Full wwPDB X-ray Structure Validation Report ⓘ

Jan 7, 2024 – 12:02 pm GMT

PDB ID	:	5OF0
Title	:	X-ray structure of human glutamate carboxypeptidase II (GCPII), the E424M inactive mutant, in complex with a inhibitor CFBzOG
Authors	:	Novakova, Z.; Motlova, L.; Barinka, C.
Deposited on	:	2017-07-10
Resolution	:	1.48 Å(reported)

This is a Full wwPDB X-ray Structure 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/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:

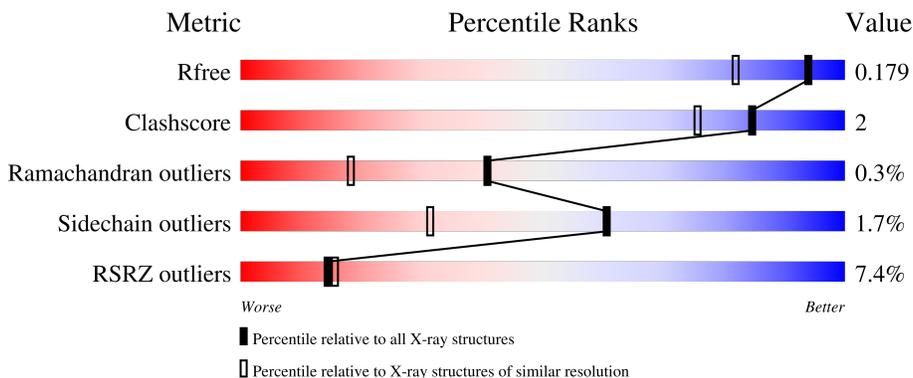|		
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1   Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
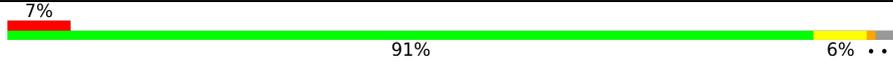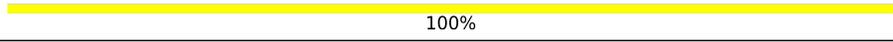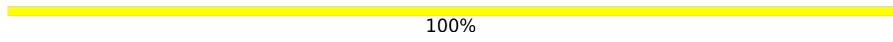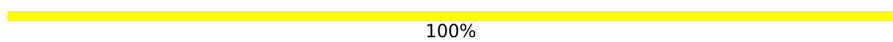*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.48 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	Percentile Ranks	Value
Rfree		0.179
Clashscore		2
Ramachandran outliers		0.3%
Sidechain outliers		1.7%
RSRZ outliers		7.4%

Worse   *Better*

∎ Percentile relative to all X-ray structures

❘ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	4690 (1.50-1.46)
Clashscore	141614	4955 (1.50-1.46)
Ramachandran outliers	138981	4846 (1.50-1.46)
Sidechain outliers	138945	4844 (1.50-1.46)
RSRZ outliers	127900	4614 (1.50-1.46)

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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	707	7% · 91% · 6% ··
2	B	2	100%
2	C	2	100%
2	D	2	50% · 50%
3	E	4	100%

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Mol	Chain	Length	Quality of chain
4	F	5	20% 80%

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	NAG	C	2	-	-	-	X

2 Entry composition ⓘ

There are 10 unique types of molecules in this entry. The entry contains 6629 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 Glutamate carboxypeptidase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	692	Total 5757	C 3694	N 967	O 1073	S 23	0	48	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	424	MET	GLU	engineered mutation	UNP Q04609

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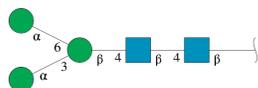

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total 28	C 16	N 2	O 10	0	0	0
2	C	2	Total 28	C 16	N 2	O 10	0	0	0
2	D	2	Total 28	C 16	N 2	O 10	0	0	0

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.
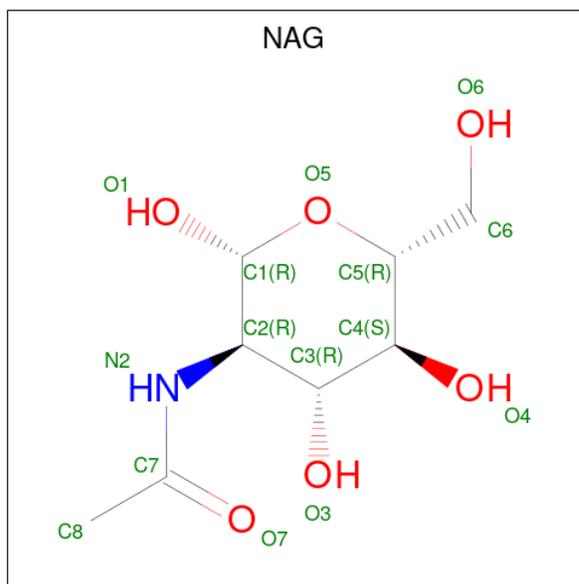
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	4	Total 50	C 28	N 2	O 20	0	0	0

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyran ose-(1-6)]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				ZeroOcc	AltConf	Trace
4	F	5	Total 61	C 34	N 2	O 25	0	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

NAG

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

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total 2	Zn 2	0	0

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total 1	Ca 1	0	0

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total 1	Cl 1	0	0

- Molecule 9 is (2 {S})-2-[[(2 {S})-6-[(4-fluorophenyl)methylamino]-1-oxidanyl-1,6-bis(oxidanylidene)hexan-2-yl]carbamoylamino]pentanedioic acid (three-letter code: 9TB) (formula: $C_{19}H_{24}FN_3O_8$).
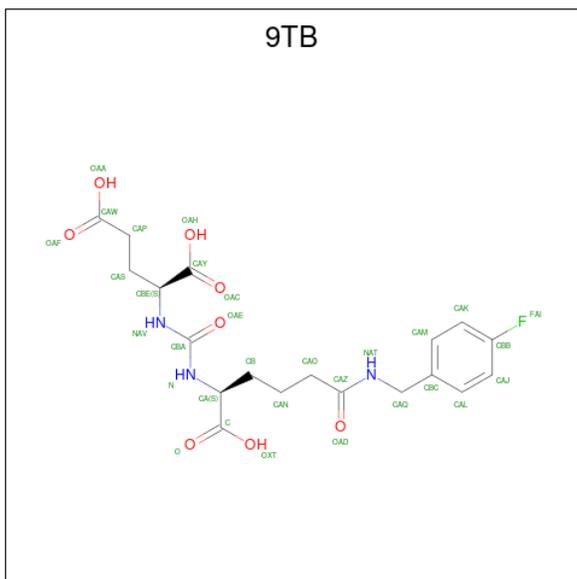
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total 31	C 19	F 1	N 3	O 8	0	0

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	614	Total 614	O 614	0	1

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 electron 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 dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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: Glutamate carboxypeptidase 2
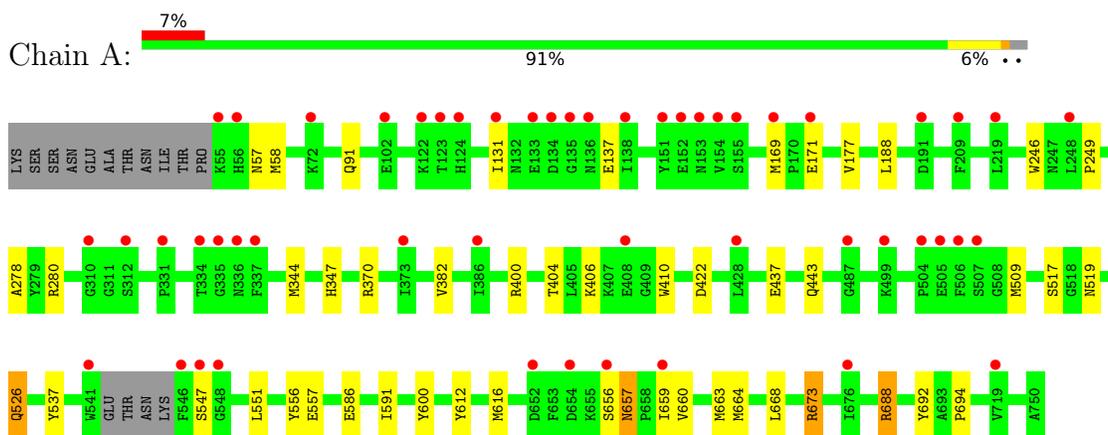
Chain A:

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

Chain B:

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

Chain C:

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

Chain D:
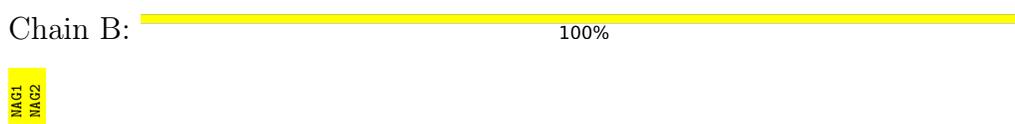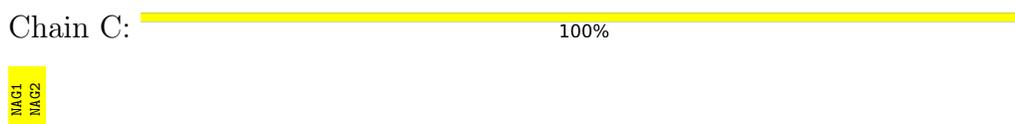
• Molecule 3: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-b eta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:

100%
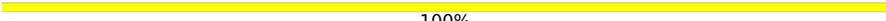
NAG1 NAG2 BMA3 MAN4

• Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyrano se-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyra nose

Chain F:

20%   80%

NAG1 NAG2 BMA3 MAN4 MAN5

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	101.47Å 130.46Å 159.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.25 – 1.48 49.25 – 1.48	Depositor EDS
% Data completeness (in resolution range)	98.8 (49.25-1.48) 98.8 (49.25-1.48)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.43 (at 1.48Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.157 , 0.172 0.164 , 0.179	Depositor DCC
R_{free} test set	3382 reflections (1.95%)	wwPDB-VP
Wilson B-factor (Å^2)	20.3	Xtriage
Anisotropy	0.596	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 55.1	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	6629	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: 9TB, ZN, CL, MAN, BMA, CA, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$|Z|$ >5	RMSZ	#$|Z|$ >5
1	A	0.68	1/6042 (0.0%)	0.84	6/8179 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	557	GLU	CD-OE2	-5.29	1.19	1.25

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	370	ARG	NE-CZ-NH1	7.95	124.28	120.30
1	A	673	ARG	NE-CZ-NH1	7.22	123.91	120.30
1	A	673	ARG	NE-CZ-NH2	-6.89	116.86	120.30
1	A	688[A]	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	A	688[B]	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	A	422	ASP	CB-CG-OD1	5.15	122.94	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2   Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5757	0	5626	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	28	0	25	0	0
2	C	28	0	25	0	0
2	D	28	0	25	0	0
3	E	50	0	43	0	0
4	F	61	0	52	0	0
5	A	28	0	26	1	0
6	A	2	0	0	0	0
7	A	1	0	0	0	0
8	A	1	0	0	0	0
9	A	31	0	0	0	0
10	A	614	0	0	7	0
All	All	6629	0	5822	27	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 2.

All (27) 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:660[A]:VAL:O	1:A:664[A]:MET:HG2	1.26	1.35
1:A:656[B]:SER:O	1:A:657[B]:ASN:HB2	1.86	0.76
1:A:660[A]:VAL:O	1:A:664[A]:MET:CG	2.22	0.69
1:A:400:ARG:O	1:A:404[B]:THR:HG23	1.96	0.66
1:A:437:GLU:OE2	10:A:901:HOH:O	2.14	0.66
1:A:91[B]:GLN:NE2	10:A:904:HOH:O	2.35	0.60
1:A:526[A]:GLN:NE2	1:A:692:TYR:O	2.37	0.58
1:A:688[B]:ARG:NH1	10:A:902:HOH:O	2.26	0.57
1:A:612:TYR:CZ	1:A:616:MET:HG3	2.46	0.51
1:A:517:SER:HB2	1:A:694:PRO:HG3	1.92	0.51
1:A:659[B]:ILE:O	1:A:663[B]:MET:HG3	2.10	0.51
1:A:443[B]:GLN:NE2	10:A:908:HOH:O	2.43	0.50
1:A:278:ALA:HB3	1:A:280[B]:ARG:NH1	2.28	0.48
1:A:58:MET:HE1	1:A:586[A]:GLU:HG2	1.95	0.48
1:A:131:ILE:HD11	1:A:171:GLU:HG3	1.96	0.47
1:A:58:MET:CE	1:A:586[A]:GLU:HG2	2.46	0.46
1:A:131:ILE:HG22	1:A:137:GLU:HG2	2.00	0.44
1:A:169:MET:HA	1:A:344:MET:O	2.19	0.43
1:A:177:VAL:HG12	1:A:188:LEU:HD11	2.02	0.41
1:A:347:HIS:HE1	10:A:1408:HOH:O	2.03	0.41
1:A:659[B]:ILE:HD13	1:A:659[B]:ILE:HA	1.85	0.41
1:A:551:LEU:HD22	1:A:556:TYR:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:TRP:CD1	5:A:808:NAG:H83	2.56	0.41
1:A:58:MET:HE1	1:A:586[A]:GLU:CG	2.52	0.40
1:A:664[A]:MET:HE1	10:A:1256:HOH:O	2.21	0.40
1:A:406:LYS:HA	1:A:410:TRP:O	2.22	0.40
1:A:591[A]:ILE:HD12	10:A:1508:HOH:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	736/707 (104%)	715 (97%)	18 (2%)	3 (0%)	34	13

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	382	VAL
1	A	657[A]	ASN
1	A	657[B]	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	637/603 (106%)	625 (98%)	12 (2%)	57	26

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	249	PRO
1	A	509	MET
1	A	519	ASN
1	A	526[A]	GLN
1	A	526[B]	GLN
1	A	537	TYR
1	A	547	SER
1	A	600	TYR
1	A	668[A]	LEU
1	A	668[B]	LEU
1	A	673	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	124	HIS
1	A	345	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

15 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	NAG	B	1	2,1	14,14,15	0.39	0	17,19,21	0.95	1 (5%)
2	NAG	B	2	2	14,14,15	0.64	0	17,19,21	1.40	1 (5%)
2	NAG	C	1	2,1	14,14,15	0.72	0	17,19,21	1.61	2 (11%)
2	NAG	C	2	2	14,14,15	0.52	0	17,19,21	0.93	1 (5%)
2	NAG	D	1	2,1	14,14,15	0.62	0	17,19,21	1.08	1 (5%)
2	NAG	D	2	2	14,14,15	0.42	0	17,19,21	0.76	0
3	NAG	E	1	3,1	14,14,15	0.45	0	17,19,21	0.94	1 (5%)
3	NAG	E	2	3	14,14,15	0.36	0	17,19,21	1.34	1 (5%)
3	BMA	E	3	3	11,11,12	0.55	0	15,15,17	1.52	1 (6%)
3	MAN	E	4	3	11,11,12	0.46	0	15,15,17	0.94	1 (6%)
4	NAG	F	1	4,1	14,14,15	0.56	0	17,19,21	1.20	1 (5%)
4	NAG	F	2	4	14,14,15	0.56	0	17,19,21	1.55	3 (17%)
4	BMA	F	3	4	11,11,12	0.54	0	15,15,17	0.80	0
4	MAN	F	4	4	11,11,12	0.42	0	15,15,17	1.10	1 (6%)
4	MAN	F	5	4	11,11,12	0.57	0	15,15,17	1.00	1 (6%)

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	NAG	B	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1
2	NAG	C	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	NAG	D	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
3	NAG	E	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	BMA	E	3	3	-	1/2/19/22	0/1/1/1
3	MAN	E	4	3	-	0/2/19/22	0/1/1/1
4	NAG	F	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	F	2	4	-	4/6/23/26	0/1/1/1
4	BMA	F	3	4	-	0/2/19/22	0/1/1/1
4	MAN	F	4	4	-	0/2/19/22	0/1/1/1
4	MAN	F	5	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	3	BMA	C1-O5-C5	4.84	118.74	112.19
2	B	2	NAG	C2-N2-C7	4.60	129.45	122.90
2	C	1	NAG	C1-C2-N2	-3.90	103.82	110.49
4	F	2	NAG	C1-O5-C5	3.71	117.22	112.19
4	F	1	NAG	O5-C1-C2	-3.32	106.05	111.29
2	C	1	NAG	C8-C7-N2	3.22	121.55	116.10
3	E	2	NAG	C8-C7-N2	3.06	121.28	116.10
4	F	2	NAG	C8-C7-N2	2.80	120.84	116.10
2	D	1	NAG	O5-C1-C2	-2.68	107.06	111.29
4	F	4	MAN	O5-C5-C6	2.64	111.35	107.20
4	F	5	MAN	O5-C5-C6	2.46	111.06	107.20
2	B	1	NAG	O5-C1-C2	-2.28	107.69	111.29
2	C	2	NAG	C1-O5-C5	2.22	115.20	112.19
4	F	2	NAG	O4-C4-C5	-2.14	103.99	109.30
3	E	4	MAN	O5-C5-C6	2.09	110.48	107.20
3	E	1	NAG	O5-C1-C2	-2.08	108.00	111.29

There are no chirality outliers.

All (16) torsion outliers are listed below:

| Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2
3	E	2	NAG	C8-C7-N2-C2
3	E	2	NAG	O7-C7-N2-C2
4	F	2	NAG	C8-C7-N2-C2
4	F	2	NAG	O7-C7-N2-C2
2	C	2	NAG	O5-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
4	F	2	NAG	C4-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6
4	F	2	NAG	O5-C5-C6-O6
4	F	1	NAG	C4-C5-C6-O6
3	E	3	BMA	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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

Oligosaccharide Chain B

Bond lengths

Bond angles

Torsions

Rings

Oligosaccharide Chain C

Bond lengths

Bond angles

Torsions

Rings

Oligosaccharide Chain D

Bond lengths

Bond angles

Torsions

Rings

Oligosaccharide Chain E

Bond lengths

Bond angles

Torsions

Rings

Oligosaccharide Chain F

Bond lengths

Bond angles

Torsions

Rings
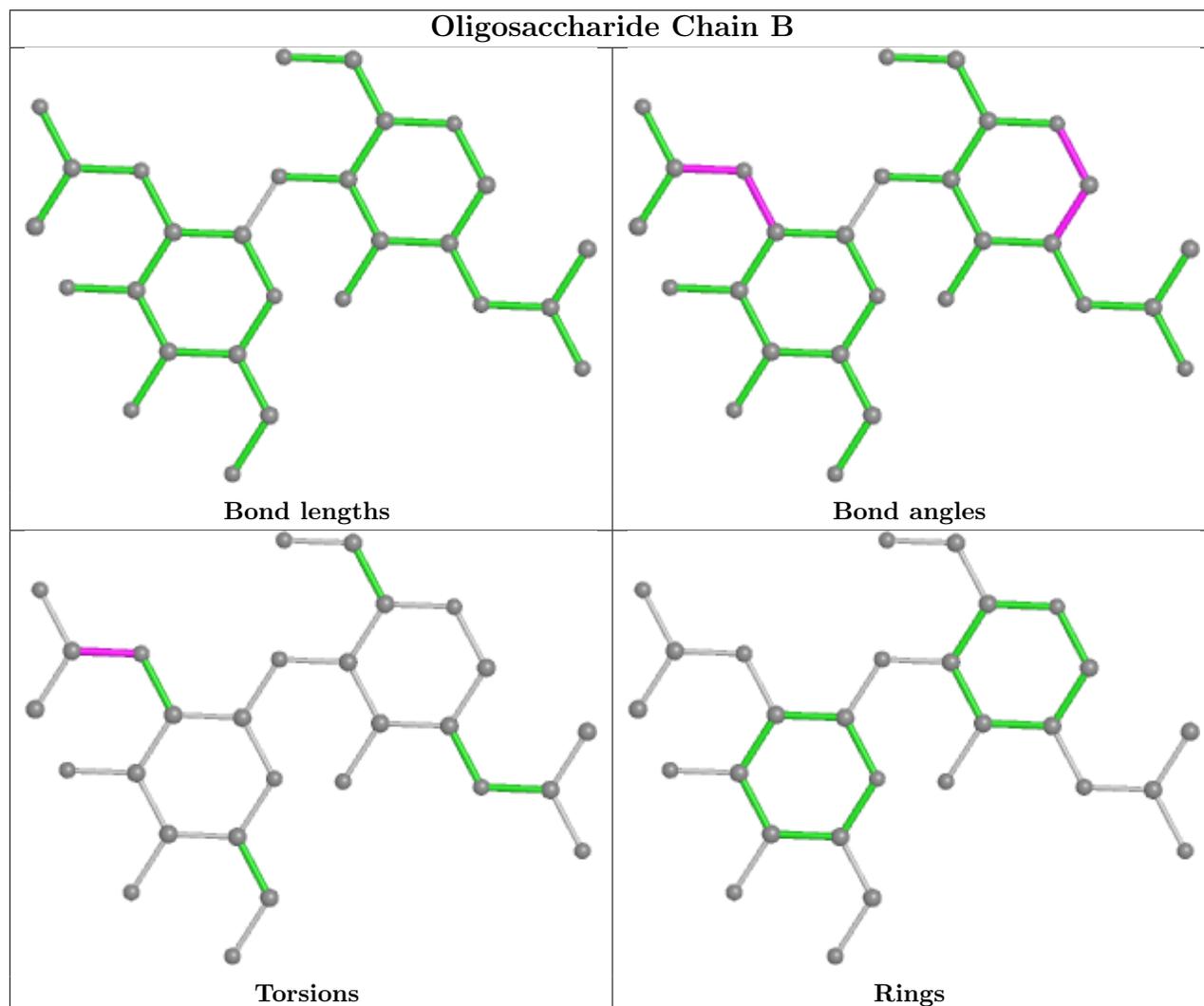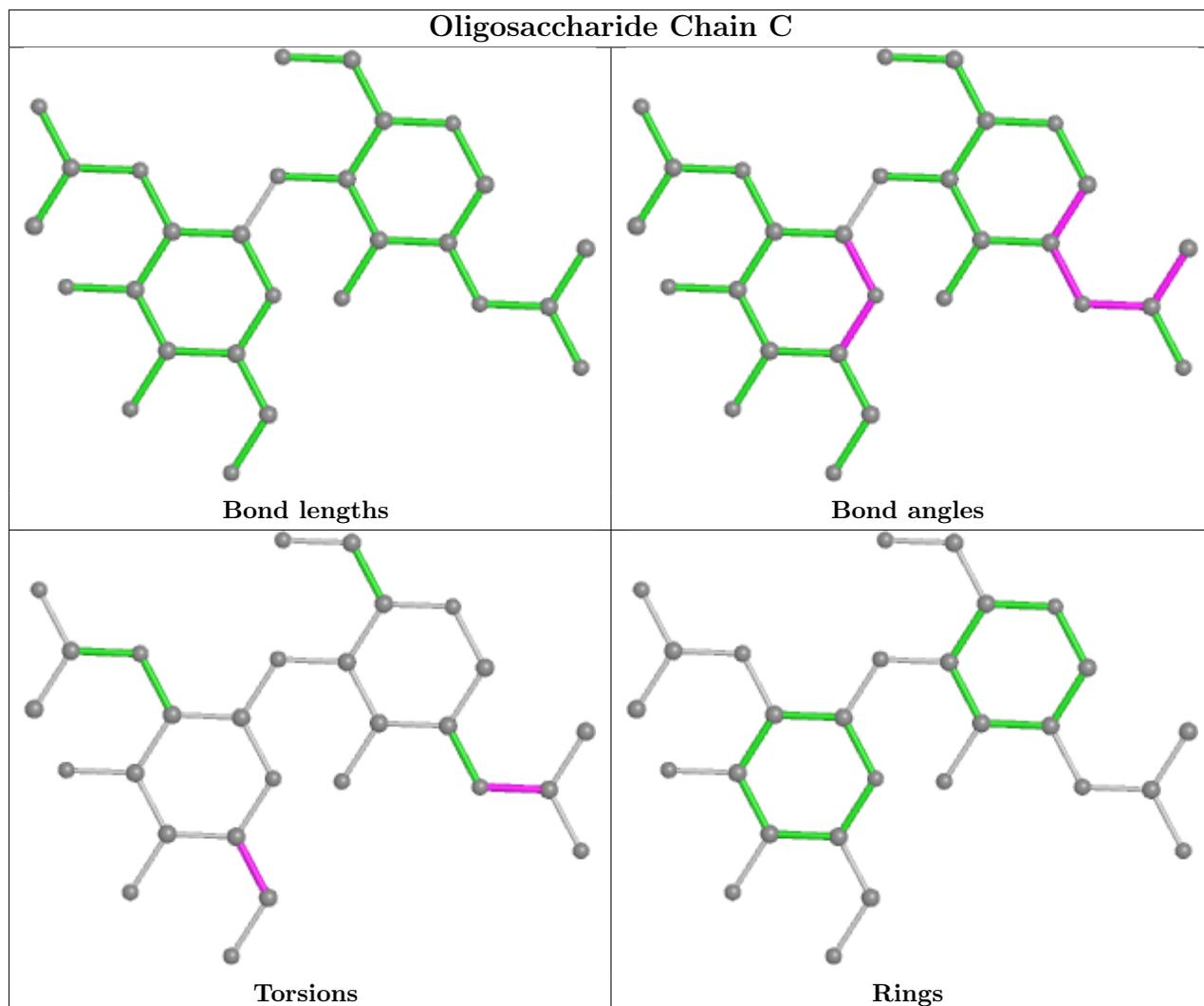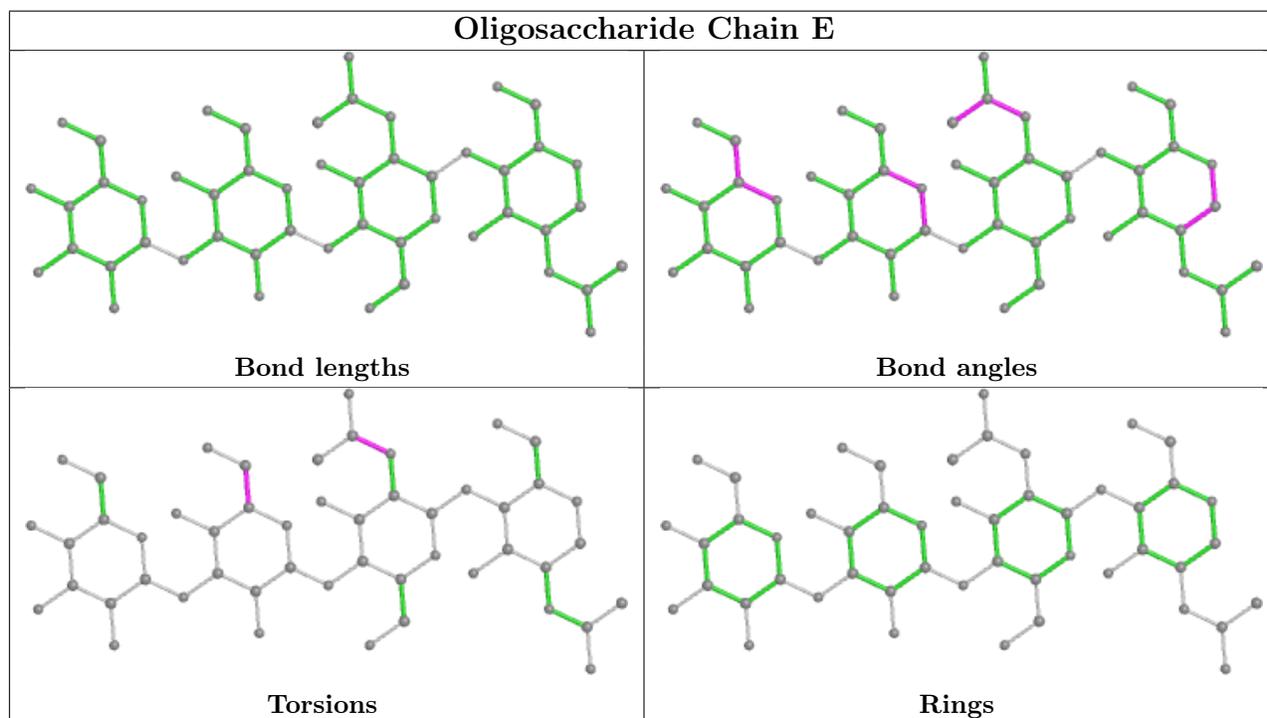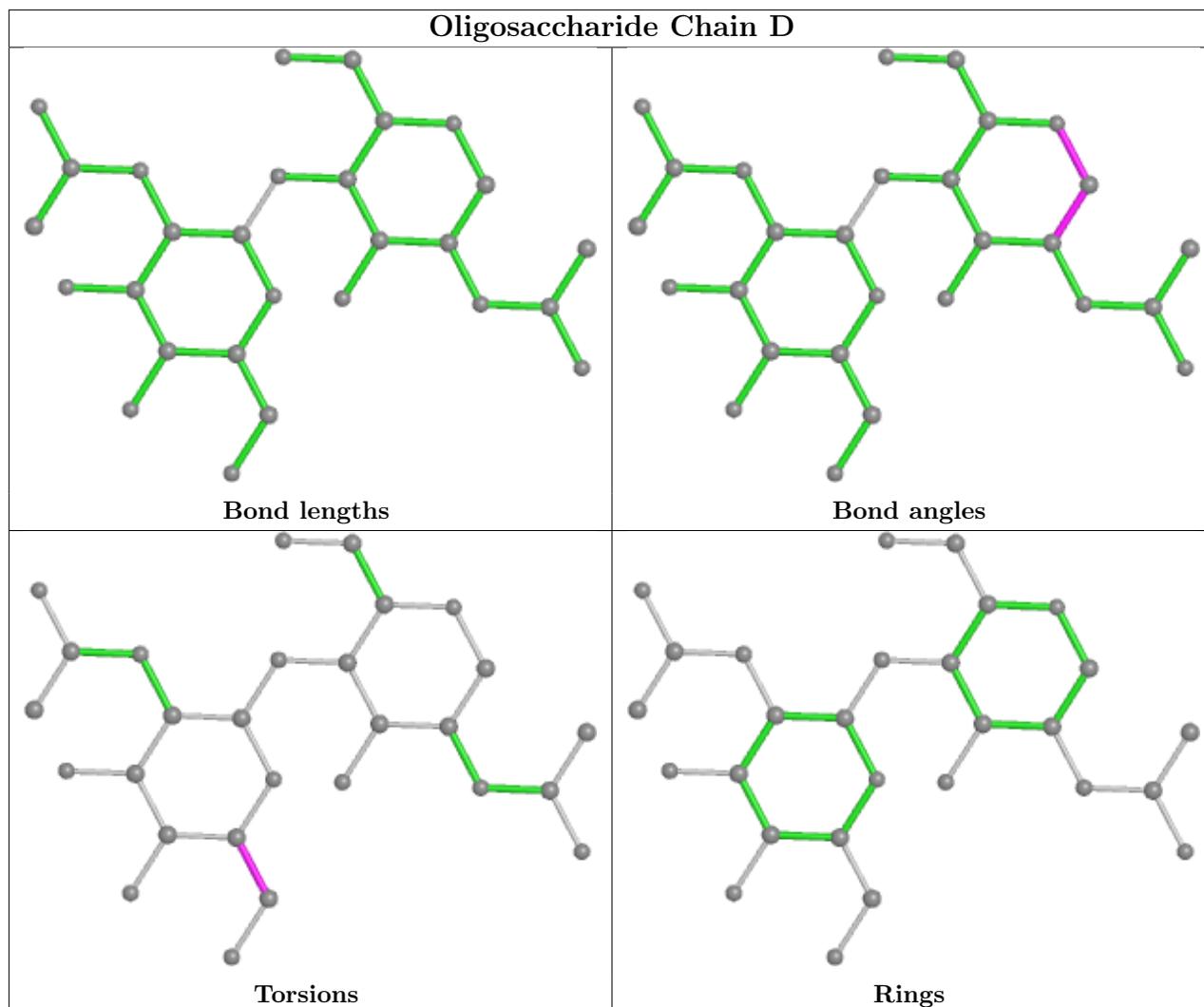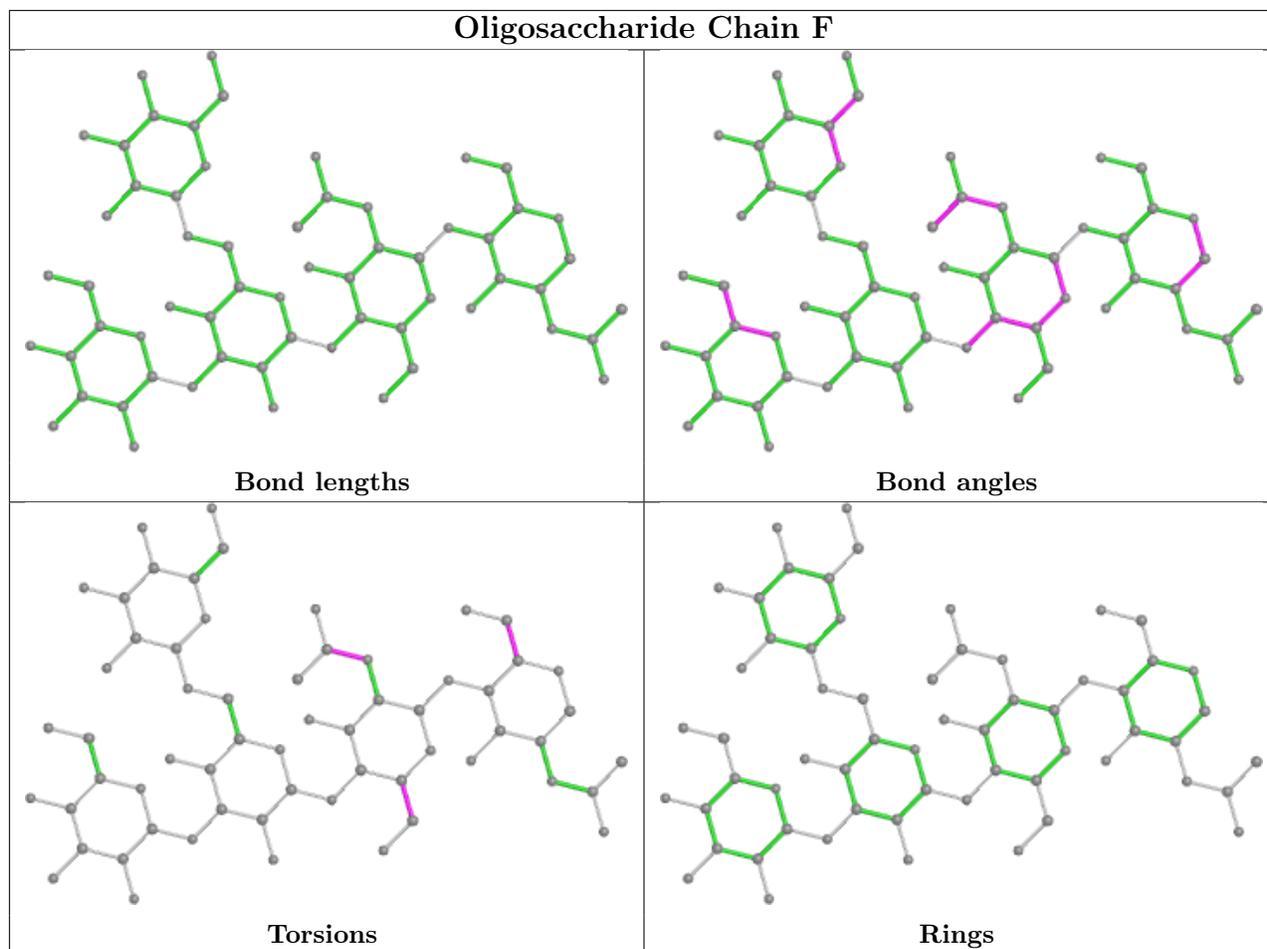
5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
9	9TB	A	822	-	31,31,31	1.90	2 (6%)	40,40,40	1.71	11 (27%)
5	NAG	A	807	1	14,14,15	0.56	0	17,19,21	2.35	5 (29%)
5	NAG	A	808	1	14,14,15	0.76	0	17,19,21	1.12	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	9TB	A	822	-	-	5/32/32/32	0/1/1/1
5	NAG	A	807	1	-	2/6/23/26	0/1/1/1
5	NAG	A	808	1	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	822	9TB	CAQ-NAT	-9.33	1.27	1.46
9	A	822	9TB	CBA-N	-2.05	1.31	1.35

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	807	NAG	C1-O5-C5	6.52	121.03	112.19
9	A	822	9TB	CAK-CBB-CAJ	-4.01	117.50	122.83
9	A	822	9TB	OAD-CAZ-CAO	-3.71	115.22	122.02
5	A	807	NAG	C8-C7-N2	3.32	121.71	116.10
9	A	822	9TB	CAO-CAZ-NAT	3.20	121.81	116.42
5	A	807	NAG	O5-C1-C2	-3.04	106.48	111.29
9	A	822	9TB	CAL-CAJ-CBB	3.03	121.50	118.36
9	A	822	9TB	CAM-CAK-CBB	2.91	121.38	118.36
9	A	822	9TB	OAE-CBA-NAV	-2.88	117.38	122.62
9	A	822	9TB	FAI-CBB-CAJ	2.70	123.12	118.54
9	A	822	9TB	CAQ-NAT-CAZ	2.69	126.53	122.34
9	A	822	9TB	OAH-CAY-CBE	2.64	122.16	113.40
5	A	807	NAG	C6-C5-C4	-2.44	107.29	113.00
9	A	822	9TB	CBC-CAQ-NAT	2.43	118.26	113.05
5	A	807	NAG	C4-C3-C2	-2.30	107.65	111.02
5	A	808	NAG	O5-C1-C2	-2.11	107.96	111.29
9	A	822	9TB	OAE-CBA-N	2.08	126.42	122.62

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	822	9TB	N-CA-CB-CAN
5	A	807	NAG	C8-C7-N2-C2
5	A	807	NAG	O7-C7-N2-C2
9	A	822	9TB	C-CA-CB-CAN

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Mol	Chain	Res	Type	Atoms
9	A	822	9TB	CAO-CAN-CB-CA
9	A	822	9TB	CAN-CAO-CAZ-NAT
9	A	822	9TB	CAN-CAO-CAZ-OAD

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	808	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand 9TB A 822

Bond lengths　　　　　Bond angles

Torsions　　　　　Rings
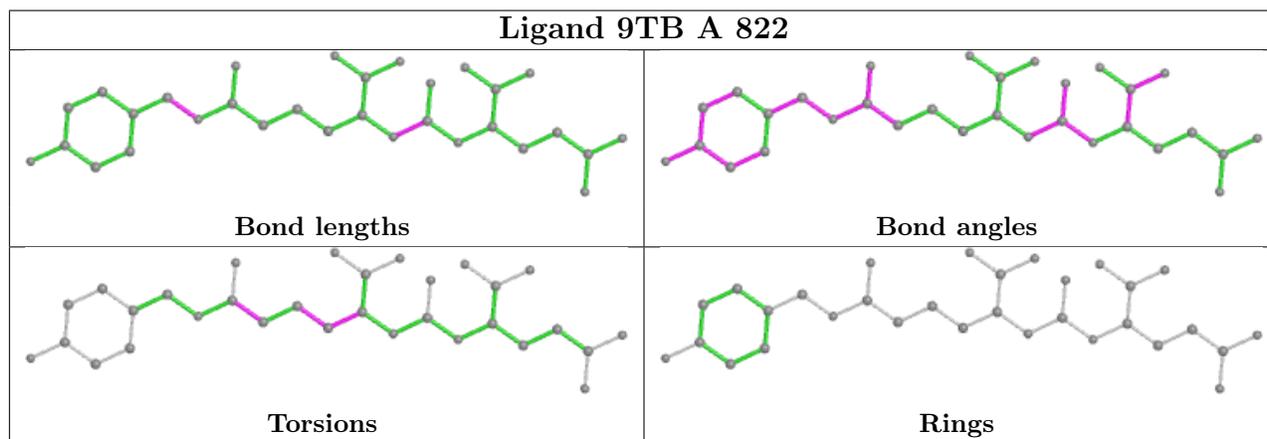
5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	692/707 (97%)	0.51	51 (7%)	14	15	26, 36, 55, 79	3 (0%)

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	546	PHE	9.8
1	A	656[A]	SER	7.5
1	A	547	SER	6.1
1	A	541	TRP	5.7
1	A	55	LYS	5.4
1	A	507	SER	5.2
1	A	155	SER	4.9
1	A	153	ASN	4.3
1	A	719	VAL	3.9
1	A	135	GLY	3.8
1	A	506	PHE	3.7
1	A	336	ASN	3.6
1	A	131	ILE	3.5
1	A	154	VAL	3.5
1	A	505	GLU	3.4
1	A	138[A]	ILE	3.4
1	A	136	ASN	3.4
1	A	134	ASP	3.4
1	A	334	THR	3.2
1	A	152	GLU	3.0
1	A	133	GLU	3.0
1	A	487	GLY	3.0
1	A	428	LEU	2.9
1	A	548	GLY	2.8
1	A	659[A]	ILE	2.7
1	A	56	HIS	2.7
1	A	171	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	312[A]	SER	2.6
1	A	72	LYS	2.5
1	A	504	PRO	2.5
1	A	337	PHE	2.5
1	A	151	TYR	2.4
1	A	335	GLY	2.4
1	A	310	GLY	2.4
1	A	676	ILE	2.4
1	A	209	PHE	2.3
1	A	386	ILE	2.3
1	A	124	HIS	2.3
1	A	123	THR	2.3
1	A	102	GLU	2.3
1	A	331	PRO	2.3
1	A	219	LEU	2.2
1	A	654	ASP	2.2
1	A	652	ASP	2.2
1	A	122	LYS	2.2
1	A	191	ASP	2.2
1	A	373	ILE	2.1
1	A	169	MET	2.1
1	A	248	LEU	2.1
1	A	499	LYS	2.0
1	A	408	GLU	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.
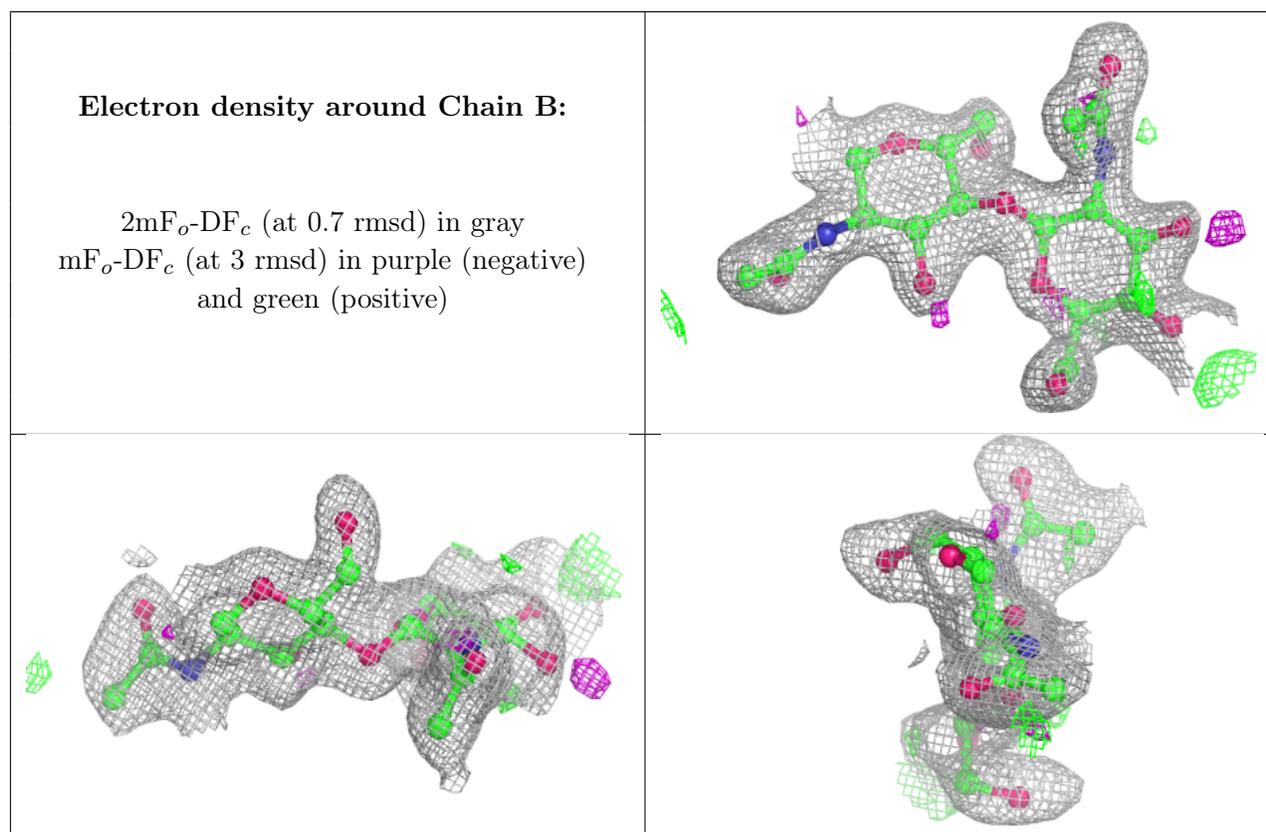
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	C	2	14/15	0.58	0.41	77,80,83,84	0
4	MAN	F	5	11/12	0.63	0.26	61,64,67,70	0
2	NAG	B	2	14/15	0.67	0.27	50,57,65,66	0
2	NAG	C	1	14/15	0.76	0.26	52,58,65,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å²)	Q<0.9
3	MAN	E	4	11/12	0.77	0.23	59,63,64,68	0
3	BMA	E	3	11/12	0.80	0.22	57,59,64,69	0
2	NAG	D	1	14/15	0.81	0.22	48,52,57,58	0
4	MAN	F	4	11/12	0.83	0.12	55,58,61,61	0
2	NAG	D	2	14/15	0.83	0.28	61,65,71,74	0
4	NAG	F	1	14/15	0.84	0.12	34,40,48,57	0
3	NAG	E	2	14/15	0.85	0.12	44,50,54,62	0
4	NAG	F	2	14/15	0.88	0.18	49,53,63,66	0
4	BMA	F	3	11/12	0.88	0.14	51,52,55,56	0
2	NAG	B	1	14/15	0.92	0.17	42,48,56,59	0
3	NAG	E	1	14/15	0.93	0.08	37,41,47,51	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.
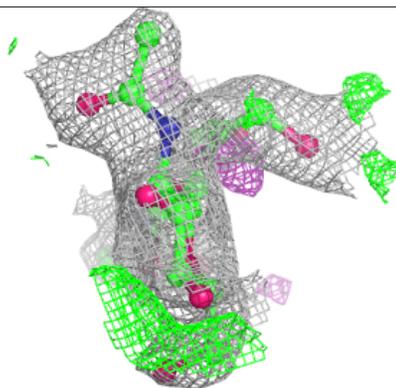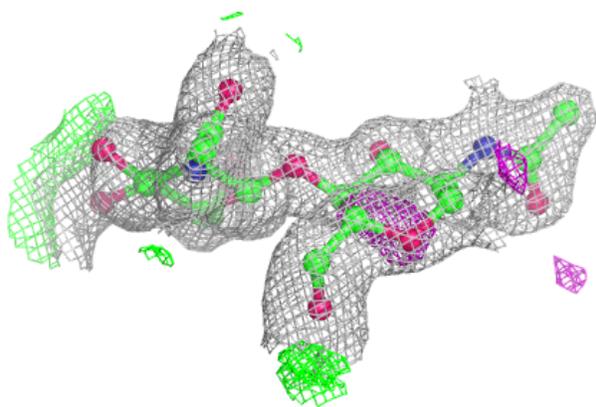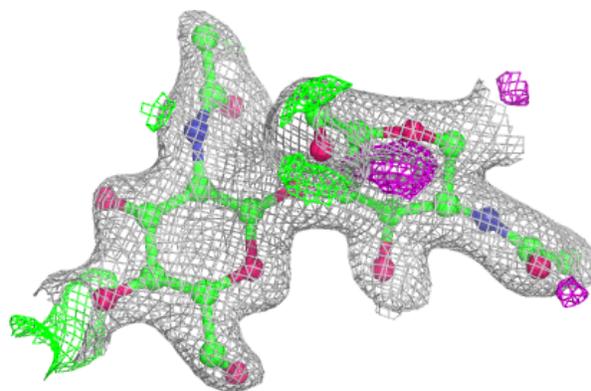

Electron density around Chain B:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

Electron density around Chain C:

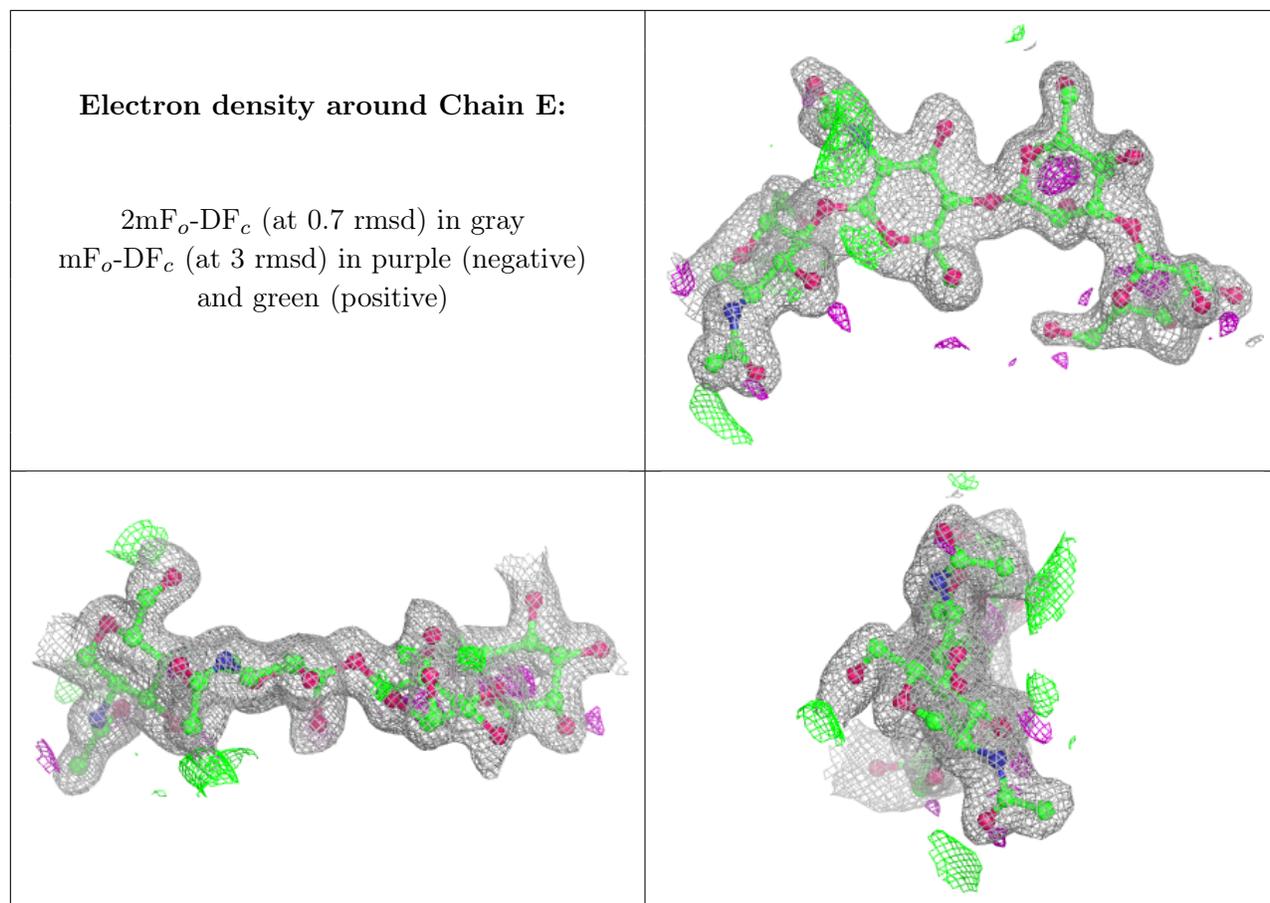$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
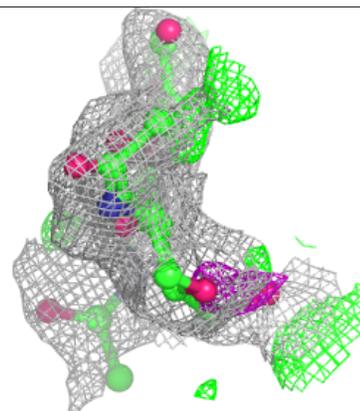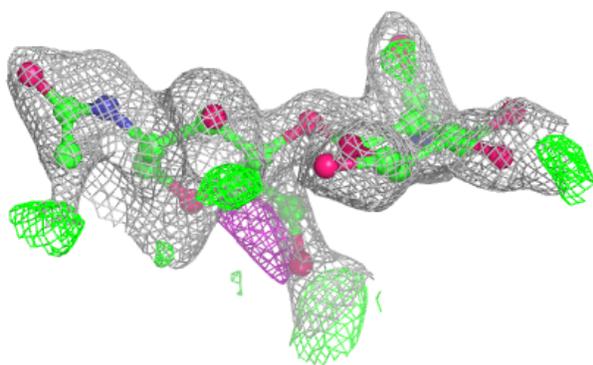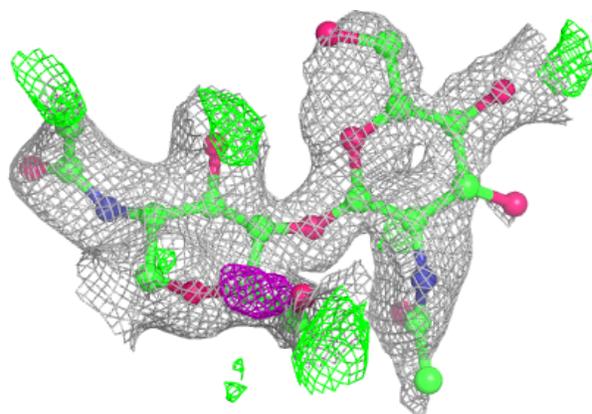
Electron density around Chain D:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around Chain E:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
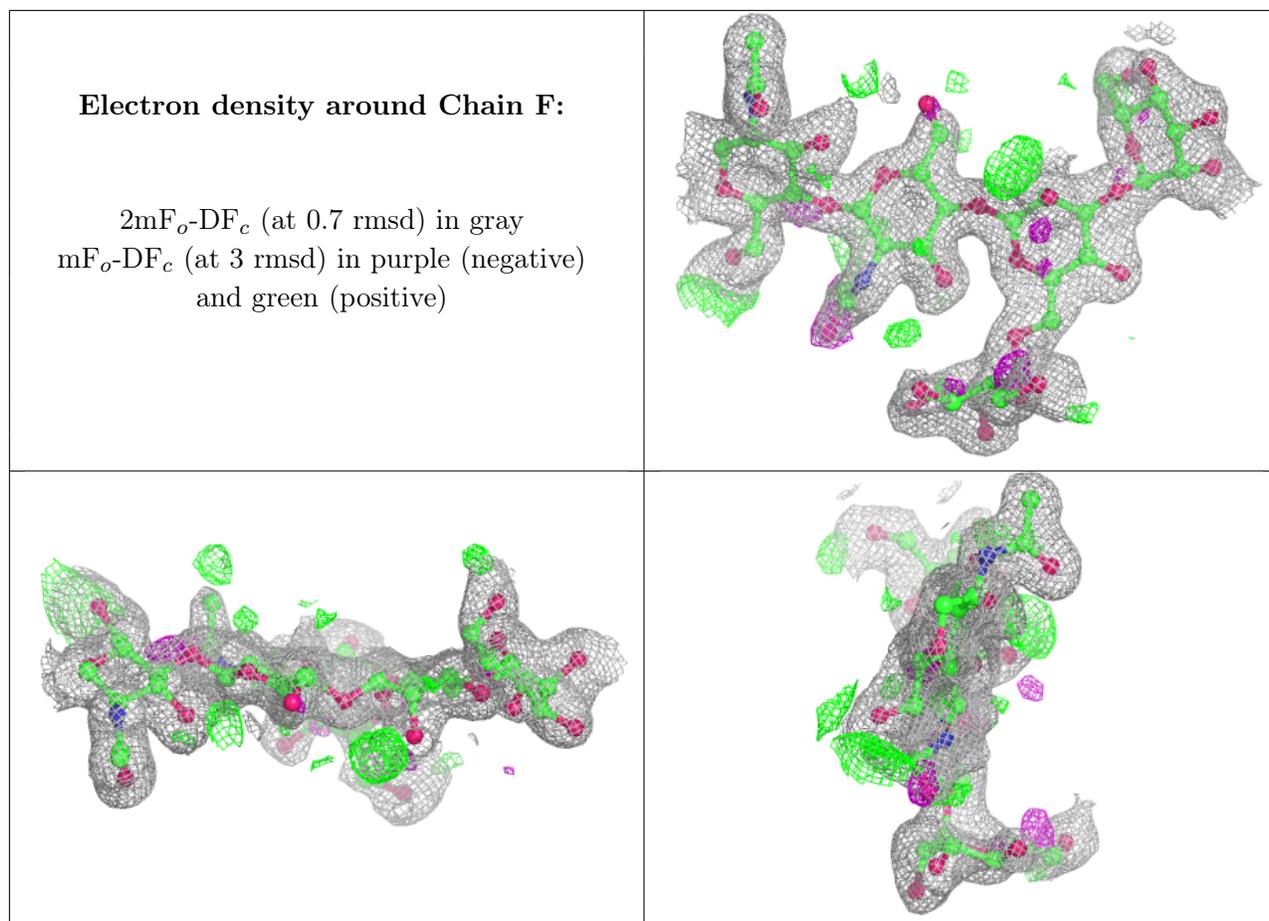and green (positive)

Electron density around Chain F:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
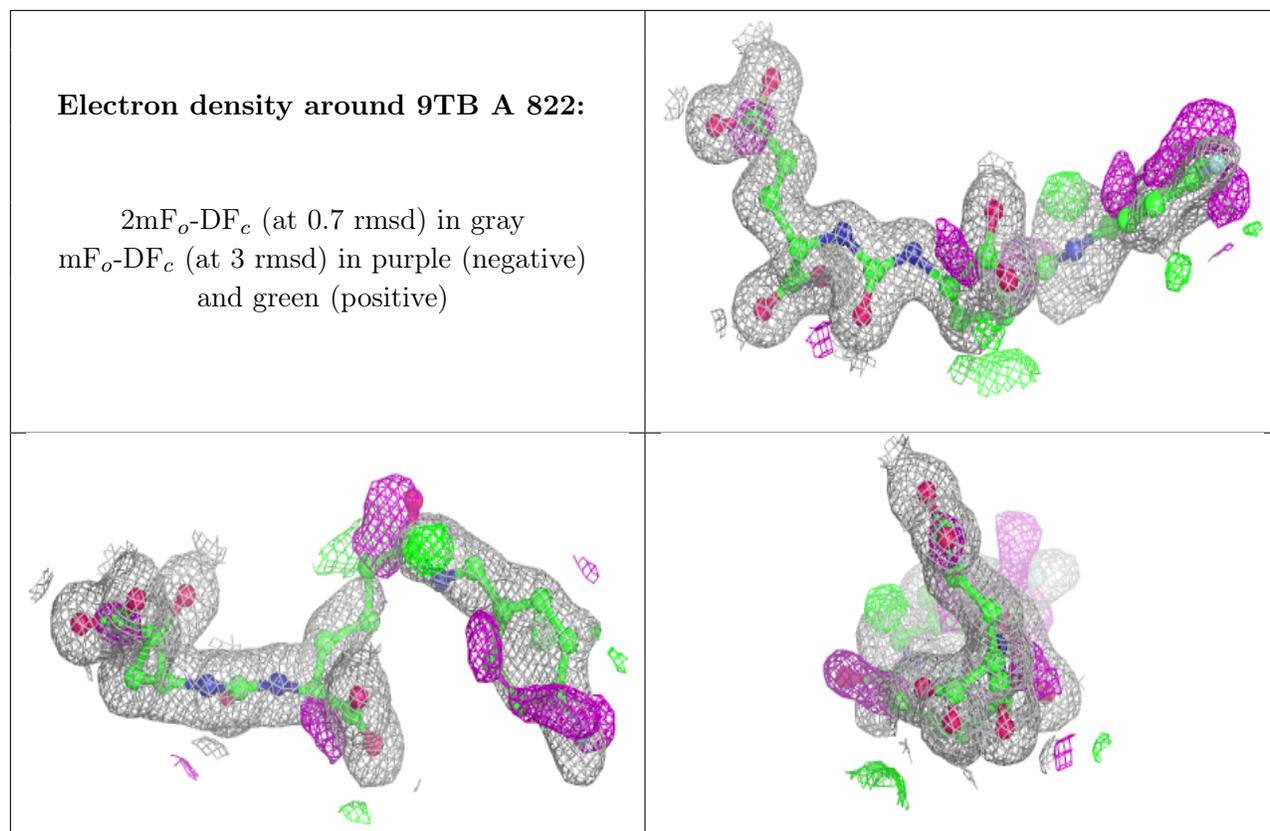mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($Å^2$)	Q<0.9
5	NAG	A	807	14/15	0.69	0.23	74,79,83,85	0
5	NAG	A	808	14/15	0.81	0.14	41,48,57,57	0
9	9TB	A	822	31/31	0.94	0.14	30,36,69,81	0
6	ZN	A	819	1/1	1.00	0.10	28,28,28,28	0
7	CA	A	820	1/1	1.00	0.11	27,27,27,27	0
8	CL	A	821	1/1	1.00	0.13	31,31,31,31	0
6	ZN	A	818	1/1	1.00	0.09	29,29,29,29	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 9TB A 822:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

6.5 Other polymers ⓘ

There are no such residues in this entry.