Full wwPDB X-ray Structure Validation Report ⓘ

Oct 1, 2023 – 11:01 PM EDT

PDB ID	:	6NB2
Title	:	CRYSTAL STRUCTURE OF ENOLASE FROM LEGIONELLA PNEUMOPHILA BOUND TO 2-PHOSPHOGLYCERIC ACID AND MAGNESIUM
Authors	:	Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on	:	2018-12-06
Resolution	:	1.85 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	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
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 (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 Å.

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

MolProbity 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 7386 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.

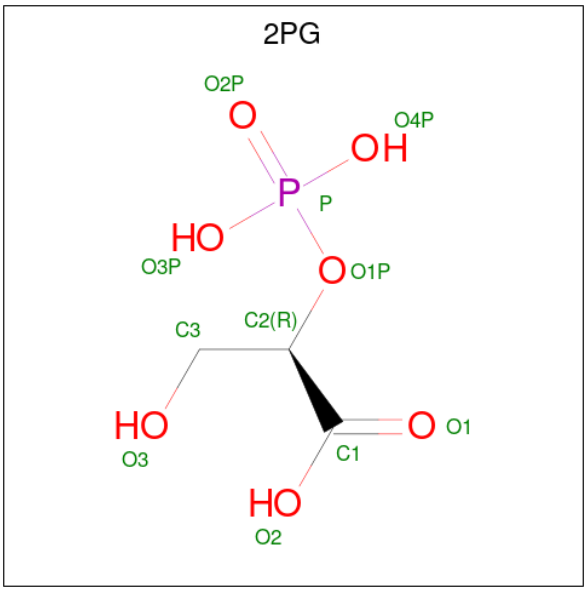
- Molecule 1 is a protein called Enolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	423	Total	C	N	O	S	0	12	0
			3294	2060	577	638	19			
1	B	424	Total	C	N	O	S	0	10	0
			3298	2059	581	639	19			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP Q5ZTX1
A	-6	ALA	-	expression tag	UNP Q5ZTX1
A	-5	HIS	-	expression tag	UNP Q5ZTX1
A	-4	HIS	-	expression tag	UNP Q5ZTX1
A	-3	HIS	-	expression tag	UNP Q5ZTX1
A	-2	HIS	-	expression tag	UNP Q5ZTX1
A	-1	HIS	-	expression tag	UNP Q5ZTX1
A	0	HIS	-	expression tag	UNP Q5ZTX1
B	-7	MET	-	initiating methionine	UNP Q5ZTX1
B	-6	ALA	-	expression tag	UNP Q5ZTX1
B	-5	HIS	-	expression tag	UNP Q5ZTX1
B	-4	HIS	-	expression tag	UNP Q5ZTX1
B	-3	HIS	-	expression tag	UNP Q5ZTX1
B	-2	HIS	-	expression tag	UNP Q5ZTX1
B	-1	HIS	-	expression tag	UNP Q5ZTX1
B	0	HIS	-	expression tag	UNP Q5ZTX1

- Molecule 2 is 2-PHOSPHOGLYCERIC ACID (three-letter code: 2PG) (formula: $C_3H_7O_7P$).

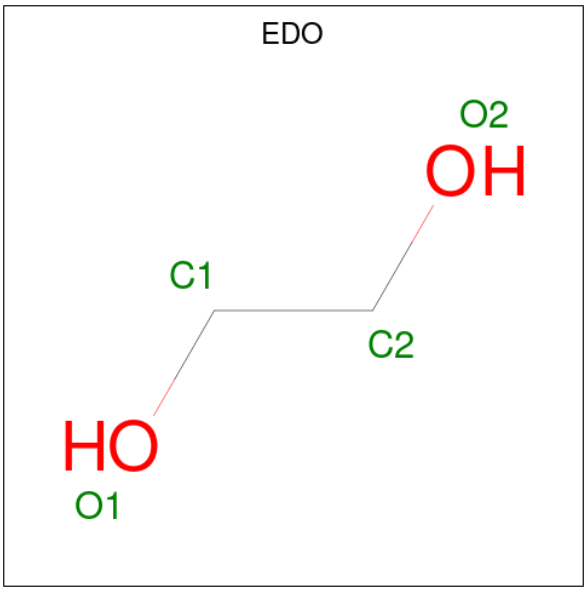


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O P 11 3 7 1	0	0
2	B	1	Total C O P 11 3 7 1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Mg 2 2	0	0
3	B	2	Total Mg 2 2	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	347	Total O 350 350	0	3
5	B	386	Total O 390 390	0	4

MolProbity 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	P 42 21 2	Depositor
Cell constants a, b, c, α, β, γ	116.45Å 116.45Å 142.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.12 – 1.85	Depositor
% Data completeness (in resolution range)	100.0 (45.12-1.85)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.56 (at 1.86Å)	Xtriage
Refinement program	PHENIX DEV_3366	Depositor
R, R_{free}	0.146 , 0.172	Depositor
Wilson B-factor (Å^2)	24.6	Xtriage
Anisotropy	0.425	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7386	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.85% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] 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

4.1 Standard geometry

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

4.2 Too-close contacts

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

4.3 Torsion angles

4.3.1 Protein backbone

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

4.3.2 Protein sidechains

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

4.3.3 RNA

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

4.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates

There are no monosaccharides in this entry.

4.6 Ligand geometry

Of 13 ligands modelled in this entry, 4 are monoatomic - leaving 9 for Mogul analysis.

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	2PG	B	502	3	9,10,10	1.38	2 (22%)	11,14,14	1.51	1 (9%)
4	EDO	B	501	-	3,3,3	0.50	0	2,2,2	0.28	0
4	EDO	A	507	-	3,3,3	0.49	0	2,2,2	0.42	0
4	EDO	B	506	-	3,3,3	0.47	0	2,2,2	0.39	0
4	EDO	A	506	-	3,3,3	0.65	0	2,2,2	0.07	0
4	EDO	A	504	-	3,3,3	0.44	0	2,2,2	0.41	0
4	EDO	A	505	-	3,3,3	0.54	0	2,2,2	0.22	0
2	2PG	A	501	3	9,10,10	1.52	2 (22%)	11,14,14	1.64	2 (18%)
4	EDO	B	505	-	3,3,3	0.49	0	2,2,2	0.27	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	2PG	B	502	3	-	0/11/11/11	-
4	EDO	B	501	-	-	0/1/1/1	-
4	EDO	A	507	-	-	1/1/1/1	-
4	EDO	B	506	-	-	0/1/1/1	-
4	EDO	A	506	-	-	1/1/1/1	-
4	EDO	A	504	-	-	0/1/1/1	-
4	EDO	A	505	-	-	0/1/1/1	-
2	2PG	A	501	3	-	2/11/11/11	-
4	EDO	B	505	-	-	0/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	2PG	P-O1P	3.11	1.65	1.59
2	B	502	2PG	C2-C1	2.43	1.54	1.52
2	A	501	2PG	C2-C1	2.38	1.54	1.52
2	B	502	2PG	P-O1P	2.08	1.63	1.59

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	502	2PG	P-O1P-C2	-3.85	114.21	123.04

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	501	2PG	P-O1P-C2	-3.68	114.60	123.04
2	A	501	2PG	O2-C1-C2	2.86	121.19	113.03

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	506	EDO	O1-C1-C2-O2
2	A	501	2PG	O1-C1-C2-C3
2	A	501	2PG	O2-C1-C2-C3
4	A	507	EDO	O1-C1-C2-O2

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

5.1 Protein, DNA and RNA chains

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

5.2 Non-standard residues in protein, DNA, RNA chains

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

5.3 Carbohydrates

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

5.4 Ligands

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

5.5 Other polymers

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