

Full wwPDB X-ray Structure Validation Report (i)

Oct 15, 2023 – 06:07 PM EDT

:	1X38
:	crystal structure of barley beta-D-glucan glucohydrolase isoenzyme exo1 in
	complex with gluco-phenylimidazole
:	Hrmova, M.; Streltsov, V.A.; Smith, B.J.; Vasella, A.; Varghese, J.N.; Fincher,
	G.B.
	2005-05-02
:	1.70 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 (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:

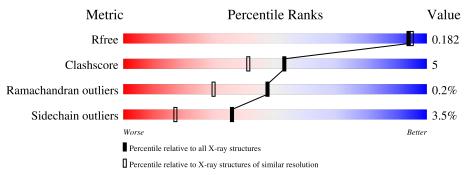
		4 001 407
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range}({\rm \AA})) \end{array}$		
R_{free}	130704	4298 (1.70-1.70)		
Clashscore	141614	4695 (1.70-1.70)		
Ramachandran outliers	138981	4610 (1.70-1.70)		
Sidechain outliers	138945	4610 (1.70-1.70)		

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length		Quality of chain						
1	А	602		91% 8%						
2	В	3	33%	33%	33%					
3	С	7		29%						
4	D	5	60%		40%					



2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 5721 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 beta-D-glucan exohydrolase isoenzyme ExoI.

Mol	Chain	Residues		Atoms					AltConf	Trace
1	А	602	Total 4566	C 2891	N 787	O 862	S 26	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	320	LYS	ASN	SEE REMARK 999	$GB \ 4566505$

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



Mo	Chain	Residues	A	Aton	ns		ZeroOcc	AltConf	Trace
2	В	3	Total 39	C 22	N 2	O 15	0	0	0

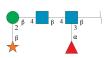
• Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alp ha-D-mannopyranose-(1-6)-[beta-D-xylopyranose-(1-2)]beta-D-mannopyranose-(1-4)-2-acet amido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deox y-beta-D-glucopyranose.



Mol	Chain	Residues	I	Aton	ns	ZeroOcc	AltConf	Trace
3	С	7	Total 83		N 3	0	0	0

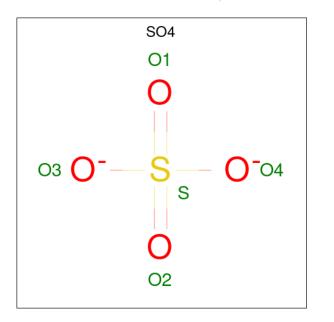


• Molecule 4 is an oligosaccharide called beta-D-xylopyranose-(1-2)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetam ido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	A	toms	ZeroOcc	AltConf	Trace
4	D	5	Total 58	C N 33 2	0	0	0

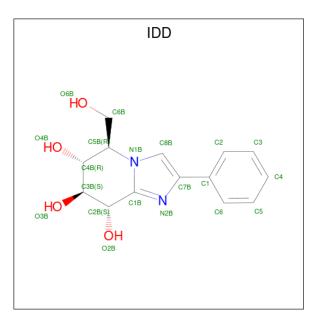
• Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Ν	ſol	Chain	Residues	Atoms			ZeroOcc	AltConf
	5	А	1	Total 5	0 4	S 1	0	0

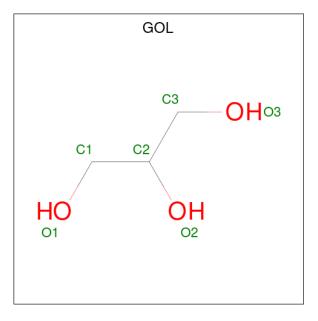
• Molecule 6 is (5R,6R,7S,8S)-5-(HYDROXYMETHYL)-2-PHENYL-5,6,7,8-TETRAHYDRO IMIDAZO[1,2-A]PYRIDINE-6,7,8-TRIOL (three-letter code: IDD) (formula: $C_{14}H_{16}N_2O_4$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	А	1	Total 20	C 14	N 2	0 4	0	0

• Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 7 & 3 & 4 \end{array}$	0	1
7	А	1	Total C O 12 6 6	0	1

• Molecule 8 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	931	Total O 931 931	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. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: beta-D-glucan exohydrolase isoenzyme ExoI

Chai	in A	-								9	1%										89	%	•		
D1 E36	T41	V 14 K63	06W	V97 H98	N101 N102	V103 R119	E134	T138	R167	<mark>գ171</mark>	<mark>զ181</mark>	K186 D187	A203	N222	N226	6229 L230	H234	K239	S247	H262	D285	D290	H331	L358	H377
R386	N394 L404	K408 K409	A410	N422	Y425	D4 <mark>37</mark> T438 G439	R440 T441	T459	Y479	Y4 <mark>89</mark>	G494	G505 L506	S507	V530	L534	F558	V582	H586	L593	T602					

• 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:	33%	33%	33%
NAG1 NAG2 BMA3			

 $\label{eq:main_optimal_state} \bullet \mbox{Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[beta-D-xylopyranose-(1-2)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose -(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose -(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose -(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose -(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose -(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose -(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose -(1-4)-[alpha-L-fucopyranose -(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose -(1-4)-[alpha-L-fucopyranose -(1-4)-[alpha-L-fucopyranose -(1-4)-[alpha-L-fucopyranose -(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose -$

Chain C:	71%	29%

NAG1 NAG2 BMA3 MAN4 NAG5 XYP6 XYP6

NA BM XY FU

 • Molecule 4: beta-D-xylopyranose-(1-2)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta a-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)] 2-acetamido-2-deoxy-beta-D-glucopyranose e

Chain D:	60%	40%
<mark>ម ម ន ៥ ម</mark>		



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants	100.56Å 100.56Å 182.41Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.30 - 1.70	Depositor
Resolution (A)	34.30 - 1.70	EDS
% Data completeness	99.8 (34.30-1.70)	Depositor
(in resolution range)	99.8 (34.30-1.70)	EDS
R _{merge}	0.05	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.38 (at 1.70 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0011	Depositor
D D	0.160 , 0.183	Depositor
R, R_{free}	0.158 , 0.182	DCC
R_{free} test set	5168 reflections (5.00%)	wwPDB-VP
Wilson B-factor $(Å^2)$	24.8	Xtriage
Anisotropy	0.332	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36, 35.5	EDS
L-test for twinning ²	$ \langle L \rangle = 0.50, \langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5721	wwPDB-VP
Average B, all atoms $(Å^2)$	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities 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: XYP, FUC, BMA, SO4, IDD, GOL, 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).

Mal	Chain	Bond	lengths	Bond	angles
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.54	0/4663	0.61	0/6334

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 (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	А	4566	0	4550	49	1
2	В	39	0	34	1	0
3	С	83	0	63	2	0
4	D	58	0	42	0	0
5	А	5	0	0	0	0
6	А	20	0	16	0	0
7	А	19	0	22	1	0
8	А	931	0	0	11	1
All	All	5721	0	4727	51	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 5.

All (51) 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:517:ARG:HB2	1:A:517:ARG:NH1	1.41	1.34
1:A:517:ARG:HH11	1:A:517:ARG:CB	1.47	1.01
1:A:41:THR:HG22	1:A:44:VAL:H	1.39	0.86
1:A:394:ASN:HD21	1:A:404:LEU:H	1.18	0.86
1:A:410:ALA:O	1:A:459:THR:HB	1.78	0.83
1:A:41:THR:HG21	8:A:6671:HOH:O	1.84	0.78
1:A:97:VAL:H	1:A:101:ASN:HD21	1.34	0.75
1:A:181:GLN:HE21	1:A:203:ALA:H	1.37	0.72
1:A:422:ASN:HD21	1:A:439:GLY:H	1.37	0.72
1:A:167:ARG:HH11	1:A:171:GLN:HE22	1.39	0.70
1:A:239:LYS:HE2	8:A:6936:HOH:O	1.91	0.70
1:A:505:GLY:N	8:A:6932:HOH:O	2.28	0.65
1:A:422:ASN:ND2	1:A:439:GLY:H	1.95	0.65
1:A:262:HIS:HE1	1:A:285:ASP:H	1.43	0.64
1:A:97:VAL:H	1:A:101:ASN:ND2	1.96	0.63
1:A:119:ARG:HE	7:A:2002[A]:GOL:H2	1.63	0.62
1:A:517:ARG:HB2	1:A:517:ARG:HH11	0.58	0.62
8:A:6766:HOH:O	3:C:7:FUC:H63	2.01	0.60
1:A:479:TYR:HB3	1:A:517:ARG:HH12	1.68	0.59
1:A:234:HIS:HE1	8:A:6196:HOH:O	1.86	0.58
1:A:386:ARG:NH1	8:A:6930:HOH:O	2.33	0.57
1:A:408:LYS:O	1:A:459:THR:HG21	2.04	0.57
1:A:167:ARG:NH1	1:A:171:GLN:HE22	2.02	0.56
1:A:167:ARG:HH11	1:A:171:GLN:NE2	2.01	0.56
1:A:234:HIS:HD2	8:A:6027:HOH:O	1.88	0.56
1:A:262:HIS:CE1	1:A:285:ASP:H	2.23	0.56
1:A:226:ASN:ND2	1:A:229:GLY:H	2.03	0.55
1:A:331:HIS:HD2	8:A:6340:HOH:O	1.90	0.55
1:A:507:SER:OG	8:A:6932:HOH:O	2.18	0.54
1:A:582:VAL:HG11	1:A:593:LEU:HB3	1.89	0.54
1:A:181:GLN:HE22	1:A:247:SER:H	1.57	0.53
1:A:186:LYS:HD3	1:A:186:LYS:H	1.75	0.52
1:A:134:GLU:OE2	1:A:377:HIS:HD2	1.94	0.51
1:A:530:VAL:HG13	1:A:534:LEU:HD22	1.92	0.51
1:A:41:THR:CG2	1:A:44:VAL:H	2.19	0.50
1:A:422:ASN:HD22	1:A:422:ASN:C	2.16	0.49
1:A:222:ASN:HB2	2:B:1:NAG:H82	1.96	0.48
1:A:226:ASN:C	1:A:226:ASN:HD22	2.19	0.46
1:A:437:ASP:HB3	1:A:441:THR:HG21	1.98	0.46
1:A:186:LYS:HD3	1:A:186:LYS:N	2.30	0.46
1:A:422:ASN:ND2	1:A:425:TYR:H	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:2:NAG:H82	3:C:4:MAN:O3	2.18	0.43
1:A:602:THR:HG21	8:A:6307:HOH:O	2.18	0.43
1:A:489:TYR:CD2	1:A:494:GLY:HA3	2.55	0.42
1:A:181:GLN:HE22	1:A:247:SER:N	2.18	0.42
1:A:63:LYS:N	1:A:63:LYS:HE3	2.35	0.42
1:A:558:PHE:HB2	8:A:6652:HOH:O	2.21	0.41
1:A:63:LYS:HE3	1:A:63:LYS:H	1.86	0.41
1:A:413:ILE:HG21	1:A:479:TYR:CZ	2.55	0.41
1:A:103:VAL:HG21	1:A:138:THR:HG21	2.03	0.40
1:A:186:LYS:H	1:A:186:LYS:CD	2.33	0.40

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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)
1:A:63:LYS:NZ	8:A:6243:HOH:O[3_554]	2.09	0.11

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	А	600/602~(100%)	584 (97%)	15~(2%)	1 (0%)	47 30

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	505	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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	485/485~(100%)	468 (96%)	17 (4%)	36 17

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	1	ASP
1	А	36	GLU
1	А	41	THR
1	А	63	LYS
1	А	90	MET
1	А	98	HIS
1	А	187	ASP
1	А	226	ASN
1	А	230	LEU
1	А	290	ASP
1	А	358	LEU
1	А	422	ASN
1	А	459	THR
1	А	517	ARG
1	А	534	LEU
1	А	582	VAL
1	А	586	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	101	ASN
1	А	112	ASN
1	А	171	GLN
1	А	181	GLN
1	А	199	ASN
1	А	226	ASN
1	А	234	HIS
1	А	240	ASN

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Mol	Chain	Res	Type
1	А	257	ASN
1	А	262	HIS
1	А	265	GLN
1	А	331	HIS
1	А	333	ASN
1	А	377	HIS
1	А	394	ASN
1	А	422	ASN
1	А	581	ASN

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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	ol Type Chain Res Link		Tink	Bo	ond leng	ths	Bond angles			
	туре	Ullalli	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
2	NAG	В	1	1,2	14,14,15	0.64	0	17,19,21	1.11	2 (11%)
2	NAG	В	2	2	14,14,15	0.50	0	17,19,21	0.83	0
2	BMA	В	3	2	11,11,12	0.65	0	$15,\!15,\!17$	0.97	1 (6%)
3	NAG	С	1	1,3	14,14,15	0.57	0	17,19,21	0.87	1 (5%)
3	NAG	С	2	3	14,14,15	0.57	0	17,19,21	1.04	0
3	BMA	С	3	3	11,11,12	0.57	0	$15,\!15,\!17$	0.76	1 (6%)
3	MAN	С	4	3	11,11,12	0.56	0	$15,\!15,\!17$	0.88	1 (6%)
3	NAG	С	5	3	14,14,15	0.42	0	17,19,21	0.92	1 (5%)



Mol	Turne	Chain	Res	Link	Bo	ond leng	\mathbf{ths}	Bond angles		
10101	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
3	XYP	С	6	3	$9,\!9,\!10$	1.21	1 (11%)	10,12,14	0.73	0
3	FUC	С	7	3	10,10,11	0.61	0	14,14,16	0.84	1 (7%)
4	NAG	D	1	1,4	14,14,15	0.57	0	17,19,21	0.83	0
4	NAG	D	2	4	$14,\!14,\!15$	0.49	0	$17,\!19,\!21$	0.60	0
4	BMA	D	3	4	$11,\!11,\!12$	0.55	0	$15,\!15,\!17$	0.79	1 (6%)
4	XYP	D	4	4	9,9,10	1.20	1 (11%)	10,12,14	1.03	1 (10%)
4	FUC	D	5	4	10,10,11	0.58	0	14,14,16	0.72	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
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	-	2/2/19/22	0/1/1/1
3	NAG	С	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	С	2	3	-	2/6/23/26	0/1/1/1
3	BMA	С	3	3	-	1/2/19/22	0/1/1/1
3	MAN	С	4	3	-	0/2/19/22	0/1/1/1
3	NAG	С	5	3	-	0/6/23/26	0/1/1/1
3	XYP	С	6	3	-	-	0/1/1/1
3	FUC	С	7	3	-	-	0/1/1/1
4	NAG	D	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1
4	BMA	D	3	4	-	0/2/19/22	0/1/1/1
4	XYP	D	4	4	-	-	0/1/1/1
4	FUC	D	5	4	-	-	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
4	D	4	XYP	O5-C1	-3.23	1.36	1.42
3	С	6	XYP	O5-C1	-3.19	1.36	1.42

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
4	D	4	XYP	C5-O5-C1	2.89	115.96	111.52
2	В	1	NAG	C1-O5-C5	2.76	115.93	112.19

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Observed(°) Ideal(°)			
	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$	

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	С	5	NAG	C1-O5-C5	2.70	115.85	112.19
2	В	1	NAG	O5-C1-C2	-2.55	107.27	111.29
3	С	7	FUC	O5-C5-C6	2.40	112.49	107.33
2	В	3	BMA	C3-C4-C5	2.20	114.17	110.24
3	С	4	MAN	C1-O5-C5	2.15	115.10	112.19
4	D	3	BMA	O5-C5-C6	2.10	110.49	107.20
3	С	3	BMA	O5-C5-C6	2.05	110.42	107.20
3	С	1	NAG	O5-C1-C2	-2.00	108.13	111.29

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There are no chirality outliers.

All (6) torsion outliers are listed below:

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

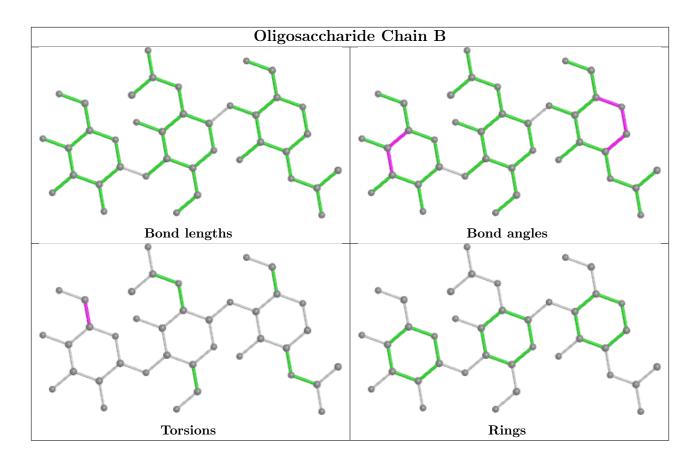
There are no ring outliers.

4 monomers are involved in 3 short contacts:

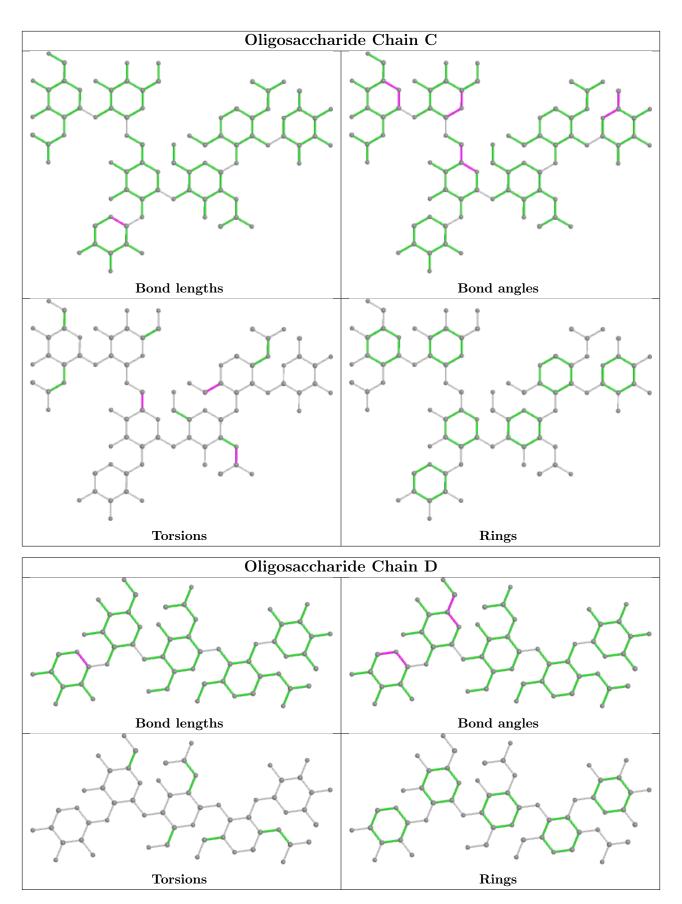
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	С	4	MAN	1	0
3	С	7	FUC	1	0
2	В	1	NAG	1	0
3	С	2	NAG	1	0

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











5.6 Ligand geometry (i)

6 ligands 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	Turne	Chain	Dec	Res Link		ond leng	ths	B	ond ang	les
	Type	Unam	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
7	GOL	А	2001[B]	-	$5,\!5,\!5$	0.52	0	$5,\!5,\!5$	0.25	0
7	GOL	А	2002[B]	-	$5,\!5,\!5$	0.34	0	5, 5, 5	0.42	0
5	SO4	А	3001	-	4,4,4	0.15	0	6,6,6	0.21	0
7	GOL	А	2001[A]	-	$5,\!5,\!5$	0.51	0	$5,\!5,\!5$	0.34	0
6	IDD	А	1001	-	19,22,22	1.20	2 (10%)	16,32,32	0.92	1 (6%)
7	GOL	А	2002[A]	-	$5,\!5,\!5$	0.43	0	$5,\!5,\!5$	0.19	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
7	GOL	А	2001[B]	-	-	2/4/4/4	-
7	GOL	А	2002[B]	-	-	2/4/4/4	-
7	GOL	А	2001[A]	-	-	0/4/4/4	-
6	IDD	А	1001	-	-	0/2/26/26	0/2/3/3
7	GOL	А	2002[A]	-	-	2/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
6	А	1001	IDD	C1B-C2B	-2.58	1.47	1.51
6	А	1001	IDD	C8B-C7B	-2.28	1.36	1.40

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
6	А	1001	IDD	O2B-C2B-C3B	2.05	112.85	108.55



There are no chirality outliers.

Mol	Chain	Res	Type	Atoms
7	А	2001[B]	GOL	O1-C1-C2-C3
7	А	2002[A]	GOL	O1-C1-C2-O2
7	А	2002[A]	GOL	O1-C1-C2-C3
7	А	2002[B]	GOL	O1-C1-C2-C3
7	А	2002[B]	GOL	O1-C1-C2-O2
7	А	2001[B]	GOL	O1-C1-C2-O2

All (6) torsion outliers are listed below:

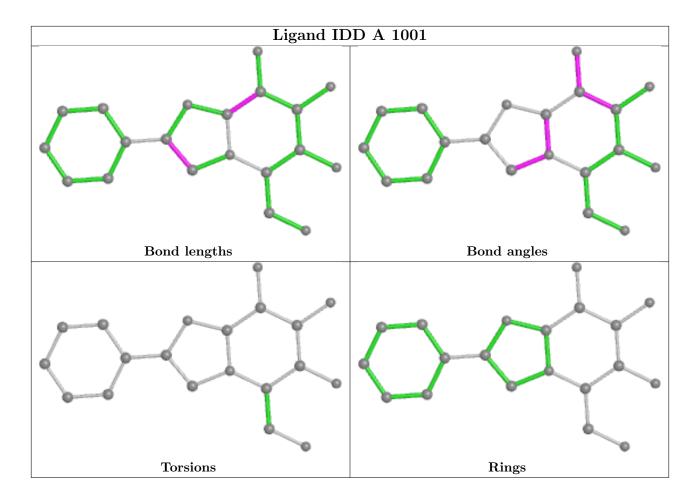
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	А	2002[A]	GOL	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)

Unable to reproduce the depositors R factor - this section is therefore empty.

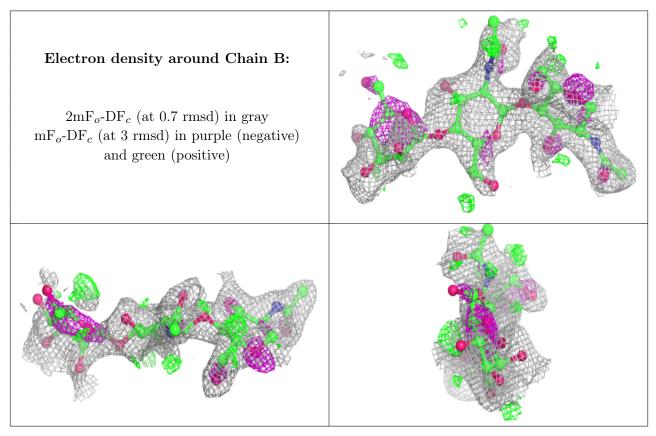
6.2 Non-standard residues in protein, DNA, RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

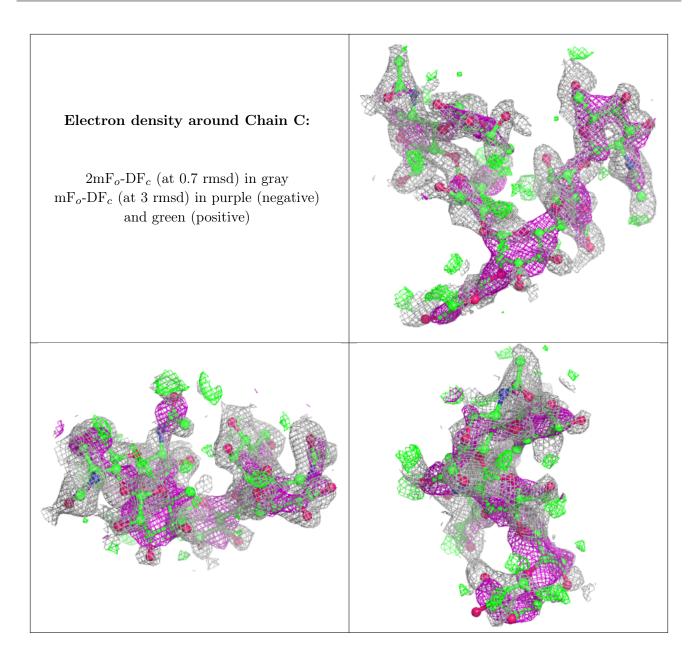
6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

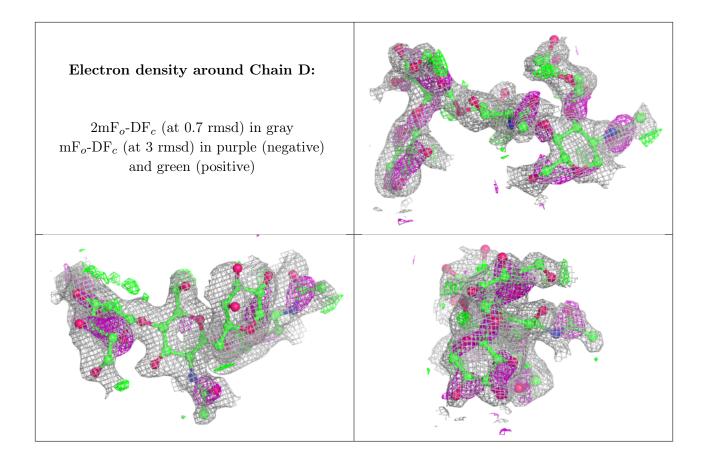
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.









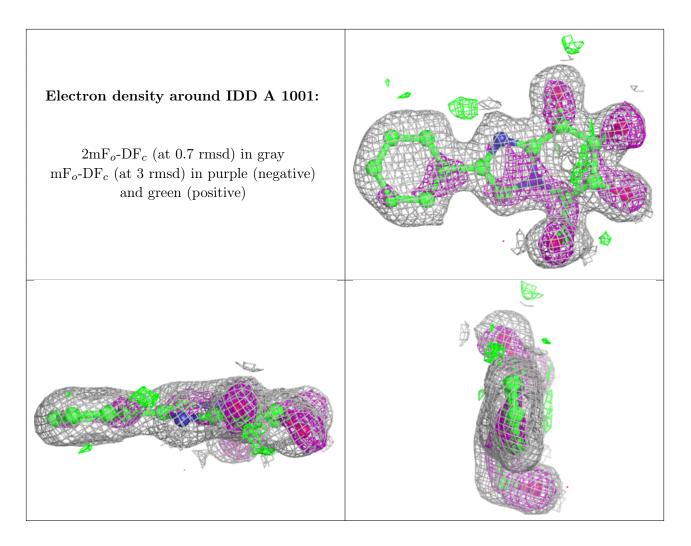


6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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)

Unable to reproduce the depositors R factor - this section is therefore empty.

