

# wwPDB X-ray Structure Validation Summary Report (i)

#### Feb 5, 2024 – 12:16 PM EST

PDB ID : 1TPH

Title : 1.8 ANGSTROMS CRYSTAL STRUCTURE OF WILD TYPE CHICKEN

TRIOSEPHOSPHATE ISOMERASE-PHOSPHOGLYCOLOHYDROXAMA

TE COMPLEX

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Deposited on : 1993-12-22

Resolution : 1.80 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 (i) 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 (i)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (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)

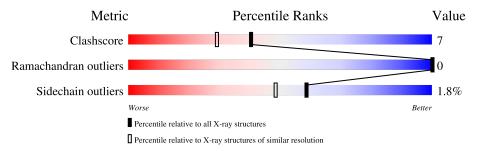
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance (i)

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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
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 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	1	247	81%	17%	
1	2	247	78%	19%	<del></del>

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
2	PGH	1	250	-	X	-	-



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3981 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.

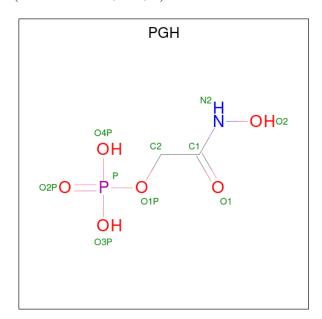
• Molecule 1 is a protein called TRIOSEPHOSPHATE ISOMERASE.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	1	245	Total	С	- 1	0	S	0	0	0
			1856	1176	325	349	6	Ů	Ŭ	
1	9	245	Total	С	N	Ο	S	0	0	0
1	1 2	240	1856	1176	325	349	6		0	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	194	THR	SER	conflict	UNP P00940
2	194	THR	SER	conflict	UNP P00940

• Molecule 2 is PHOSPHOGLYCOLOHYDROXAMIC ACID (three-letter code: PGH) (formula: C<sub>2</sub>H<sub>6</sub>NO<sub>6</sub>P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	1	1	Total 10	C 2	N 1	O 6	P 1	0	0

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Mo	ol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2		2	1	Total	С	N	О	Р	0	0
		4	1	10	2	1	6	1		U

#### • Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	1	119	Total O 119 119	0	0
3	2	130	Total O 130 130	0	0

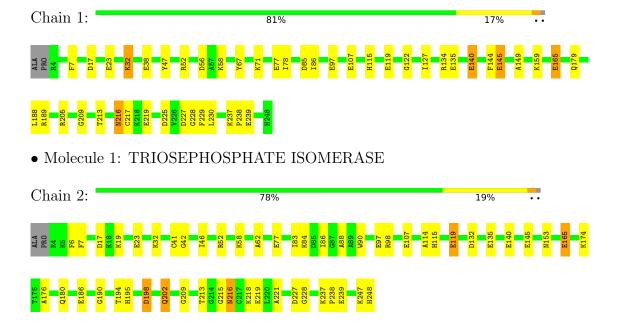


# 3 Residue-property plots (i)

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: TRIOSEPHOSPHATE ISOMERASE





# 4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	136.40Å 74.00Å 57.20Å	Donositon	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor	
Resolution (Å)	6.00 - 1.80	Depositor	
% Data completeness	(Not available) (6.00-1.80)	Depositor	
(in resolution range)	(1101 available) (0.00 1.00)		
$R_{merge}$	(Not available)	Depositor	
$R_{sym}$	(Not available)	Depositor	
Refinement program	PROLSQ	Depositor	
$R, R_{free}$	0.185 , (Not available)	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	3981	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	15.0	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: PGH

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	Bo	nd lengths	Bond angles		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	1	1.13	$12/1891 \ (0.6\%)$	1.51	15/2552~(0.6%)	
1	2	1.13	13/1891 (0.7%)	1.50	$12/2552 \ (0.5\%)$	
All	All	1.13	$25/3782 \ (0.7\%)$	1.51	$27/5104 \ (0.5\%)$	

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(Å)
1	1	97	GLU	CD-OE2	8.85	1.35	1.25
1	1	145	GLU	CD-OE2	8.10	1.34	1.25
1	2	23	GLU	CD-OE2	7.94	1.34	1.25
1	1	239	GLU	CD-OE1	7.05	1.33	1.25
1	2	216	ASN	CA-CB	6.91	1.71	1.53

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}(^{o})$
1	1	205	ARG	NE-CZ-NH1	13.75	127.17	120.30
1	2	216	ASN	CB-CA-C	-8.17	94.05	110.40
1	2	215	GLY	C-N-CA	8.14	142.06	121.70
1	1	227	ASP	CB-CG-OD2	7.97	125.48	118.30
1	2	41	CYS	O-C-N	7.21	135.46	123.20

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	$\mathbf{H}(\mathbf{model})$	H(added)	Clashes	Symm-Clashes
1	1	1856	0	1863	26	0
1	2	1856	0	1862	30	0
2	1	10	0	4	0	0
2	2	10	0	4	1	0
3	1	119	0	0	2	0
3	2	130	0	0	4	0
All	All	3981	0	3733	54	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 54 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:1:32:LYS:CE	1:1:32:LYS:H	1.91	0.84
1:1:32:LYS:H	1:1:32:LYS:HE3	1.45	0.82
1:1:145:GLU:HG3	3:1:481:HOH:O	1.84	0.77
1:2:176:ALA:HB1	1:2:180:GLN:HG3	1.72	0.72
1:1:216:ASN:C	1:1:216:ASN:HD22	1.94	0.71

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	Perce	$\mathbf{ntiles}$
1	1	243/247~(98%)	236 (97%)	7 (3%)	0	100	100
1	2	243/247~(98%)	235 (97%)	8 (3%)	0	100	100
All	All	486/494 (98%)	471 (97%)	15 (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	1	191/192 (100%)	187 (98%)	4 (2%)	53 42		
1	2	191/192 (100%)	188 (98%)	3 (2%)	62 54		
All	All	382/384 (100%)	375 (98%)	7 (2%)	59 48		

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	216	ASN
1	2	58	LYS
1	2	202	GLN
1	2	86	ILE
1	1	86	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	2	111	GLN
1	2	115	HIS
1	2	248	HIS
1	2	179	GLN
1	1	202	GLN

#### 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)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

2 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	Trme	Chain	Chain	Dec	T 2 1-	Bond lengths			В	ond ang	cles
IVIOI	Type		Res	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
2	PGH	2	250	-	9,9,9	3.03	4 (44%)	10,12,12	1.42	2 (20%)	
2	PGH	1	250	-	9,9,9	2.97	5 (55%)	10,12,12	2.84	5 (50%)	

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.

N	Aol	$\mathbf{Type}$	Chain	Res	Link	Chirals	Torsions	Rings
	2	PGH	2	250	-	-	1/8/8/8	-
	2	PGH	1	250	-	-	2/8/8/8	-

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\text{\AA})$
2	2	250	PGH	P-O4P	6.16	1.78	1.54
2	1	250	PGH	P-O1P	4.84	1.75	1.60
2	1	250	PGH	P-O2P	4.07	1.63	1.50
2	2	250	PGH	P-O1P	3.93	1.72	1.60
2	1	250	PGH	P-O3P	3.91	1.69	1.54

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
2	1	250	PGH	O1-C1-N2	6.36	131.08	123.27

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Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	1	250	PGH	O4P-P-O1P	3.49	116.03	106.73
2	1	250	PGH	O3P-P-O2P	-2.77	99.83	110.68
2	2	250	PGH	O1-C1-N2	2.60	126.47	123.27
2	1	250	PGH	C2-C1-N2	-2.45	112.12	116.37

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	1	250	PGH	C2-O1P-P-O3P
2	2	250	PGH	O1-C1-C2-O1P
2	1	250	PGH	O1-C1-C2-O1P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	250	PGH	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.

