



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2025 – 04:38 PM EDT

PDB ID : 9NWF / pdb_00009nwf
Title : Structure of an inactive beta-D-glucuronate dehydratase mutant in complex with chondrosine
Authors : Boraston, A.B.; Alvarez, B.; Canil, O.
Deposited on : 2025-03-22
Resolution : 2.60 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0rc1
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

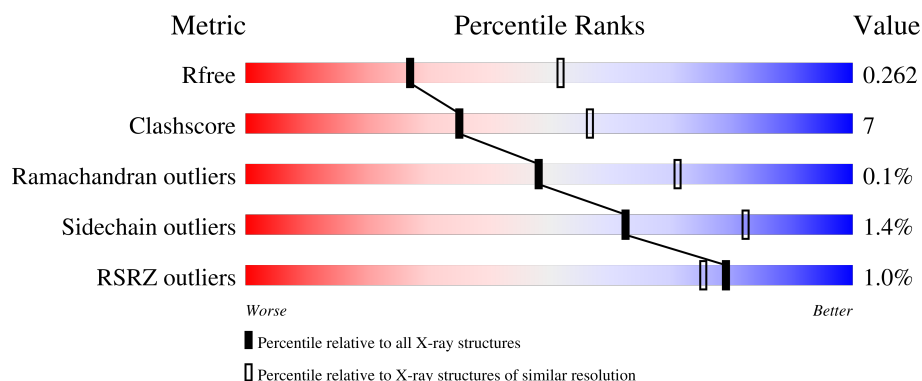
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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.




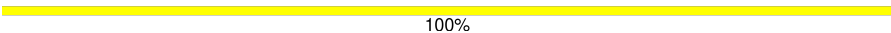
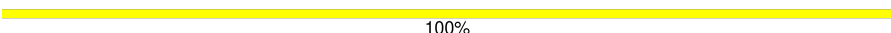
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	3775 (2.60-2.60)
Clashscore	180529	4181 (2.60-2.60)
Ramachandran outliers	177936	4129 (2.60-2.60)
Sidechain outliers	177891	4129 (2.60-2.60)
RSRZ outliers	164620	3775 (2.60-2.60)

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 $\leq 5\%$. 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	405	<div> <div></div> <div>81%</div> <div>14%</div> <div>5%</div> </div>
1	B	405	<div> <div></div> <div>75%</div> <div>21%</div> <div>•</div> </div>
1	C	405	<div> <div></div> <div>80%</div> <div>15%</div> <div>• 5%</div> </div>
1	D	405	<div> <div></div> <div>79%</div> <div>16%</div> <div>5%</div> </div>
2	E	2	<div> <div></div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
2	G	2	 50%50%
2	I	2	 100%
2	J	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	IOD	C	503	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12912 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.

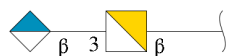
- Molecule 1 is a protein called Glucuronate dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	385	Total	C	N	O	S	0	0	0
			3078	1966	530	566	16			
1	B	387	Total	C	N	O	S	0	0	0
			3088	1972	532	568	16			
1	C	385	Total	C	N	O	S	0	0	0
			3078	1966	530	566	16			
1	D	385	Total	C	N	O	S	0	7	0
			3133	1998	542	577	16			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP A0A174GN40
A	2	SER	-	expression tag	UNP A0A174GN40
A	3	HIS	-	expression tag	UNP A0A174GN40
A	4	MET	-	expression tag	UNP A0A174GN40
A	285	ALA	ARG	engineered mutation	UNP A0A174GN40
B	1	GLY	-	expression tag	UNP A0A174GN40
B	2	SER	-	expression tag	UNP A0A174GN40
B	3	HIS	-	expression tag	UNP A0A174GN40
B	4	MET	-	expression tag	UNP A0A174GN40
B	285	ALA	ARG	engineered mutation	UNP A0A174GN40
C	1	GLY	-	expression tag	UNP A0A174GN40
C	2	SER	-	expression tag	UNP A0A174GN40
C	3	HIS	-	expression tag	UNP A0A174GN40
C	4	MET	-	expression tag	UNP A0A174GN40
C	285	ALA	ARG	engineered mutation	UNP A0A174GN40
D	1	GLY	-	expression tag	UNP A0A174GN40
D	2	SER	-	expression tag	UNP A0A174GN40
D	3	HIS	-	expression tag	UNP A0A174GN40
D	4	MET	-	expression tag	UNP A0A174GN40
D	285	ALA	ARG	engineered mutation	UNP A0A174GN40

- Molecule 2 is an oligosaccharide called beta-D-glucopyranuronic acid-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	2	Total	C	N	O	0	0	0
			24	12	1	11			
2	G	2	Total	C	N	O	0	0	0
			24	12	1	11			
2	I	2	Total	C	N	O	0	0	0
			24	12	1	11			
2	J	2	Total	C	N	O	0	0	0
			24	12	1	11			

- Molecule 3 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	I	0	0
			9	9		
3	B	6	Total	I	0	0
			6	6		
3	C	7	Total	I	0	0
			7	7		
3	D	5	Total	I	0	0
			5	5		

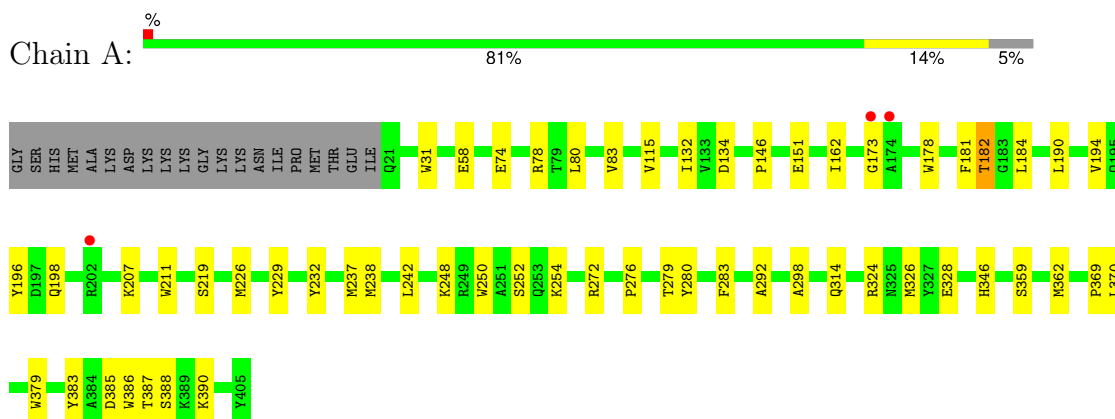
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	92	Total	O	0	0
			92	92		
4	B	98	Total	O	0	0
			98	98		
4	C	115	Total	O	0	0
			115	115		
4	D	107	Total	O	0	0
			107	107		

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.

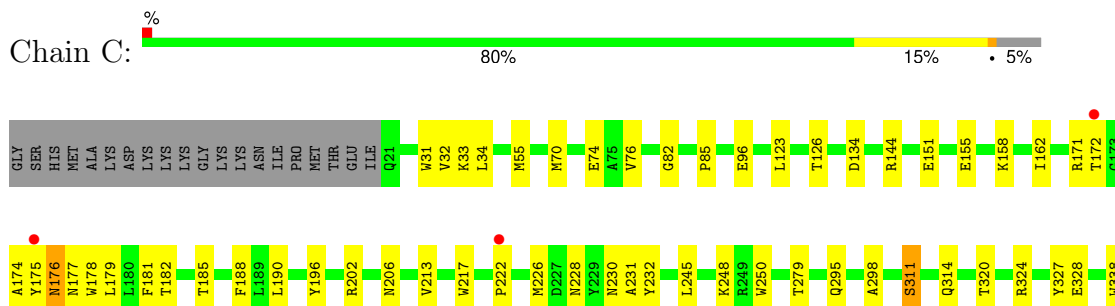
- Molecule 1: Glucuronate dehydratase

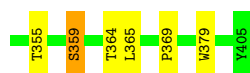


- Molecule 1: Glucuronate dehydratase

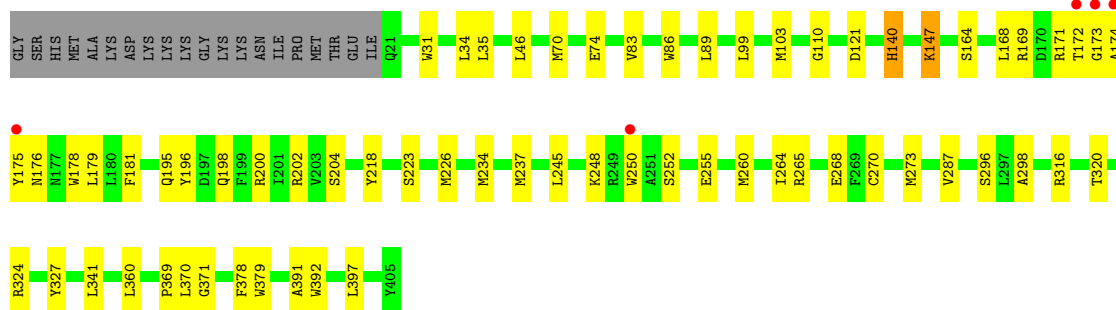
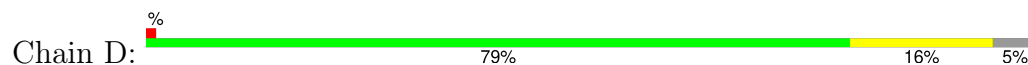


- Molecule 1: Glucuronate dehydratase





- Molecule 1: Glucuronate dehydratase



- Molecule 2: beta-D-glucopyranuronic acid-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose



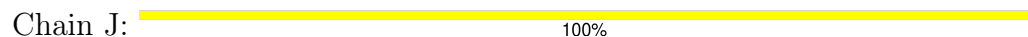
- Molecule 2: beta-D-glucopyranuronic acid-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose



- Molecule 2: beta-D-glucopyranuronic acid-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose



- Molecule 2: beta-D-glucopyranuronic acid-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.54Å 105.84Å 179.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 2.60 19.96 – 2.60	Depositor EDS
% Data completeness (in resolution range)	91.4 (19.96-2.60) 91.1 (19.96-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 2.59Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.191 , 0.262 0.191 , 0.262	Depositor DCC
R_{free} test set	2996 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	46.9	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 40.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12912	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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: IOD, BDP, 1GN

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	0.36	0/3164	0.54	0/4295
1	B	0.36	0/3174	0.52	0/4309
1	C	0.36	0/3164	0.56	0/4295
1	D	0.37	0/3220	0.54	0/4371
All	All	0.36	0/12722	0.54	0/17270

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	A	3078	0	2992	42	0
1	B	3088	0	2996	58	0
1	C	3078	0	2992	41	0
1	D	3133	0	3040	48	0
2	E	24	0	19	0	0
2	G	24	0	19	2	0
2	I	24	0	18	0	0
2	J	24	0	19	0	0
3	A	9	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	6	0	0	2	0
3	C	7	0	0	4	0
3	D	5	0	0	0	0
4	A	92	0	0	1	0
4	B	98	0	0	3	0
4	C	115	0	0	1	0
4	D	107	0	0	2	0
All	All	12912	0	12095	180	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 7.

The worst 5 of 180 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:290:ARG:HB3	1:B:326:MET:HE1	1.46	0.96
1:D:202:ARG:HH22	1:D:250:TRP:HE3	1.21	0.88
1:D:179:LEU:HD21	1:D:204:SER:HA	1.55	0.88
1:A:226:MET:HE2	1:D:226:MET:HE2	1.63	0.80
1:A:254:LYS:HD2	1:A:254:LYS:H	1.45	0.79

There are no symmetry-related clashes.

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	383/405 (95%)	365 (95%)	18 (5%)	0	100	100
1	B	385/405 (95%)	367 (95%)	18 (5%)	0	100	100
1	C	383/405 (95%)	367 (96%)	15 (4%)	1 (0%)	37	59
1	D	390/405 (96%)	371 (95%)	19 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1541/1620 (95%)	1470 (95%)	70 (4%)	1 (0%)	48 71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	176	ASN

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	322/340 (95%)	318 (99%)	4 (1%)	67 85
1	B	322/340 (95%)	318 (99%)	4 (1%)	67 85
1	C	322/340 (95%)	318 (99%)	4 (1%)	67 85
1	D	327/340 (96%)	321 (98%)	6 (2%)	54 77
All	All	1293/1360 (95%)	1275 (99%)	18 (1%)	62 82

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	164	SER
1	D	296	SER
1	D	287	VAL
1	C	126	THR
1	D	147	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	195	GLN
1	D	228	ASN
1	B	309	HIS
1	B	398	HIS

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Mol	Chain	Res	Type
1	C	206	ASN

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 ⓘ

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
2	1GN	E	1	2	12,12,12	1.74	3 (25%)	16,17,17	1.30	2 (12%)
2	BDP	E	2	2	12,12,13	1.21	1 (8%)	14,17,19	1.10	1 (7%)
2	1GN	G	1	2	12,12,12	1.64	3 (25%)	16,17,17	1.16	2 (12%)
2	BDP	G	2	2	12,12,13	1.17	1 (8%)	14,17,19	1.20	1 (7%)
2	1GN	I	1	2	12,12,12	1.71	4 (33%)	16,17,17	1.24	2 (12%)
2	BDP	I	2	2	12,12,13	1.21	1 (8%)	14,17,19	1.38	1 (7%)
2	1GN	J	1	2	12,12,12	1.62	3 (25%)	16,17,17	0.99	1 (6%)
2	BDP	J	2	2	12,12,13	1.26	2 (16%)	14,17,19	1.35	2 (14%)

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	1GN	E	1	2	-	2/2/22/22	0/1/1/1
2	BDP	E	2	2	-	2/4/21/24	0/1/1/1
2	1GN	G	1	2	-	2/2/22/22	0/1/1/1
2	BDP	G	2	2	-	2/4/21/24	0/1/1/1
2	1GN	I	1	2	-	0/2/22/22	0/1/1/1
2	BDP	I	2	2	-	2/4/21/24	0/1/1/1
2	1GN	J	1	2	-	2/2/22/22	0/1/1/1
2	BDP	J	2	2	-	2/4/21/24	0/1/1/1

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	1GN	C3-C2	-3.96	1.48	1.53
2	G	1	1GN	C3-C2	-3.33	1.49	1.53
2	I	1	1GN	C3-C2	-3.21	1.49	1.53
2	J	1	1GN	C3-C2	-3.20	1.49	1.53
2	I	1	1GN	O5-C1	2.68	1.49	1.42

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	2	BDP	O3-C3-C2	-3.43	103.06	110.05
2	E	1	1GN	O5-C1-C2	3.25	113.30	109.51
2	J	2	BDP	O3-C3-C2	-3.03	103.88	110.05
2	G	2	BDP	O4-C4-C3	-2.36	104.82	110.38
2	E	1	1GN	O5-C5-C4	2.35	113.94	109.70

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

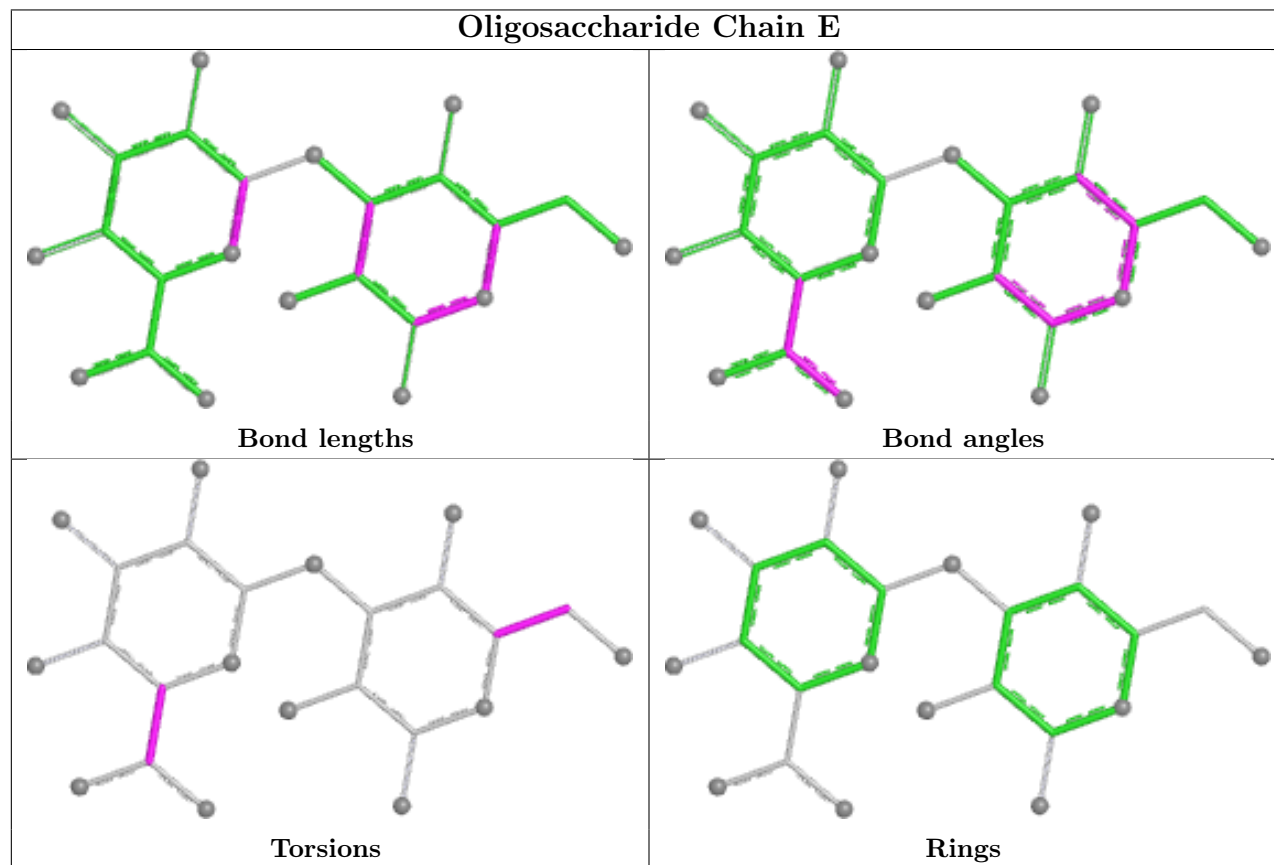
Mol	Chain	Res	Type	Atoms
2	E	2	BDP	C4-C5-C6-O6A
2	E	2	BDP	C4-C5-C6-O6B
2	G	2	BDP	C4-C5-C6-O6A
2	G	2	BDP	C4-C5-C6-O6B
2	I	2	BDP	C4-C5-C6-O6A

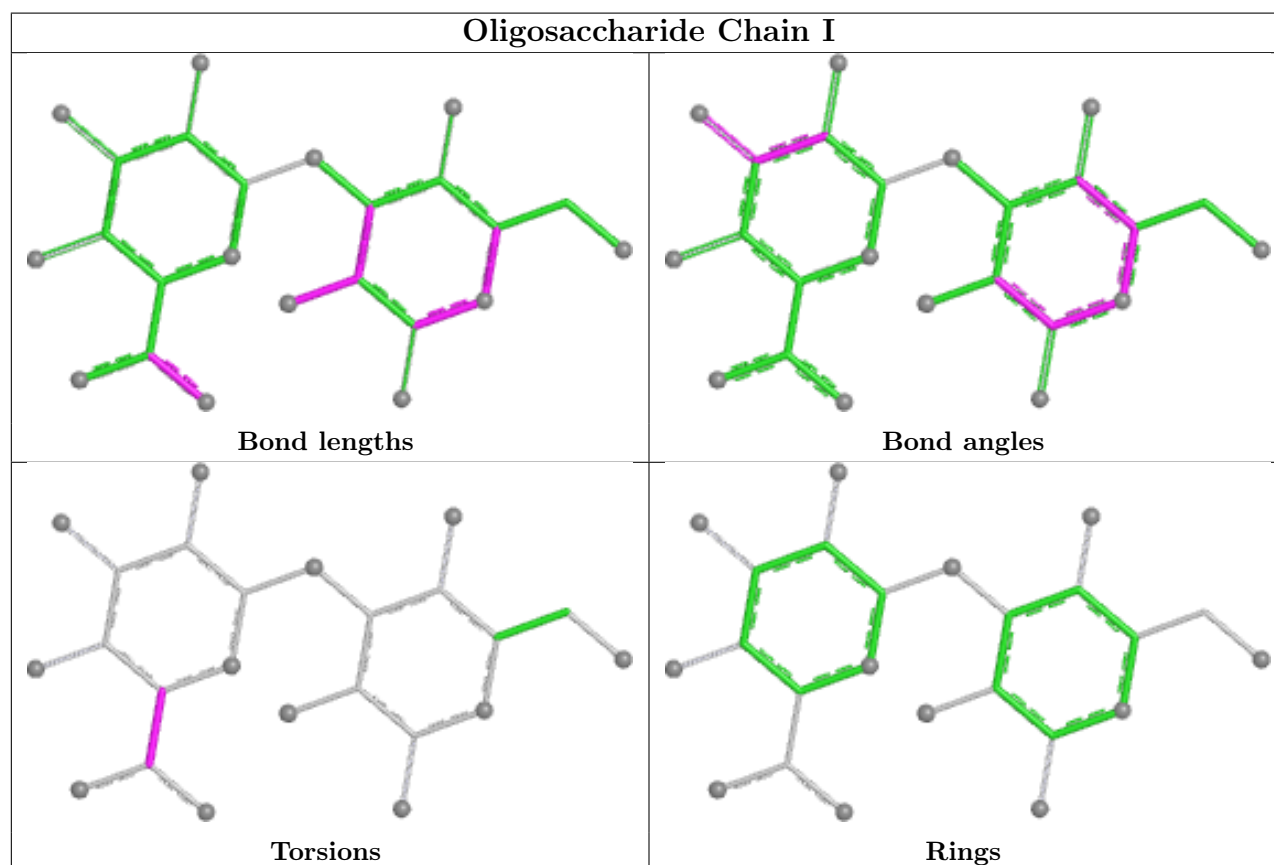
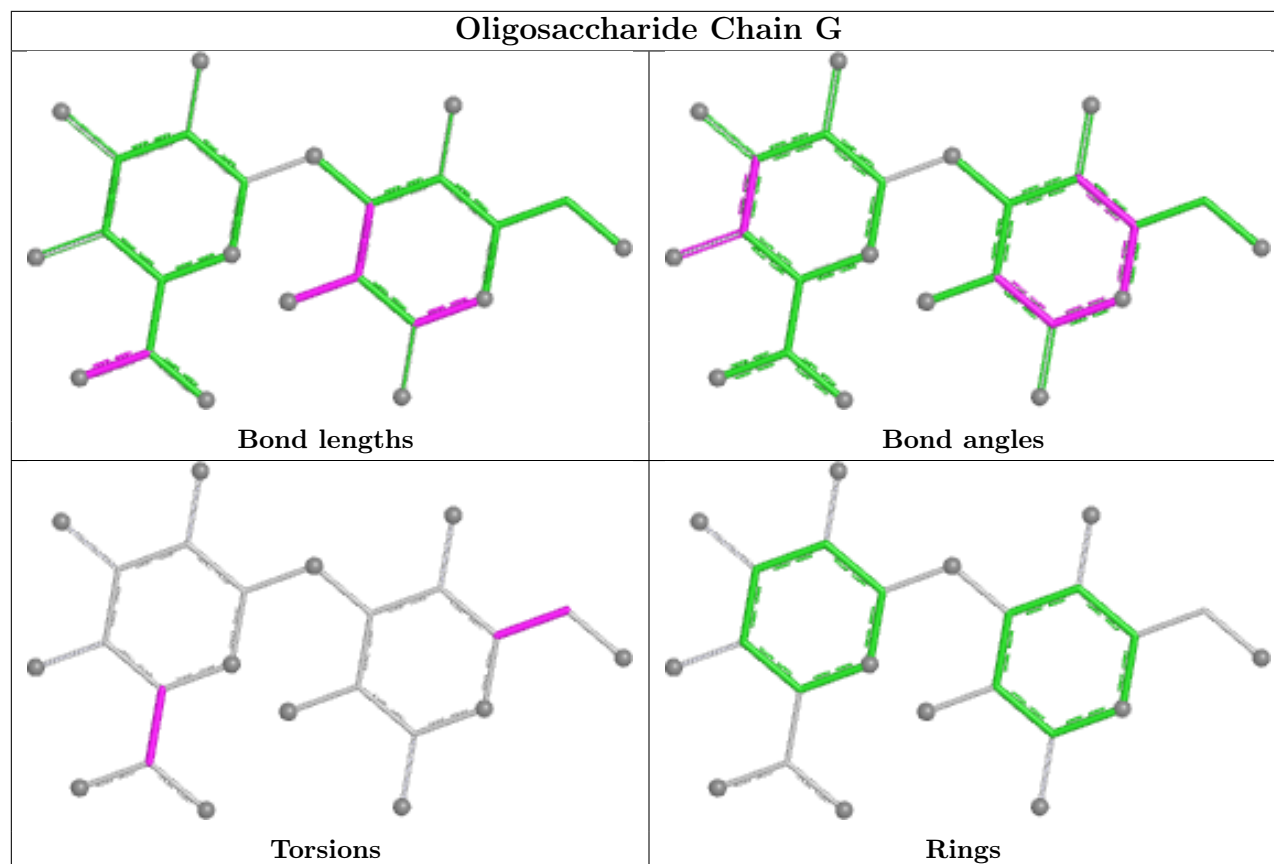
There are no ring outliers.

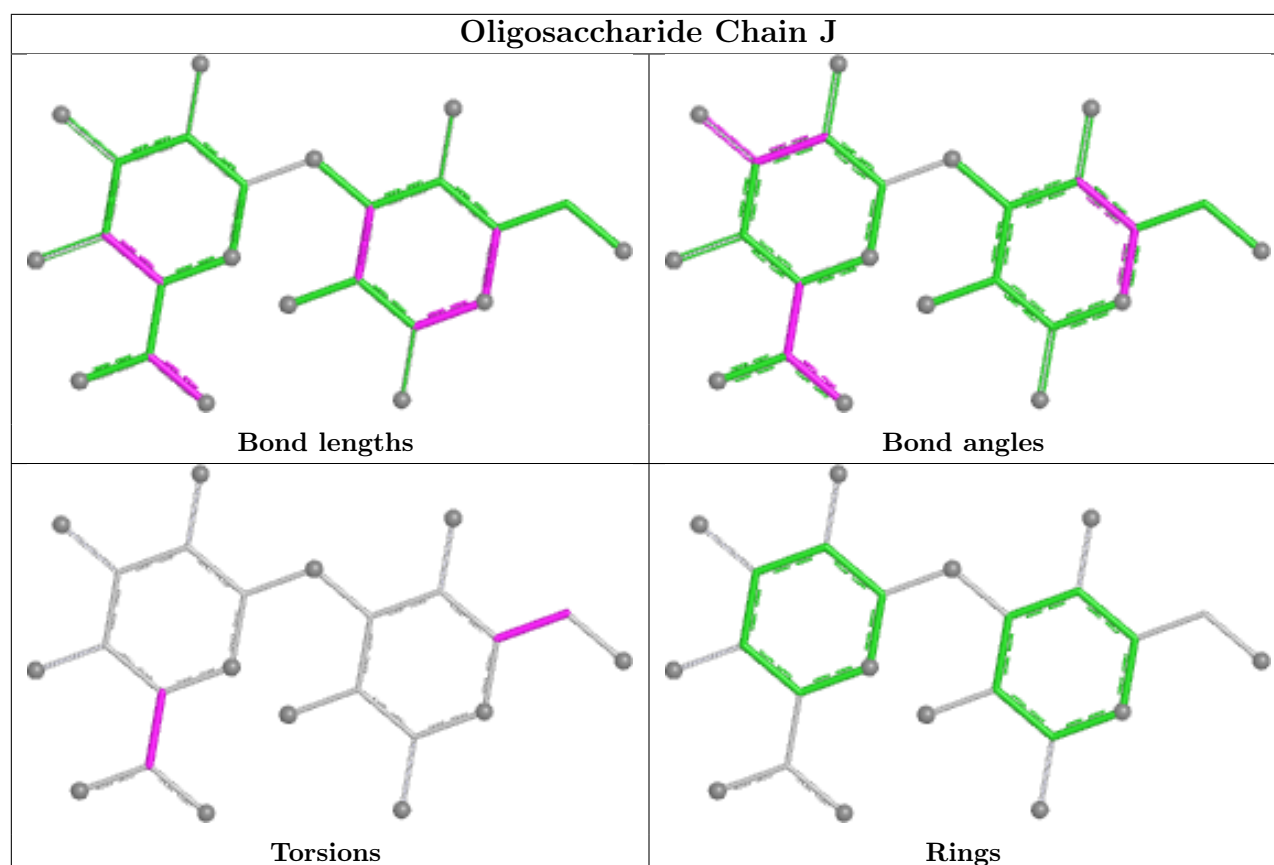
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	1	1GN	2	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](#)

Of 27 ligands modelled in this entry, 27 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	385/405 (95%)	-0.54	3 (0%) 82 79	34, 43, 59, 80	0
1	B	387/405 (95%)	-0.39	4 (1%) 79 75	29, 47, 62, 88	0
1	C	385/405 (95%)	-0.53	3 (0%) 82 79	33, 45, 60, 80	0
1	D	385/405 (95%)	-0.52	5 (1%) 74 70	28, 43, 57, 81	7 (1%)
All	All	1542/1620 (95%)	-0.50	15 (0%) 79 75	28, 45, 60, 88	7 (0%)

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	172[A]	THR	5.5
1	D	175[A]	TYR	5.4
1	B	174	ALA	3.7
1	D	173[A]	GLY	3.4
1	C	172	THR	3.4

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](#)

SUGAR-RSR INFOmissingINFO

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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	IOD	C	503	1/1	0.82	0.19	143,143,143,143	0
3	IOD	B	506	1/1	0.84	0.20	177,177,177,177	0
3	IOD	A	508	1/1	0.88	0.14	162,162,162,162	0
3	IOD	B	503	1/1	0.92	0.15	138,138,138,138	0
3	IOD	C	507	1/1	0.93	0.16	138,138,138,138	0
3	IOD	C	506	1/1	0.94	0.13	114,114,114,114	0
3	IOD	C	505	1/1	0.95	0.14	118,118,118,118	0
3	IOD	B	502	1/1	0.95	0.12	118,118,118,118	0
3	IOD	A	507	1/1	0.95	0.13	115,115,115,115	0
3	IOD	D	502	1/1	0.95	0.12	135,135,135,135	0
3	IOD	A	505	1/1	0.96	0.08	112,112,112,112	0
3	IOD	D	505	1/1	0.96	0.08	109,109,109,109	0
3	IOD	C	504	1/1	0.97	0.16	115,115,115,115	0
3	IOD	B	504	1/1	0.97	0.13	122,122,122,122	0
3	IOD	A	509	1/1	0.97	0.13	98,98,98,98	0
3	IOD	C	501	1/1	0.97	0.10	112,112,112,112	0
3	IOD	C	502	1/1	0.97	0.13	98,98,98,98	0
3	IOD	D	503	1/1	0.97	0.17	126,126,126,126	0
3	IOD	B	501	1/1	0.97	0.13	100,100,100,100	0
3	IOD	A	503	1/1	0.98	0.04	71,71,71,71	0
3	IOD	A	504	1/1	0.98	0.06	94,94,94,94	0
3	IOD	D	501	1/1	0.98	0.09	93,93,93,93	0
3	IOD	A	501	1/1	0.98	0.13	128,128,128,128	0
3	IOD	B	505	1/1	0.98	0.12	113,113,113,113	0
3	IOD	D	504	1/1	0.98	0.11	117,117,117,117	0
3	IOD	A	506	1/1	0.98	0.14	129,129,129,129	0
3	IOD	A	502	1/1	1.00	0.01	59,59,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.