



# wwPDB X-ray Structure Validation Summary Report

Oct 5, 2023 – 01:17 AM EDT

PDB ID : 6V09  
Title : Crystal structure of human recombinant Beta-2 glycoprotein I short tag (ST-B2GPI)  
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Deposited on : 2019-11-18  
Resolution : 2.99 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](mailto: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>.

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

MolProbity : **FAILED**  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : **FAILED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

# 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 2.99 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2768 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-2-glycoprotein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	324	2517	1601	417	473	26	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	GLU	-	expression tag	UNP P02749
A	-10	ASP	-	expression tag	UNP P02749
A	-9	GLN	-	expression tag	UNP P02749
A	-8	VAL	-	expression tag	UNP P02749
A	-7	ASP	-	expression tag	UNP P02749
A	-6	PRO	-	expression tag	UNP P02749
A	-5	ARG	-	expression tag	UNP P02749
A	-4	LEU	-	expression tag	UNP P02749
A	-3	ILE	-	expression tag	UNP P02749
A	-2	ASP	-	expression tag	UNP P02749
A	-1	GLY	-	expression tag	UNP P02749
A	0	LYS	-	expression tag	UNP P02749

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	3	39	22	2	15	0	0	0
2	C	3	39	22	2	15	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

- Molecule 4 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



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

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

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	15	Total	O	0	0
			15	15		

MolProbity and EDS failed to run properly - this section is therefore empty.

### 3 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	160.25Å 171.16Å 113.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	116.98 – 2.99	Depositor
% Data completeness (in resolution range)	98.5 (116.98-2.99)	Depositor
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.58 (at 3.00Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.223 , 0.246	Depositor
Wilson B-factor (Å <sup>2</sup> )	64.2	Xtriage
Anisotropy	0.046	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2768	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.75% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical 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.

## 4 Model quality [i](#)

### 4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.3 Torsion angles [i](#)

#### 4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 4.5 Carbohydrates [i](#)

6 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	B	1	2,1	14,14,15	0.56	0	17,19,21	1.70	3 (17%)
2	NAG	B	2	2	14,14,15	1.11	1 (7%)	17,19,21	1.95	4 (23%)
2	BMA	B	3	2	11,11,12	1.06	2 (18%)	15,15,17	2.19	5 (33%)
2	NAG	C	1	2,1	14,14,15	0.69	0	17,19,21	0.94	1 (5%)
2	NAG	C	2	2	14,14,15	0.81	0	17,19,21	0.79	0
2	BMA	C	3	2	11,11,12	1.33	2 (18%)	15,15,17	0.58	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	B	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	1/6/23/26	0/1/1/1
2	BMA	B	3	2	-	2/2/19/22	0/1/1/1
2	NAG	C	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	BMA	C	3	2	-	2/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	NAG	C1-C2	2.53	1.56	1.52
2	C	3	BMA	C1-C2	2.45	1.57	1.52
2	B	3	BMA	C2-C3	2.25	1.55	1.52
2	B	3	BMA	C1-C2	2.21	1.57	1.52
2	C	3	BMA	C2-C3	2.02	1.55	1.52

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3	BMA	C1-C2-C3	6.56	117.73	109.67
2	B	2	NAG	O5-C5-C6	3.93	113.36	107.20
2	B	1	NAG	O5-C5-C6	3.66	112.94	107.20
2	B	2	NAG	C2-N2-C7	3.55	127.95	122.90
2	B	1	NAG	C1-O5-C5	3.45	116.86	112.19

There are no chirality outliers.

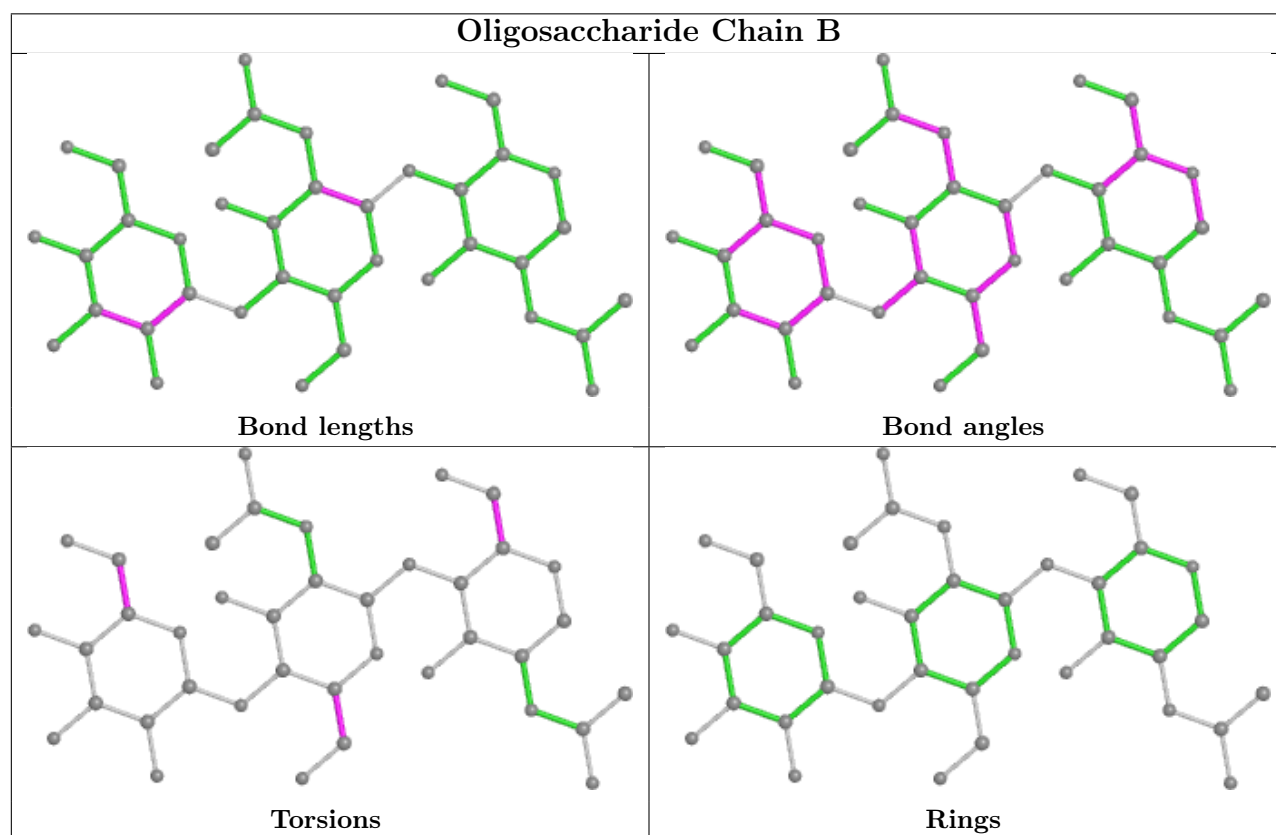
5 of 9 torsion outliers are listed below:

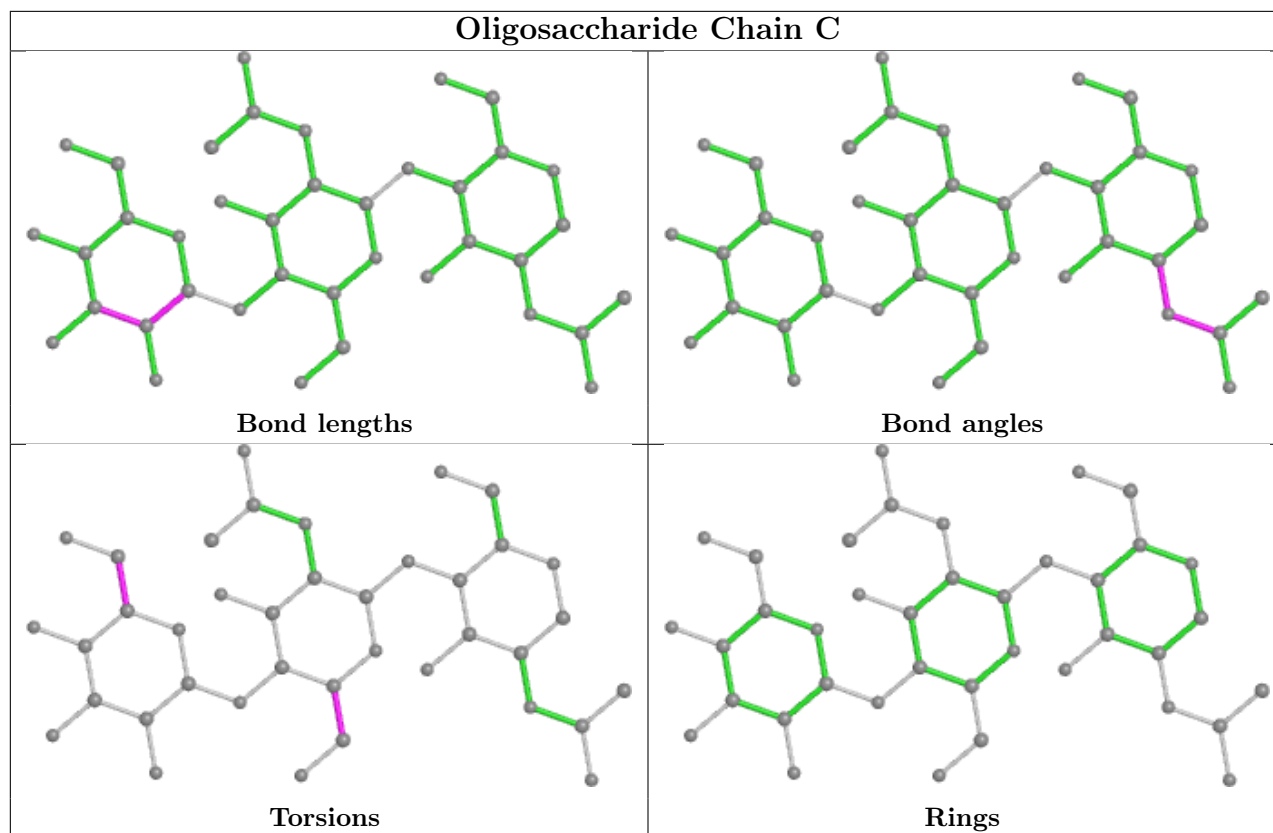
Mol	Chain	Res	Type	Atoms
2	B	3	BMA	O5-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
2	C	3	BMA	O5-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
2	C	3	BMA	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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





## 4.6 Ligand geometry [i](#)

28 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	SO4	A	422	-	4,4,4	0.37	0	6,6,6	0.19	0
4	SO4	A	423	-	4,4,4	0.37	0	6,6,6	0.20	0
4	SO4	A	432	-	4,4,4	0.37	0	6,6,6	0.09	0
4	SO4	A	413	-	4,4,4	0.32	0	6,6,6	0.27	0
4	SO4	A	409	-	4,4,4	0.36	0	6,6,6	0.55	0
4	SO4	A	415	-	4,4,4	0.35	0	6,6,6	0.12	0
4	SO4	A	430	-	4,4,4	0.35	0	6,6,6	0.06	0
4	SO4	A	420	-	4,4,4	0.39	0	6,6,6	0.18	0
4	SO4	A	421	-	4,4,4	0.32	0	6,6,6	0.33	0
4	SO4	A	410	-	4,4,4	0.40	0	6,6,6	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	SO4	A	427	-	4,4,4	0.37	0	6,6,6	0.12	0
4	SO4	A	428	-	4,4,4	0.29	0	6,6,6	0.20	0
4	SO4	A	433	-	4,4,4	0.37	0	6,6,6	0.16	0
4	SO4	A	424	-	4,4,4	0.35	0	6,6,6	0.10	0
4	SO4	A	434	-	4,4,4	0.33	0	6,6,6	0.08	0
4	SO4	A	419	-	4,4,4	0.36	0	6,6,6	0.12	0
4	SO4	A	425	-	4,4,4	0.35	0	6,6,6	0.12	0
3	NAG	A	402	1	14,14,15	0.99	1 (7%)	17,19,21	2.01	4 (23%)
4	SO4	A	416	-	4,4,4	0.32	0	6,6,6	0.14	0
4	SO4	A	411	-	4,4,4	0.38	0	6,6,6	0.26	0
3	NAG	A	401	1	14,14,15	0.69	0	17,19,21	0.94	1 (5%)
4	SO4	A	412	-	4,4,4	0.36	0	6,6,6	0.29	0
4	SO4	A	417	-	4,4,4	0.36	0	6,6,6	0.20	0
4	SO4	A	426	-	4,4,4	0.35	0	6,6,6	0.10	0
4	SO4	A	414	-	4,4,4	0.34	0	6,6,6	0.07	0
4	SO4	A	418	-	4,4,4	0.39	0	6,6,6	0.20	0
4	SO4	A	431	-	4,4,4	0.36	0	6,6,6	0.13	0
4	SO4	A	429	-	4,4,4	0.33	0	6,6,6	0.07	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	A	402	1	-	2/6/23/26	0/1/1/1
3	NAG	A	401	1	-	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)
3	A	402	NAG	C1-C2	2.01	1.55	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	NAG	C1-O5-C5	5.22	119.27	112.19
3	A	402	NAG	O5-C5-C6	3.59	112.83	107.20
3	A	402	NAG	C1-C2-N2	3.38	116.27	110.49
3	A	401	NAG	C2-N2-C7	-3.01	118.62	122.90
3	A	402	NAG	C2-N2-C7	2.74	126.80	122.90

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	NAG	O5-C5-C6-O6
3	A	402	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

#### 4.7 Other polymers [i](#)

There are no such residues in this entry.

#### 4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 5 Fit of model and data

### 5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

### 5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

### 5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

### 5.4 Ligands

EDS failed to run properly - this section is therefore empty.

### 5.5 Other polymers

EDS failed to run properly - this section is therefore empty.