



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 04:36 am GMT

PDB ID : 2G9R
Title : The crystal structure of glycogen phosphorylase b in complex with (3R,4R,5R)-5-hydroxymethyl-1-(3-phenylpropyl)-piperidine-3,4-diol
Authors : Oikonomakos, N.G.; Tiraidis, C.; Leonidas, D.D.; Zographos, S.E.
Deposited on : 2006-03-07
Resolution : 2.07 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

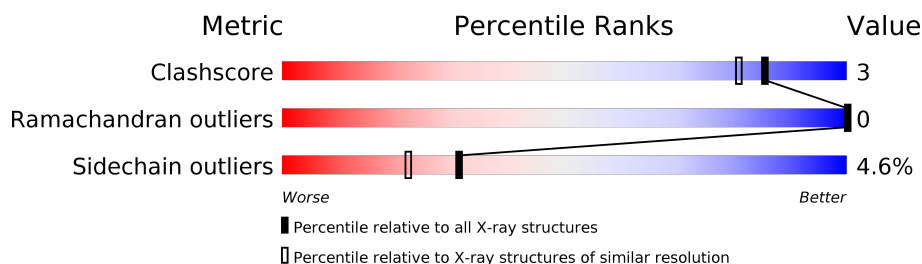
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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	112137	2143 (2.08-2.04)
Ramachandran outliers	110173	2126 (2.08-2.04)
Sidechain outliers	110143	2126 (2.08-2.04)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	842	 87% 8% . .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6894 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.

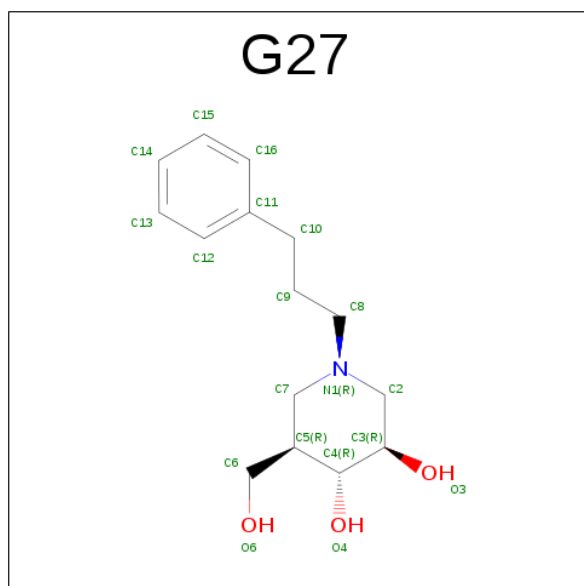
- Molecule 1 is a protein called Glycogen phosphorylase, muscle form.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	810	6604	4209	1161	1204	1	29	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	680	LLP	LYS	MODIFIED RESIDUE	UNP P00489

- Molecule 2 is (3R,4R,5R)-5-(HYDROXYMETHYL)-1-(3-PHENYLPROPYL)PIPERIDINE-3,4-DIOL (three-letter code: G27) (formula: C₁₅H₂₃NO₃).



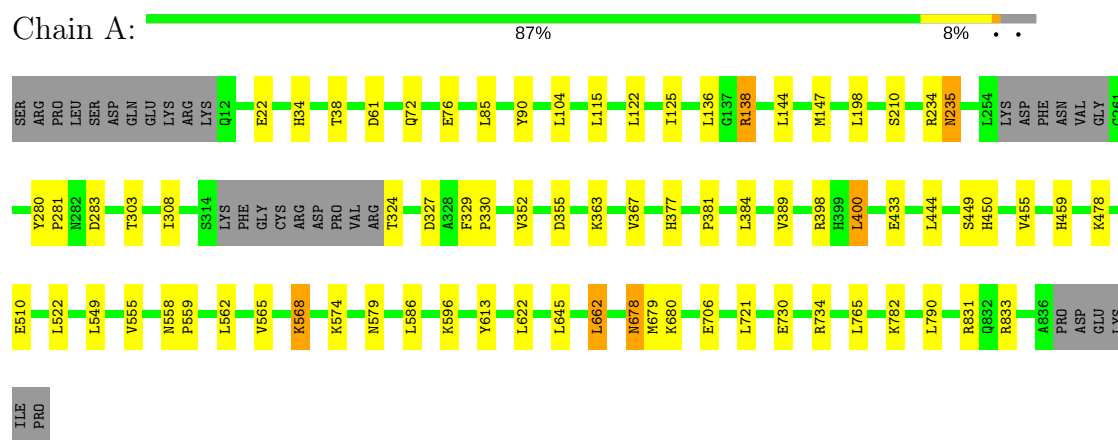
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	19	15	1	3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	271	Total 271	O 271	0	0

Note EDS was not executed.

- Molecule 1: Glycogen phosphorylase, muscle form



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	128.36 Å 128.36 Å 116.26 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	90.91 – 2.07	Depositor
% Data completeness (in resolution range)	99.2 (90.91-2.07)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.188 , 0.220	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6894	wwPDB-VP
Average B, all atoms (Å ²)	34.0	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: G27, LLP

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	0.37	0/6726	0.53	0/9102

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	6604	0	6539	34	0
2	A	19	0	23	1	0
3	A	271	0	0	2	0
All	All	6894	0	6562	34	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 3.

All (34) 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:455:VAL:H	1:A:459:HIS:HD2	1.33	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:ARG:O	1:A:138:ARG:HD3	1.94	0.68
1:A:730:GLU:O	1:A:734:ARG:HG3	1.94	0.68
1:A:355:ASP:OD1	1:A:398:ARG:HD3	1.92	0.67
1:A:568:LYS:HE2	3:A:1029:HOH:O	1.97	0.63
1:A:568:LYS:HE3	1:A:574:LYS:HZ2	1.64	0.63
1:A:34:HIS:HE1	1:A:61:ASP:OD1	1.86	0.58
1:A:678:ASN:HD22	1:A:679:MET:H	1.50	0.57
1:A:363:LYS:HE3	1:A:367:VAL:HG23	1.89	0.54
1:A:283:ASP:O	2:A:998:G27:H12	2.07	0.53
1:A:450:HIS:HE1	3:A:1126:HOH:O	1.92	0.52
1:A:72:GLN:O	1:A:76:GLU:HG2	2.09	0.52
1:A:34:HIS:HD2	1:A:38:THR:OG1	1.94	0.51
1:A:308:ILE:HD13	1:A:352:VAL:HG11	1.92	0.50
1:A:678:ASN:N	1:A:678:ASN:HD22	2.08	0.50
1:A:562:LEU:HD21	1:A:662:LEU:HB2	1.93	0.50
1:A:329:PHE:HB3	1:A:330:PRO:HD3	1.96	0.48
1:A:449:SER:O	1:A:478:LYS:HE2	2.14	0.48
1:A:680:LLP:NZ	1:A:680:LLP:O3	2.47	0.46
1:A:144:LEU:HD23	1:A:147:MET:CE	2.45	0.45
1:A:122:LEU:HA	1:A:125:ILE:HD12	1.99	0.45
1:A:136:LEU:HD13	1:A:377:HIS:CE1	2.52	0.44
1:A:235:ASN:H	1:A:235:ASN:HD22	1.64	0.44
1:A:549:LEU:HB3	1:A:555:VAL:HG23	2.00	0.44
1:A:568:LYS:HG3	1:A:574:LYS:HD3	2.01	0.43
1:A:678:ASN:ND2	1:A:679:MET:H	2.16	0.42
1:A:327:ASP:OD2	1:A:363:LYS:HE2	2.20	0.41
1:A:389:VAL:HG13	1:A:400:LEU:HD11	2.01	0.41
1:A:678:ASN:HD22	1:A:679:MET:N	2.18	0.41
1:A:280:TYR:HA	1:A:281:PRO:HD3	1.88	0.41
1:A:558:ASN:HA	1:A:559:PRO:HD3	1.89	0.40
1:A:678:ASN:N	1:A:678:ASN:ND2	2.68	0.40
1:A:85:LEU:HD11	1:A:303:THR:HG21	2.02	0.40
1:A:381:PRO:HA	1:A:384:LEU:HG	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	803/842 (95%)	780 (97%)	23 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	700/730 (96%)	668 (95%)	32 (5%)	31	22

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	GLU
1	A	90	TYR
1	A	104	LEU
1	A	115	LEU
1	A	138	ARG
1	A	198	LEU
1	A	210	SER
1	A	234	ARG
1	A	235	ASN
1	A	324	THR
1	A	400	LEU
1	A	433	GLU
1	A	444	LEU

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Mol	Chain	Res	Type
1	A	510	GLU
1	A	522	LEU
1	A	565	VAL
1	A	568	LYS
1	A	579	ASN
1	A	586	LEU
1	A	596	LYS
1	A	613	TYR
1	A	622	LEU
1	A	645	LEU
1	A	662	LEU
1	A	678	ASN
1	A	706	GLU
1	A	721	LEU
1	A	765	LEU
1	A	782	LYS
1	A	790	LEU
1	A	831	ARG
1	A	833	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	HIS
1	A	235	ASN
1	A	253	ASN
1	A	412	ASN
1	A	450	HIS
1	A	459	HIS
1	A	481	ASN
1	A	484	ASN
1	A	539	GLN
1	A	566	GLN
1	A	579	ASN
1	A	678	ASN
1	A	767	HIS
1	A	768	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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$
1	LLP	A	680	1	24,24,25	1.73	5 (20%)	28,32,34	1.32	4 (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
1	LLP	A	680	1	-	0/15/17/19	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	680	LLP	O3-C3	-5.42	1.24	1.37
1	A	680	LLP	C4'-NZ	2.17	1.33	1.27
1	A	680	LLP	C2-N1	2.28	1.38	1.33
1	A	680	LLP	C4-C4'	2.72	1.51	1.46
1	A	680	LLP	CA-C	3.10	1.54	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	680	LLP	CE-NZ-C4'	-2.90	110.61	119.03
1	A	680	LLP	C4-C4'-NZ	-2.39	113.07	124.66
1	A	680	LLP	C5-C6-N1	-2.37	119.86	123.87
1	A	680	LLP	OP4-C5'-C5	2.13	113.59	109.32

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	680	LLP	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	G27	A	998	-	20,20,20	0.97	0	23,26,26	0.73	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	G27	A	998	-	-	0/8/24/24	0/2/2/2

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	998	G27	1	0

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.