



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 10:59 PM UTC

PDB ID : 4ZA0 / pdb_00004za0
Title : Structure of Human Enolase 2 in complex with Phosphonoacetohydroxamate
Authors : Leonard, P.G.; Maxwell, D.; Czako, B.; Muller, F.L.
Deposited on : 2015-04-13
Resolution : 2.31 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) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

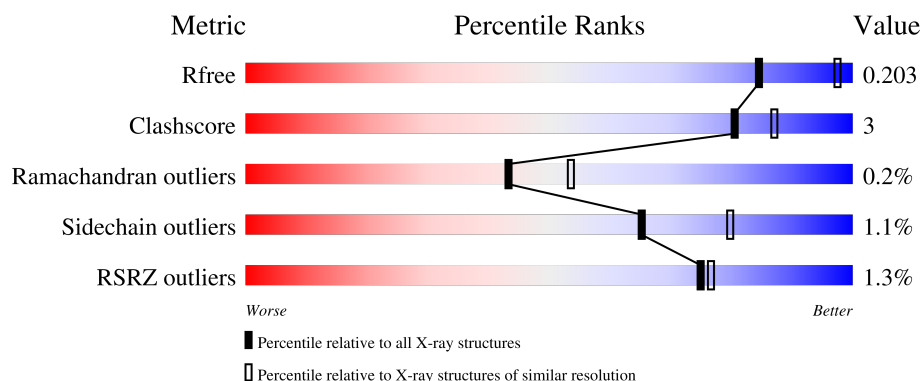
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

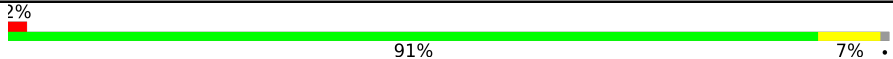
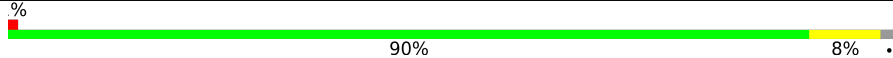
The reported resolution of this entry is 2.31 Å.

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))
R_{free}	180053	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
Ramachandran outliers	187476	8303 (2.34-2.30)
Sidechain outliers	187428	8303 (2.34-2.30)
RSRZ outliers	180081	7760 (2.34-2.30)

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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	440	
1	B	440	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7139 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 Gamma-enolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	434	Total	C	N	O	S	0	0	0
			3322	2089	569	650	14			
1	B	432	Total	C	N	O	S	0	0	0
			3307	2078	567	648	14			

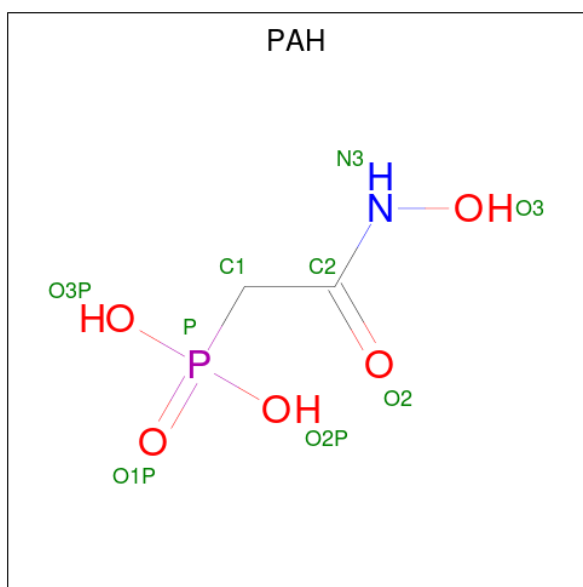
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	435	HIS	-	expression tag	UNP P09104
A	436	HIS	-	expression tag	UNP P09104
A	437	HIS	-	expression tag	UNP P09104
A	438	HIS	-	expression tag	UNP P09104
A	439	HIS	-	expression tag	UNP P09104
A	440	HIS	-	expression tag	UNP P09104
B	435	HIS	-	expression tag	UNP P09104
B	436	HIS	-	expression tag	UNP P09104
B	437	HIS	-	expression tag	UNP P09104
B	438	HIS	-	expression tag	UNP P09104
B	439	HIS	-	expression tag	UNP P09104
B	440	HIS	-	expression tag	UNP P09104

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 3 is PHOSPHONOACETOHYDROXAMIC ACID (CCD ID: PAH) (formula: C₂H₆NO₅P).

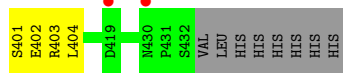


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			9	2	1	5	1		
3	B	1	Total	C	N	O	P	0	0
			9	2	1	5	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	229	Total	O	0	0
			229	229		
4	B	259	Total	O	0	0
			259	259		

- Molecule 1: Gamma-enolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.79Å 108.67Å 112.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.02 – 2.31 58.02 – 2.31	Depositor EDS
% Data completeness (in resolution range)	99.9 (58.02-2.31) 100.0 (58.02-2.31)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.99 (at 2.32Å)	Xtriage
Refinement program	PHENIX 1.9-1692	Depositor
R, R_{free}	0.164 , 0.204 0.167 , 0.203	Depositor DCC
R_{free} test set	1942 reflections (5.22%)	wwPDB-VP
Wilson B-factor (Å ²)	18.4	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for -h,l,k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7139	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: PAH, MG

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	0.30	1/3377 (0.0%)	0.70	2/4568 (0.0%)
1	B	0.31	1/3362 (0.0%)	0.71	1/4547 (0.0%)
All	All	0.31	2/6739 (0.0%)	0.71	3/9115 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	371	HIS	C-O	-6.23	1.16	1.23
1	A	371	HIS	C-O	-6.01	1.16	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	29	GLY	N-CA-C	5.93	117.55	111.56
1	A	266	ASP	CA-C-N	5.22	124.89	119.56
1	A	266	ASP	C-N-CA	5.22	124.89	119.56

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	3322	0	3298	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3307	0	3278	19	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	9	0	3	0	0
3	B	9	0	3	0	0
4	A	229	0	0	1	0
4	B	259	0	0	3	0
All	All	7139	0	6582	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:262:LYS:HB3	1:B:202:LYS:HE2	1.72	0.69
1:B:153:ILE:HB	1:B:168:PHE:HB2	1.83	0.60
1:A:401:SER:HB2	1:B:402:GLU:HB3	1.88	0.56
1:B:345:ASN:OD1	4:B:601:HOH:O	2.18	0.54
1:A:167:GLU:HB2	1:A:245:ASP:HB3	1.90	0.53
1:A:153:ILE:HB	1:A:168:PHE:HB2	1.92	0.51
1:A:390:THR:C	1:A:431:PRO:HG3	2.35	0.51
1:B:167:GLU:HB2	1:B:245:ASP:HB3	1.93	0.50
1:B:228:LYS:NZ	4:B:610:HOH:O	2.43	0.50
1:A:402:GLU:HB3	1:B:401:SER:HB2	1.93	0.49
1:A:295:PRO:HD2	1:A:304:TRP:CH2	2.48	0.48
1:B:165:MET:HG2	1:B:246:VAL:HG13	1.95	0.47
1:B:371:HIS:CG	1:B:395:THR:HA	2.49	0.47
1:B:295:PRO:HD2	1:B:304:TRP:CH2	2.49	0.47
1:B:69:ILE:HA	1:B:73:ILE:HB	1.98	0.46
1:B:166:GLN:HG2	1:B:167:GLU:HG3	1.97	0.46
1:A:202:LYS:HB3	1:A:202:LYS:HE2	1.80	0.45
1:A:371:HIS:CE1	1:A:396:GLY:N	2.84	0.45
1:B:396:GLY:HA3	1:B:403:ARG:HD2	2.00	0.44
1:A:396:GLY:HA3	1:A:403:ARG:HD2	1.98	0.44
1:A:294:ASP:OD2	1:A:318:ASP:HB3	2.17	0.44
1:B:294:ASP:OD2	1:B:318:ASP:HB3	2.18	0.44
1:B:162:LYS:HG2	4:B:789:HOH:O	2.17	0.43
1:A:25:TYR:CZ	1:A:30:LEU:HD13	2.54	0.43
1:A:238:GLU:H	1:A:238:GLU:CD	2.25	0.43
1:B:151:ASN:O	1:B:397:ALA:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:371:HIS:H	1:B:371:HIS:CD2	2.37	0.43
1:A:245:ASP:HA	1:A:293:GLU:HB3	2.00	0.43
1:A:151:ASN:O	1:A:397:ALA:HB2	2.20	0.42
1:A:329:GLU:HG3	1:A:359:LEU:HD21	2.02	0.42
1:A:103:LYS:NZ	4:A:618:HOH:O	2.50	0.42
1:B:329:GLU:HG3	1:B:359:LEU:HD21	2.03	0.41
1:A:371:HIS:CG	1:A:395:THR:HA	2.56	0.41
1:B:193:LYS:HB2	1:B:213:PHE:CZ	2.56	0.41

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	432/440 (98%)	420 (97%)	11 (2%)	1 (0%)	43	53
1	B	430/440 (98%)	419 (97%)	10 (2%)	1 (0%)	43	53
All	All	862/880 (98%)	839 (97%)	21 (2%)	2 (0%)	43	53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	400	ARG
1	B	400	ARG

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	351/357 (98%)	348 (99%)	3 (1%)	70	83
1	B	349/357 (98%)	344 (99%)	5 (1%)	59	75
All	All	700/714 (98%)	692 (99%)	8 (1%)	65	80

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	327	ARG
1	A	404	LEU
1	A	433	VAL
1	B	54	LYS
1	B	144	ILE
1	B	238	GLU
1	B	327	ARG
1	B	404	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	151	ASN
1	A	314	GLN
1	A	392	GLN
1	B	151	ASN
1	B	190	HIS
1	B	206	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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
3	PAH	B	503	2	8,8,8	3.38	1 (12%)	10,11,11	2.16	2 (20%)
3	PAH	A	503	2	8,8,8	3.40	1 (12%)	10,11,11	2.21	2 (20%)

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	PAH	B	503	2	-	3/7/7/7	-
3	PAH	A	503	2	-	3/7/7/7	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	503	PAH	C2-N3	9.10	1.42	1.32
3	B	503	PAH	C2-N3	9.00	1.42	1.32

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	PAH	C1-C2-N3	5.26	120.75	114.87
3	B	503	PAH	C1-C2-N3	5.21	120.69	114.87
3	A	503	PAH	O2-C2-N3	-3.42	119.07	123.27
3	B	503	PAH	O2-C2-N3	-3.39	119.11	123.27

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503	PAH	C2-C1-P-O1P
3	B	503	PAH	C2-C1-P-O1P
3	A	503	PAH	C2-C1-P-O2P
3	A	503	PAH	C2-C1-P-O3P
3	B	503	PAH	C2-C1-P-O2P
3	B	503	PAH	C2-C1-P-O3P

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	434/440 (98%)	-0.25	7 (1%) 70 72	10, 19, 34, 55	0
1	B	432/440 (98%)	-0.40	4 (0%) 81 82	10, 16, 31, 58	0
All	All	866/880 (98%)	-0.33	11 (1%) 75 76	10, 18, 33, 58	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	433	VAL	4.7
1	A	430	ASN	3.9
1	A	142	ASP	3.6
1	B	430	ASN	3.1
1	A	432	SER	2.9
1	A	434	LEU	2.5
1	A	419	ASP	2.3
1	A	1	MET	2.3
1	B	1	MET	2.2
1	B	142	ASP	2.2
1	B	419	ASP	2.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MG	B	502	1/1	0.97	0.04	8,8,8,8	0
3	PAH	A	503	9/9	0.97	0.06	12,13,15,15	0
3	PAH	B	503	9/9	0.97	0.06	11,12,15,16	0
2	MG	A	502	1/1	0.98	0.04	7,7,7,7	0
2	MG	B	501	1/1	1.00	0.13	1,1,1,1	0
2	MG	A	501	1/1	1.00	0.13	1,1,1,1	0

6.5 Other polymers [i](#)

There are no such residues in this entry.