



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 09:41 AM UTC

PDB ID : 1AFC / pdb_00001afc
Title : STRUCTURAL STUDIES OF THE BINDING OF THE ANTI-ULCER
DRUG SUCROSE OCTASULFATE TO ACIDIC FIBROBLAST GROWTH
FACTOR
Authors : Zhu, X.; Hsu, B.T.; Rees, D.C.
Deposited on : 1993-07-13
Resolution : 2.70 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

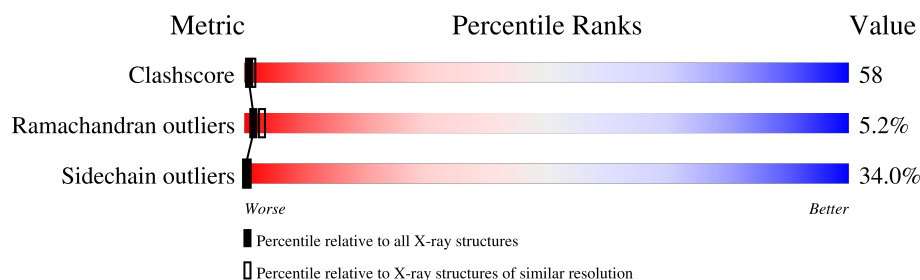
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)

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	140	9% 31% 31% 20% 9%
1	B	140	7% 36% 30% 18% 9%
1	C	140	11% 25% 34% 21% 9%
1	D	140	16% 27% 36% 11% 9%
1	E	140	14% 24% 31% 22% 9%
1	F	140	11% 25% 31% 23% 9%
1	G	140	9% 32% 31% 18% 9%
1	H	140	11% 24% 29% 26% 9%

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Mol	Chain	Length	Quality of chain
2	I	2	 100%
2	J	2	 100%
2	K	2	 100%
2	L	2	 100%
2	M	2	 100%
2	N	2	 100%
2	O	2	 100%
2	P	2	 100%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GU4	I	1	-	-	X	-
2	YYJ	I	2	-	-	X	-
2	GU4	K	1	-	-	X	-
2	YYJ	K	2	-	-	X	-
2	YYJ	L	2	-	-	X	-
2	GU4	M	1	-	-	X	-
2	YYJ	M	2	-	-	X	-
2	YYJ	N	2	-	-	X	-
2	GU4	O	1	-	-	X	-
2	YYJ	O	2	-	-	X	-
2	GU4	P	1	-	-	X	-
2	YYJ	P	2	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8304 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.

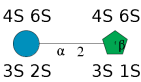
- Molecule 1 is a protein called ACIDIC FIBROBLAST GROWTH FACTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	127	Total	C	N	O	S	0	0	0
			983	630	168	182	3			
1	B	127	Total	C	N	O	S	0	0	0
			983	630	168	182	3			
1	C	127	Total	C	N	O	S	0	0	0
			983	630	168	182	3			
1	D	127	Total	C	N	O	S	0	0	0
			983	630	168	182	3			
1	E	127	Total	C	N	O	S	0	0	0
			983	630	168	182	3			
1	F	127	Total	C	N	O	S	0	0	0
			983	630	168	182	3			
1	G	127	Total	C	N	O	S	0	0	0
			983	630	168	182	3			
1	H	127	Total	C	N	O	S	0	0	0
			983	630	168	182	3			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	ALA	CYS	conflict	UNP P03968
B	47	ALA	CYS	conflict	UNP P03968
C	47	ALA	CYS	conflict	UNP P03968
D	47	ALA	CYS	conflict	UNP P03968
E	47	ALA	CYS	conflict	UNP P03968
F	47	ALA	CYS	conflict	UNP P03968
G	47	ALA	CYS	conflict	UNP P03968
H	47	ALA	CYS	conflict	UNP P03968

- Molecule 2 is an oligosaccharide called 1,3,4,6-tetra-O-sulfo-beta-D-fructofuranose-(2-1)-2,3,4,6-tetra-O-sulfonato-alpha-D-glucopyranose.



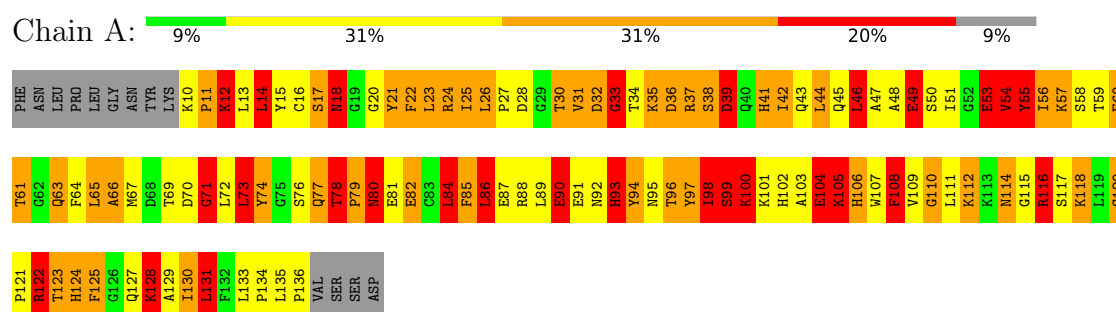
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	I	2	Total	C	O	S	0	0	0
			55	12	35	8			
2	J	2	Total	C	O	S	0	0	0
			55	12	35	8			
2	K	2	Total	C	O	S	0	0	0
			55	12	35	8			
2	L	2	Total	C	O	S	0	0	0
			55	12	35	8			
2	M	2	Total	C	O	S	0	0	0
			55	12	35	8			
2	N	2	Total	C	O	S	0	0	0
			55	12	35	8			
2	O	2	Total	C	O	S	0	0	0
			55	12	35	8			
2	P	2	Total	C	O	S	0	0	0
			55	12	35	8			

3 Residue-property plots

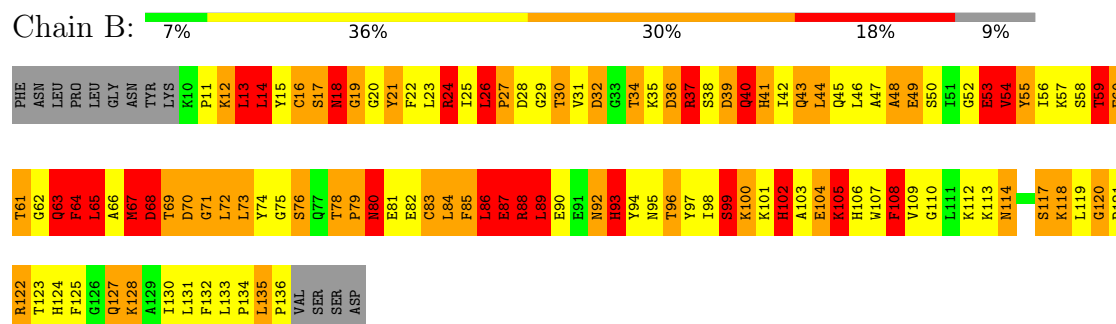
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

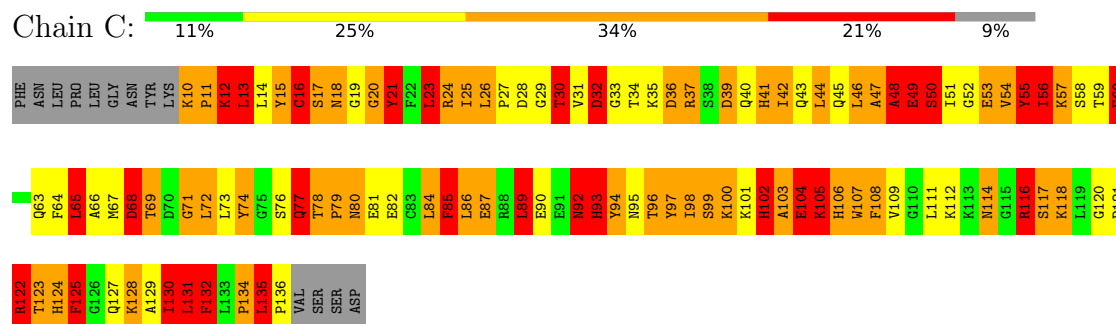
• Molecule 1: ACIDIC FIBROBLAST GROWTH FACTOR



• Molecule 1: ACIDIC FIBROBLAST GROWTH FACTOR

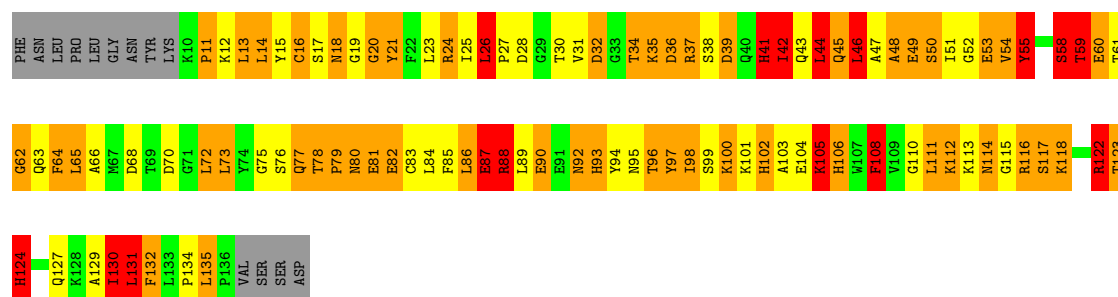


• Molecule 1: ACIDIC FIBROBLAST GROWTH FACTOR



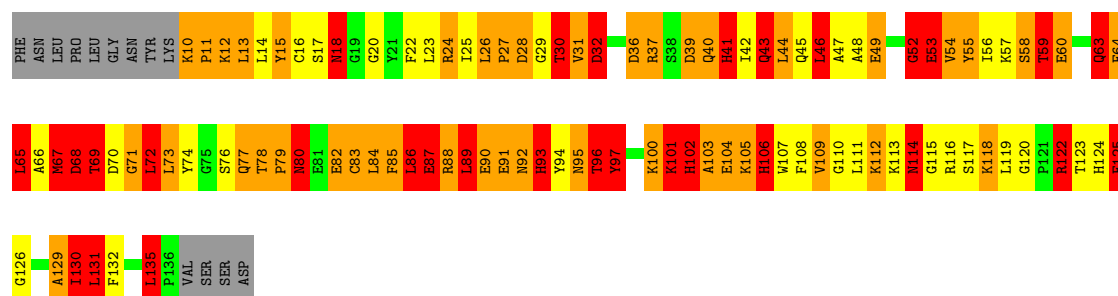
• Molecule 1: ACIDIC FIBROBLAST GROWTH FACTOR

Chain D: 

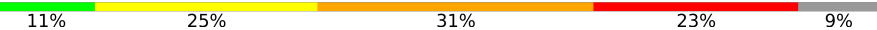


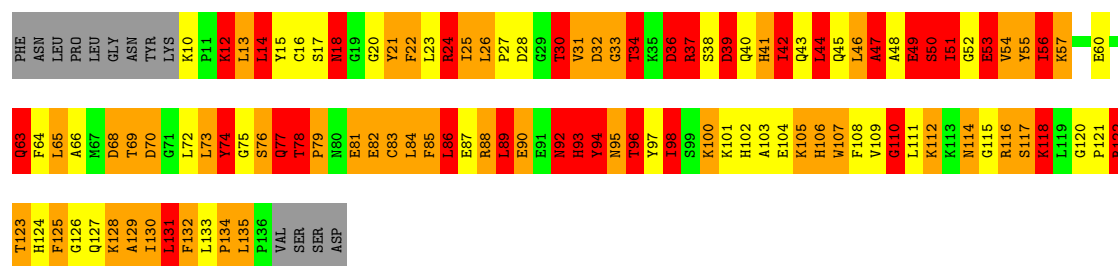
• Molecule 1: ACIDIC FIBROBLAST GROWTH FACTOR

Chain E: 



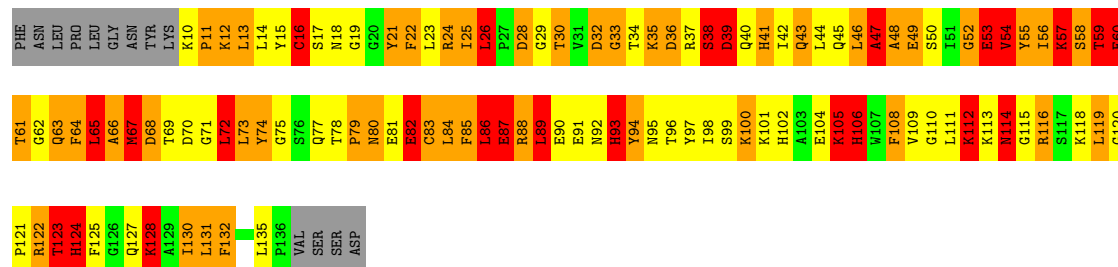
• Molecule 1: ACIDIC FIBROBLAST GROWTH FACTOR

Chain F: 

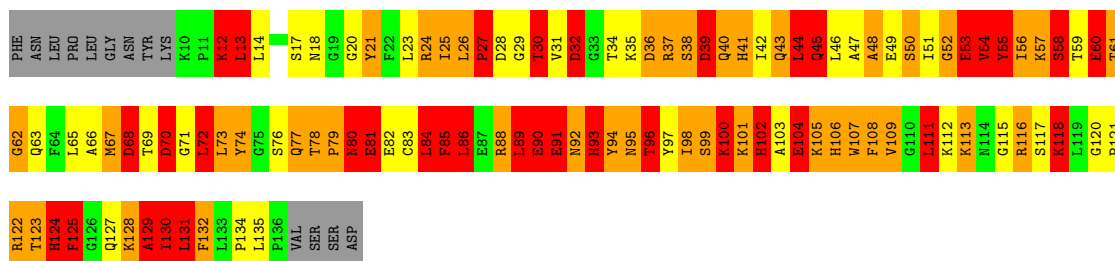


• Molecule 1: ACIDIC FIBROBLAST GROWTH FACTOR

Chain G: 



• Molecule 1: ACIDIC FIBROBLAST GROWTH FACTOR



- GU41
YYJ2

- GU41
YYJ2

- GU41
YYJ2

- GU41
YYJ2

- GU41
YYJ2

- Molecule 2: 1,3,4,6-tetra-O-sulfo-beta-D-fructofuranose-(2-1)-2,3,4,6-tetra-O-sulfonato-alpha-D-glucopyranose

Chain N:  100%

CH01
YY02

- Molecule 2: 1,3,4,6-tetra-O-sulfo-beta-D-fructofuranose-(2-1)-2,3,4,6-tetra-O-sulfonato-alpha-D-glucopyranose

Chain O:  100%

CH01
YY02

- Molecule 2: 1,3,4,6-tetra-O-sulfo-beta-D-fructofuranose-(2-1)-2,3,4,6-tetra-O-sulfonato-alpha-D-glucopyranose

Chain P:  100%

CH01
YY02

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	110.60Å 110.60Å 172.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.204 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8304	wwPDB-VP
Average B, all atoms (Å ²)	13.0	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: YYJ, GU4

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	1.20	3/1007 (0.3%)	2.06	35/1363 (2.6%)
1	B	1.25	5/1007 (0.5%)	2.04	31/1363 (2.3%)
1	C	1.23	8/1007 (0.8%)	2.05	41/1363 (3.0%)
1	D	1.23	6/1007 (0.6%)	1.92	21/1363 (1.5%)
1	E	1.26	4/1007 (0.4%)	2.00	32/1363 (2.3%)
1	F	1.28	5/1007 (0.5%)	2.04	35/1363 (2.6%)
1	G	1.21	5/1007 (0.5%)	2.01	33/1363 (2.4%)
1	H	1.23	6/1007 (0.6%)	2.04	37/1363 (2.7%)
All	All	1.24	42/8056 (0.5%)	2.02	265/10904 (2.4%)

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	89
1	B	0	77
1	C	0	76
1	D	0	76
1	E	0	74
1	F	0	78
1	G	0	67
1	H	0	83
All	All	0	620

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	106	HIS	CD2-NE2	-7.23	1.29	1.37
1	F	106	HIS	CD2-NE2	-6.91	1.30	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	41	HIS	CD2-NE2	-6.86	1.30	1.37
1	D	106	HIS	CD2-NE2	-6.85	1.30	1.37
1	B	106	HIS	CD2-NE2	-6.74	1.30	1.37

The worst 5 of 265 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	125	PHE	CA-CB-CG	-11.62	102.18	113.80
1	C	36	ASP	CA-CB-CG	11.40	124.00	112.60
1	G	33	GLY	O-C-N	-10.21	114.71	123.60
1	H	125	PHE	CA-CB-CG	-9.88	103.92	113.80
1	D	32	ASP	CA-C-N	-9.31	114.44	121.61

There are no chirality outliers.

5 of 620 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	10	LYS	Mainchain
1	A	11	PRO	Mainchain
1	A	12	LYS	Mainchain
1	A	14	LEU	Mainchain
1	A	15	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	983	0	944	109	0
1	B	983	0	944	98	0
1	C	983	0	944	116	0
1	D	983	0	944	97	0
1	E	983	0	944	92	0
1	F	983	0	944	88	0
1	G	983	0	944	128	0
1	H	983	0	944	123	0
2	I	55	0	6	24	0
2	J	55	0	6	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	55	0	6	13	0
2	L	55	0	6	21	0
2	M	55	0	6	19	0
2	N	55	0	6	14	0
2	O	55	0	6	26	0
2	P	55	0	6	18	0
All	All	8304	0	7600	925	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 58.

The worst 5 of 925 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:ASN:HD21	1:A:116:ARG:NH1	1.43	1.16
1:G:24:ARG:HH11	1:G:26:LEU:HD11	1.01	1.14
1:H:27:PRO:HB3	1:H:61:THR:HG21	1.31	1.12
1:D:86:LEU:HD21	1:D:100:LYS:HG3	1.30	1.11
1:F:24:ARG:HD2	1:F:26:LEU:HD11	1.30	1.11

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 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	125/140 (89%)	104 (83%)	17 (14%)	4 (3%)	3	7
1	B	125/140 (89%)	112 (90%)	9 (7%)	4 (3%)	3	7
1	C	125/140 (89%)	103 (82%)	18 (14%)	4 (3%)	3	7
1	D	125/140 (89%)	104 (83%)	16 (13%)	5 (4%)	2	5
1	E	125/140 (89%)	102 (82%)	16 (13%)	7 (6%)	1	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	125/140 (89%)	105 (84%)	11 (9%)	9 (7%)	1	1
1	G	125/140 (89%)	105 (84%)	15 (12%)	5 (4%)	2	5
1	H	125/140 (89%)	92 (74%)	19 (15%)	14 (11%)	0	0
All	All	1000/1120 (89%)	827 (83%)	121 (12%)	52 (5%)	1	3

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	81	GLU
1	B	18	ASN
1	B	68	ASP
1	D	18	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	101/122 (83%)	65 (64%)	36 (36%)	0	0
1	B	101/122 (83%)	65 (64%)	36 (36%)	0	0
1	C	101/122 (83%)	63 (62%)	38 (38%)	0	0
1	D	101/122 (83%)	75 (74%)	26 (26%)	0	2
1	E	101/122 (83%)	65 (64%)	36 (36%)	0	0
1	F	101/122 (83%)	70 (69%)	31 (31%)	0	1
1	G	101/122 (83%)	62 (61%)	39 (39%)	0	0
1	H	101/122 (83%)	68 (67%)	33 (33%)	0	1
All	All	808/976 (83%)	533 (66%)	275 (34%)	0	0

5 of 275 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	84	LEU

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Mol	Chain	Res	Type
1	G	122	ARG
1	H	84	LEU
1	C	92	ASN
1	C	86	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	43	GLN
1	H	63	GLN
1	H	102	HIS
1	E	63	GLN
1	E	43	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 ⓘ

16 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	GU4	I	1	2	27,27,28	1.48	4 (14%)	32,43,45	2.16	7 (21%)
2	YYJ	I	2	2	27,28,28	2.10	6 (22%)	33,46,46	1.52	3 (9%)
2	GU4	J	1	2	27,27,28	1.46	5 (18%)	32,43,45	1.75	7 (21%)
2	YYJ	J	2	2	27,28,28	1.80	5 (18%)	33,46,46	1.28	2 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GU4	K	1	2	27,27,28	1.50	4 (14%)	32,43,45	2.14	7 (21%)
2	YYJ	K	2	2	27,28,28	1.81	4 (14%)	33,46,46	1.56	6 (18%)
2	GU4	L	1	2	27,27,28	1.92	5 (18%)	32,43,45	1.70	4 (12%)
2	YYJ	L	2	2	27,28,28	1.46	5 (18%)	33,46,46	1.29	5 (15%)
2	GU4	M	1	2	27,27,28	1.66	5 (18%)	32,43,45	2.34	11 (34%)
2	YYJ	M	2	2	27,28,28	1.77	4 (14%)	33,46,46	1.19	4 (12%)
2	GU4	N	1	2	27,27,28	1.53	5 (18%)	32,43,45	1.52	5 (15%)
2	YYJ	N	2	2	27,28,28	1.55	4 (14%)	33,46,46	1.44	5 (15%)
2	GU4	O	1	2	27,27,28	1.46	4 (14%)	32,43,45	1.98	10 (31%)
2	YYJ	O	2	2	27,28,28	1.43	4 (14%)	33,46,46	1.34	2 (6%)
2	GU4	P	1	2	27,27,28	1.86	5 (18%)	32,43,45	1.61	5 (15%)
2	YYJ	P	2	2	27,28,28	1.74	5 (18%)	33,46,46	1.72	5 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GU4	I	1	2	-	8/21/38/41	0/1/1/1
2	YYJ	I	2	2	-	7/23/42/42	0/1/1/1
2	GU4	J	1	2	-	12/21/38/41	0/1/1/1
2	YYJ	J	2	2	-	15/23/42/42	0/1/1/1
2	GU4	K	1	2	-	10/21/38/41	0/1/1/1
2	YYJ	K	2	2	-	6/23/42/42	0/1/1/1
2	GU4	L	1	2	-	12/21/38/41	0/1/1/1
2	YYJ	L	2	2	-	8/23/42/42	0/1/1/1
2	GU4	M	1	2	-	13/21/38/41	0/1/1/1
2	YYJ	M	2	2	-	14/23/42/42	0/1/1/1
2	GU4	N	1	2	-	10/21/38/41	0/1/1/1
2	YYJ	N	2	2	-	12/23/42/42	0/1/1/1
2	GU4	O	1	2	-	12/21/38/41	0/1/1/1
2	YYJ	O	2	2	-	13/23/42/42	0/1/1/1
2	GU4	P	1	2	-	9/21/38/41	0/1/1/1
2	YYJ	P	2	2	-	8/23/42/42	0/1/1/1

The worst 5 of 74 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	2	YYJ	O3-S3	-5.95	1.39	1.57
2	L	1	GU4	O6-S6	-4.95	1.43	1.56
2	J	2	YYJ	O3-S3	-4.89	1.42	1.57
2	P	1	GU4	O4-S4	-4.85	1.42	1.57
2	P	1	GU4	O2-S2	-4.71	1.43	1.57

The worst 5 of 88 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	1	GU4	C1-O5-C5	-8.15	101.27	112.19
2	I	1	GU4	O2-C2-C3	6.87	114.26	106.65
2	M	1	GU4	C1-O5-C5	-5.83	104.38	112.19
2	M	1	GU4	O6-C6-C5	5.59	117.53	107.57
2	L	1	GU4	O4-C4-C3	-5.47	96.61	108.56

There are no chirality outliers.

5 of 169 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	I	1	GU4	C4-C5-C6-O6
2	I	2	YYJ	C2-C1-O1-S1
2	I	2	YYJ	C6-O6-S6-O1S6
2	J	1	GU4	C2-O2-S2-O10
2	J	2	YYJ	C2-C1-O1-S1

There are no ring outliers.

16 monomers are involved in 142 short contacts:

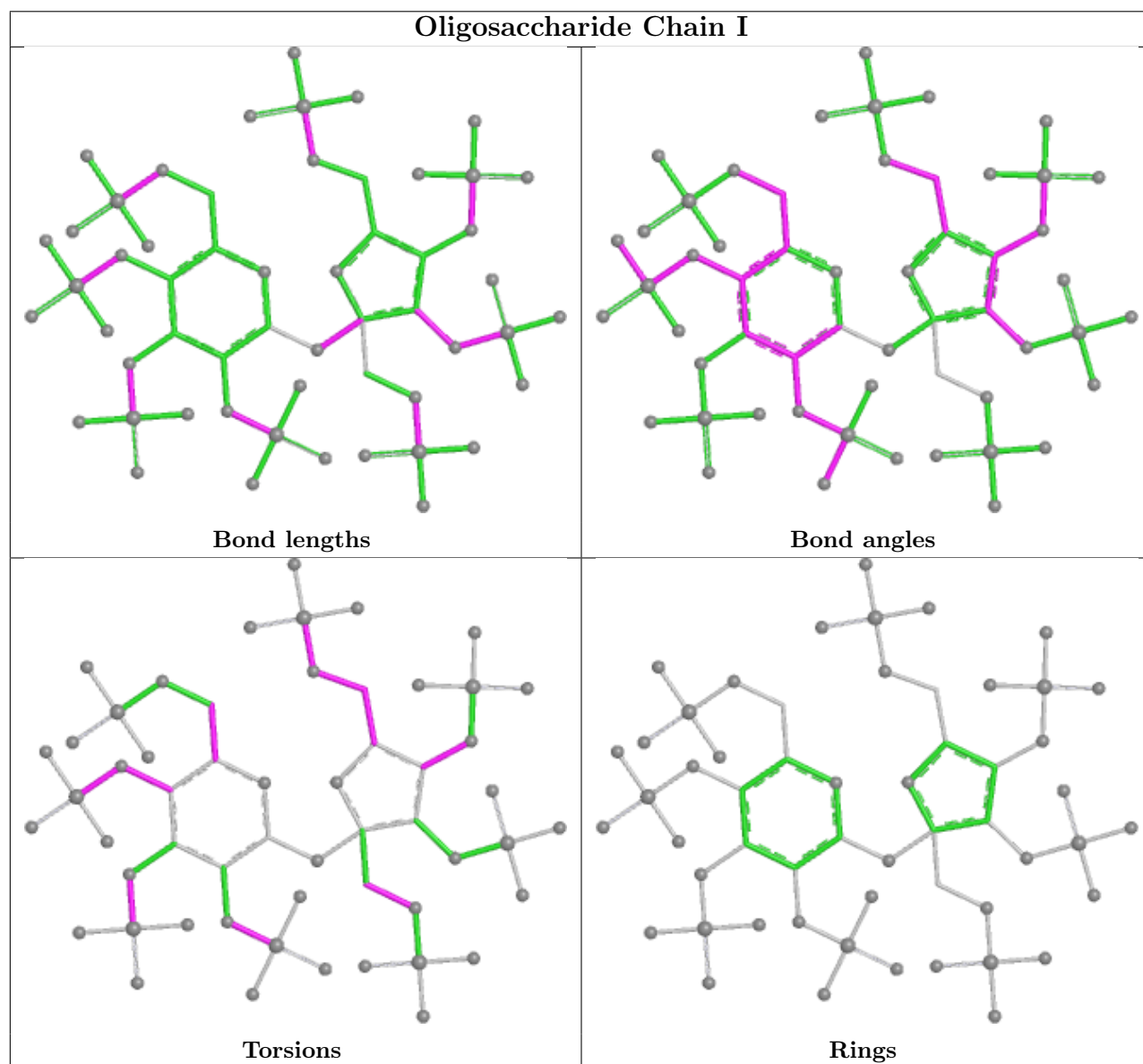
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	J	1	GU4	2	0
2	P	1	GU4	13	0
2	O	2	YYJ	21	0
2	K	2	YYJ	9	0
2	L	1	GU4	8	0
2	M	2	YYJ	14	0
2	I	1	GU4	15	0
2	L	2	YYJ	15	0
2	N	2	YYJ	13	0
2	O	1	GU4	13	0
2	M	1	GU4	9	0

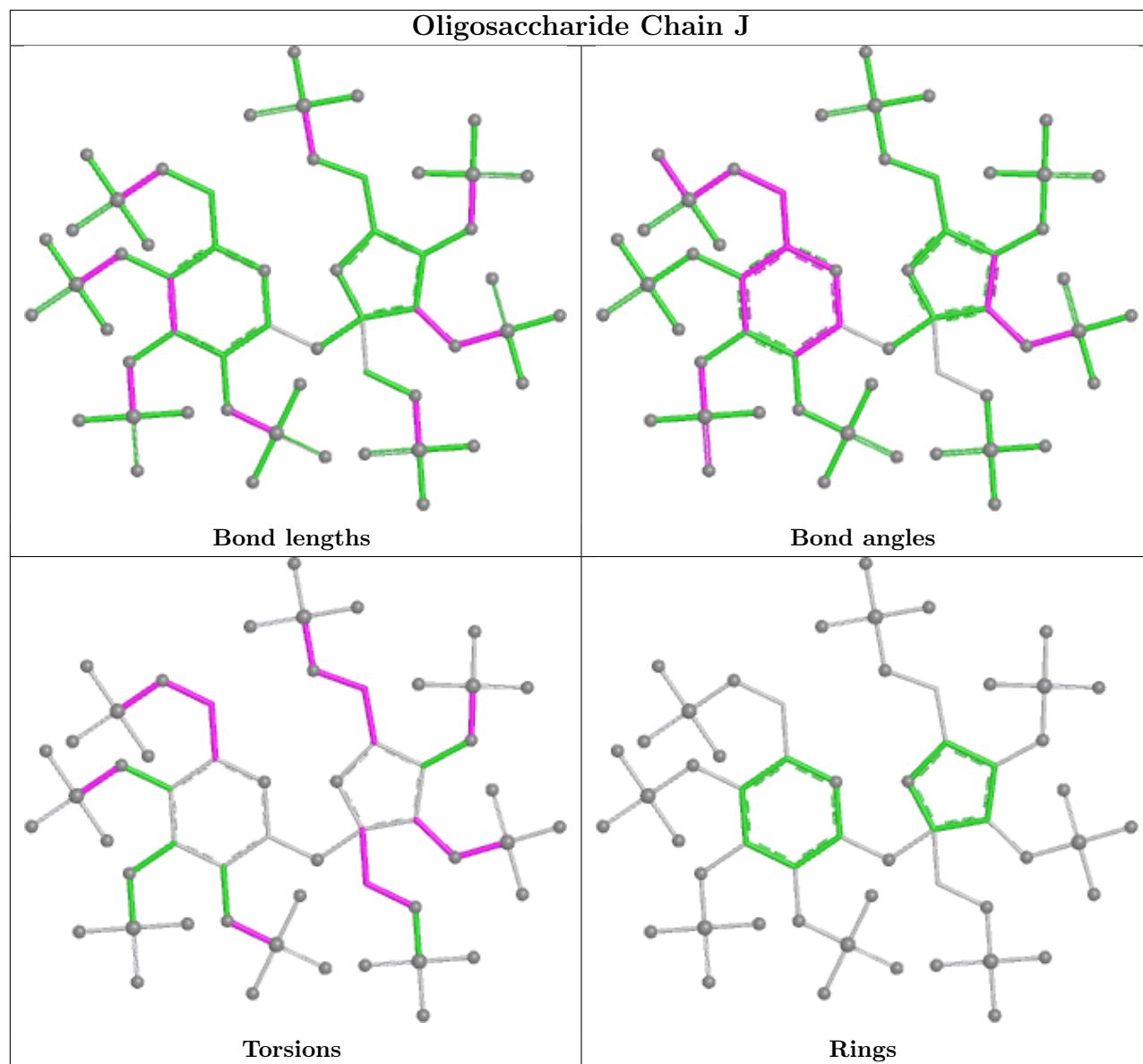
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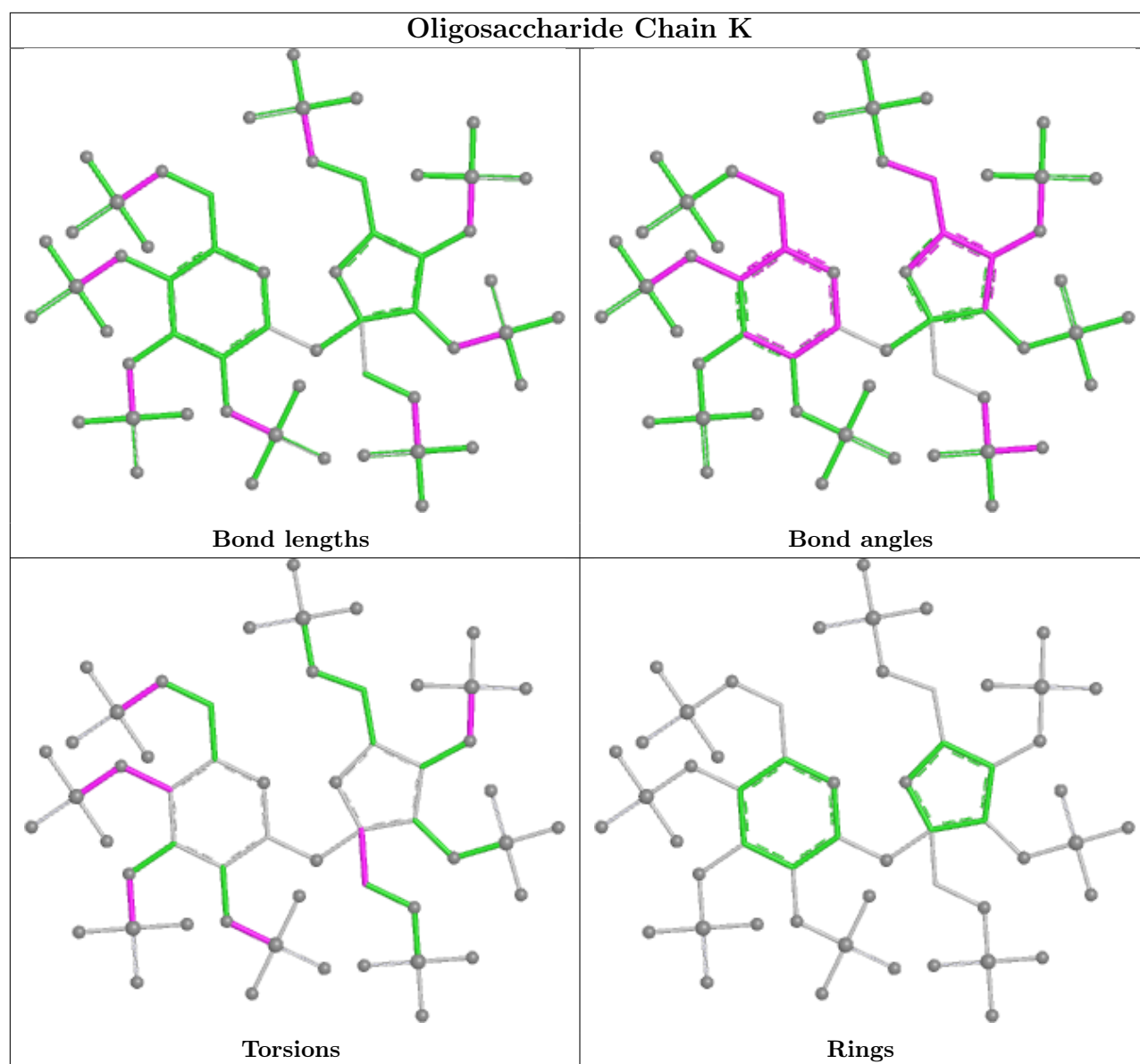
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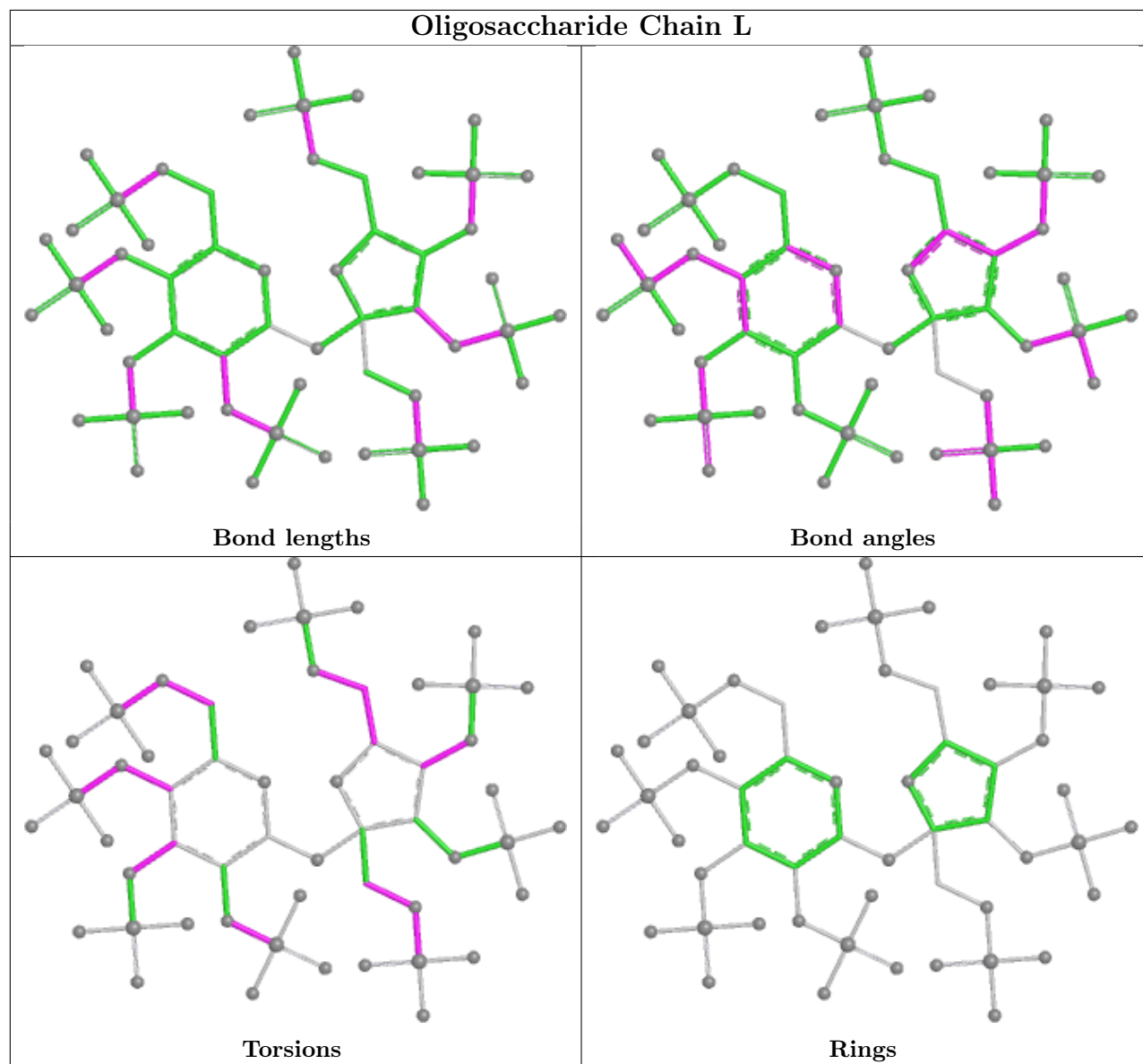
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	2	YYJ	11	0
2	I	2	YYJ	21	0
2	K	1	GU4	9	0
2	N	1	GU4	4	0
2	J	2	YYJ	6	0

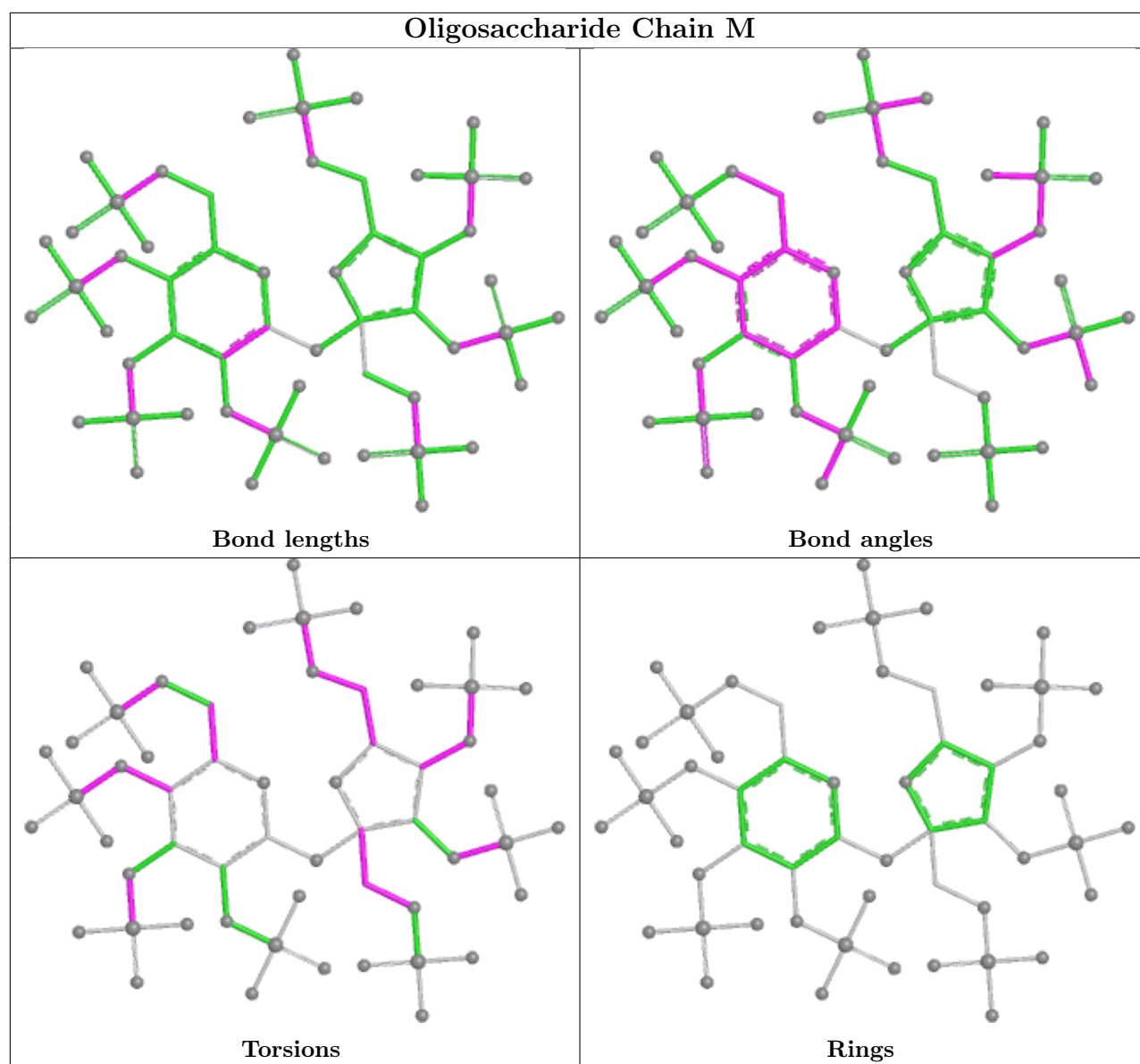
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

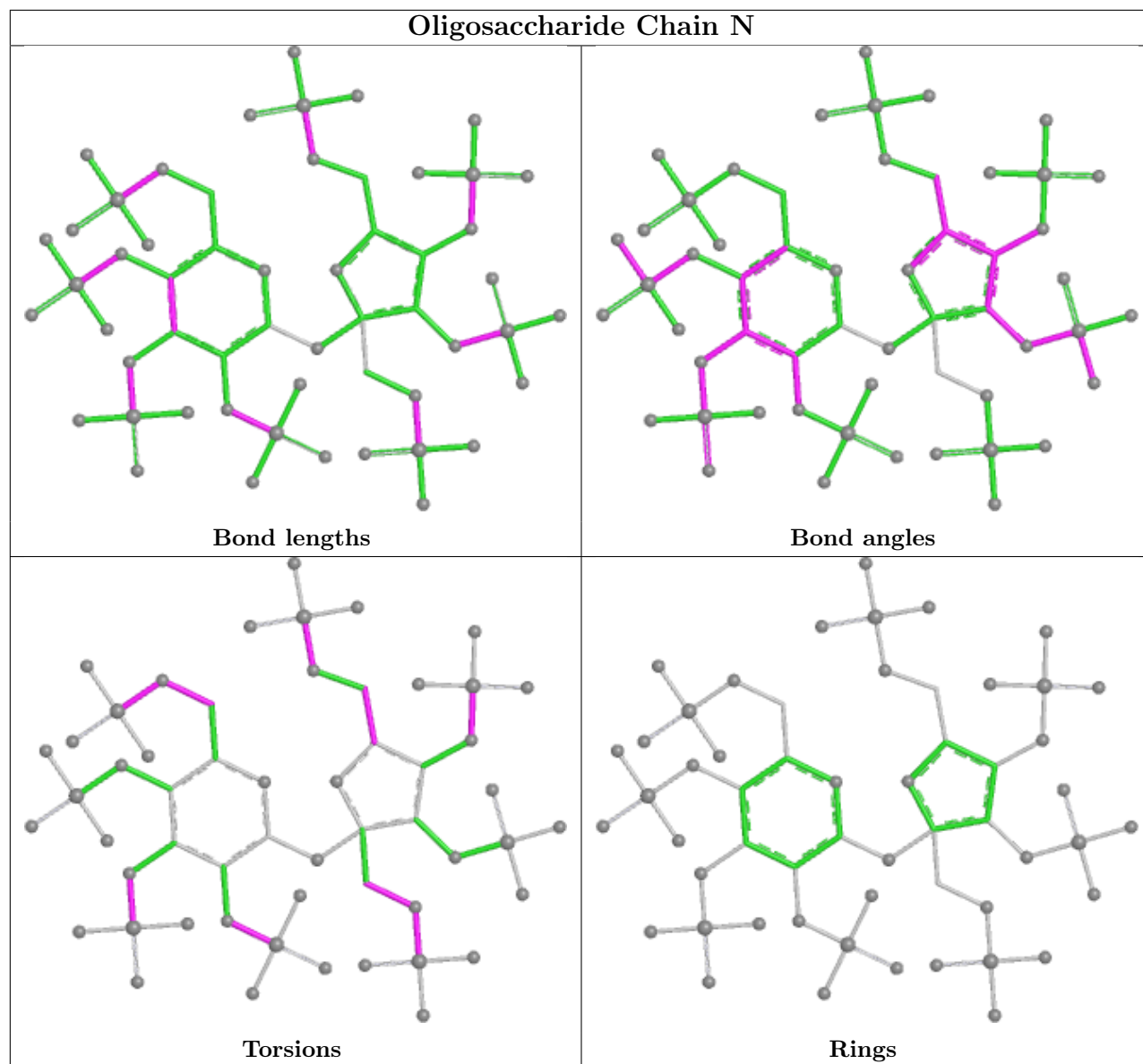


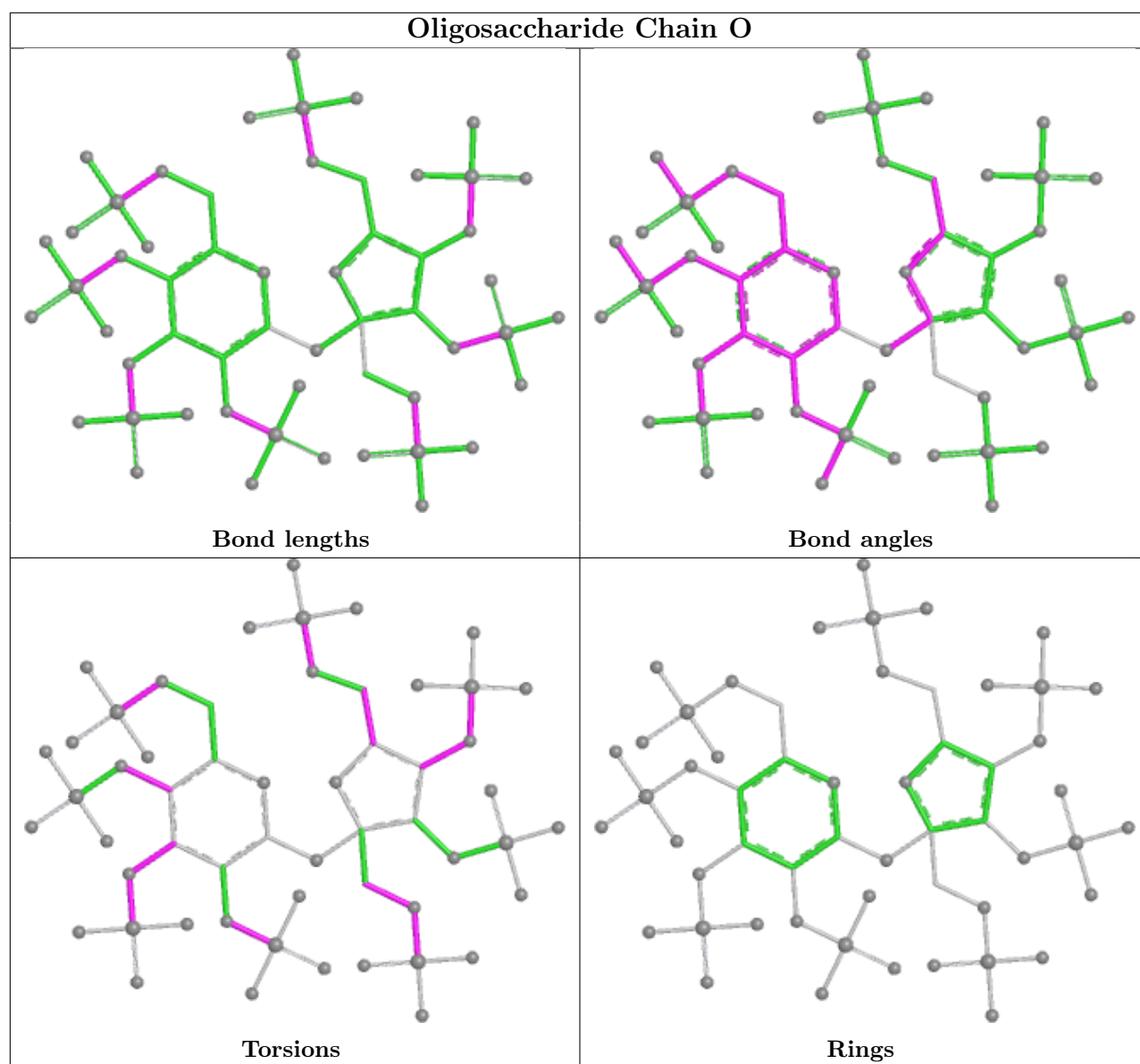


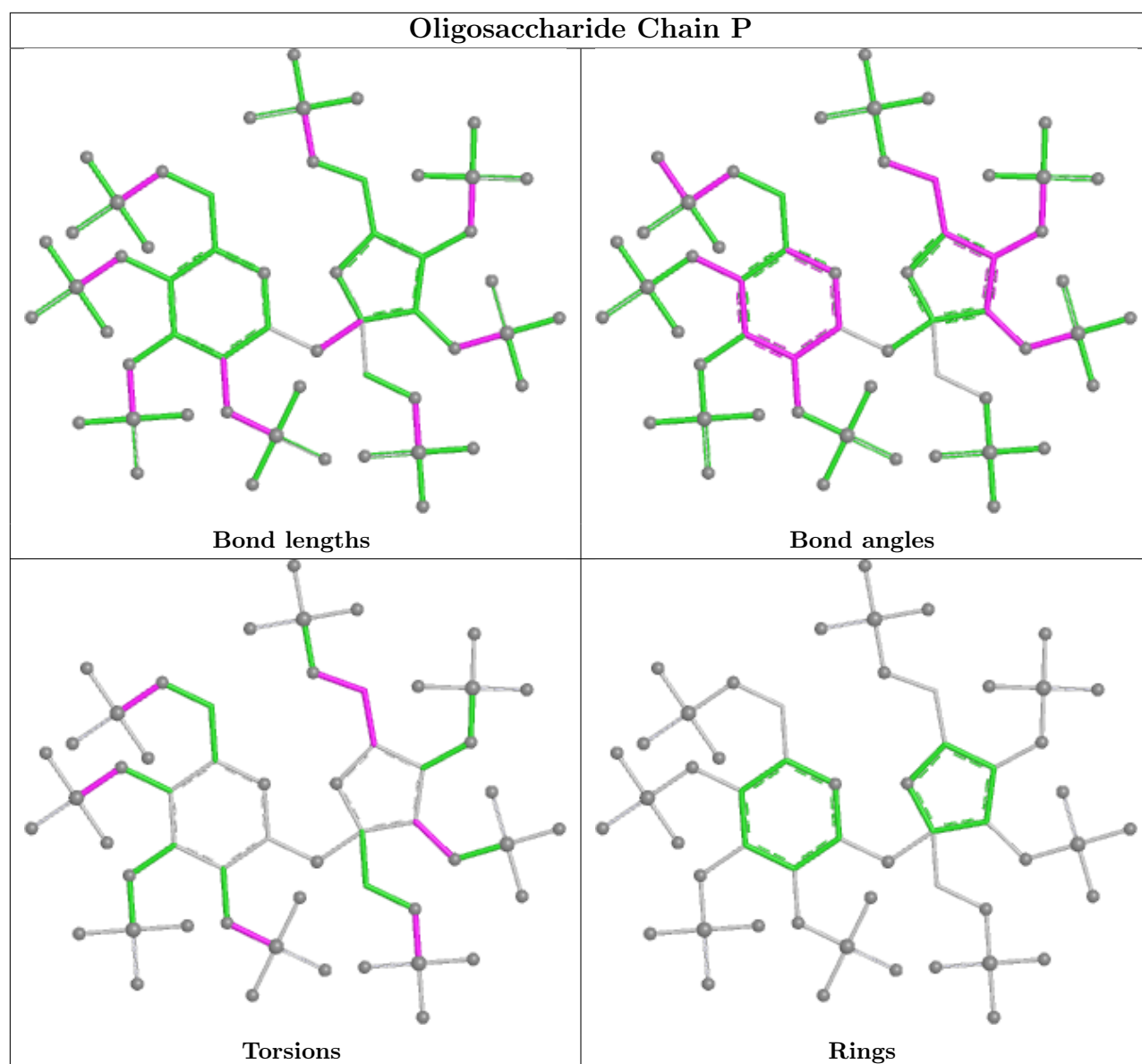












5.6 Ligand geometry [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.