



# Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1J8R  
Title : BINARY COMPLEX OF THE PAPG RECEPTOR-BINDING DOMAIN BOUND TO GBO4 RECEPTOR  
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Deposited on : 2001-05-22  
Resolution : 1.80 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](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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
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) : 2.13.1

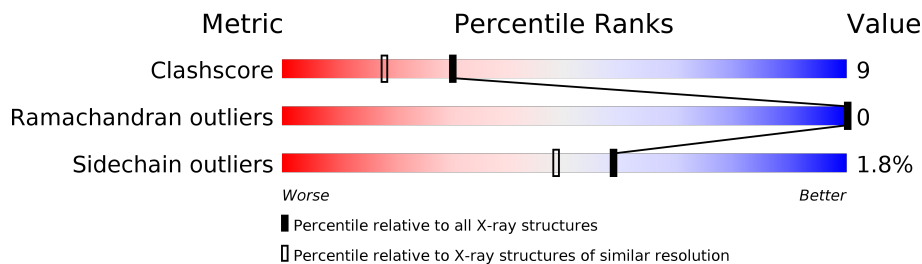
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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))
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	196	
2	B	4	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1835 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 PYELONEPHRITIC ADHESIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	196	1605	1047	264	289	2	3	0	0	0

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-galactopyranose-(1-3)-alpha-D-galactopyranose-(1-4)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	4	48	26	1	21	0	0	0

- Molecule 3 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	182	182	182	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.

Note EDS was not executed.

- Molecule 1: PYELONEPHRITIC ADHESIN

Chain A:  89% 10%



- Molecule 2: 2-acetamido-2-deoxy-beta-D-galactopyranose-(1-3)-alpha-D-galactopyranose-(1-4)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain B:  25% 25% 50%



## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.08Å 79.67Å 158.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.63 – 1.80	Depositor
% Data completeness (in resolution range)	91.0 (31.63-1.80)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.220 , 0.242	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	1835	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

## 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: BGC, GLA, GAL, NGA

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	0.51	0/1655	0.71	0/2243

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	1605	0	1534	29	0
2	B	48	0	41	2	0
3	A	182	0	0	2	0
All	All	1835	0	1575	30	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 9.

All (30) 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:21:VAL:CG2	1:A:196:GLY:HA3	2.06	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:ASN:HD21	1:A:46:GLY:H	1.33	0.77
1:A:21:VAL:HG23	1:A:196:GLY:HA3	1.69	0.72
1:A:21:VAL:HG23	1:A:195:GLY:O	1.99	0.62
1:A:81:GLU:OE1	1:A:137:LYS:HE3	2.01	0.61
1:A:146:LEU:HD11	1:A:195:GLY:HA2	1.82	0.60
1:A:110:ARG:HG2	1:A:110:ARG:HH11	1.67	0.59
1:A:74:ASN:H	1:A:74:ASN:HD22	1.50	0.58
1:A:146:LEU:HD23	3:A:364:HOH:O	2.05	0.57
1:A:146:LEU:N	1:A:146:LEU:HD22	2.19	0.57
1:A:74:ASN:N	1:A:74:ASN:HD22	2.03	0.57
1:A:21:VAL:HG23	1:A:196:GLY:CA	2.37	0.55
1:A:21:VAL:CG1	1:A:24:GLN:HG3	2.38	0.54
1:A:1:TRP:NE1	1:A:165:SER:HB3	2.26	0.50
1:A:3:ASN:ND2	1:A:46:GLY:H	2.07	0.49
1:A:21:VAL:HG13	1:A:24:GLN:HG3	1.95	0.48
1:A:4:ILE:HG12	1:A:171:PHE:CD2	2.51	0.46
1:A:1:TRP:CE2	1:A:165:SER:HB3	2.51	0.46
1:A:146:LEU:N	1:A:146:LEU:CD2	2.79	0.45
1:A:74:ASN:ND2	1:A:74:ASN:H	2.13	0.45
1:A:21:VAL:HG23	1:A:195:GLY:C	2.35	0.45
1:A:146:LEU:H	1:A:146:LEU:CD2	2.30	0.45
1:A:68:LYS:HG2	1:A:99:TYR:CE1	2.52	0.45
1:A:21:VAL:CG2	1:A:196:GLY:CA	2.88	0.43
1:A:3:ASN:HD21	1:A:46:GLY:N	2.08	0.43
1:A:107:TRP:CE3	2:B:2:GAL:H5	2.54	0.43
1:A:110:ARG:HG2	1:A:110:ARG:NH1	2.30	0.43
1:A:146:LEU:HD11	1:A:195:GLY:CA	2.47	0.42
3:A:406:HOH:O	2:B:4:NGA:H81	2.19	0.42
1:A:27:GLN:HA	1:A:137:LYS:HA	2.00	0.42

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	194/196 (99%)	191 (98%)	3 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	168/165 (102%)	165 (98%)	3 (2%)	59	48

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	ASN
1	A	113	ASP
1	A	180	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	3	ASN
1	A	73	GLN
1	A	74	ASN
1	A	92	ASN
1	A	96	ASN
1	A	119	GLN
1	A	176	ASN
1	A	185	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](#)

4 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	BGC	B	1	2	12,12,12	0.78	0	17,17,17	0.63	0
2	GAL	B	2	2	11,11,12	1.43	2 (18%)	15,15,17	4.02	3 (20%)
2	GLA	B	3	2	11,11,12	1.89	3 (27%)	15,15,17	1.53	2 (13%)
2	NGA	B	4	2	14,14,15	1.47	2 (14%)	17,19,21	1.42	3 (17%)

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	BGC	B	1	2	-	0/2/22/22	0/1/1/1
2	GAL	B	2	2	-	1/2/19/22	0/1/1/1
2	GLA	B	3	2	-	0/2/19/22	0/1/1/1
2	NGA	B	4	2	-	2/6/23/26	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3	GLA	O5-C5	4.33	1.52	1.43
2	B	4	NGA	C4-C5	3.89	1.61	1.53
2	B	2	GAL	C4-C5	3.61	1.60	1.53
2	B	3	GLA	C4-C3	2.65	1.59	1.52
2	B	2	GAL	O5-C5	2.53	1.48	1.43
2	B	4	NGA	C1-C2	-2.45	1.48	1.52
2	B	3	GLA	O2-C2	-2.01	1.39	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	GAL	O4-C4-C3	11.90	137.85	110.35
2	B	2	GAL	O4-C4-C5	-9.16	86.55	109.30
2	B	3	GLA	C1-O5-C5	5.01	118.98	112.19
2	B	4	NGA	C6-C5-C4	2.74	119.42	113.00
2	B	2	GAL	C6-C5-C4	2.66	119.24	113.00
2	B	4	NGA	C8-C7-N2	2.16	119.75	116.10
2	B	3	GLA	O5-C5-C6	2.05	110.42	107.20
2	B	4	NGA	O4-C4-C5	2.05	114.38	109.30

There are no chirality outliers.

All (3) torsion outliers are listed below:

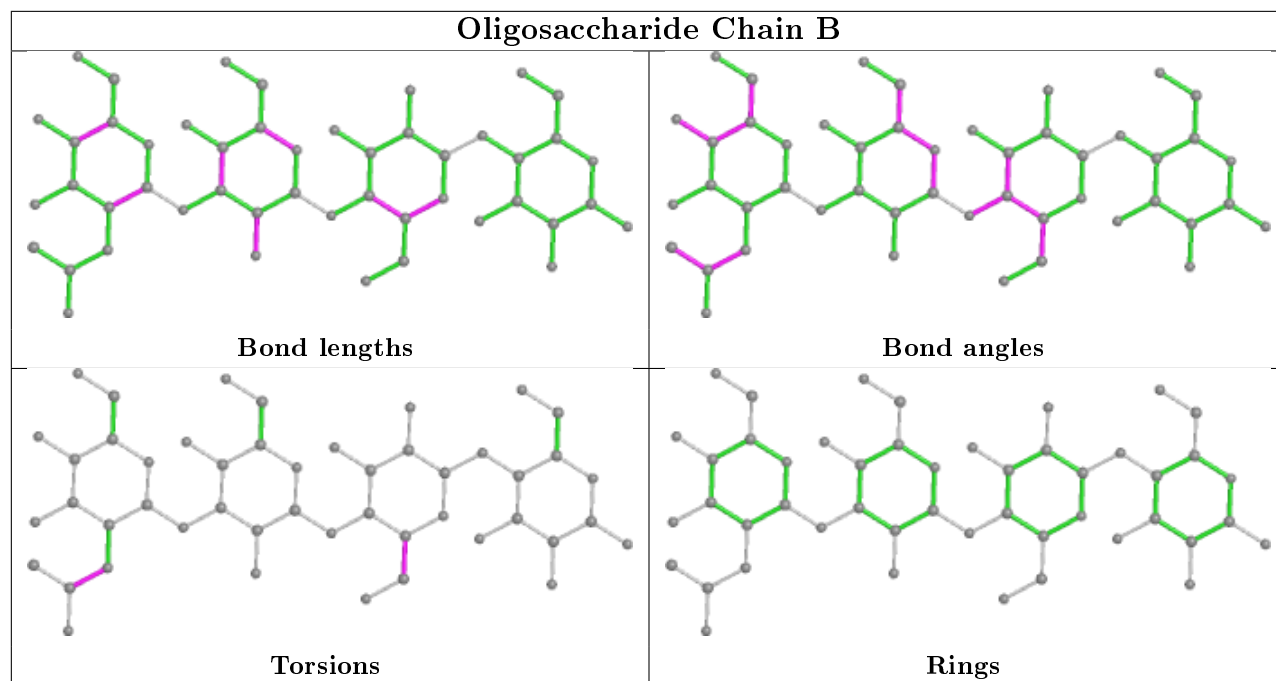
Mol	Chain	Res	Type	Atoms
2	B	4	NGA	C8-C7-N2-C2
2	B	4	NGA	O7-C7-N2-C2
2	B	2	GAL	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	4	NGA	1	0
2	B	2	GAL	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](#)

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.