

# wwPDB X-ray Structure Validation Summary Report (i)

Nov 20, 2023 – 03:21 pm GMT

PDB ID : 8BOW

Title: X-ray structure of human glutamate carboxypeptidase II (GCPII) in complex

with an inhibitor 617

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Deposited on : 2022-11-15

Resolution : 1.58 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 (i) 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 (1)) 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)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

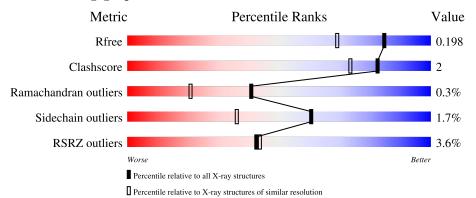
Validation Pipeline (wwPDB-VP) : 2.36

### 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.58 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	5534 (1.60-1.56)
Clashscore	141614	5861 (1.60-1.56)
Ramachandran outliers	138981	5708 (1.60-1.56)
Sidechain outliers	138945	5703 (1.60-1.56)
RSRZ outliers	127900	5431 (1.60-1.56)

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	91%	7% ••
2	В	3	100%	
2	F	3	33% 67%	
3	С	5	100%	
4	D	2	100%	

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Mol	Chain	Length		Quality of chain	
5	E	4	25%	75%	

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	BMA	В	3	-	-	-	X
4	NAG	D	2	-	-	-	X



# 2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 6787 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.

Mo	l Chain	Residues		Atoms				ZeroOcc	AltConf	Trace
1	A	692	Total 5830	C 3739	N 983	O 1086	S 22	0	42	0

• Molecule 2 is an oligosaccharide called 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		
2	В	3	Total 39	C 22			0	0	0
2	F	3	Total 39		N 2		0	0	0

• Molecule 3 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	1	Aton	ns		ZeroOcc	AltConf	Trace
3	С	5	Total 61			O 25	0	0	0

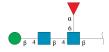
• Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.





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

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



Mol	Chain	Residues	I	Ator	ns		ZeroOcc	AltConf	Trace
5	E	4	Total 49	C 28	N 2	O 19	0	0	0

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

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

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

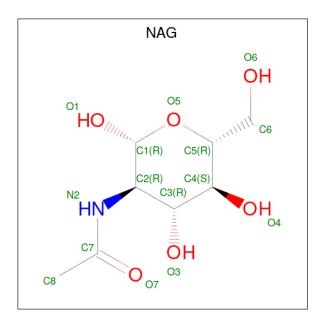
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Ca 1 1	0	0

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

$\mathbf{M}$	ol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	,	A	1	Total C	1	0	0

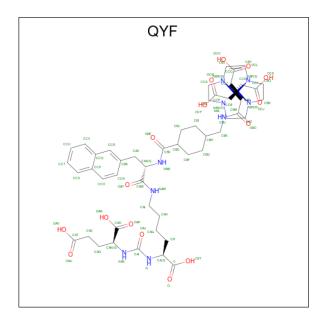
• Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).





Mol	Chain	Residues	A	ton	ns		ZeroOcc	AltConf
9	A	1	Total 14				0	0
9	A	1	Total 14	C 8	N 1	O 5	0	0

• Molecule 10 is  $(2 \{S\})$ -2-[[ $(2 \{S\})$ -6-[[ $(2 \{S\})$ -3-naphthalen-2-yl-2-[[4-[[2-[(11 \{Z\})-4,7,10-tris (2-hydroxy-2-oxoethyl)-1,4,7,10-tetrazacyclododec-11-en-1-yl]ethanoylamino]methyl]cyclohe xyl]carbonylamino]propanoyl]amino]-1-oxidanyl-1-oxidanylidene-hexan-2-yl]carbamoylamino]pentanedioic acid (three-letter code: QYF) (formula:  $C_{49}H_{69}N_9O_{16}$ ) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	A				ZeroOcc	AltConf
10	A	1	Total 74	C 49	N 9	O 16	0	0

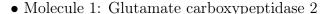
#### • Molecule 11 is water.

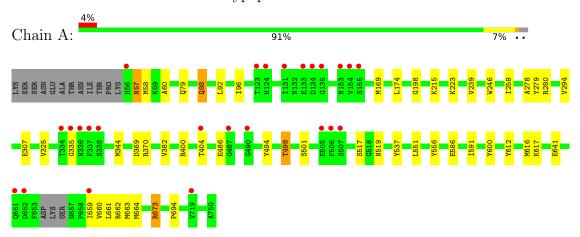
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	635	Total O 635 635	0	0



### 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B: 100%

NAG1 NAG2 BMA3

 $\bullet \ \, \text{Molecule 2: beta-D-mannopyranose-} (1\text{-}4)\text{-}2\text{-}acetamido-2\text{-}deoxy-beta-D-glucopyranose-} (1\text{-}4)\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}2\text{-}acetamido-2\text{-}$ 

Chain F: 33% 67%

NAG1 NAG2 BMA3

 $\bullet \ \, Molecule \ 3: \ alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)] beta-D-mannopyranose-(1-6)] beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-$ 

Chain C: 100%

NAG1 NAG2 BMA3 MAN4 MAN5



• Molecule 4: 2-acetan	nido-2-deoxy-beta-D-gluc	copyranose-(1-4)-2-acc	etamido-2-deoxy-	beta-D-gluc
opyranose				

Chain D:

100%

NAG1

 $\bullet \ \, Molecule \ 5: \ beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose$ 

Chain E:

25%

75%

NAG1 NAG2 BMA3



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants	101.28Å 130.00Å 159.49Å	Donogitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.25 - 1.58	Depositor
Resolution (A)	45.25 - 1.58	EDS
% Data completeness	99.6 (45.25-1.58)	Depositor
(in resolution range)	99.6 (45.25-1.58)	EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.24 (at 1.58Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
D D.	0.181 , 0.198	Depositor
$R, R_{free}$	0.180 , 0.198	DCC
$R_{free}$ test set	2100 reflections (1.46%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.6	Xtriage
Anisotropy	0.585	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.35, 44.9	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.48, < 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	6787	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.65% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: CA, FUC, CL, QYF, NAG, BMA, MAN, ZN

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	
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.61	0/5997	0.73	3/8120 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}(^{o})$
1	A	673	ARG	NE-CZ-NH2	-6.82	116.89	120.30
1	A	370	ARG	NE-CZ-NH1	5.66	123.13	120.30
1	A	673	ARG	NE-CZ-NH1	5.21	122.90	120.30

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	5830	0	5665	30	0
2	В	39	0	34	0	0
2	F	39	0	34	0	0
3	С	61	0	52	0	0
4	D	28	0	25	0	0
5	Ε	49	0	43	0	0
6	A	2	0	0	0	0
7	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	1	0	0	0	0
9	A	28	0	26	1	0
10	A	74	0	0	0	0
11	A	635	0	0	4	1
All	All	6787	0	5879	30	1

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.

The worst 5 of 30 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ (\rm \AA) \end{array}$	Clash overlap (Å)
1:A:660[A]:VAL:O	1:A:664[A]:MET:HG2	1.34	1.23
1:A:494:TYR:O	1:A:498[A]:THR:HG23	1.85	0.75
1:A:641:GLU:HG3	11:A:1355:HOH:O	1.90	0.70
1:A:88:GLN:H	1:A:88:GLN:HE21	1.41	0.67
1:A:486[A]:GLU:OE1	1:A:486[A]:GLU:N	2.29	0.66

All (1) 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-1 Atom-2		Clash overlap (Å)
11:A:905:HOH:O	11:A:1058:HOH:O[2_565]	1.85	0.35

#### 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	Perce	ntiles
1	A	727/707 (103%)	713 (98%)	12 (2%)	2 (0%)	41	21

All (2) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	382	VAL
1	A	335	GLY

#### 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 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	Analysed Rotameric		Percentiles	
1	A	629/603 (104%)	617 (98%)	12 (2%)	57 31	

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	501	SER
1	A	519	ASN
1	A	673	ARG
1	A	537	TYR
1	A	239[A]	VAL

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	88	GLN
1	A	303	GLN

#### 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)

17 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	Во	ond leng	ths	В	ond ang	les
WIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	В	1	1,2	14,14,15	0.38	0	17,19,21	1.18	2 (11%)
2	NAG	В	2	2	14,14,15	0.51	0	17,19,21	1.02	1 (5%)
2	BMA	В	3	2	11,11,12	0.64	0	15,15,17	1.24	2 (13%)
3	NAG	С	1	1,3	14,14,15	0.54	0	17,19,21	1.30	3 (17%)
3	NAG	С	2	3	14,14,15	0.43	0	17,19,21	1.39	1 (5%)
3	BMA	С	3	3	11,11,12	0.45	0	15,15,17	0.94	1 (6%)
3	MAN	С	4	3	11,11,12	0.64	0	15,15,17	1.11	2 (13%)
3	MAN	С	5	3	11,11,12	0.63	0	15,15,17	0.86	1 (6%)
4	NAG	D	1	4,1	14,14,15	0.65	0	17,19,21	1.53	1 (5%)
4	NAG	D	2	4	14,14,15	0.68	0	17,19,21	1.44	3 (17%)
5	NAG	Е	1	5,1	14,14,15	0.62	0	17,19,21	1.34	2 (11%)
5	NAG	Е	2	5	14,14,15	0.70	0	17,19,21	0.98	1 (5%)
5	BMA	Е	3	5	11,11,12	0.79	0	15,15,17	2.07	4 (26%)
5	FUC	Е	4	5	10,10,11	0.84	0	14,14,16	0.73	0
2	NAG	F	1	1,2	14,14,15	0.48	0	17,19,21	0.99	1 (5%)
2	NAG	F	2	2	14,14,15	0.41	0	17,19,21	0.66	0
2	BMA	F	3	2	11,11,12	0.55	0	15,15,17	1.04	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	В	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	В	2	2	-	0/6/23/26	0/1/1/1
2	BMA	В	3	2	-	0/2/19/22	0/1/1/1
3	NAG	С	1	1,3	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	С	2	3	-	2/6/23/26	0/1/1/1
3	BMA	С	3	3	-	0/2/19/22	0/1/1/1
3	MAN	С	4	3	-	0/2/19/22	0/1/1/1
3	MAN	С	5	3	-	0/2/19/22	0/1/1/1
4	NAG	D	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
5	NAG	E	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	E	2	5	-	2/6/23/26	0/1/1/1
5	BMA	Е	3	5	-	0/2/19/22	0/1/1/1
5	FUC	E	4	5	-	-	0/1/1/1
2	NAG	F	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
2	BMA	F	3	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
5	Е	3	BMA	C1-O5-C5	5.23	119.28	112.19
4	D	1	NAG	C1-O5-C5	5.22	119.27	112.19
3	С	2	NAG	C1-O5-C5	4.74	118.61	112.19
5	Е	3	BMA	C3-C4-C5	4.05	117.47	110.24
5	Е	1	NAG	C2-N2-C7	3.46	127.83	122.90

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

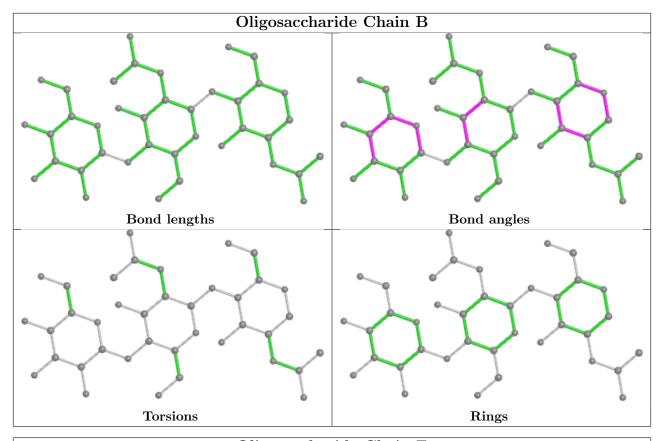
Mol	Chain	Res	Type	Atoms
5	Е	1	NAG	C8-C7-N2-C2
5	Е	1	NAG	O7-C7-N2-C2
5	Е	2	NAG	C4-C5-C6-O6
3	С	2	NAG	C4-C5-C6-O6
5	Е	2	NAG	O5-C5-C6-O6

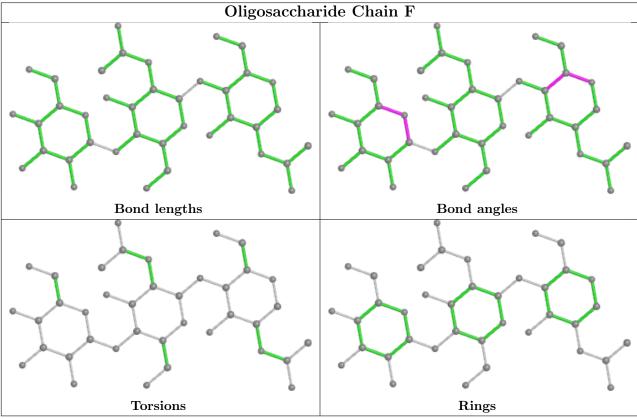
There are no ring outliers.

No monomer is involved in short contacts.

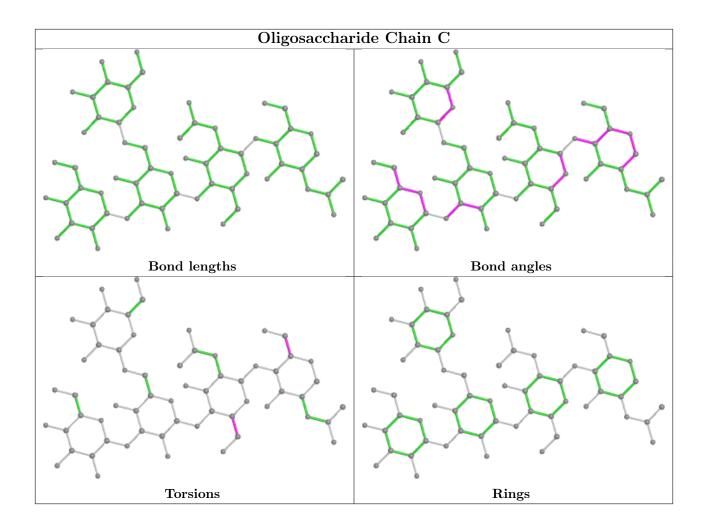
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



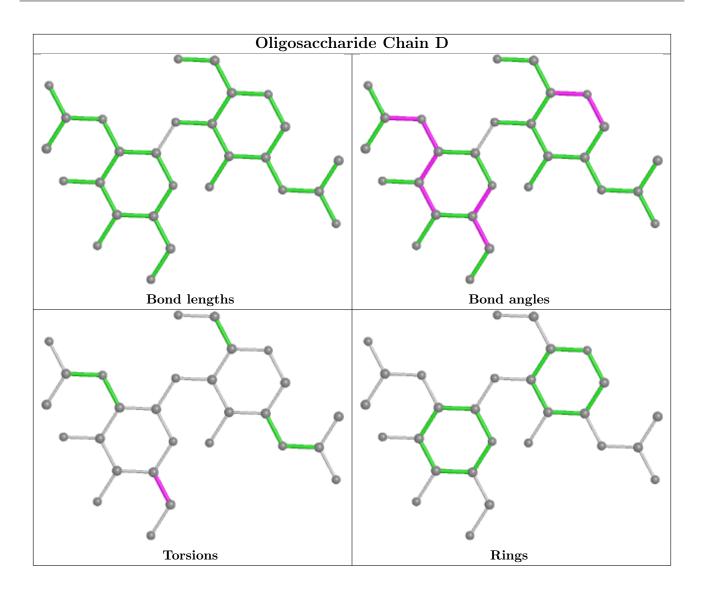




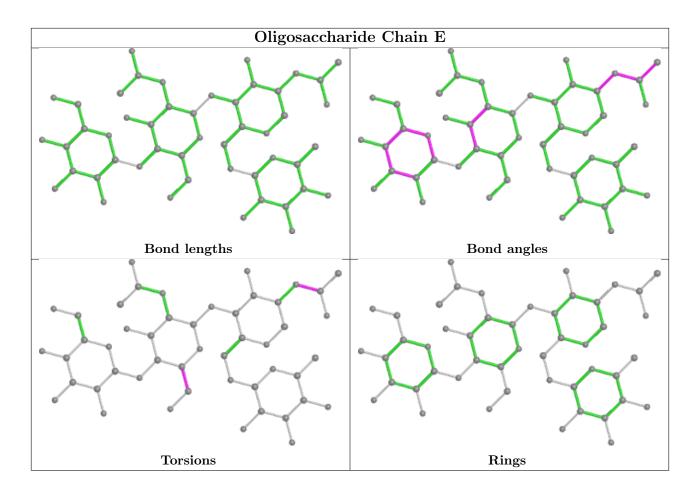












### 5.6 Ligand geometry (i)

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).

Mal	Mol Type Chain	Chain	Res	Link	Bond lengths			Bond angles		
MIOI		rtes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
9	NAG	A	805	1	14,14,15	0.72	0	17,19,21	1.55	2 (11%)
10	QYF	A	807	6	77,77,77	1.77	8 (10%)	98,102,102	1.42	13 (13%)
9	NAG	A	806	1	14,14,15	0.65	0	17,19,21	1.61	2 (11%)

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.



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′-′ means	no	outhers	of that	, kind	were	identified	

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	A	805	1	-	2/6/23/26	0/1/1/1
10	QYF	A	807	6	-	23/86/96/96	0/3/4/4
9	NAG	A	806	1	-	2/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(A)	$Ideal(\AA)$
10	A	807	QYF	CBY-CBX	8.73	1.56	1.34
10	A	807	QYF	CBY-NBP	4.93	1.48	1.33
10	A	807	QYF	CBX-NBW	4.93	1.48	1.33
10	A	807	QYF	CAZ-CBA	-2.90	1.44	1.51
10	A	807	QYF	CCB-NBP	2.61	1.48	1.45

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
10	A	807	QYF	CBN-NBW-CCA	-5.75	106.55	116.52
9	A	806	NAG	C1-O5-C5	4.58	118.40	112.19
10	A	807	QYF	CBQ-NBP-CBY	-4.29	106.28	121.14
9	A	805	NAG	C1-O5-C5	4.14	117.80	112.19
10	A	807	QYF	CCB-NBP-CBQ	-3.85	109.84	116.52

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	807	QYF	CBI-CBH-CBK-NBL
10	A	807	QYF	CBM-CBN-NBW-CCA
10	A	807	QYF	CBZ-CCA-NBW-CBN
10	A	807	QYF	CBY-CBX-NBW-CBN
10	A	807	QYF	CBY-CBX-NBW-CCA

There are no ring outliers.

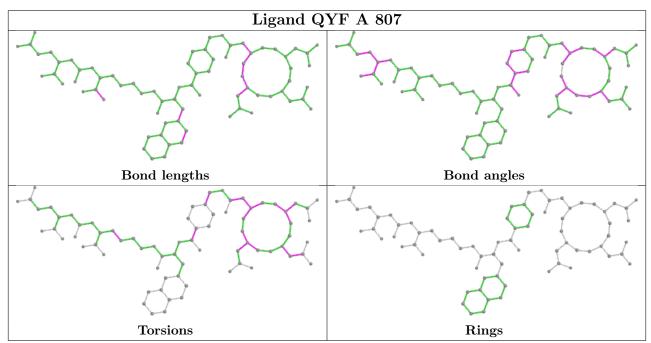
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	806	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.



### 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)

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,  $95^{th}$  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	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$			$OWAB(A^2)$	Q < 0.9
1	A	692/707 (97%)	0.03	25 (3%)	42	44	13, 22, 38, 68	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	335	GLY	3.8
1	A	135	GLY	3.3
1	A	153	ASN	3.2
1	A	506	PHE	3.1
1	A	507	SER	2.9

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

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

#### 6.3 Carbohydrates (i)

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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	BMA	В	3	11/12	0.43	0.44	74,84,87,88	0
5	BMA	Е	3	11/12	0.54	0.40	86,89,92,93	0
4	NAG	D	2	14/15	0.60	0.44	80,84,89,94	0
4	NAG	D	1	14/15	0.69	0.26	46,53,62,74	0
5	FUC	Е	4	10/11	0.69	0.38	54,60,62,64	0
2	BMA	F	3	11/12	0.73	0.24	55,61,68,75	0
3	MAN	С	5	11/12	0.78	0.21	61,67,73,73	0

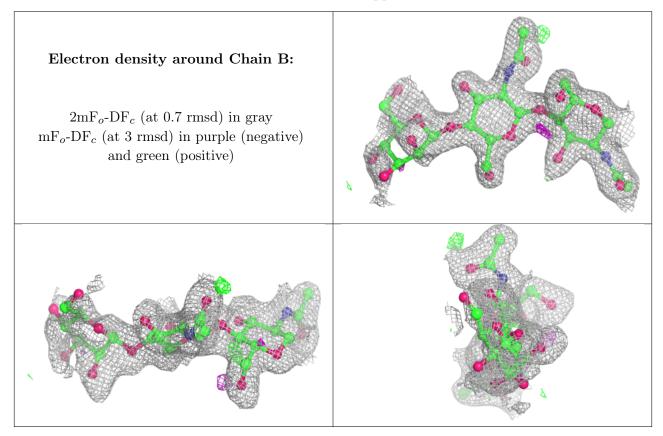
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
5	NAG	E	2	14/15	0.78	0.26	50,58,67,79	0
2	NAG	В	2	14/15	0.80	0.23	36,48,54,64	0
5	NAG	Е	1	14/15	0.84	0.16	39,41,45,50	0
3	NAG	С	2	14/15	0.86	0.12	37,40,43,53	0
3	MAN	С	4	11/12	0.88	0.10	44,45,47,48	0
3	BMA	С	3	11/12	0.89	0.09	40,42,49,53	0
2	NAG	F	2	14/15	0.92	0.11	31,39,45,49	0
2	NAG	В	1	14/15	0.93	0.12	30,35,40,44	0
3	NAG	С	1	14/15	0.93	0.08	19,26,35,42	0
2	NAG	F	1	14/15	0.94	0.08	25,27,29,32	0

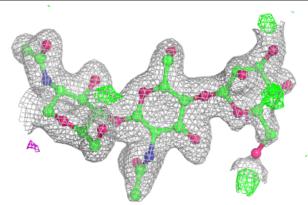
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

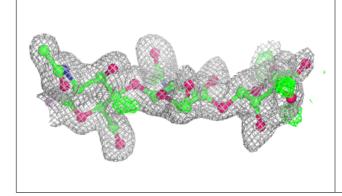


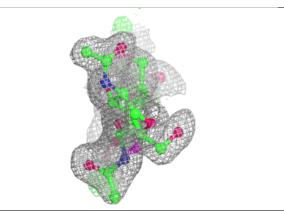


# Electron density around Chain F:

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

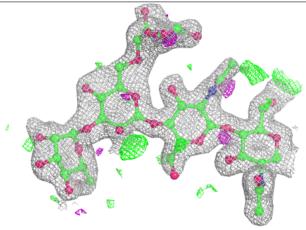


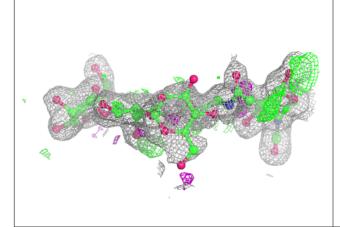


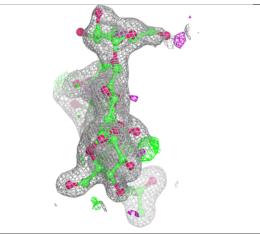


#### Electron density around Chain C:

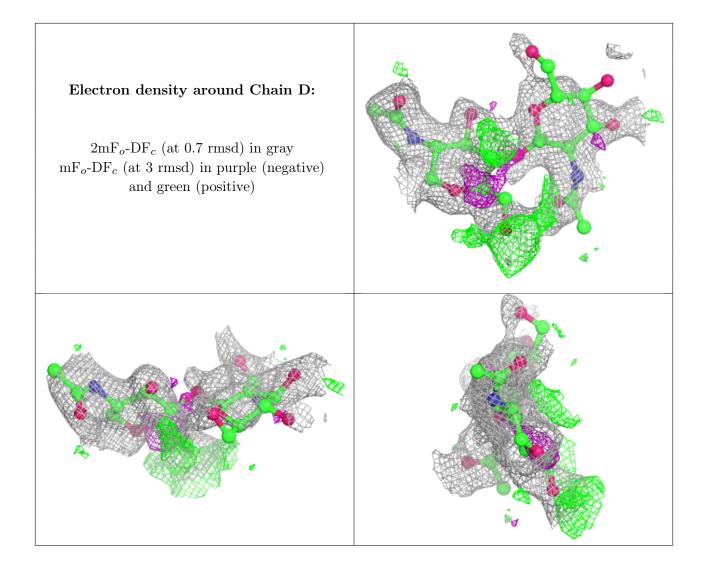
 $2 {
m mF}_o {
m -DF}_c$  (at 0.7 rmsd) in gray  ${
m mF}_o {
m -DF}_c$  (at 3 rmsd) in purple (negative) and green (positive)



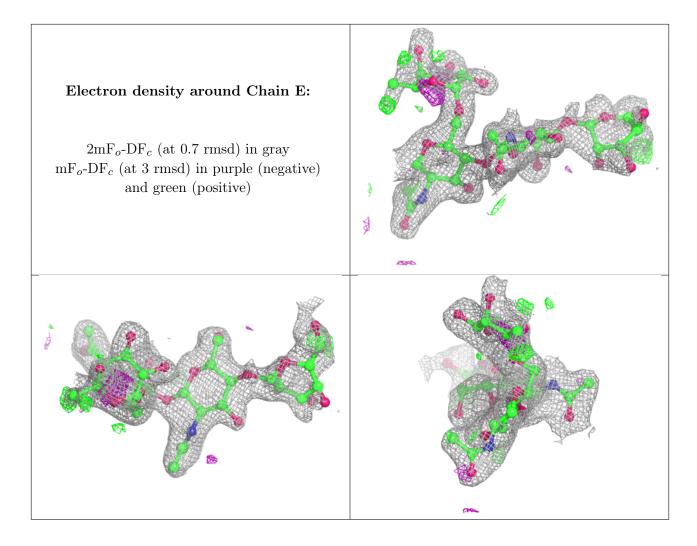












### 6.4 Ligands (i)

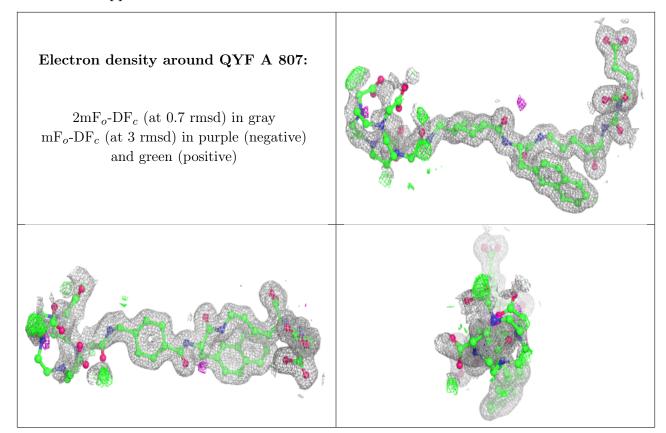
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
9	NAG	A	805	14/15	0.80	0.22	62,67,71,74	0
9	NAG	A	806	14/15	0.86	0.15	29,48,65,68	0
10	QYF	A	807	74/74	0.94	0.15	14,19,115,118	0
8	CL	A	804	1/1	0.99	0.10	19,19,19,19	0
6	ZN	A	802	1/1	1.00	0.04	16,16,16,16	0
7	CA	A	803	1/1	1.00	0.07	15,15,15,15	0
6	ZN	A	801	1/1	1.00	0.07	15,15,15,15	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.



## 6.5 Other polymers (i)

There are no such residues in this entry.

