wwPDB X-ray Structure Validation Summary Report (i)

Nov 23, 2022 – 03:29 pm GMT

PDB ID	:	8A49
Title	:	Endoglycosidase S in complex with IgG1 Fc
Authors	:	Sudol, A.S.L.; Tews, I.; Crispin, M.
Deposited on	:	2022-06-10
Resolution	:	3.45 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 (i)) were used in the production of this report:

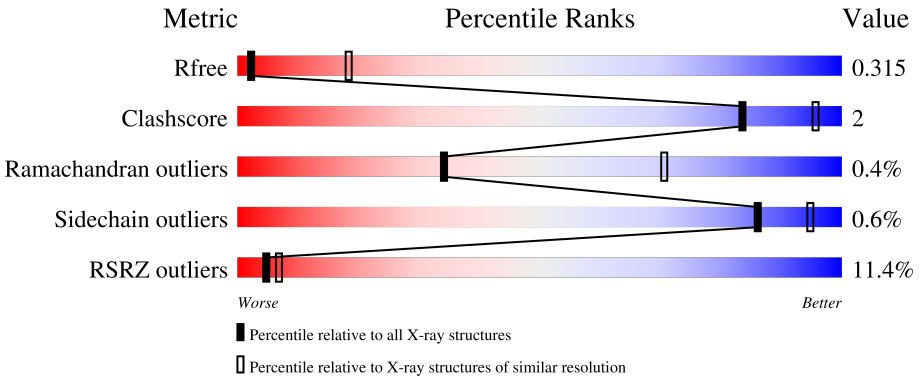
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.3
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

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 3.45 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	1291 (3.52-3.40)
Clashscore	141614	1372 (3.52-3.40)
Ramachandran outliers	138981	1337 (3.52-3.40)
Sidechain outliers	138945	1338 (3.52-3.40)
RSRZ outliers	127900	1205 (3.52-3.40)

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	227	14% 84% 7% 9%
1	B	227	14% 81% 10% 9%
2	C	906	6% 91% 7%
2	D	906	14% 91% 6%
3	E	8	100%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 33731 atoms, of which 16644 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 IgG1 Fc.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	207	Total	C	H	N	O	S	110	0	0
			3265	1048	1618	279	313	7			
1	B	207	Total	C	H	N	O	S	113	0	0
			3224	1035	1601	276	305	7			

- Molecule 2 is a protein called Secreted endoglycosidase EndoS.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	884	Total	C	H	N	O	S	422	0	0
			13643	4361	6754	1150	1362	16			
2	D	879	Total	C	H	N	O	S	428	0	0
			13339	4270	6578	1133	1342	16			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	99	MET	-	initiating methionine	UNP Q9APG4
C	233	ALA	ASP	engineered mutation	UNP Q9APG4
C	235	LEU	GLU	engineered mutation	UNP Q9APG4
C	996	LEU	-	expression tag	UNP Q9APG4
C	997	LEU	-	expression tag	UNP Q9APG4
C	998	GLU	-	expression tag	UNP Q9APG4
C	999	HIS	-	expression tag	UNP Q9APG4
C	1000	HIS	-	expression tag	UNP Q9APG4
C	1001	HIS	-	expression tag	UNP Q9APG4
C	1002	HIS	-	expression tag	UNP Q9APG4
C	1003	HIS	-	expression tag	UNP Q9APG4
C	1004	HIS	-	expression tag	UNP Q9APG4
D	99	MET	-	initiating methionine	UNP Q9APG4
D	233	ALA	ASP	engineered mutation	UNP Q9APG4
D	235	LEU	GLU	engineered mutation	UNP Q9APG4
D	996	LEU	-	expression tag	UNP Q9APG4

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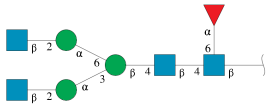
Chain	Residue	Modelled	Actual	Comment	Reference
D	997	LEU	-	expression tag	UNP Q9APG4
D	998	GLU	-	expression tag	UNP Q9APG4
D	999	HIS	-	expression tag	UNP Q9APG4
D	1000	HIS	-	expression tag	UNP Q9APG4
D	1001	HIS	-	expression tag	UNP Q9APG4
D	1002	HIS	-	expression tag	UNP Q9APG4
D	1003	HIS	-	expression tag	UNP Q9APG4
D	1004	HIS	-	expression tag	UNP Q9APG4

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]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	Atoms					ZeroOcc	AltConf	Trace
3	E	8	Total	C	H	N	O	20	0	0
			192	56	93	4	39			

- Molecule 4 is water.

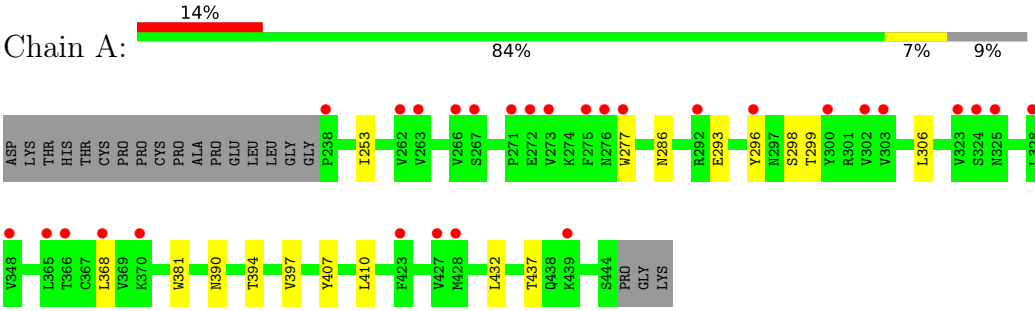
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	6	Total	O	0	0
			6	6		
4	C	31	Total	O	0	0
			31	31		
4	D	17	Total	O	0	0
			17	17		
4	B	14	Total	O	0	0
			14	14		

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.

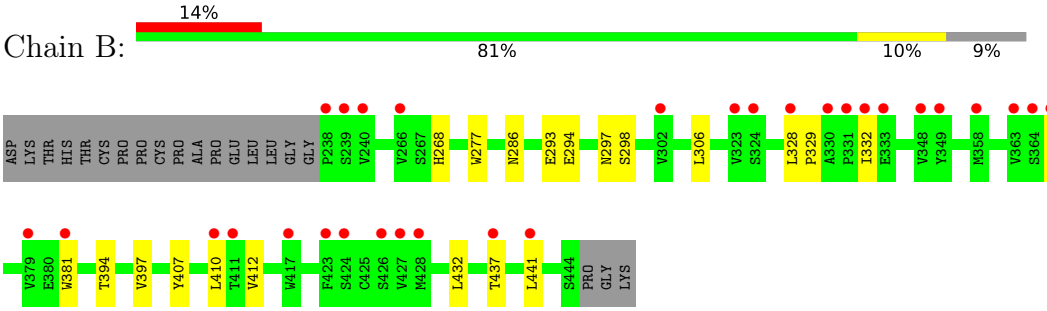
• Molecule 1: IgG1 Fc

Chain A:



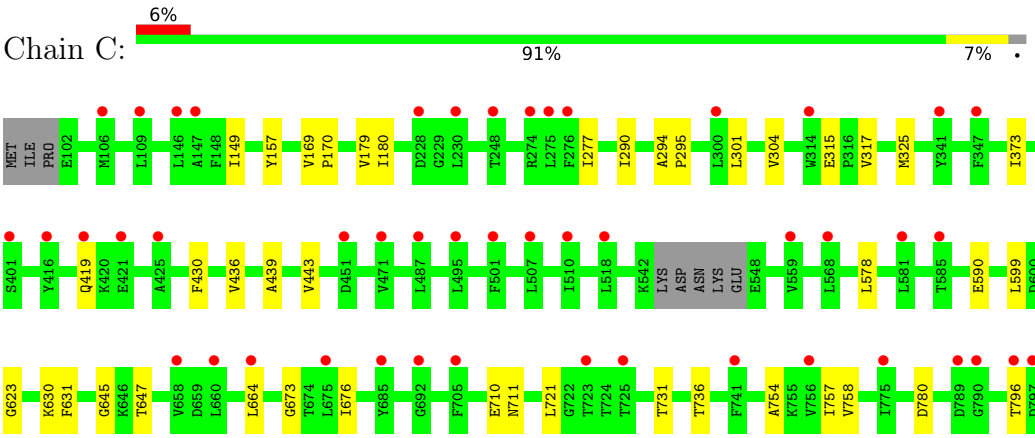
• Molecule 1: IgG1 Fc

Chain B:



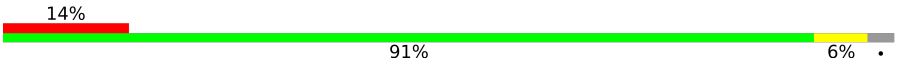
• Molecule 2: Secreted endoglycosidase EndoS

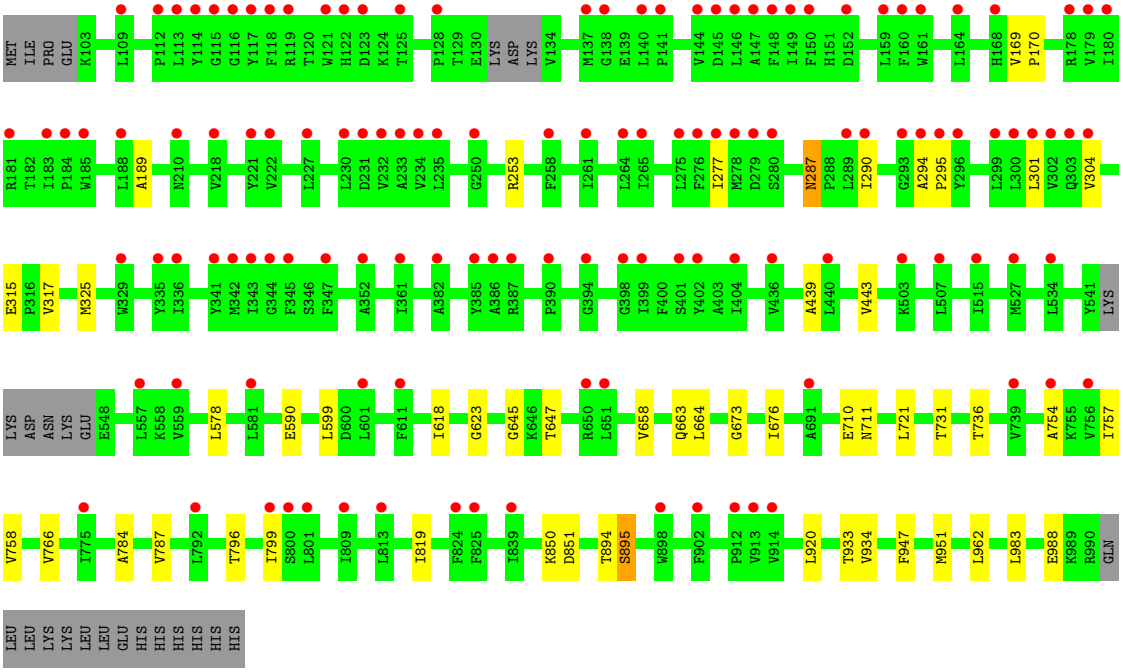
Chain C:



• Molecule 2: Secreted endoglycosidase EndoS

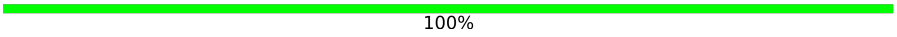
Chain D:





• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]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:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	96.53Å 174.29Å 193.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.78 – 3.45 49.78 – 3.45	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.78-3.45) 93.6 (49.78-3.45)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.61 (at 3.48Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.253 , 0.311 0.257 , 0.315	Depositor DCC
R_{free} test set	2118 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å^2)	116.4	Xtriage
Anisotropy	0.278	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	33731	wwPDB-VP
Average B, all atoms (Å^2)	152.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.66% 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: BMA, FUC, MAN, 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	0.25	0/1693	0.45	0/2308
1	B	0.25	0/1668	0.46	0/2275
2	C	0.25	0/7031	0.43	0/9538
2	D	0.25	0/6898	0.43	0/9368
All	All	0.25	0/17290	0.44	0/23489

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1647	1618	1603	9	0
1	B	1623	1601	1575	13	0
2	C	6889	6754	6676	34	1
2	D	6761	6578	6463	31	1
3	E	99	93	85	0	0
4	A	6	0	0	0	0
4	B	14	0	0	0	0
4	C	31	0	0	0	0
4	D	17	0	0	1	0
All	All	17087	16644	16402	80	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 80 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)
2:D:796:THR:HG22	1:B:286:ASN:HD22	1.42	0.83
1:A:286:ASN:HD22	2:C:796:THR:HG22	1.53	0.71
2:D:294:ALA:HB3	2:D:295:PRO:HD3	1.79	0.63
2:C:294:ALA:HB3	2:C:295:PRO:HD3	1.80	0.62
1:B:328:LEU:HD21	1:B:332:ILE:HG13	1.81	0.62

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-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:856:ASN:HD22	2:D:850:LYS:O[2_355]	1.39	0.21

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	205/227 (90%)	196 (96%)	8 (4%)	1 (0%)	29	66
1	B	205/227 (90%)	193 (94%)	10 (5%)	2 (1%)	15	52
2	C	880/906 (97%)	812 (92%)	65 (7%)	3 (0%)	41	75
2	D	873/906 (96%)	807 (92%)	64 (7%)	2 (0%)	47	80
All	All	2163/2266 (96%)	2008 (93%)	147 (7%)	8 (0%)	34	70

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	298	SER

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Mol	Chain	Res	Type
1	B	297	ASN
1	B	298	SER
2	C	895	SER
2	D	895	SER

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	Rotameric	Outliers	Percentiles	
1	A	190/210 (90%)	186 (98%)	4 (2%)	53	78
1	B	184/210 (88%)	183 (100%)	1 (0%)	88	95
2	C	738/792 (93%)	735 (100%)	3 (0%)	91	97
2	D	711/792 (90%)	708 (100%)	3 (0%)	91	97
All	All	1823/2004 (91%)	1812 (99%)	11 (1%)	86	95

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	287	ASN
2	D	851	ASP
1	B	268	HIS
2	D	988	GLU
2	C	157	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	286	ASN
1	B	384	ASN
1	B	421	ASN
1	A	421	ASN
2	C	798	ASN

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)

8 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	$\#\|Z\| > 2$
3	NAG	E	1	1,3	14,14,15	0.38	0	17,19,21	0.90	0
3	NAG	E	2	3	14,14,15	0.30	0	17,19,21	0.61	0
3	BMA	E	3	3	11,11,12	0.29	0	15,15,17	0.57	0
3	MAN	E	4	3	11,11,12	0.26	0	15,15,17	0.71	0
3	NAG	E	5	3	14,14,15	0.24	0	17,19,21	0.42	0
3	MAN	E	6	3	11,11,12	0.27	0	15,15,17	0.54	0
3	NAG	E	7	3	14,14,15	0.32	0	17,19,21	0.48	0
3	FUC	E	8	3	10,10,11	0.30	0	14,14,16	0.75	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
3	NAG	E	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	1/6/23/26	0/1/1/1
3	BMA	E	3	3	-	2/2/19/22	0/1/1/1
3	MAN	E	4	3	-	0/2/19/22	0/1/1/1
3	NAG	E	5	3	-	0/6/23/26	0/1/1/1
3	MAN	E	6	3	-	0/2/19/22	0/1/1/1
3	NAG	E	7	3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FUC	E	8	3	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

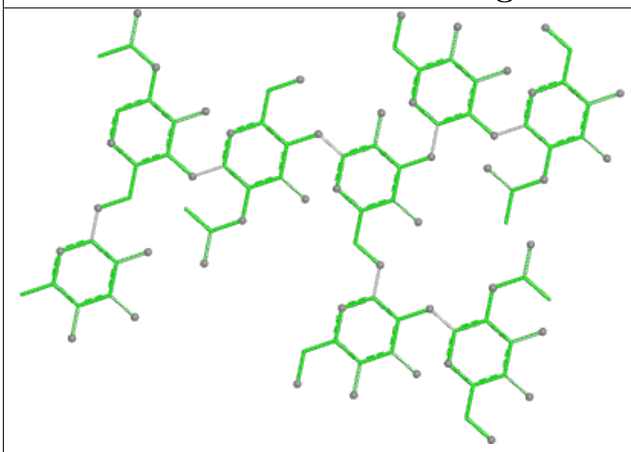
Mol	Chain	Res	Type	Atoms
3	E	3	BMA	O5-C5-C6-O6
3	E	3	BMA	C4-C5-C6-O6
3	E	2	NAG	C1-C2-N2-C7

There are no ring outliers.

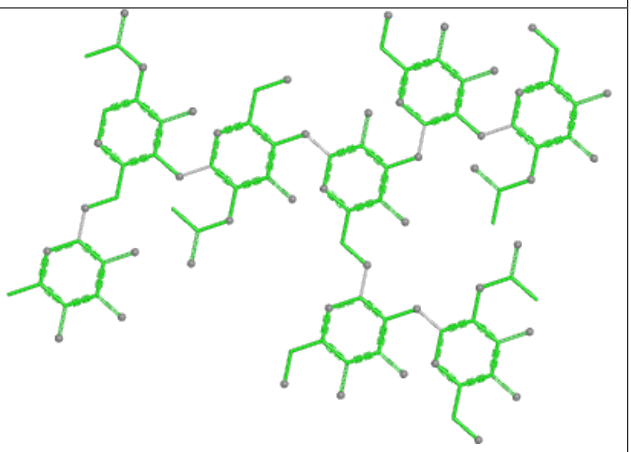
No monomer is involved in short contacts.

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

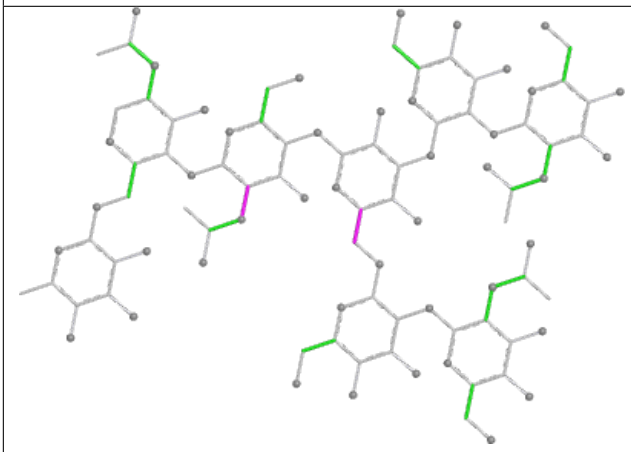
Oligosaccharide Chain E



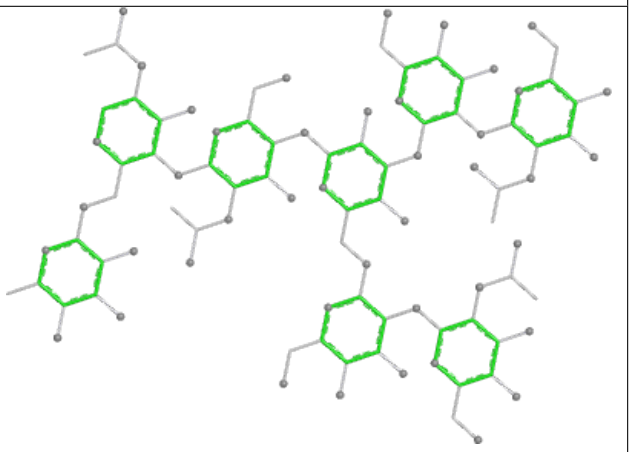
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	207/227 (91%)	0.97	31 (14%) 2 3	99, 132, 170, 208	0
1	B	207/227 (91%)	0.87	32 (15%) 2 3	99, 134, 184, 238	0
2	C	884/906 (97%)	0.66	58 (6%) 18 19	97, 143, 179, 214	0
2	D	879/906 (97%)	0.78	128 (14%) 2 3	112, 180, 231, 267	0
All	All	2177/2266 (96%)	0.76	249 (11%) 5 7	97, 152, 217, 267	0

The worst 5 of 249 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	147	ALA	19.9
2	D	116	GLY	11.3
2	D	148	PHE	11.2
2	D	222	VAL	8.1
2	D	221	TYR	8.1

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
3	NAG	E	1	14/15	0.70	0.26	30,158,163,163	1
3	NAG	E	7	14/15	0.81	0.36	30,164,171,173	3

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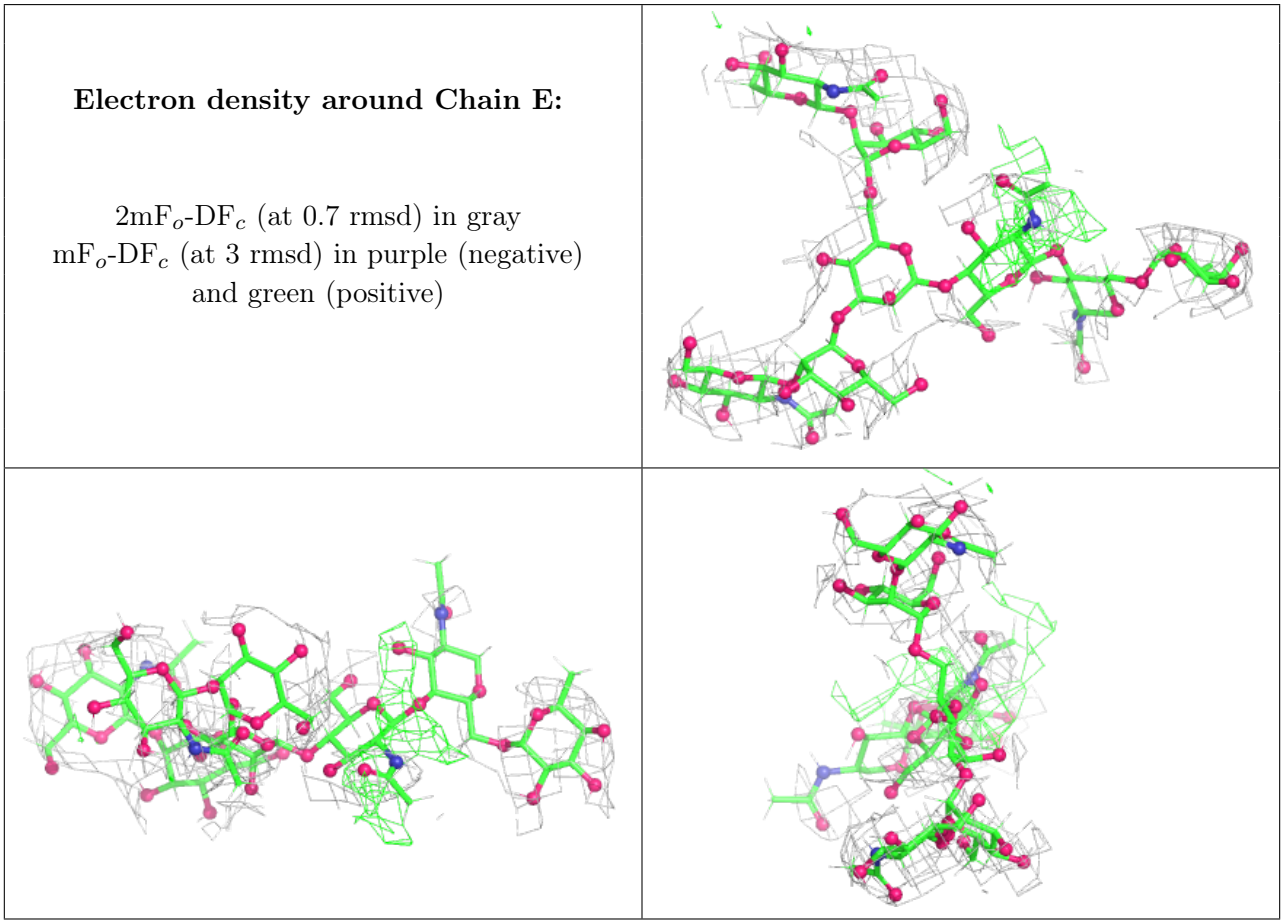
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MAN	E	6	11/12	0.87	0.26	30,159,161,167	3
3	BMA	E	3	11/12	0.88	0.28	30,151,155,156	2
3	NAG	E	5	14/15	0.92	0.27	30,159,163,166	3
3	NAG	E	2	14/15	0.92	0.35	30,168,173,174	2
3	MAN	E	4	11/12	0.92	0.25	30,143,148,154	3
3	FUC	E	8	10/11	0.92	0.29	30,133,136,136	3

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 E:

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



6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.