



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 06:46 PM UTC

PDB ID : 2G9V / pdb_00002g9v
Title : The crystal structure of glycogen phosphorylase in complex with (3R,4R,5R)-5-hydroxymethylpiperidine-3,4-diol and phosphate
Authors : Oikonomakos, N.G.; Tiraidis, C.; Leonidas, D.D.; Zographos, S.E.
Deposited on : 2006-03-07
Resolution : 2.15 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 ⓘ 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 Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

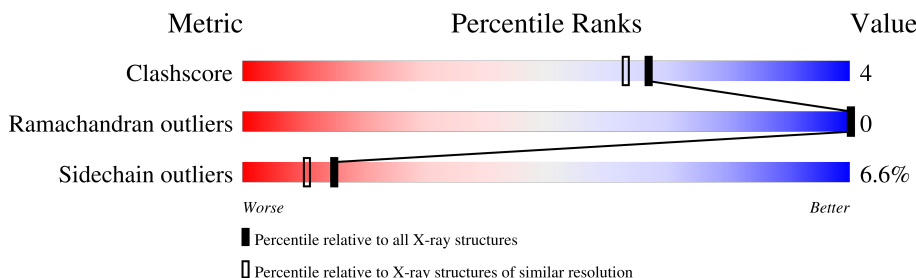
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	842	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6823 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
1	A	807	Total	C	N	O	P	S	0	0	0
			6579	4196	1156	1197	1	29			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	680	LLP	LYS	modified residue	UNP P00489

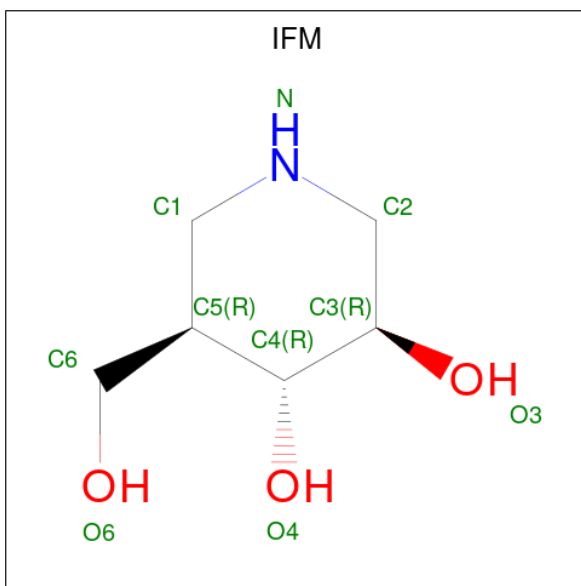
- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

- Molecule 3 is 5-HYDROXYMETHYL-3,4-DIHYDROXYPIPERIDINE (CCD ID: IFM)

(formula: $C_6H_{13}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	6	1	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	224	Total	O	0	0
			224	224		

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	128.64Å 128.64Å 116.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	90.91 – 2.15	Depositor
% Data completeness (in resolution range)	95.8 (90.91-2.15)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.193 , 0.235	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6823	wwPDB-VP
Average B, all atoms (Å ²)	40.0	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: LLP, PO4, IFM

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	0/6700	0.83	1/9065 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	565	VAL	N-CA-C	5.22	115.64	108.12

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	6579	0	6520	49	0
2	A	10	0	0	1	0
3	A	10	0	13	0	0
4	A	224	0	0	4	0
All	All	6823	0	6533	49	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 4.

All (49) 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:93:ARG:NH2	1:A:126:GLU:O	2.18	0.77
1:A:235:ASN:HA	1:A:833:ARG:HG3	1.68	0.75
1:A:367:VAL:O	1:A:371:THR:HG23	1.87	0.75
1:A:138:ARG:O	1:A:138:ARG:HD3	1.92	0.70
1:A:455:VAL:H	1:A:459:HIS:HD2	1.39	0.68
1:A:601:ARG:HD2	4:A:1018:HOH:O	1.95	0.65
1:A:355:ASP:OD1	1:A:398:ARG:HD3	1.98	0.63
1:A:311:PHE:O	1:A:314:SER:HB3	2.02	0.60
1:A:34:HIS:HE1	1:A:61:ASP:OD1	1.84	0.60
1:A:678:ASN:HD22	1:A:679:MET:H	1.50	0.58
1:A:329:PHE:HD1	1:A:371:THR:HG21	1.72	0.54
1:A:493:VAL:CG2	1:A:512:ILE:HD12	2.37	0.54
1:A:449:SER:O	1:A:478:LYS:HE2	2.09	0.53
1:A:14:SER:HB3	1:A:16:ARG:HG3	1.90	0.52
1:A:716:GLU:H	1:A:716:GLU:CD	2.19	0.51
1:A:575:ARG:HD3	1:A:666:ILE:O	2.10	0.50
1:A:678:ASN:HD22	1:A:678:ASN:N	2.08	0.50
1:A:81:ARG:HG2	1:A:155:TYR:HE2	1.77	0.50
1:A:111:ALA:O	1:A:115:LEU:HD22	2.12	0.50
1:A:545:PHE:CZ	1:A:656:VAL:HG22	2.46	0.49
1:A:329:PHE:CD1	1:A:371:THR:HG21	2.48	0.49
1:A:545:PHE:CE1	1:A:656:VAL:HG22	2.48	0.48
1:A:325:ASN:ND2	1:A:327:ASP:OD1	2.47	0.47
1:A:730:GLU:O	1:A:734:ARG:CG	2.64	0.46
1:A:34:HIS:HD2	1:A:38:THR:OG1	1.99	0.46
1:A:569:ARG:NH2	2:A:997:PO4:O3	2.48	0.46
1:A:235:ASN:H	1:A:235:ASN:HD22	1.64	0.46
1:A:562:LEU:HD21	1:A:662:LEU:HB2	1.97	0.46
1:A:546:ALA:HA	1:A:557:ILE:HD11	1.96	0.46
1:A:329:PHE:HB3	1:A:330:PRO:HD3	1.99	0.45
1:A:450:HIS:HD2	4:A:1135:HOH:O	1.99	0.45
1:A:493:VAL:HG21	1:A:512:ILE:HD12	1.98	0.45
1:A:680:LLP:O3	1:A:680:LLP:NZ	2.48	0.45
1:A:568:LYS:HG3	1:A:574:LYS:HD2	1.97	0.45
1:A:138:ARG:HD3	1:A:138:ARG:C	2.42	0.45
1:A:43:ARG:HA	1:A:43:ARG:HD2	1.87	0.44
1:A:739:ARG:O	1:A:743:GLU:HG3	2.18	0.44
1:A:732:TYR:CZ	1:A:739:ARG:HG3	2.53	0.44
1:A:456:ALA:C	1:A:481:ASN:HD21	2.26	0.43
1:A:678:ASN:ND2	1:A:679:MET:H	2.15	0.43
1:A:730:GLU:O	1:A:734:ARG:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:SER:C	1:A:16:ARG:H	2.26	0.43
1:A:379:VAL:HG22	4:A:1060:HOH:O	2.18	0.43
1:A:450:HIS:HE1	4:A:1087:HOH:O	2.02	0.42
1:A:493:VAL:HG22	1:A:512:ILE:HD12	2.01	0.42
1:A:726:TYR:OH	1:A:774:PHE:HB2	2.20	0.41
1:A:85:LEU:HD11	1:A:303:THR:HG21	2.03	0.41
1:A:232:GLY:HA3	1:A:235:ASN:HD21	1.87	0.40
1:A:558:ASN:HA	1:A:559:PRO:HD3	1.87	0.40

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	798/842 (95%)	771 (97%)	27 (3%)	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	697/730 (96%)	651 (93%)	46 (7%)	15	10

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	ARG
1	A	18	LEU
1	A	22	GLU
1	A	39	LEU
1	A	102	LEU
1	A	104	LEU
1	A	115	LEU
1	A	122	LEU
1	A	138	ARG
1	A	198	LEU
1	A	234	ARG
1	A	235	ASN
1	A	271	LEU
1	A	282	ASN
1	A	292	ARG
1	A	306	ASP
1	A	325	ASN
1	A	363	LYS
1	A	371	THR
1	A	384	LEU
1	A	391	LEU
1	A	398	ARG
1	A	400	LEU
1	A	430	LEU
1	A	444	LEU
1	A	467	ILE
1	A	522	LEU
1	A	536	LYS
1	A	544	LYS
1	A	549	LEU
1	A	565	VAL
1	A	568	LYS
1	A	586	LEU
1	A	596	LYS
1	A	622	LEU
1	A	643	ILE
1	A	645	LEU
1	A	662	LEU
1	A	678	ASN
1	A	706	GLU
1	A	716	GLU
1	A	721	LEU
1	A	734	ARG

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Mol	Chain	Res	Type
1	A	765	LEU
1	A	790	LEU
1	A	803	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	HIS
1	A	72	GLN
1	A	211	GLN
1	A	235	ASN
1	A	253	ASN
1	A	270	ASN
1	A	390	HIS
1	A	412	ASN
1	A	450	HIS
1	A	459	HIS
1	A	481	ASN
1	A	558	ASN
1	A	566	GLN
1	A	579	ASN
1	A	678	ASN
1	A	727	ASN
1	A	767	HIS
1	A	832	GLN

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	23,24,25	1.61	4 (17%)	25,32,34	1.31	3 (12%)

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	-	2/16/17/19	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	680	LLP	O3-C3	-5.46	1.24	1.36
1	A	680	LLP	C4-C4'	2.43	1.51	1.46
1	A	680	LLP	C2-N1	2.22	1.37	1.33
1	A	680	LLP	C4'-NZ	2.07	1.34	1.27

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	680	LLP	CE-NZ-C4'	-2.81	109.72	118.72
1	A	680	LLP	C5-C6-N1	-2.60	119.61	123.83
1	A	680	LLP	C4-C4'-NZ	-2.32	113.34	124.04

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	680	LLP	C6-C5-C5'-OP4
1	A	680	LLP	C4-C5-C5'-OP4

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
2	PO4	A	996	-	4,4,4	0.89	0	6,6,6	0.61	0
2	PO4	A	997	-	4,4,4	1.22	0	6,6,6	0.70	0
3	IFM	A	998	-	10,10,10	1.52	1 (10%)	9,13,13	0.68	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	IFM	A	998	-	-	0/2/16/16	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	998	IFM	C2-C3	3.64	1.55	1.52

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	997	PO4	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.