17,19,21	0.79	0
8	NAG	C	1209	1	14,14,15	1.63	2 (14%)	17,19,21	0.65	0
8	NAG	C	1204	1	14,14,15	1.62	2 (14%)	17,19,21	0.66	0
8	NAG	C	1210	1	14,14,15	1.56	2 (14%)	17,19,21	0.73	0
8	NAG	A	1307	1	14,14,15	0.28	0	17,19,21	0.67	0
8	NAG	A	1309	1	14,14,15	0.28	0	17,19,21	0.66	0
8	NAG	B	1208	1	14,14,15	1.53	2 (14%)	17,19,21	0.74	0
8	NAG	C	1205	1	14,14,15	1.69	3 (21%)	17,19,21	1.52	2 (11%)
8	NAG	B	1206	1	14,14,15	1.63	2 (14%)	17,19,21	0.78	0
8	NAG	A	1302	1	14,14,15	1.70	3 (21%)	17,19,21	1.52	2 (11%)
8	NAG	A	1308	1	14,14,15	0.24	0	17,19,21	0.72	0
8	NAG	A	1305	1	14,14,15	1.51	2 (14%)	17,19,21	0.75	0
8	NAG	A	1310	1	14,14,15	0.26	0	17,19,21	0.63	0
8	NAG	C	1203	1	14,14,15	1.67	2 (14%)	17,19,21	0.80	0
8	NAG	B	1205	1	14,14,15	1.58	2 (14%)	17,19,21	0.72	0
8	NAG	B	1209	1	14,14,15	1.66	2 (14%)	17,19,21	0.79	0
8	NAG	A	1301	1	14,14,15	1.61	2 (14%)	17,19,21	0.65	0
8	NAG	C	1202	1	14,14,15	1.50	2 (14%)	17,19,21	0.74	0
8	NAG	A	1303	1	14,14,15	1.66	2 (14%)	17,19,21	0.71	0
8	NAG	B	1201	1	14,14,15	1.63	2 (14%)	17,19,21	0.73	0
8	NAG	B	1210	1	14,14,15	1.61	2 (14%)	17,19,21	0.66	0
8	NAG	B	1207	1	14,14,15	1.53	2 (14%)	17,19,21	0.74	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
8	NAG	B	1204	1	-	1/6/23/26	0/1/1/1
8	NAG	B	1202	1	-	0/6/23/26	0/1/1/1
8	NAG	C	1208	1	-	0/6/23/26	0/1/1/1
8	NAG	B	1211	1	-	1/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	C	1201	1	-	0/6/23/26	0/1/1/1
8	NAG	C	1207	1	-	0/6/23/26	0/1/1/1
8	NAG	A	1304	1	-	0/6/23/26	0/1/1/1
8	NAG	C	1206	1	-	0/6/23/26	0/1/1/1
8	NAG	B	1203	1	-	0/6/23/26	0/1/1/1
8	NAG	A	1306	1	-	2/6/23/26	0/1/1/1
8	NAG	C	1209	1	-	1/6/23/26	0/1/1/1
8	NAG	C	1204	1	-	0/6/23/26	0/1/1/1
8	NAG	C	1210	1	-	0/6/23/26	0/1/1/1
8	NAG	A	1307	1	-	2/6/23/26	0/1/1/1
8	NAG	A	1309	1	-	3/6/23/26	0/1/1/1
8	NAG	B	1208	1	-	1/6/23/26	0/1/1/1
8	NAG	C	1205	1	-	1/6/23/26	0/1/1/1
8	NAG	B	1206	1	-	0/6/23/26	0/1/1/1
8	NAG	A	1302	1	-	1/6/23/26	0/1/1/1
8	NAG	A	1308	1	-	3/6/23/26	0/1/1/1
8	NAG	A	1305	1	-	1/6/23/26	0/1/1/1
8	NAG	A	1310	1	-	4/6/23/26	0/1/1/1
8	NAG	C	1203	1	-	2/6/23/26	0/1/1/1
8	NAG	B	1205	1	-	0/6/23/26	0/1/1/1
8	NAG	B	1209	1	-	2/6/23/26	0/1/1/1
8	NAG	A	1301	1	-	0/6/23/26	0/1/1/1
8	NAG	C	1202	1	-	1/6/23/26	0/1/1/1
8	NAG	A	1303	1	-	0/6/23/26	0/1/1/1
8	NAG	B	1201	1	-	0/6/23/26	0/1/1/1
8	NAG	B	1210	1	-	0/6/23/26	0/1/1/1
8	NAG	B	1207	1	-	0/6/23/26	0/1/1/1

All (57) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1303	NAG	C1-C2	4.75	1.58	1.52
8	B	1206	NAG	C1-C2	4.72	1.58	1.52
8	C	1207	NAG	C1-C2	4.72	1.58	1.52
8	C	1201	NAG	C1-C2	4.72	1.58	1.52
8	A	1306	NAG	C1-C2	4.71	1.58	1.52
8	C	1203	NAG	C1-C2	4.68	1.58	1.52
8	B	1209	NAG	C1-C2	4.67	1.58	1.52
8	B	1202	NAG	C1-C2	4.67	1.58	1.52
8	B	1210	NAG	C1-C2	4.60	1.58	1.52
8	B	1201	NAG	C1-C2	4.59	1.58	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	1204	NAG	C1-C2	4.59	1.58	1.52
8	A	1301	NAG	C1-C2	4.55	1.58	1.52
8	C	1209	NAG	C1-C2	4.50	1.58	1.52
8	C	1208	NAG	C1-C2	4.48	1.58	1.52
8	C	1206	NAG	C1-C2	4.44	1.58	1.52
8	A	1304	NAG	C1-C2	4.44	1.58	1.52
8	B	1205	NAG	C1-C2	4.43	1.58	1.52
8	B	1204	NAG	C1-C2	4.42	1.58	1.52
8	B	1203	NAG	C1-C2	4.38	1.58	1.52
8	B	1211	NAG	C1-C2	4.38	1.58	1.52
8	B	1208	NAG	C1-C2	4.37	1.58	1.52
8	C	1210	NAG	C1-C2	4.36	1.58	1.52
8	A	1302	NAG	C1-C2	4.34	1.58	1.52
8	C	1205	NAG	C1-C2	4.34	1.58	1.52
8	C	1202	NAG	C1-C2	4.31	1.58	1.52
8	A	1305	NAG	C1-C2	4.31	1.58	1.52
8	B	1207	NAG	C1-C2	4.23	1.58	1.52
8	B	1201	NAG	O5-C5	2.56	1.48	1.43
8	A	1303	NAG	O5-C5	2.52	1.48	1.43
8	A	1302	NAG	O5-C5	2.52	1.48	1.43
8	C	1205	NAG	O5-C5	2.50	1.48	1.43
8	C	1207	NAG	O5-C5	2.49	1.48	1.43
8	C	1209	NAG	O5-C5	2.49	1.48	1.43
8	B	1211	NAG	O5-C5	2.45	1.48	1.43
8	C	1203	NAG	O5-C5	2.45	1.48	1.43
8	B	1204	NAG	O5-C5	2.45	1.48	1.43
8	C	1206	NAG	O5-C5	2.45	1.48	1.43
8	B	1202	NAG	O5-C5	2.44	1.48	1.43
8	B	1203	NAG	O5-C5	2.44	1.48	1.43
8	B	1207	NAG	O5-C5	2.43	1.48	1.43
8	C	1210	NAG	O5-C5	2.39	1.48	1.43
8	C	1208	NAG	O5-C5	2.39	1.48	1.43
8	A	1306	NAG	O5-C5	2.38	1.48	1.43
8	B	1209	NAG	O5-C5	2.36	1.48	1.43
8	A	1304	NAG	O5-C5	2.35	1.48	1.43
8	B	1205	NAG	O5-C5	2.34	1.48	1.43
8	C	1201	NAG	O5-C5	2.28	1.47	1.43
8	B	1206	NAG	O5-C5	2.27	1.47	1.43
8	B	1210	NAG	O5-C5	2.26	1.47	1.43
8	A	1301	NAG	O5-C5	2.26	1.47	1.43
8	C	1204	NAG	O5-C5	2.25	1.47	1.43
8	A	1302	NAG	C2-N2	2.13	1.49	1.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	1208	NAG	O5-C5	2.09	1.47	1.43
8	B	1211	NAG	C2-N2	2.07	1.49	1.46
8	A	1305	NAG	O5-C5	2.04	1.47	1.43
8	C	1202	NAG	O5-C5	2.03	1.47	1.43
8	C	1205	NAG	C2-N2	2.01	1.49	1.46

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	1205	NAG	C2-N2-C7	5.05	129.67	122.90
8	A	1302	NAG	C2-N2-C7	5.03	129.64	122.90
8	B	1211	NAG	C2-N2-C7	5.01	129.62	122.90
8	A	1302	NAG	C1-C2-N2	-2.20	106.97	110.43
8	C	1205	NAG	C1-C2-N2	-2.19	106.99	110.43
8	B	1211	NAG	C1-C2-N2	-2.17	107.01	110.43

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1302	NAG	C3-C2-N2-C7
8	A	1308	NAG	C1-C2-N2-C7
8	A	1308	NAG	C8-C7-N2-C2
8	A	1308	NAG	O7-C7-N2-C2
8	A	1309	NAG	C1-C2-N2-C7
8	A	1309	NAG	C8-C7-N2-C2
8	A	1309	NAG	O7-C7-N2-C2
8	A	1310	NAG	C1-C2-N2-C7
8	A	1310	NAG	C8-C7-N2-C2
8	A	1310	NAG	O7-C7-N2-C2
8	B	1211	NAG	C3-C2-N2-C7
8	C	1205	NAG	C3-C2-N2-C7
8	A	1307	NAG	C8-C7-N2-C2
8	A	1307	NAG	O7-C7-N2-C2
8	A	1305	NAG	O5-C5-C6-O6
8	B	1208	NAG	O5-C5-C6-O6
8	C	1202	NAG	O5-C5-C6-O6
8	A	1306	NAG	C4-C5-C6-O6
8	B	1209	NAG	C4-C5-C6-O6
8	C	1203	NAG	C4-C5-C6-O6
8	A	1310	NAG	O5-C5-C6-O6
8	A	1306	NAG	O5-C5-C6-O6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
8	C	1203	NAG	O5-C5-C6-O6
8	B	1209	NAG	O5-C5-C6-O6
8	B	1204	NAG	C4-C5-C6-O6
8	C	1209	NAG	C4-C5-C6-O6

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	C	1208	NAG	1	0
8	C	1201	NAG	1	0
8	A	1304	NAG	1	0
8	B	1203	NAG	1	0
8	B	1206	NAG	1	0
8	A	1310	NAG	1	0

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.

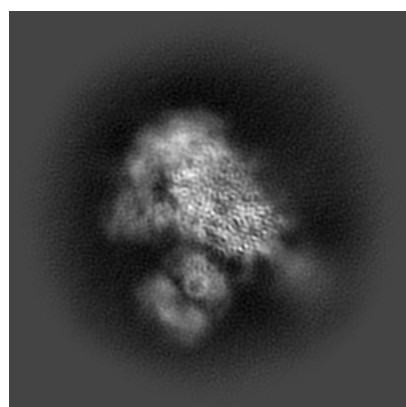
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23094. These allow visual inspection of the internal detail of the map and identification of artifacts.

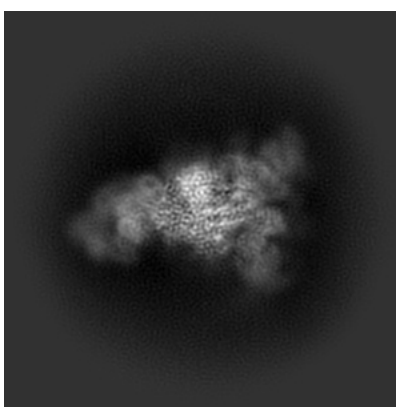
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

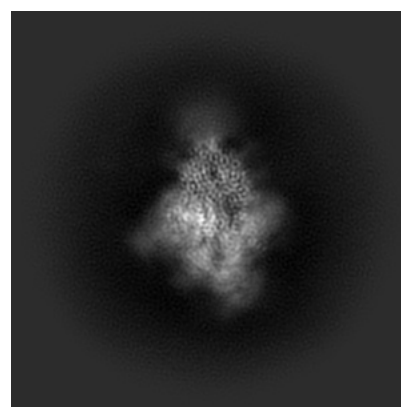
6.1.1 Primary map



X



Y

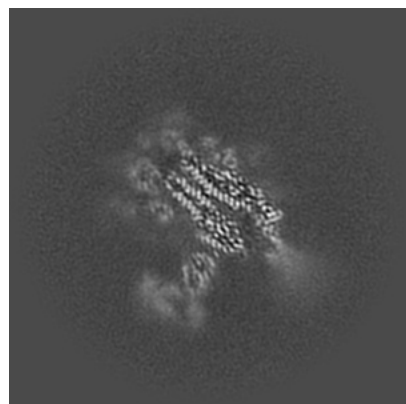


Z

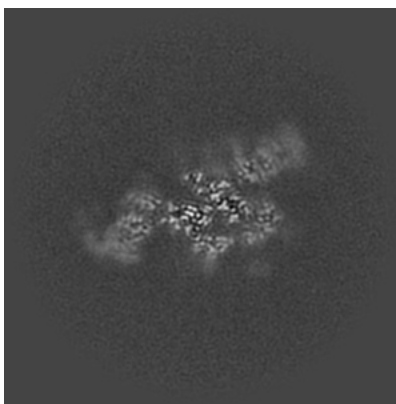
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

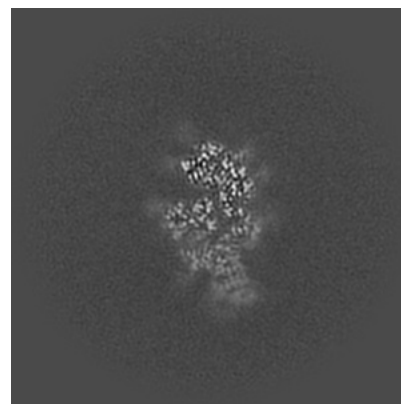
6.2.1 Primary map



X Index: 160



Y Index: 160

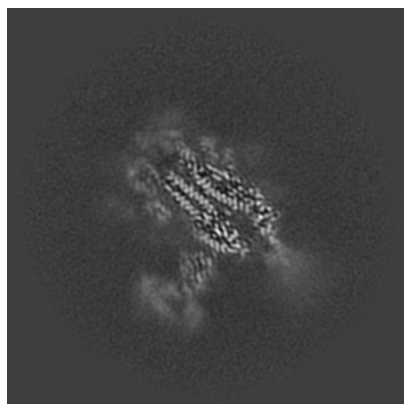


Z Index: 160

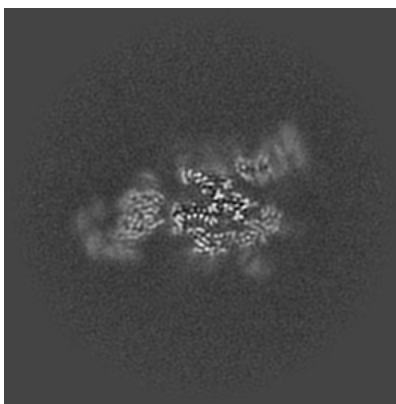
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

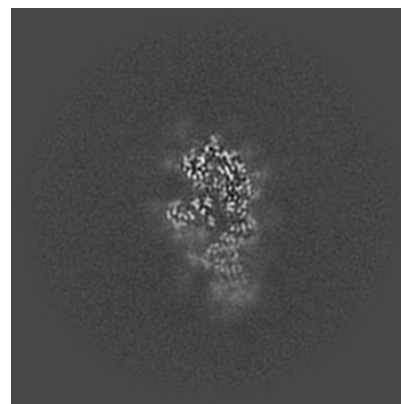
6.3.1 Primary map



X Index: 159



Y Index: 156

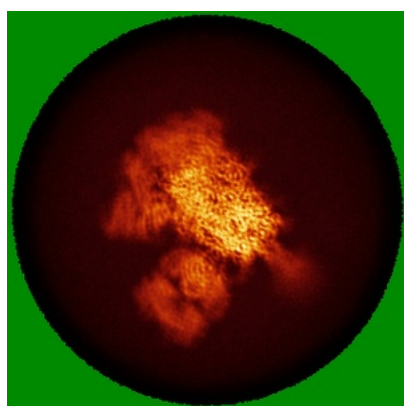


Z Index: 157

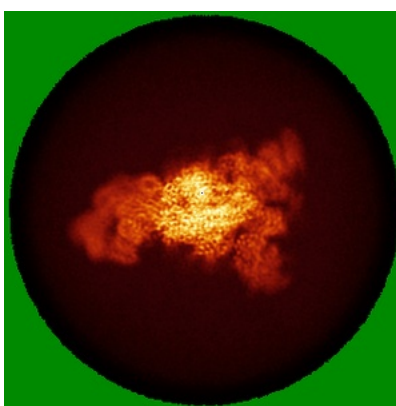
The images above show the largest variance slices of the map in three orthogonal directions.

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

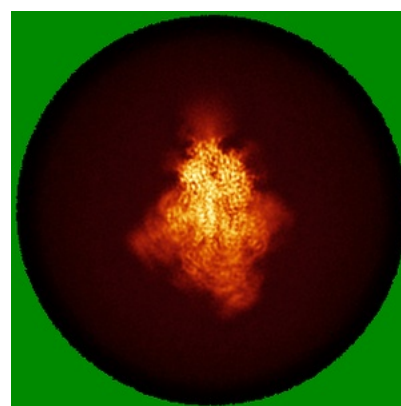
6.4.1 Primary map



X



Y

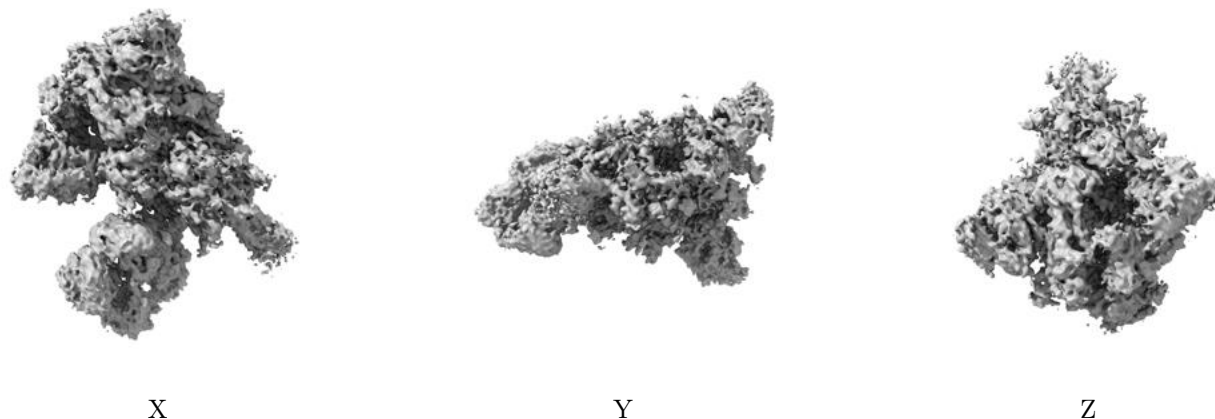


Z

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 0.184. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

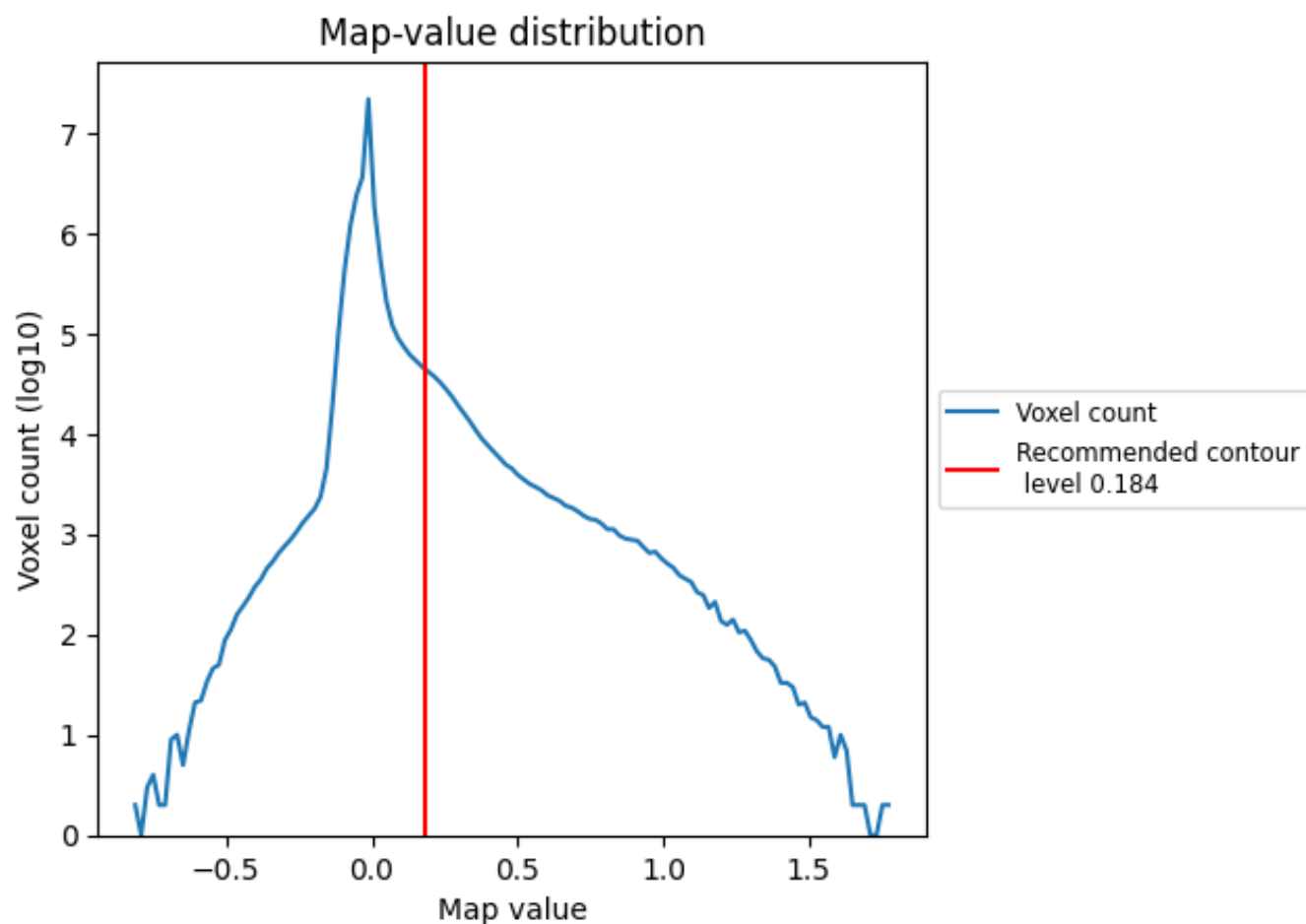
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

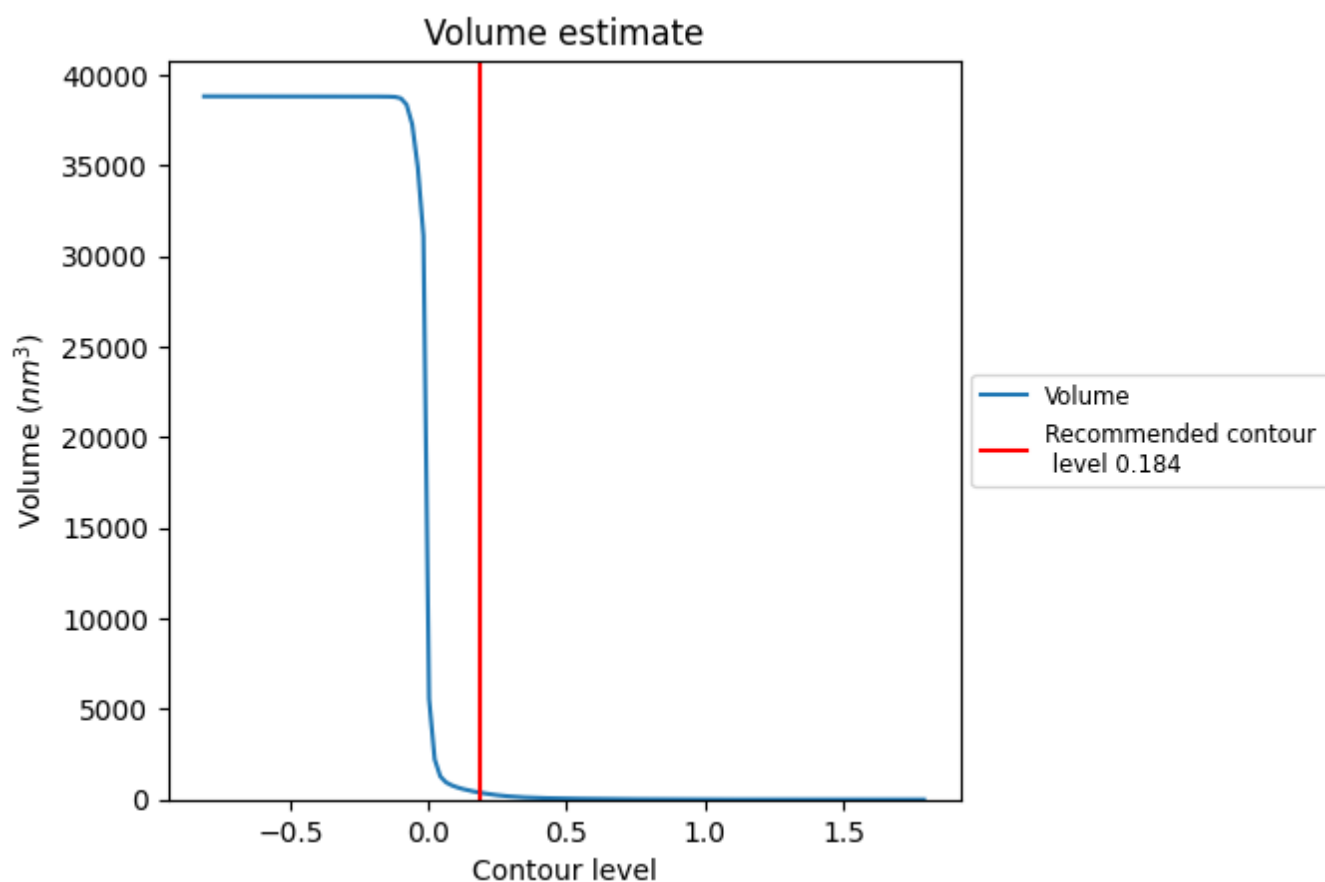
This section contains the results of statistical analysis of the map.

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.

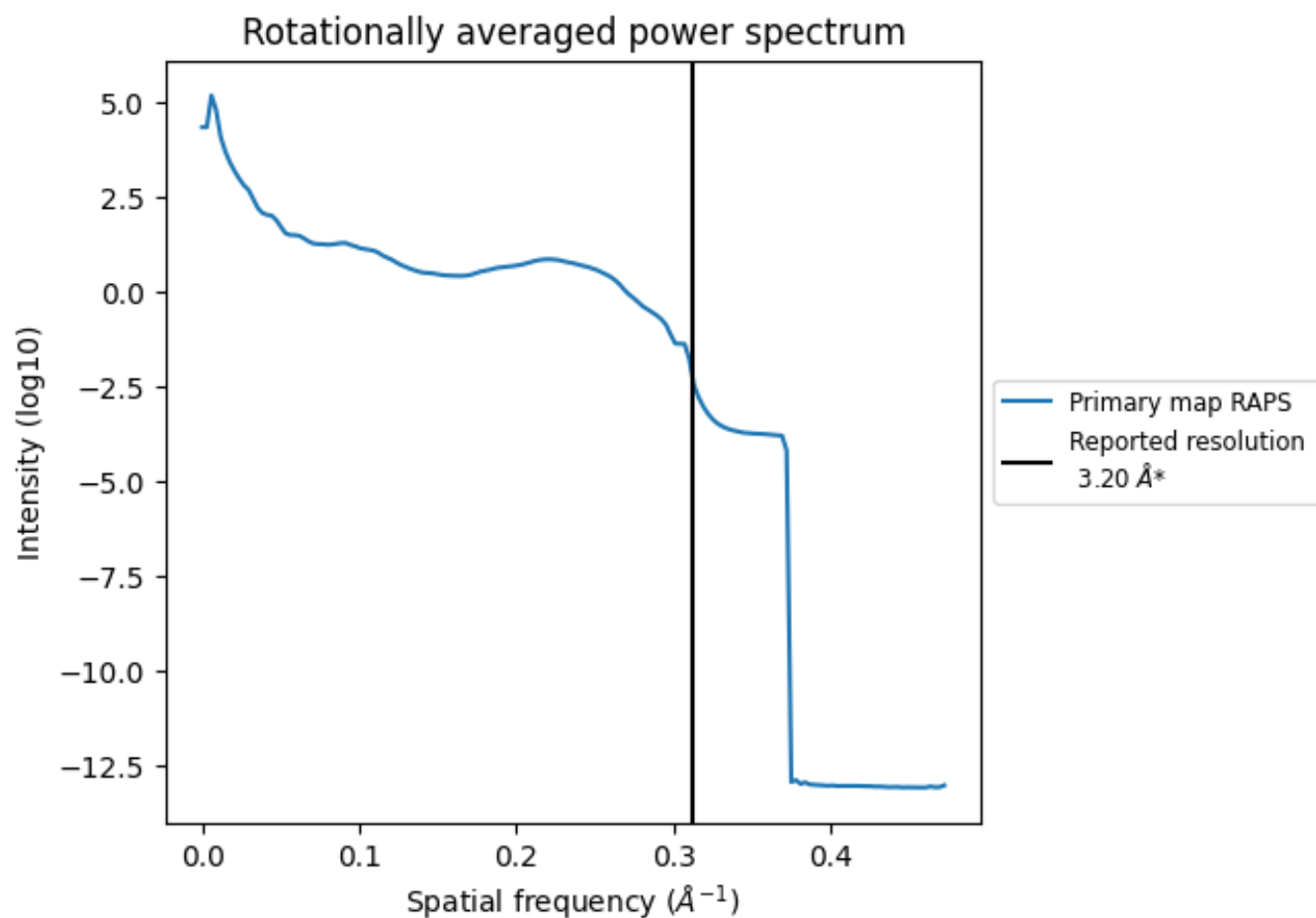
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 388 nm³; this corresponds to an approximate mass of 350 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 0.312 Å⁻¹

8 Fourier-Shell correlation

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

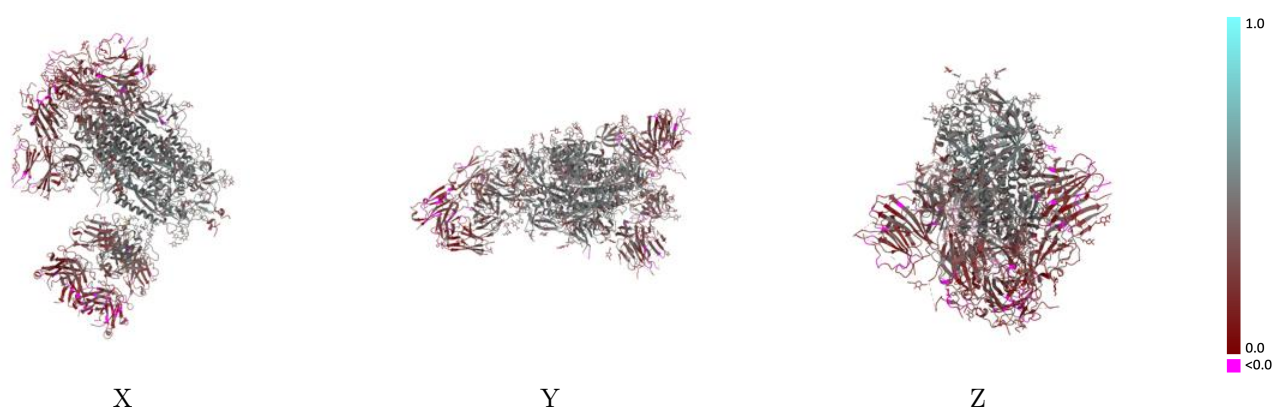
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23094 and PDB model 7L02. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

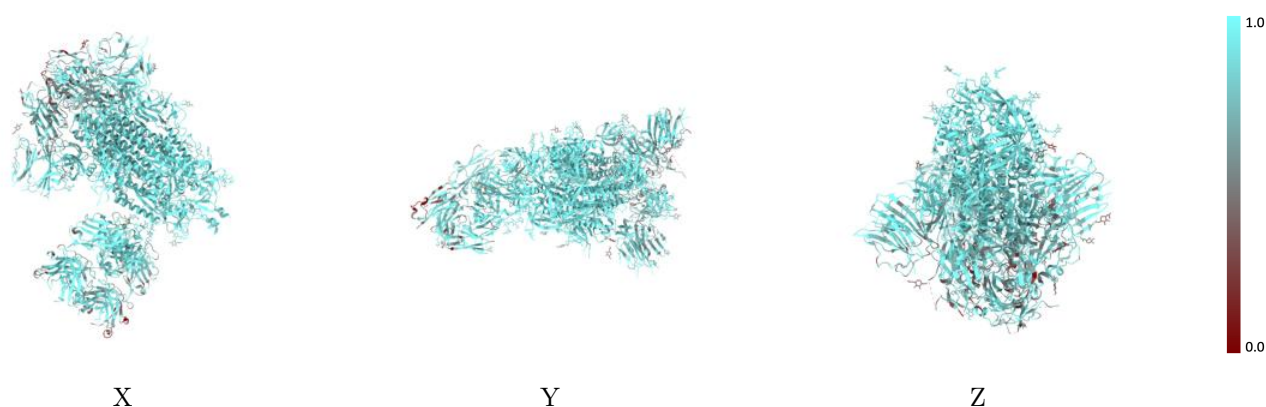
This section was not generated.

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



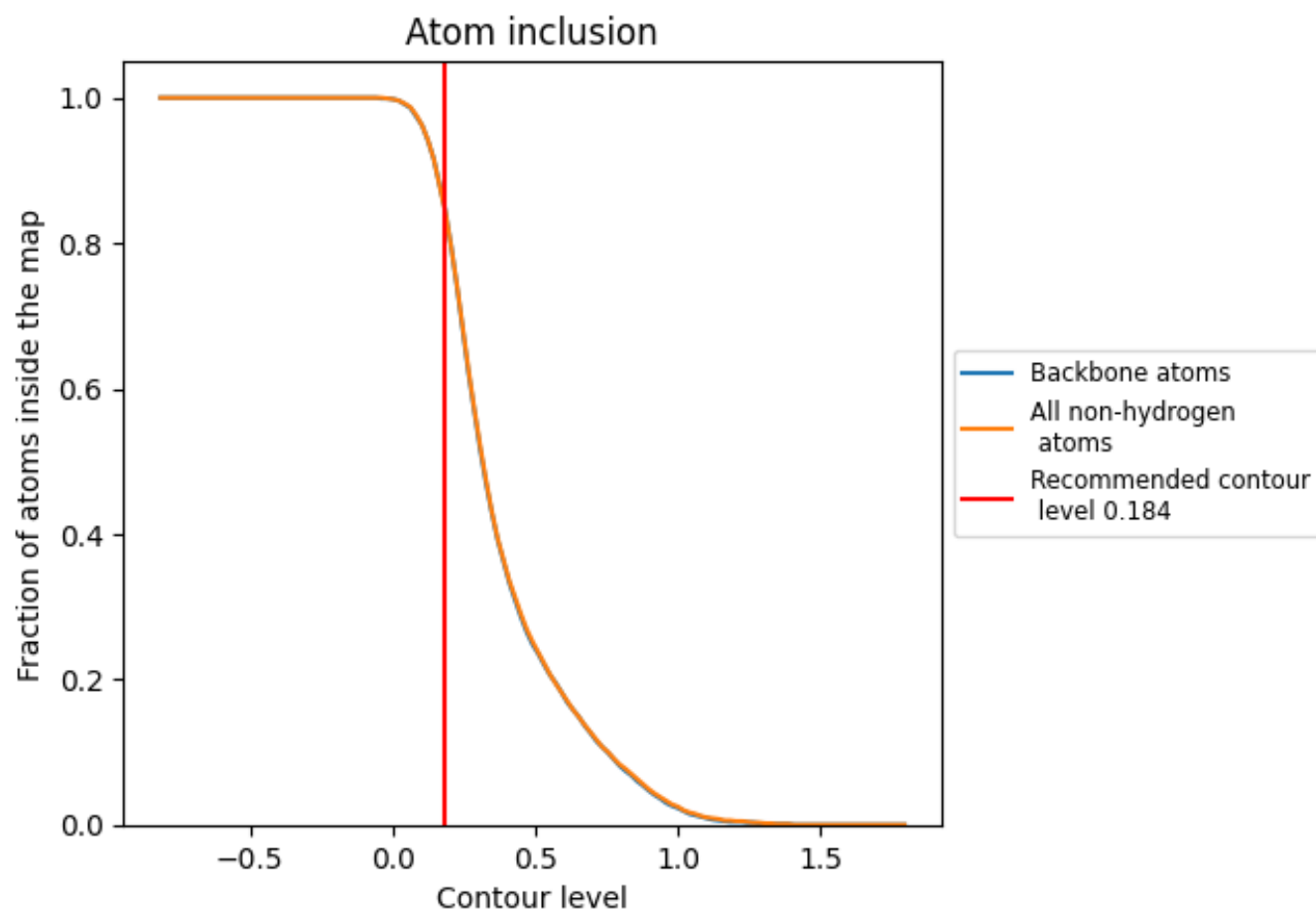
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.184).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 85% 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 (0.184) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.3410
A	 0.8600	 0.3690
B	 0.8460	 0.3540
C	 0.8590	 0.3590
D	 0.8210	 0.3480
E	 1.0000	 0.4790
F	 0.8830	 0.4460
G	 0.9640	 0.4030
H	 0.8660	 0.3110
I	 0.8930	 0.4630
J	 0.8930	 0.3870
K	 0.8550	 0.2630
L	 0.8190	 0.1910
M	 0.8180	 0.2990
N	 0.9640	 0.3810
O	 0.7860	 0.3010
P	 0.8930	 0.4350
Q	 0.7860	 0.3380
R	 0.9290	 0.4030
S	 0.8210	 0.3590
T	 0.8850	 0.3830

