wwPDB X-ray Structure Validation Summary Report (i)

Aug 9, 2020 – 03:07 PM BST

PDB ID	:	6G21
Title	:	Crystal structure of an esterase from Aspergillus oryzae
Authors	:	Moroz, O.V.; Blagova, E.; Davies, G.J.; Wilson, K.S.
Deposited on	:	2018-03-22
Resolution	:	2.10 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 following versions of software and data (see references (1)) were used in the production of this report:

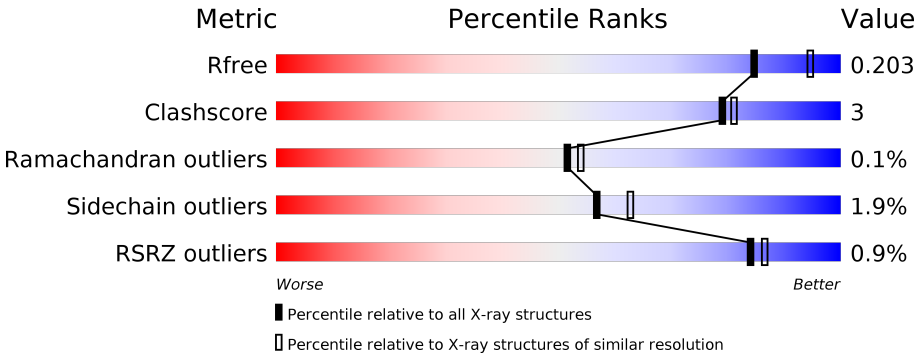
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 2.10 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))
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 on 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	507	92% 7%
1	B	507	% 89% 10%
2	C	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
3	NAG	B	605	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8444 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.

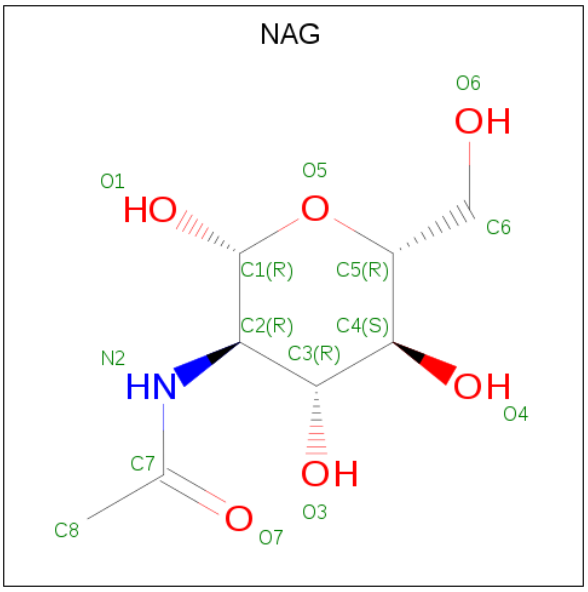
- Molecule 1 is a protein called Probable feruloyl esterase B-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	504	Total	C	N	O	S	0	1	0
			3887	2457	653	754	23			
1	B	504	Total	C	N	O	S	0	1	0
			3908	2468	661	756	23			

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

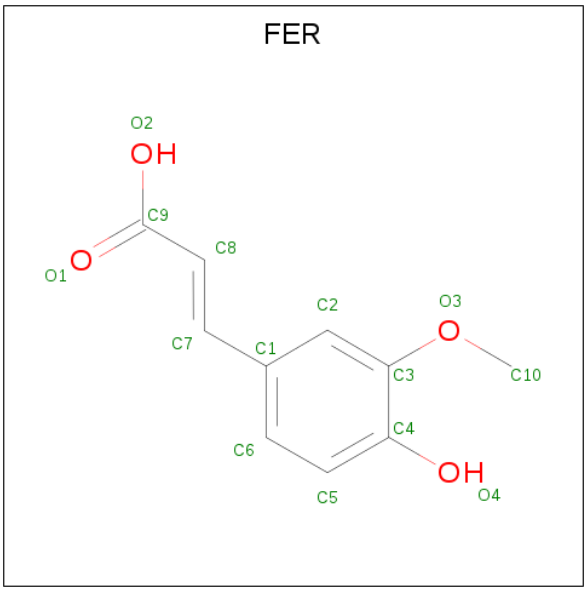
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



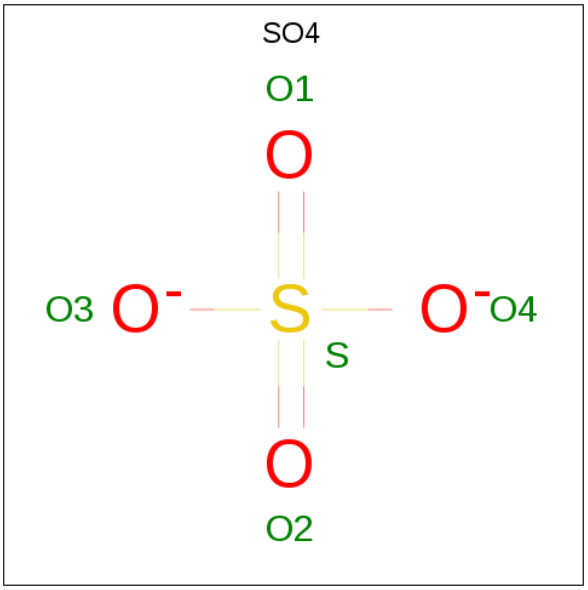
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 14 8 1 5	0	0
3	A	1	Total C N O 14 8 1 5	0	0
3	A	1	Total C N O 14 8 1 5	0	0
3	A	1	Total C N O 14 8 1 5	0	0
3	A	1	Total C N O 14 8 1 5	0	0
3	B	1	Total C N O 14 8 1 5	0	0
3	B	1	Total C N O 14 8 1 5	0	0
3	B	1	Total C N O 14 8 1 5	0	0
3	B	1	Total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

- Molecule 4 is 3-(4-HYDROXY-3-METHOXYPHENYL)-2-PROPENOIC ACID (three-letter code: FER) (formula: $C_{10}H_{10}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			14	10	4		
4	B	1	Total	C	O	0	0
			14	10	4		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total O S 5 4 1	0	0

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total Ca 1 1	0	0
6	A	1	Total Ca 1 1	0	0

- Molecule 7 is water.

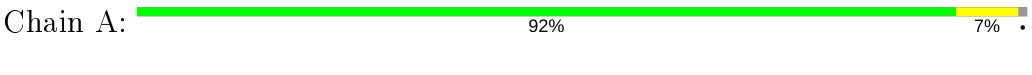
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	235	Total O 235 235	0	0
7	B	201	Total O 201 201	0	0

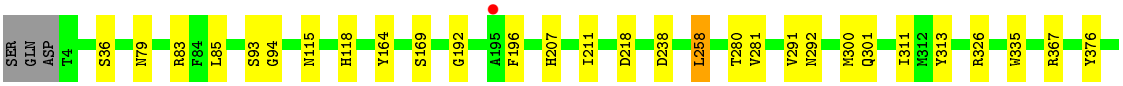
3 Residue-property plots (i)

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 1: Probable feruloyl esterase B-2

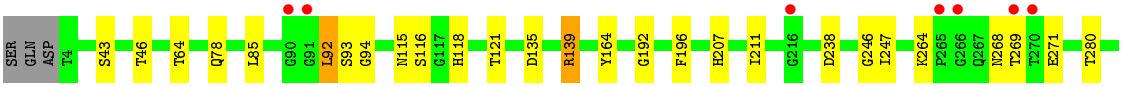
Chain A:

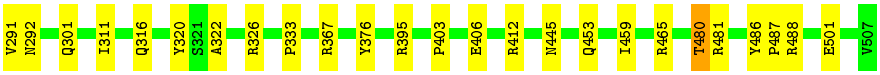




• Molecule 1: Probable feruloyl esterase B-2

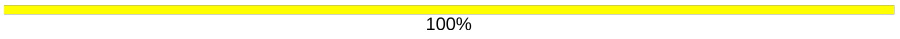
Chain B:





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

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α, β, γ	119.47Å 119.47Å 142.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	37.72 – 2.10 37.72 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (37.72-2.10) 100.0 (37.72-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.42 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0218	Depositor
R, R_{free}	0.154 , 0.194 0.165 , 0.203	Depositor DCC
R_{free} test set	3246 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å^2)	27.9	Xtriage
Anisotropy	0.150	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 47.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.045 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8444	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% of the height of the origin peak. No significant pseudotranslation is detected.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, FER, NAG, SO4

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	0.81	1/3990 (0.0%)	0.85	11/5431 (0.2%)
1	B	0.79	0/4011	0.88	11/5455 (0.2%)
All	All	0.80	1/8001 (0.0%)	0.86	22/10886 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	386	SER	CB-OG	5.29	1.49	1.42

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	139	ARG	NE-CZ-NH1	9.91	125.26	120.30
1	B	139	ARG	NE-CZ-NH2	-9.48	115.56	120.30
1	B	395	ARG	NE-CZ-NH1	6.45	123.53	120.30
1	B	488	ARG	NE-CZ-NH1	6.29	123.45	120.30
1	A	258	LEU	CA-CB-CG	-6.27	100.89	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	93	SER	Peptide
1	B	93	SER	Peptide

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	3887	0	3639	14	0
1	B	3908	0	3686	28	0
2	C	28	0	25	0	0
3	A	70	0	65	0	0
3	B	70	0	65	2	0
4	A	14	0	8	0	0
4	B	14	0	8	1	0
5	A	10	0	0	0	0
5	B	5	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	235	0	0	1	0
7	B	201	0	0	5	0
All	All	8444	0	7496	44	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 3.

The worst 5 of 44 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:92:LEU:HD12	1:B:320:TYR:HB3	1.37	1.03
1:B:92:LEU:CD1	1:B:320:TYR:HB3	2.03	0.88
1:B:480:THR:CG2	1:B:501:GLU:OE2	2.26	0.82
1:B:135:ASP:OD1	1:B:139:ARG:HD2	1.80	0.80
1:B:92:LEU:HD12	1:B:320:TYR:CB	2.11	0.79

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	503/507 (99%)	485 (96%)	17 (3%)	1 (0%)	47 49
1	B	503/507 (99%)	482 (96%)	21 (4%)	0	100 100
All	All	1006/1014 (99%)	967 (96%)	38 (4%)	1 (0%)	51 54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	169	SER

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	412/423 (97%)	406 (98%)	6 (2%)	65 71
1	B	418/423 (99%)	408 (98%)	10 (2%)	49 53
All	All	830/846 (98%)	814 (98%)	16 (2%)	57 63

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	78	GLN
1	B	116	SER
1	B	291	VAL
1	B	46	THR
1	B	301	GLN

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

Mol	Chain	Res	Type
1	B	78	GLN
1	B	434	GLN
1	B	505	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

2 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	C	1	1,2	14,14,15	0.46	0	17,19,21	1.18	1 (5%)
2	NAG	C	2	2	14,14,15	1.16	1 (7%)	17,19,21	1.52	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
2	NAG	C	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	NAG	C1-C2	2.61	1.56	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	2	NAG	C1-O5-C5	5.10	119.10	112.19
2	C	1	NAG	C2-N2-C7	2.12	125.92	122.90

There are no chirality outliers.

All (2) torsion outliers are listed below:

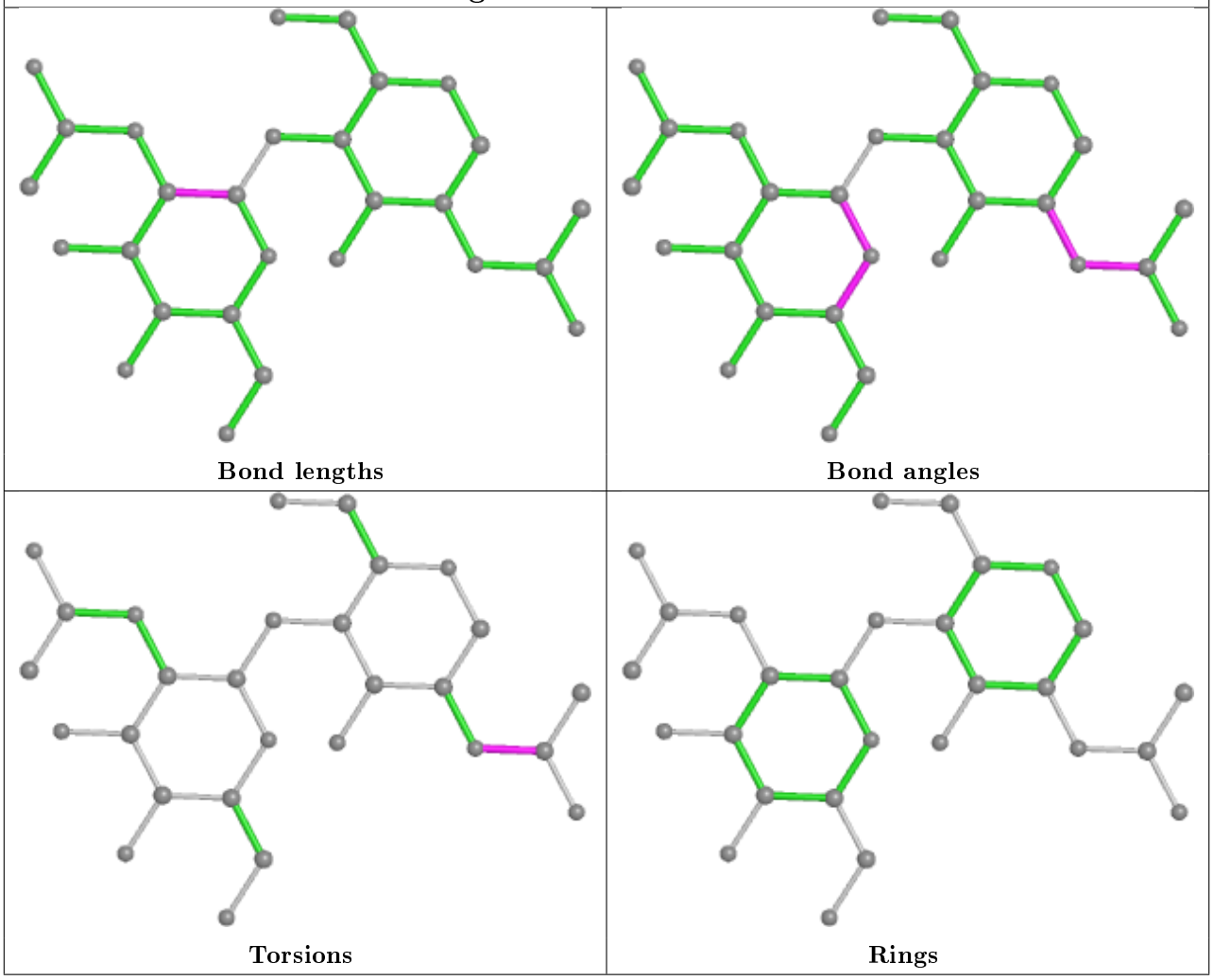
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2

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 C



5.6 Ligand geometry

Of 17 ligands modelled in this entry, 2 are monoatomic - leaving 15 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	$\#\|Z\| > 2$
4	FER	A	608	-	11,14,14	1.49	1 (9%)	15,18,18	3.29	7 (46%)
5	SO4	A	609	-	4,4,4	0.49	0	6,6,6	0.38	0
4	FER	B	606	-	11,14,14	1.76	1 (9%)	15,18,18	4.17	8 (53%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	NAG	B	601	1	14,14,15	0.49	0	17,19,21	2.51	8 (47%)
3	NAG	A	605	1	14,14,15	0.31	0	17,19,21	1.02	1 (5%)
3	NAG	B	605	1	14,14,15	0.47	0	17,19,21	1.58	4 (23%)
3	NAG	B	602	1	14,14,15	0.57	0	17,19,21	2.74	5 (29%)
5	SO4	B	607	-	4,4,4	0.40	0	6,6,6	0.53	0
3	NAG	A	602	1	14,14,15	0.74	0	17,19,21	1.57	2 (11%)
3	NAG	A	606	1	14,14,15	0.75	0	17,19,21	1.54	2 (11%)
3	NAG	A	601	1	14,14,15	0.41	0	17,19,21	1.57	3 (17%)
3	NAG	B	604	1	14,14,15	0.46	0	17,19,21	1.58	3 (17%)
3	NAG	B	603	1	14,14,15	1.12	1 (7%)	17,19,21	1.56	2 (11%)
3	NAG	A	607	1	14,14,15	0.54	0	17,19,21	1.19	1 (5%)
5	SO4	A	610	-	4,4,4	0.34	0	6,6,6	0.79	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	FER	A	608	-	-	2/5/7/7	0/1/1/1
4	FER	B	606	-	-	2/5/7/7	0/1/1/1
3	NAG	B	601	1	-	3/6/23/26	0/1/1/1
3	NAG	A	605	1	-	0/6/23/26	0/1/1/1
3	NAG	B	605	1	-	2/6/23/26	0/1/1/1
3	NAG	B	602	1	-	0/6/23/26	0/1/1/1
3	NAG	A	602	1	-	0/6/23/26	0/1/1/1
3	NAG	A	606	1	-	0/6/23/26	0/1/1/1
3	NAG	A	601	1	-	0/6/23/26	0/1/1/1
3	NAG	B	604	1	-	0/6/23/26	0/1/1/1
3	NAG	B	603	1	-	0/6/23/26	0/1/1/1
3	NAG	A	607	1	-	2/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	606	FER	C4-C3	5.08	1.49	1.40
4	A	608	FER	C4-C3	4.29	1.48	1.40
3	B	603	NAG	C1-C2	2.71	1.56	1.52

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	606	FER	C9-C8-C7	-9.44	103.52	123.69
3	B	602	NAG	C1-O5-C5	9.35	124.86	112.19
4	A	608	FER	C9-C8-C7	-8.00	106.58	123.69
4	B	606	FER	O3-C3-C4	7.55	125.51	114.57
4	B	606	FER	C6-C1-C2	6.18	126.42	118.71

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	601	NAG	C3-C2-N2-C7
4	B	606	FER	C4-C3-O3-C10
4	B	606	FER	C2-C3-O3-C10
3	B	601	NAG	C8-C7-N2-C2
3	B	601	NAG	O7-C7-N2-C2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	606	FER	1	0
3	B	601	NAG	1	0
3	B	605	NAG	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 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, 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	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	504/507 (99%)	-0.49	2 (0%)	92	93	21, 28, 42, 58	0
1	B	504/507 (99%)	-0.35	7 (1%)	75	78	21, 29, 51, 71	0
All	All	1008/1014 (99%)	-0.42	9 (0%)	84	86	21, 28, 47, 71	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	90	GLY	2.8
1	B	269	THR	2.7
1	B	270	THR	2.5
1	B	216	GLY	2.4
1	A	472	GLY	2.4

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

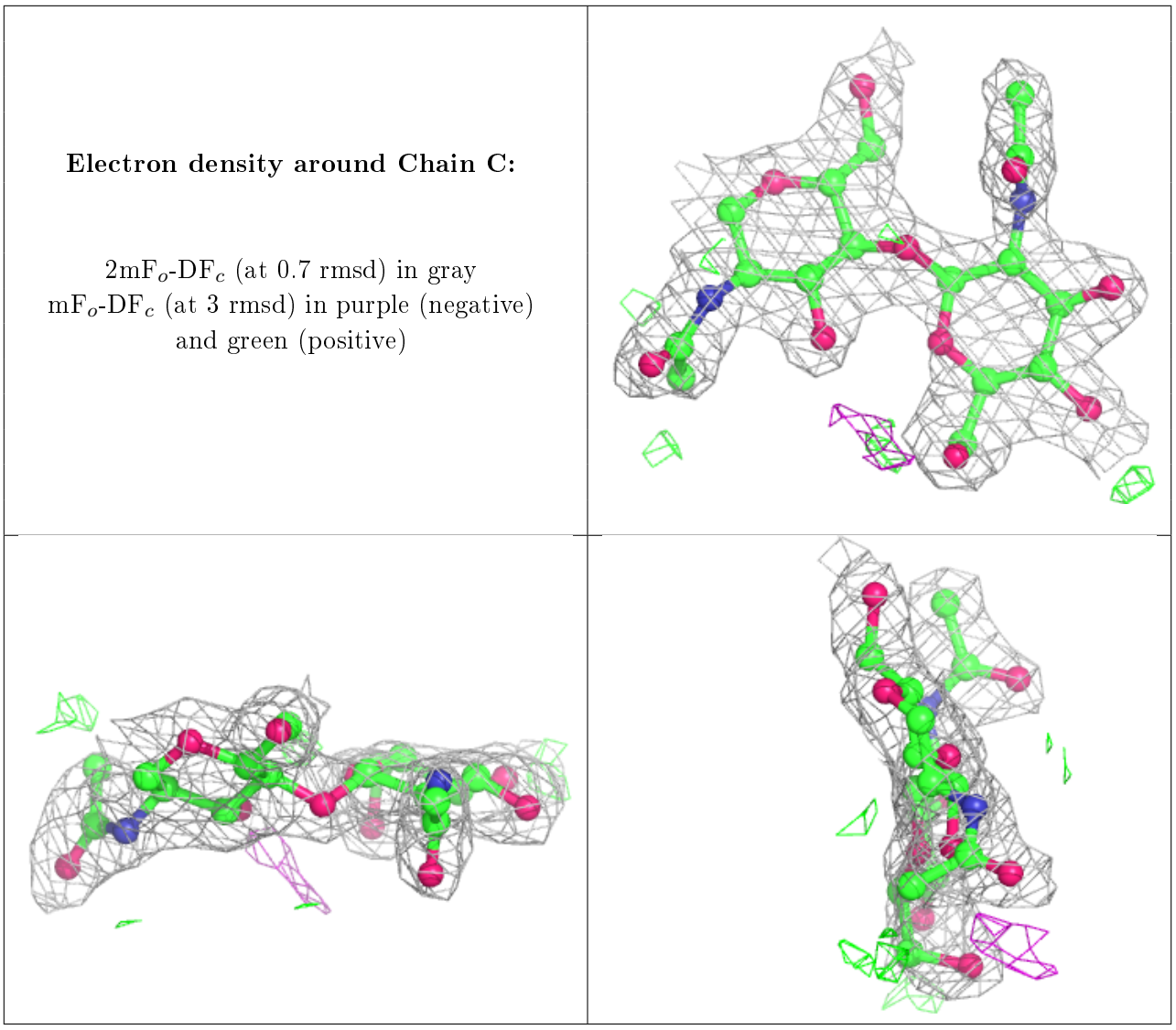
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	C	2	14/15	0.74	0.28	45,56,61,62	0
2	NAG	C	1	14/15	0.95	0.15	39,43,46,53	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 C:

$2mF_o$-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, 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	B-factors(Å^2)	Q<0.9
5	SO4	A	609	5/5	0.55	0.33	91,97,112,113	0
4	FER	A	608	14/14	0.69	0.22	51,64,76,78	0
3	NAG	B	603	14/15	0.77	0.30	55,66,71,75	0
3	NAG	B	605	14/15	0.80	0.41	58,68,78,80	0
4	FER	B	606	14/14	0.80	0.19	47,65,72,73	0
3	NAG	B	604	14/15	0.82	0.28	50,58,66,71	0
3	NAG	B	602	14/15	0.82	0.22	49,67,79,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	NAG	A	607	14/15	0.84	0.32	57,65,69,72	0
3	NAG	A	602	14/15	0.88	0.23	40,46,51,52	0
3	NAG	B	601	14/15	0.92	0.20	52,57,64,66	0
3	NAG	A	601	14/15	0.93	0.12	45,50,59,59	0
3	NAG	A	606	14/15	0.93	0.18	36,43,47,47	0
3	NAG	A	605	14/15	0.95	0.25	41,51,60,67	0
6	CA	A	611	1/1	0.99	0.05	26,26,26,26	0
5	SO4	B	607	5/5	0.99	0.09	29,33,37,38	0
5	SO4	A	610	5/5	0.99	0.07	29,33,35,37	0
6	CA	B	608	1/1	1.00	0.06	24,24,24,24	0

6.5 Other polymers (i)

There are no such residues in this entry.