



# wwPDB X-ray Structure Validation Summary Report i

Oct 3, 2023 – 05:22 AM EDT

PDB ID : 6PD3  
Title : Crystal Structure of a H5N1 influenza virus hemagglutinin at pH 5.5  
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Deposited on : 2019-06-18  
Resolution : 2.30 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 i 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](#) i) were used in the production of this report:

MolProbit	: <b>FAILED</b>
Mogul	: 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	: 1.13
EDS	: <b>FAILED</b>
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 2.30 Å.

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

MolProbit 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 4193 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.

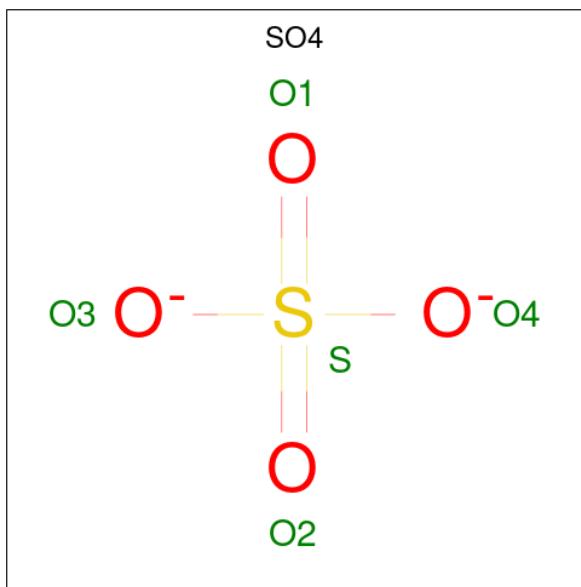
- Molecule 1 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	A	491	Total	C 3937	N 2471	O 681	S 761	24	0	1	0

There are 21 discrepancies between the modelled and reference sequences:

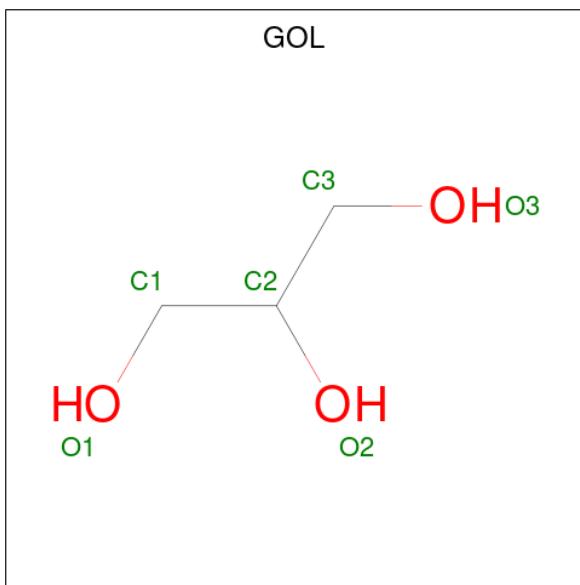
Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	LEU	-	expression tag	UNP Q1KHJ8
A	-3	LEU	-	expression tag	UNP Q1KHJ8
A	-2	ALA	-	expression tag	UNP Q1KHJ8
A	-1	ALA	-	expression tag	UNP Q1KHJ8
A	0	ALA	-	expression tag	UNP Q1KHJ8
A	1	ALA	-	expression tag	UNP Q1KHJ8
A	2	HIS	-	expression tag	UNP Q1KHJ8
A	3	SER	-	expression tag	UNP Q1KHJ8
A	4	ALA	-	expression tag	UNP Q1KHJ8
A	5	PHE	-	expression tag	UNP Q1KHJ8
A	6	ALA	-	expression tag	UNP Q1KHJ8
A	7	ALA	-	expression tag	UNP Q1KHJ8
A	8	ASP	-	expression tag	UNP Q1KHJ8
A	9	PRO	-	expression tag	UNP Q1KHJ8
A	10	GLY	-	expression tag	UNP Q1KHJ8
A	1042	SER	-	expression tag	UNP Q1KHJ8
A	1043	ARG	-	expression tag	UNP Q1KHJ8
A	1044	LEU	-	expression tag	UNP Q1KHJ8
A	1045	VAL	-	expression tag	UNP Q1KHJ8
A	1046	PRO	-	expression tag	UNP Q1KHJ8
A	1047	ARG	-	expression tag	UNP Q1KHJ8

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



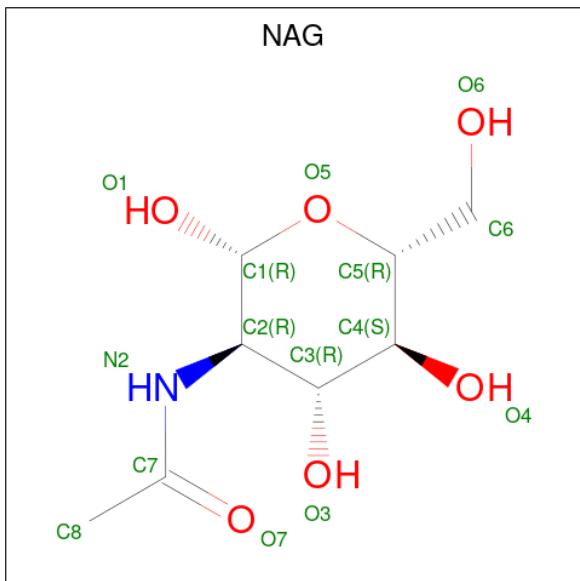
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $\text{C}_3\text{H}_8\text{O}_3$ ).



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

- Molecule 4 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
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	122	Total O 122 122	0	0

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

### 3 Data and refinement statistics i

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

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.38 Å    109.38 Å    421.04 Å 90.00°    90.00°    120.00°	Depositor
Resolution (Å)	29.79 – 2.30	Depositor
% Data completeness (in resolution range)	97.4 (29.79-2.30)	Depositor
R <sub>merge</sub>	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) >$ <sup>1</sup>	1.31 (at 2.31 Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R <sub>free</sub>	0.199 , 0.229	Depositor
Wilson B-factor (Å <sup>2</sup> )	56.8	Xtriage
Anisotropy	0.114	Xtriage
L-test for twinning <sup>2</sup>	$<  L  > = 0.48$ , $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4193	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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  $< |L| >$ ,  $< L^2 >$  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 [\(i\)](#)

There are no monosaccharides in this entry.

### 4.6 Ligand geometry [\(i\)](#)

19 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	SO4	A	1102	-	4,4,4	0.40	0	6,6,6	0.14	0
2	SO4	A	1111	-	4,4,4	0.37	0	6,6,6	0.08	0
2	SO4	A	1110	-	4,4,4	0.38	0	6,6,6	0.05	0
4	NAG	A	1119	1	14,14,15	0.74	1 (7%)	17,19,21	2.82	5 (29%)
2	SO4	A	1101	-	4,4,4	0.32	0	6,6,6	0.14	0
2	SO4	A	1108	-	4,4,4	0.39	0	6,6,6	0.05	0
2	SO4	A	1105	-	4,4,4	0.38	0	6,6,6	0.09	0
2	SO4	A	1106	-	4,4,4	0.33	0	6,6,6	0.09	0
3	GOL	A	1113	-	5,5,5	0.11	0	5,5,5	0.38	0
2	SO4	A	1103	-	4,4,4	0.37	0	6,6,6	0.11	0
4	NAG	A	1118	1	14,14,15	0.52	0	17,19,21	1.36	2 (11%)
3	GOL	A	1114	-	5,5,5	0.12	0	5,5,5	0.37	0
2	SO4	A	1107	-	4,4,4	0.37	0	6,6,6	0.10	0
2	SO4	A	1109	-	4,4,4	0.38	0	6,6,6	0.05	0
4	NAG	A	1116	1	14,14,15	0.66	0	17,19,21	2.26	5 (29%)
2	SO4	A	1112	-	4,4,4	0.37	0	6,6,6	0.06	0
3	GOL	A	1115	-	5,5,5	0.10	0	5,5,5	0.22	0
4	NAG	A	1117	1	14,14,15	0.35	0	17,19,21	1.04	2 (11%)
2	SO4	A	1104	-	4,4,4	0.38	0	6,6,6	0.09	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	GOL	A	1114	-	-	0/4/4/4	-
4	NAG	A	1119	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1116	1	-	2/6/23/26	0/1/1/1
3	GOL	A	1113	-	-	3/4/4/4	-
3	GOL	A	1115	-	-	2/4/4/4	-
4	NAG	A	1117	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1118	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)
4	A	1119	NAG	C1-C2	2.03	1.55	1.52

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1119	NAG	C1-O5-C5	6.55	121.07	112.19
4	A	1119	NAG	C1-C2-N2	6.43	121.47	110.49
4	A	1116	NAG	C1-O5-C5	5.68	119.88	112.19
4	A	1119	NAG	O5-C5-C6	4.62	114.45	107.20
4	A	1118	NAG	C1-O5-C5	3.67	117.16	112.19

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1113	GOL	O1-C1-C2-C3
3	A	1113	GOL	C1-C2-C3-O3
3	A	1115	GOL	O1-C1-C2-C3
3	A	1113	GOL	O1-C1-C2-O2
4	A	1116	NAG	C3-C2-N2-C7

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 [\(i\)](#)

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

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

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

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

### 5.3 Carbohydrates [\(i\)](#)

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

### 5.4 Ligands [\(i\)](#)

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

### 5.5 Other polymers [\(i\)](#)

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