



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 12:41 AM UTC

PDB ID : 1YPZ / pdb_00001ypz
Title : Immune receptor
Authors : Adams, E.J.; Garcia, K.C.
Deposited on : 2005-01-31
Resolution : 3.40 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

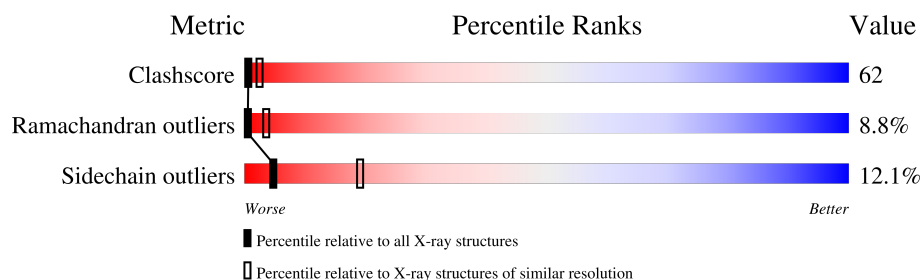
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)

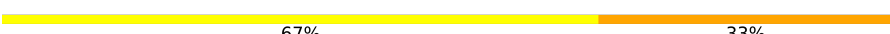
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	260	23% 57% 18% .
1	C	260	20% 62% 17% .
2	B	102	32% 57% 10% .
2	D	102	22% 62% 16% .
3	E	207	28% 53% 17% .
3	G	207	35% 49% 14% .
4	F	230	27% 52% 18% .
4	H	230	34% 50% 14% .

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Mol	Chain	Length	Quality of chain
5	I	3	 33% 67%
5	L	3	 67% 33%
6	J	2	 100%
6	K	2	 50% 50%
7	M	3	 67% 33%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NAG	I	1	X	-	X	-
5	NAG	L	1	X	-	X	-
6	NAG	J	1	X	-	X	-
6	NAG	K	1	-	-	X	-
7	NAG	M	1	X	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12984 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 H2-T22 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	0	0
			2106	1330	363	402	11			
1	C	260	Total	C	N	O	S	0	0	0
			2106	1330	363	402	11			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	102	Total	C	N	O	S	0	0	0
			849	540	143	163	3			
2	D	102	Total	C	N	O	S	0	0	0
			849	540	143	163	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	ASP	-	cloning artifact	UNP P61769
B	0	PRO	-	cloning artifact	UNP P61769
D	-1	ASP	-	cloning artifact	UNP P61769
D	0	PRO	-	cloning artifact	UNP P61769

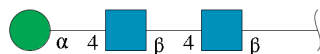
- Molecule 3 is a protein called T cell receptor delta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	207	Total	C	N	O	S	0	0	0
			1603	1000	276	321	6			
3	G	207	Total	C	N	O	S	281	0	0
			1592	992	274	321	5			

- Molecule 4 is a protein called T-cell receptor gamma chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	230	Total	C	N	O	S	0	0	0
			1852	1187	305	353	7			
4	H	230	Total	C	N	O	S	371	0	0
			1844	1181	303	353	7			

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



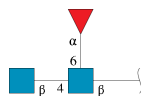
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	I	3	Total	C	N	O	0	0	0
			42	22	2	18			
5	L	3	Total	C	N	O	0	0	0
			42	22	2	18			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	J	2	Total	C	N	O	0	0	0
			30	16	2	12			
6	K	2	Total	C	N	O	0	0	0
			30	16	2	12			

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



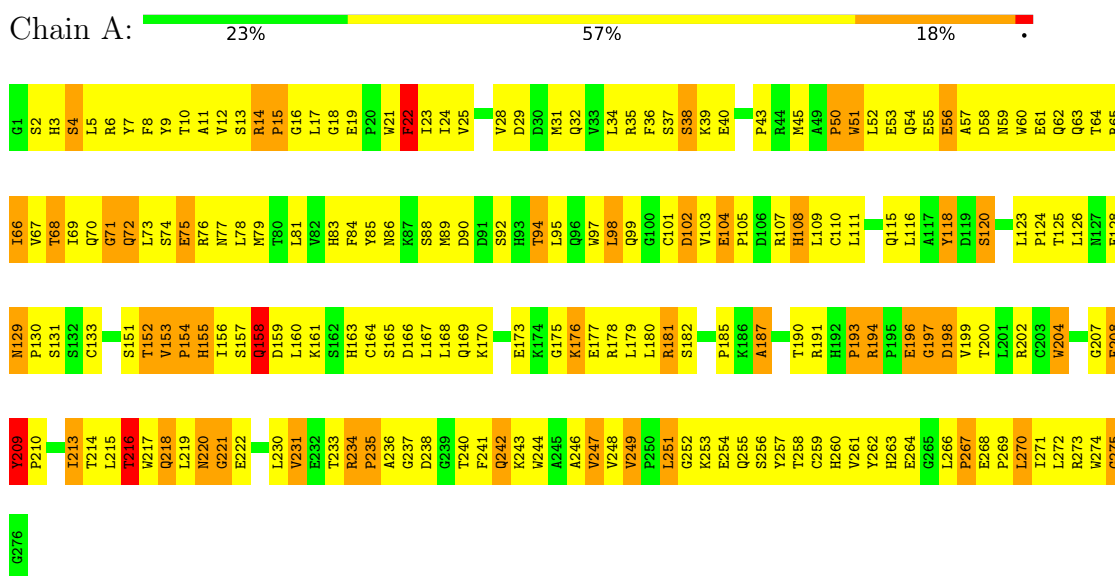
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	M	3	Total	C	N	O	0	0	0
			39	22	2	15			

3 Residue-property plots

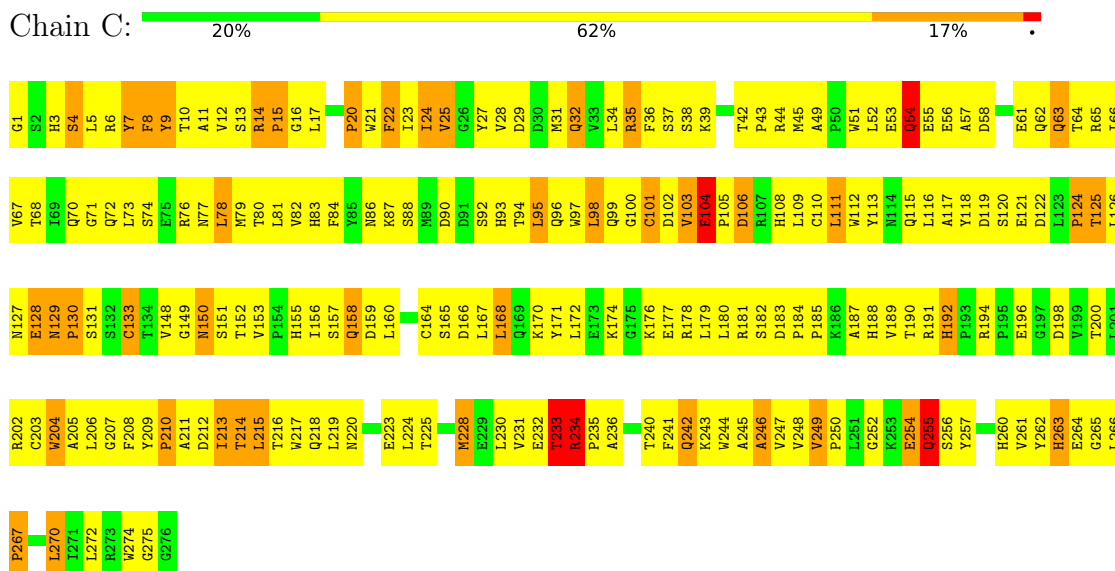
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS was not executed.

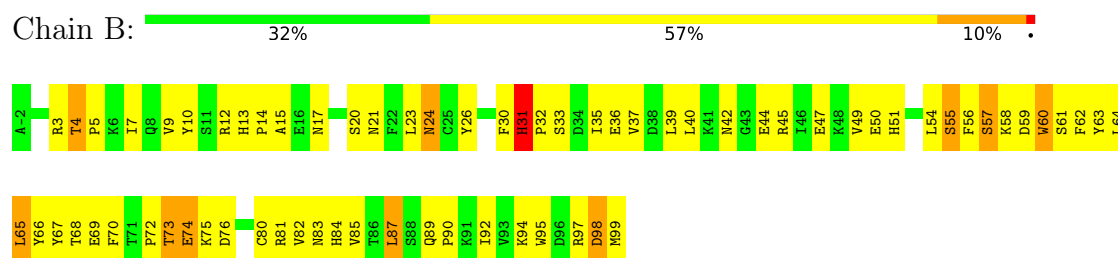
• Molecule 1: H2-T22 protein



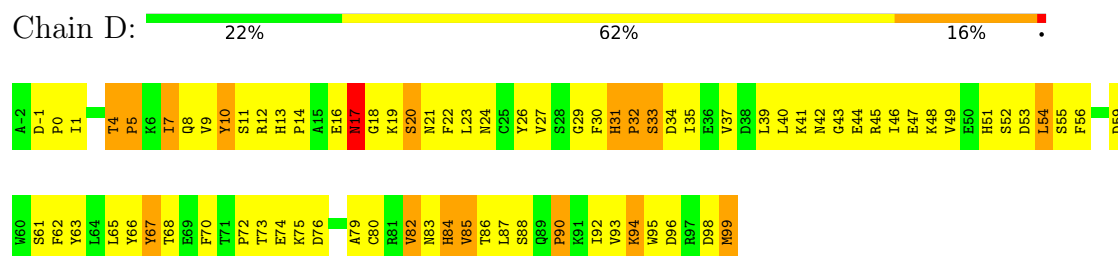
• Molecule 1: H2-T22 protein



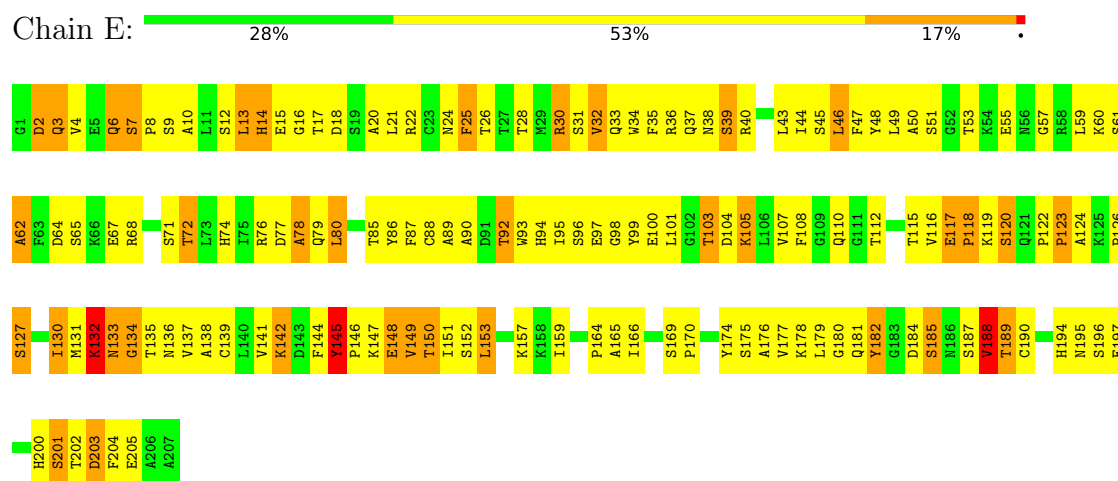
- Molecule 2: Beta-2-microglobulin



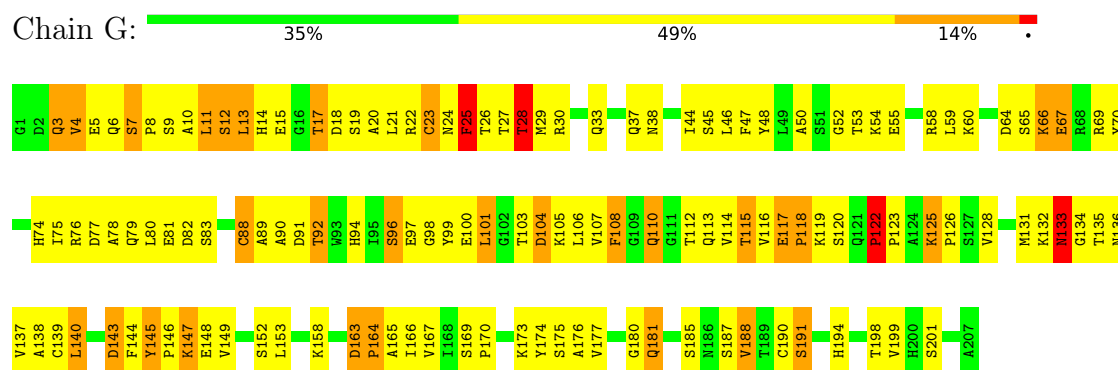
- Molecule 2: Beta-2-microglobulin



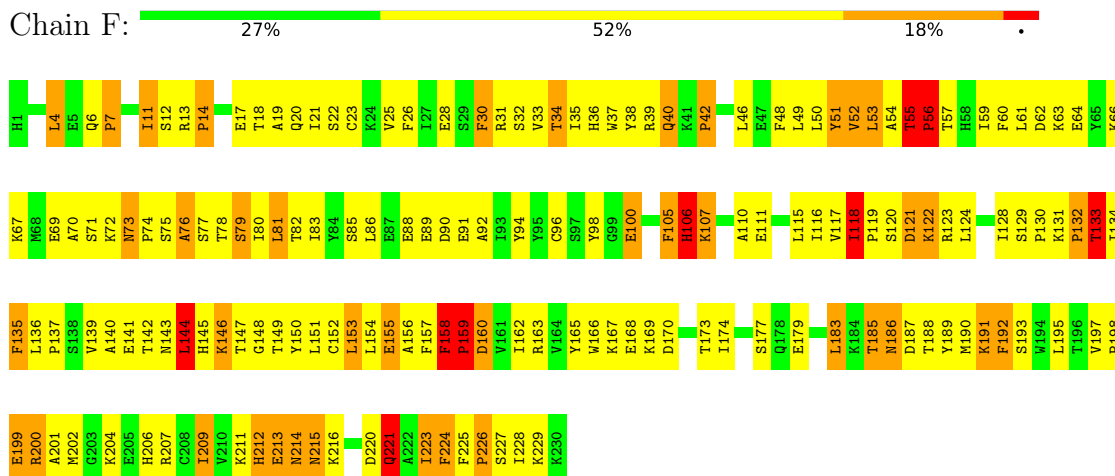
- Molecule 3: T cell receptor delta



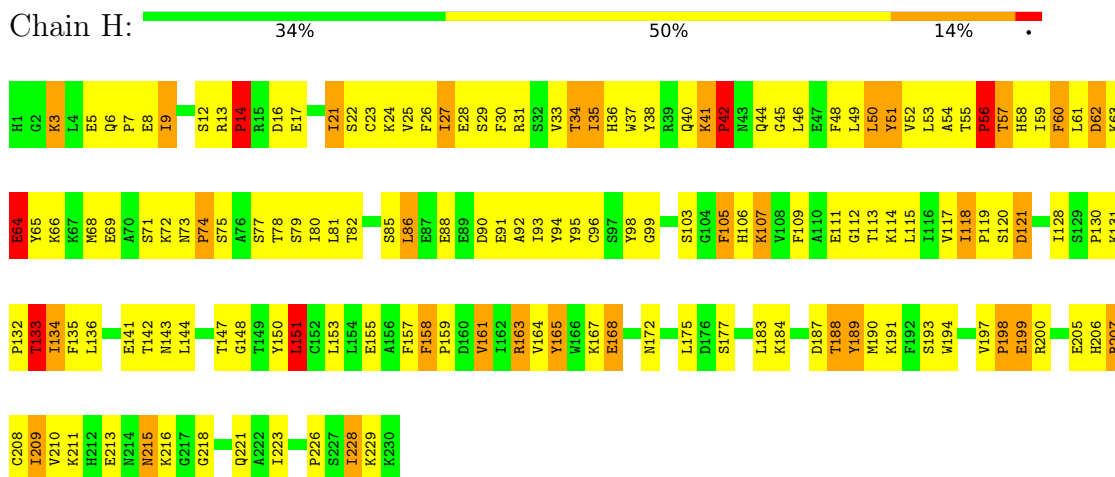
- Molecule 3: T cell receptor delta



- Molecule 4: T-cell receptor gamma chain



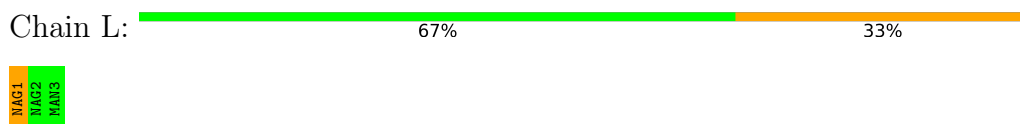
- Molecule 4: T-cell receptor gamma chain



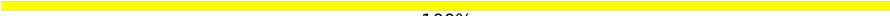
- Molecule 5: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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

Chain J:  100%

NAG1
NAG2

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

Chain K:  50% 50%

NAG1
NAG2

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

Chain M:  67% 33%

NAG1
NAG2
FUC3

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	110.53Å 113.05Å 167.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.40	Depositor
% Data completeness (in resolution range)	97.4 (20.00-3.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.264 , 0.330	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12984	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

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, FUC, MAN

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	0.76	1/2166 (0.0%)	1.31	29/2951 (1.0%)
1	C	0.64	1/2166 (0.0%)	1.32	35/2951 (1.2%)
2	B	0.58	0/873	1.22	7/1182 (0.6%)
2	D	0.52	0/873	1.07	8/1182 (0.7%)
3	E	0.71	0/1636	1.29	22/2212 (1.0%)
3	G	0.67	0/1625	1.33	27/2201 (1.2%)
4	F	0.67	0/1898	1.29	21/2565 (0.8%)
4	H	0.58	0/1889	1.32	26/2553 (1.0%)
All	All	0.66	2/13126 (0.0%)	1.29	175/17797 (1.0%)

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
2	D	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	155	HIS	CB-CG	5.58	1.57	1.50
1	C	228	MET	SD-CE	-5.25	1.66	1.79

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	29	SER	N-CA-C	-10.95	99.50	112.86
1	C	32	GLN	OE1-CD-NE2	-10.94	111.66	122.60
1	A	158	GLN	OE1-CD-NE2	-10.79	111.81	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	234	ARG	CA-C-N	10.77	133.47	120.23
1	C	234	ARG	C-N-CA	10.77	133.47	120.23

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	63	TYR	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2106	0	2006	291	1
1	C	2106	0	2009	289	4
2	B	849	0	810	85	0
2	D	849	0	810	123	0
3	E	1603	0	1554	203	1
3	G	1592	0	1524	168	0
4	F	1852	0	1832	246	4
4	H	1844	0	1816	171	0
5	I	42	0	38	10	0
5	L	42	0	36	7	0
6	J	30	0	27	9	0
6	K	30	0	27	22	0
7	M	39	0	36	12	0
All	All	12984	0	12525	1504	5

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 62.

The worst 5 of 1504 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)
3:G:24:ASN:HD21	7:M:1:NAG:C1	1.10	1.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:186:ASN:HD22	6:K:1:NAG:C1	0.99	1.57
3:E:133:ASN:HD21	5:I:1:NAG:C1	0.88	1.53
1:A:155:HIS:CD2	1:A:157:SER:N	1.88	1.41
4:F:186:ASN:CB	6:K:1:NAG:O1	1.67	1.38

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:255:GLN:NE2	4:F:66:LYS:CE[1_545]	1.35	0.85
1:A:53:GLU:OE2	3:E:157:LYS:NZ[1_455]	1.36	0.84
1:C:255:GLN:CD	4:F:66:LYS:NZ[1_545]	1.96	0.24
1:C:255:GLN:CD	4:F:66:LYS:CE[1_545]	2.13	0.07
1:C:255:GLN:NE2	4:F:66:LYS:NZ[1_545]	2.17	0.03

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 X-ray entries followed by that with respect to entries of similar resolution.

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	258/260 (99%)	181 (70%)	55 (21%)	22 (8%)	0	4
1	C	258/260 (99%)	192 (74%)	45 (17%)	21 (8%)	1	4
2	B	100/102 (98%)	86 (86%)	9 (9%)	5 (5%)	1	10
2	D	100/102 (98%)	79 (79%)	12 (12%)	9 (9%)	0	3
3	E	205/207 (99%)	157 (77%)	30 (15%)	18 (9%)	0	3
3	G	205/207 (99%)	158 (77%)	29 (14%)	18 (9%)	0	3
4	F	228/230 (99%)	167 (73%)	37 (16%)	24 (10%)	0	2
4	H	228/230 (99%)	172 (75%)	34 (15%)	22 (10%)	0	3
All	All	1582/1598 (99%)	1192 (75%)	251 (16%)	139 (9%)	0	3

5 of 139 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	14	ARG
1	A	15	PRO
1	A	51	TRP
1	A	56	GLU
1	A	129	ASN

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	233/233 (100%)	205 (88%)	28 (12%)	5	19
1	C	233/233 (100%)	208 (89%)	25 (11%)	6	23
2	B	96/96 (100%)	85 (88%)	11 (12%)	5	20
2	D	96/96 (100%)	88 (92%)	8 (8%)	10	35
3	E	180/180 (100%)	163 (91%)	17 (9%)	8	29
3	G	177/180 (98%)	152 (86%)	25 (14%)	3	13
4	F	206/206 (100%)	175 (85%)	31 (15%)	3	11
4	H	204/206 (99%)	176 (86%)	28 (14%)	3	14
All	All	1425/1430 (100%)	1252 (88%)	173 (12%)	5	19

5 of 173 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	F	212	HIS
3	G	191	SER
4	F	224	PHE
3	G	92	THR
4	H	51	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
4	F	6	GLN
3	G	3	GLN
4	F	36	HIS
4	F	186	ASN
3	G	24	ASN

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 ⓘ

13 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	I	1	5,3	15,15,15	0.56	0	21,21,21	0.77	0
5	NAG	I	2	5	15,15,15	0.47	0	21,21,21	0.70	0
5	MAN	I	3	5	12,12,12	0.44	0	17,17,17	0.45	0
6	NAG	J	1	3,6	15,15,15	0.56	0	21,21,21	0.79	0
6	NAG	J	2	6	15,15,15	0.48	0	21,21,21	0.70	0
6	NAG	K	1	4,6	15,15,15	0.56	0	21,21,21	1.13	2 (9%)
6	NAG	K	2	6	15,15,15	0.48	0	21,21,21	0.70	0
5	NAG	L	1	5,3	15,15,15	0.57	0	21,21,21	0.97	1 (4%)
5	NAG	L	2	5	15,15,15	0.48	0	21,21,21	0.70	0
5	MAN	L	3	5	12,12,12	0.44	0	17,17,17	0.45	0
7	NAG	M	1	3,7	15,15,15	1.20	1 (6%)	21,21,21	1.79	5 (23%)
7	NAG	M	2	7	14,14,15	0.78	0	17,19,21	0.84	0
7	FUC	M	3	7	10,10,11	0.97	1 (10%)	14,14,16	2.01	2 (14%)

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	I	1	5,3	1/1/6/7	0/6/26/26	0/1/1/1
5	NAG	I	2	5	-	4/6/26/26	0/1/1/1
5	MAN	I	3	5	-	2/2/22/22	0/1/1/1
6	NAG	J	1	3,6	1/1/6/7	0/6/26/26	0/1/1/1
6	NAG	J	2	6	-	4/6/26/26	0/1/1/1
6	NAG	K	1	4,6	-	0/6/26/26	0/1/1/1
6	NAG	K	2	6	-	4/6/26/26	0/1/1/1
5	NAG	L	1	5,3	1/1/6/7	0/6/26/26	0/1/1/1
5	NAG	L	2	5	-	4/6/26/26	0/1/1/1
5	MAN	L	3	5	-	2/2/22/22	0/1/1/1
7	NAG	M	1	3,7	1/1/6/7	5/6/26/26	0/1/1/1
7	NAG	M	2	7	-	5/6/23/26	0/1/1/1
7	FUC	M	3	7	-	-	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	M	1	NAG	C1-C2	-3.52	1.48	1.52
7	M	3	FUC	C1-C2	2.20	1.57	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	M	3	FUC	C1-C2-C3	6.49	119.10	109.64
7	M	1	NAG	C3-C4-C5	4.12	117.70	110.23
7	M	1	NAG	C1-C2-C3	-3.60	105.63	110.54
6	K	1	NAG	O1-C1-C2	-3.27	102.42	109.22
7	M	1	NAG	C4-C3-C2	2.54	114.09	110.40

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	I	1	NAG	C1
5	L	1	NAG	C1
6	J	1	NAG	C1
7	M	1	NAG	C1

5 of 30 torsion outliers are listed below:

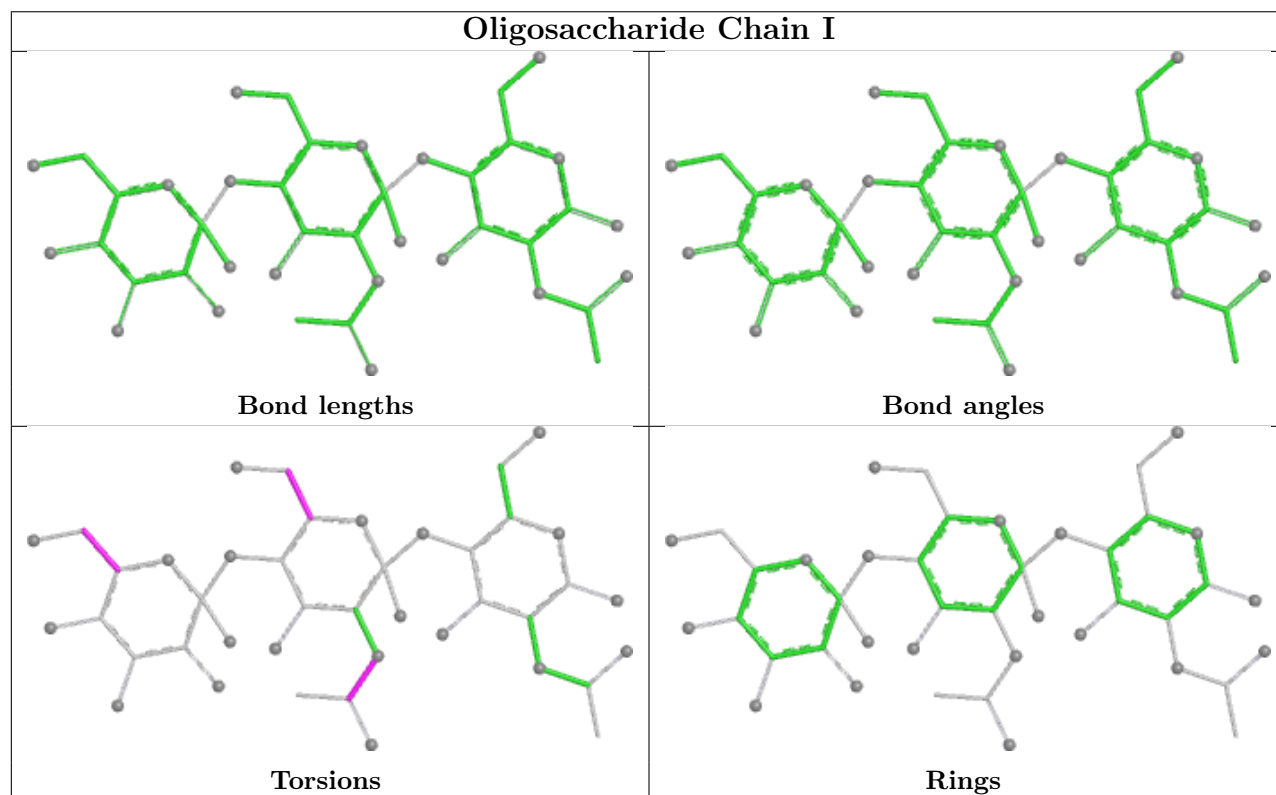
Mol	Chain	Res	Type	Atoms
5	I	2	NAG	C8-C7-N2-C2
5	I	2	NAG	O7-C7-N2-C2
5	L	2	NAG	C8-C7-N2-C2
5	L	2	NAG	O7-C7-N2-C2
6	J	2	NAG	C8-C7-N2-C2

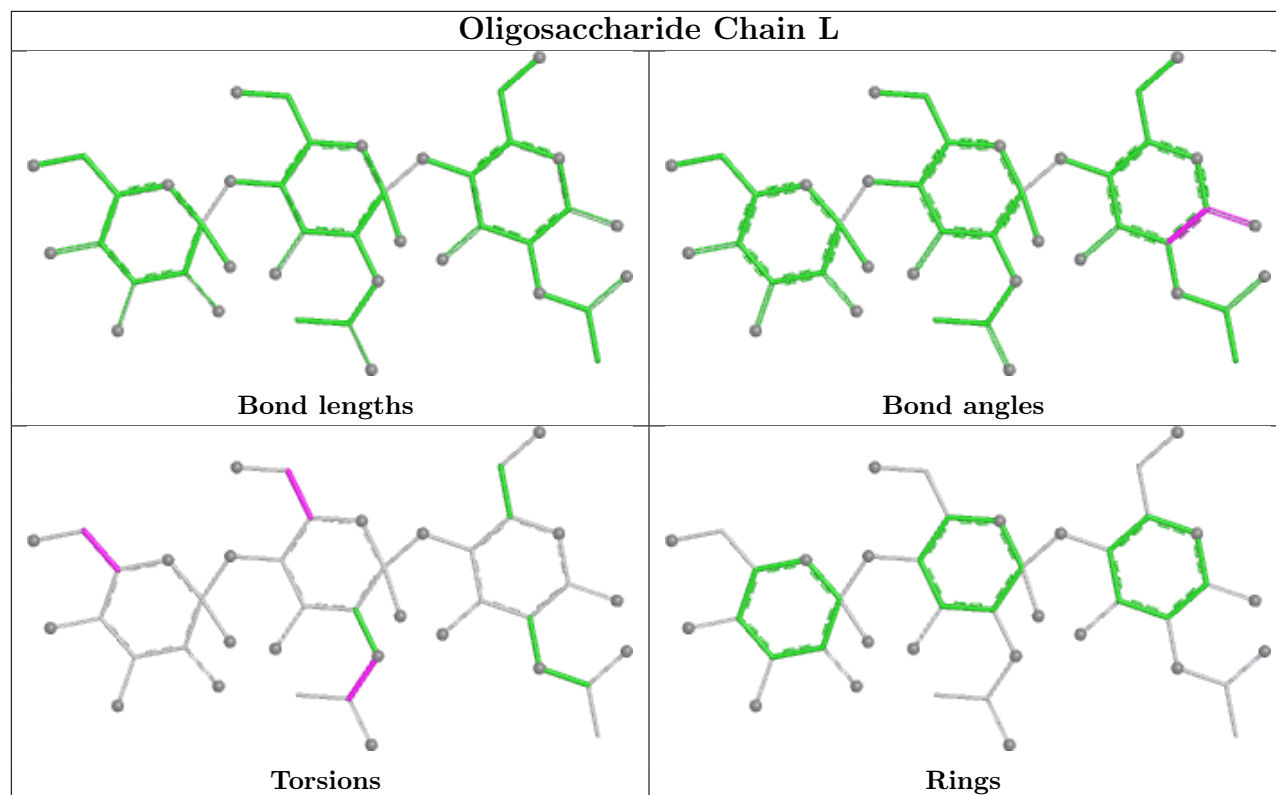
There are no ring outliers.

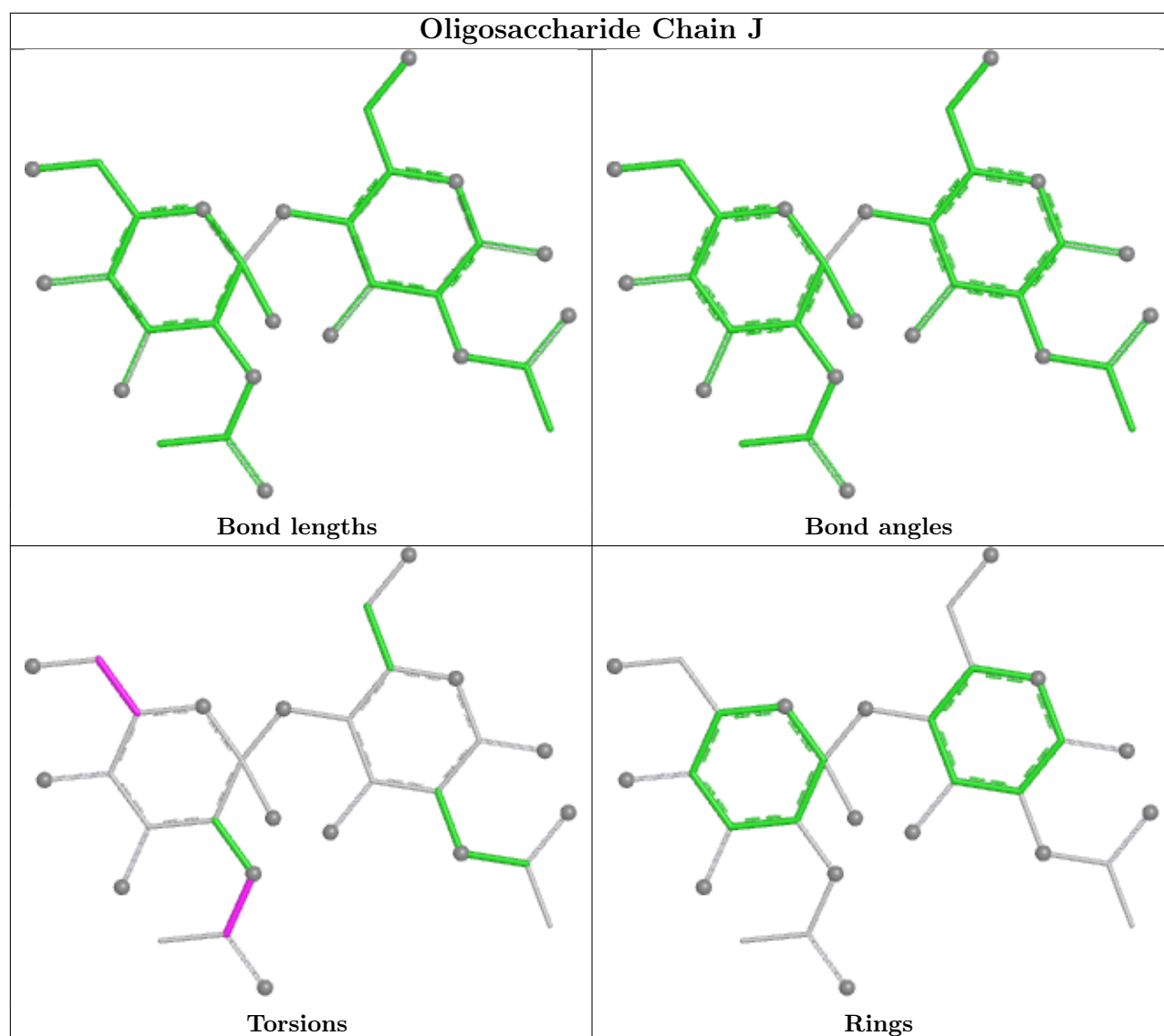
8 monomers are involved in 60 short contacts:

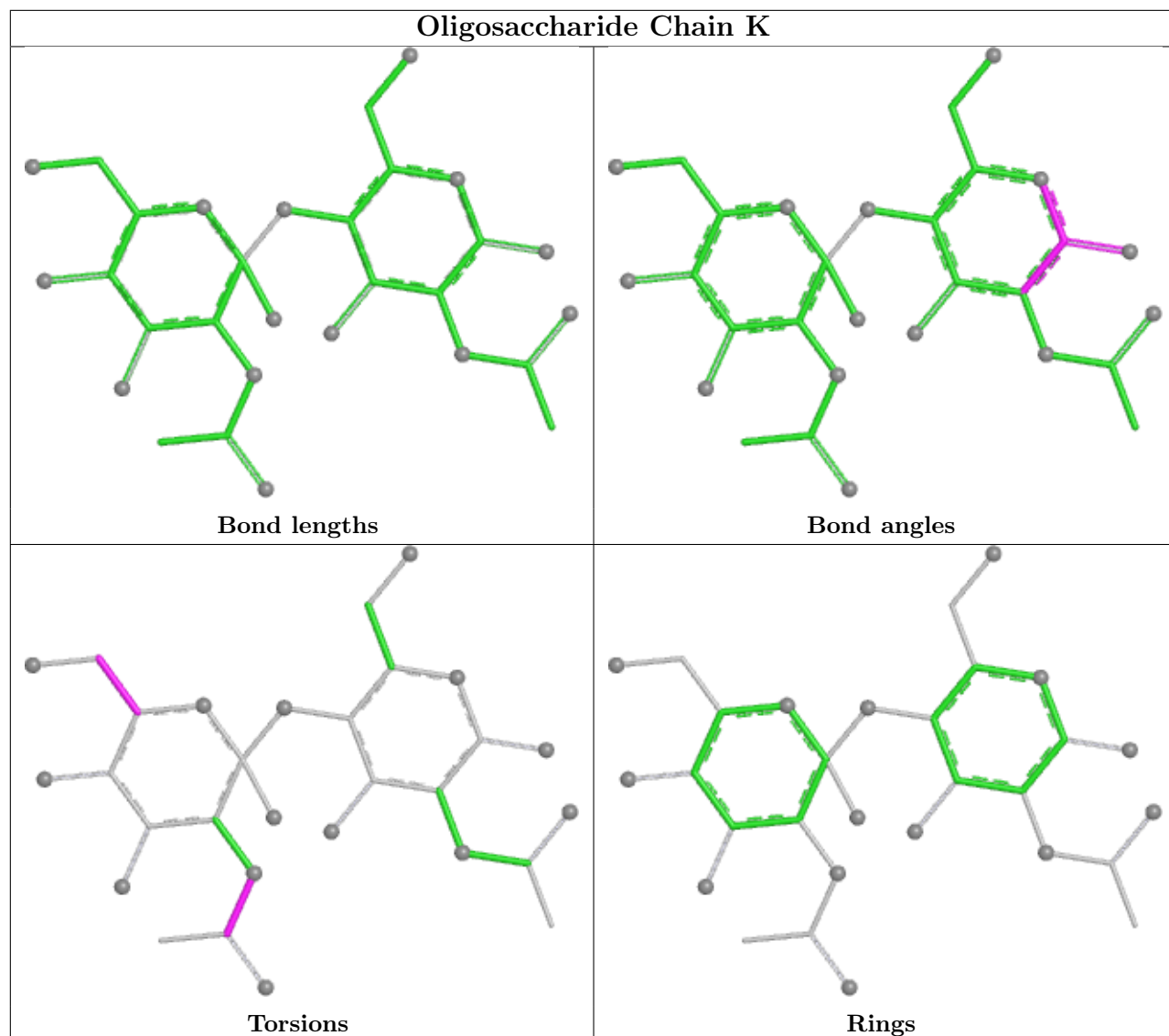
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	J	2	NAG	1	0
5	I	3	MAN	3	0
7	M	2	NAG	2	0
6	K	1	NAG	22	0
5	L	1	NAG	7	0
6	J	1	NAG	8	0
7	M	1	NAG	10	0
5	I	1	NAG	7	0

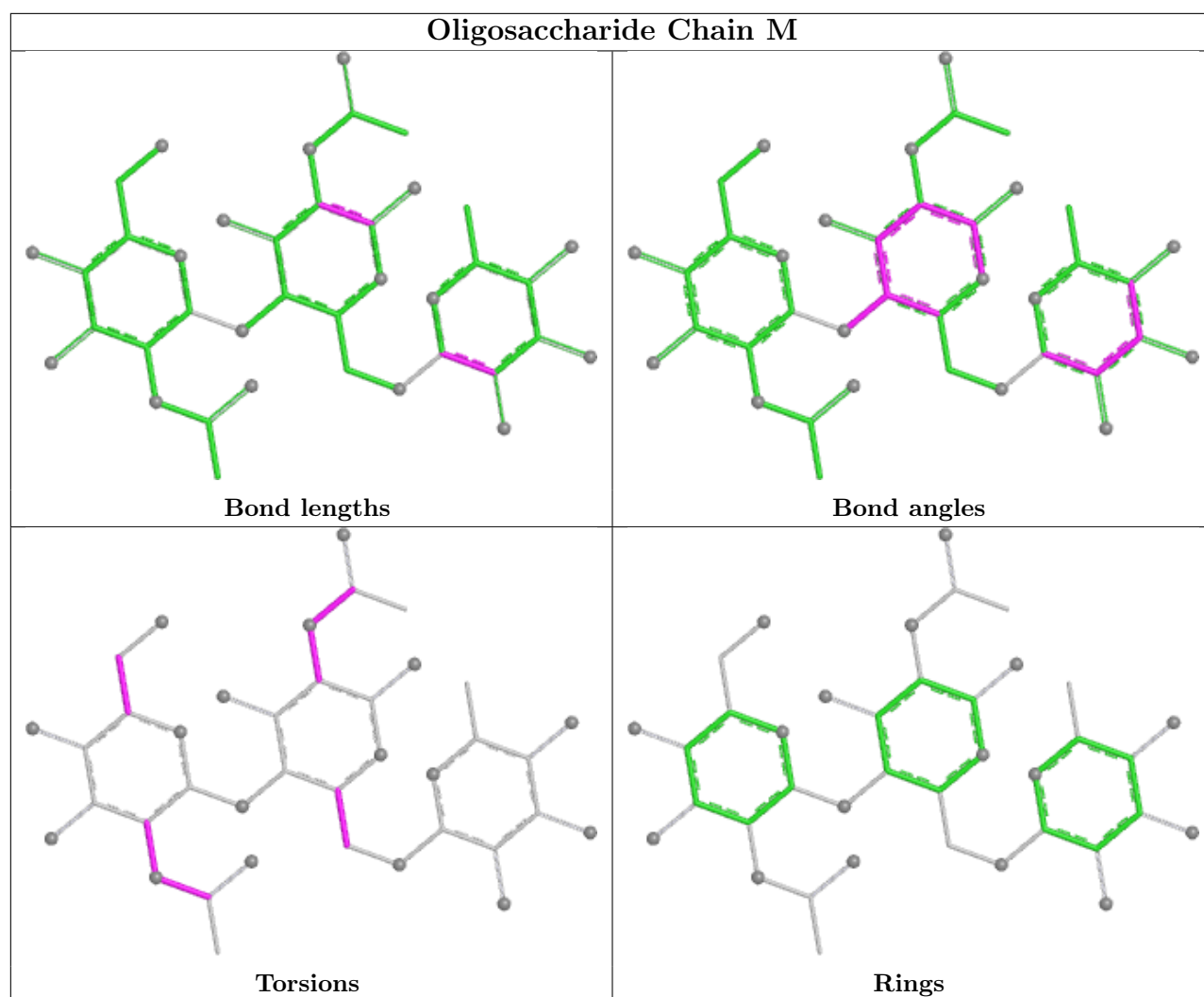
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.