

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

#### Aug 8, 2023 – 11:13 AM EDT

PDB ID : 1NX6

Title : Crystal Structure of Aspartate Semialdehyde Dehydrogenase from

Haemophilus influenzae as a Tetrahedral Hemithiocetal Reaction inter-

mediate with Phosphate at 2.15 A

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Deposited on : 2003-02-09

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 (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 (1)) were used in the production of this report:

MolProbity: 4.02b-467

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

Xtriage (Phenix) : 1.13 EDS : 2.35

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

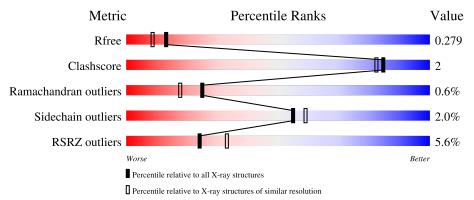
Validation Pipeline (wwPDB-VP) : 2.35

# 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 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	Similar resolution
Metric	$(\#  ext{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (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 <=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	
Ī	1	Λ	971	5%	
	1	A	371	91%	5%



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2915 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.

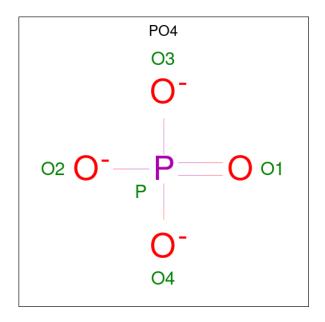
• Molecule 1 is a protein called Aspartate-Semialdehyde Dehydrogenase.

Mol	Chain	Residues		$\mathbf{At}$	oms			ZeroOcc	AltConf	Trace
1	A	357	Total 2761	C 1762	N 464	O 520	S 15	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	136	HTI	CYS	modified residue	UNP P44801

• Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



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

• Molecule 3 is water.



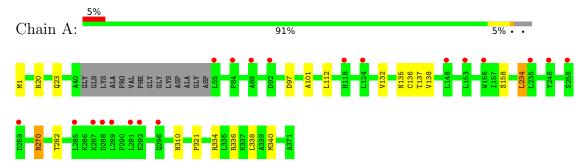
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	144	Total O 144 144	0	0



# 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

• Molecule 1: Aspartate-Semialdehyde Dehydrogenase





# 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 21 21 2	Depositor	
Cell constants	113.75Å 54.85Å 57.69Å	Donositon	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor	
Resolution (Å)	40.50 - 2.15	Depositor	
Resolution (A)	49.41 - 2.15	EDS	
% Data completeness	97.0 (40.50-2.15)	Depositor	
(in resolution range)	97.1 (49.41-2.15)	EDS	
$R_{merge}$	0.07	Depositor	
$R_{sym}$	(Not available)	Depositor	
$< I/\sigma(I) > 1$	5.35 (at 2.16Å)	Xtriage	
Refinement program	CNS 1.0	Depositor	
D.D.	0.228 , 0.284	Depositor	
$R, R_{free}$	0.224 , $0.279$	DCC	
$R_{free}$ test set	1945 reflections (9.59%)	wwPDB-VP	
Wilson B-factor (Å <sup>2</sup> )	30.2	Xtriage	
Anisotropy	0.037	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.33, 29.4	EDS	
L-test for twinning <sup>2</sup>	$< L >=0.49, < L^2>=0.32$	Xtriage	
Estimated twinning fraction	0.029 for -h,l,k	Xtriage	
$F_o, F_c$ correlation	0.93	EDS	
Total number of atoms	2915	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.96% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: HTI, PO4

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).

Mal	Chain	Bond	lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.59	0/2795	0.74	1/3780 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$
1	A	234	LEU	CA-CB-CG	5.74	128.50	115.30

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	2761	0	2819	13	0
2	A	10	0	0	1	0
3	A	144	0	0	0	0
All	All	2915	0	2819	13	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 2.

All (13) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	$egin{aligned} &  ext{Interatomic} \ &  ext{distance} \ &  ext{(Å)} \end{aligned}$	Clash overlap (Å)
1:A:310:ASN:HD21	1:A:334:ARG:HE	1.46	0.63
1:A:310:ASN:ND2	1:A:334:ARG:HE	1.96	0.61
1:A:135:ASN:HD22	1:A:138:VAL:HG23	1.75	0.51
1:A:336:ARG:HH12	1:A:338:LEU:HD23	1.76	0.51
1:A:135:ASN:HD22	1:A:138:VAL:H	1.61	0.49
1:A:136:HTI:CAM	1:A:270:ARG:HH22	2.27	0.47
1:A:20:ARG:HH11	1:A:23:GLN:HE21	1.62	0.47
1:A:20:ARG:HH11	1:A:23:GLN:NE2	2.16	0.44
1:A:158:SER:HB3	1:A:282:THR:HB	2.00	0.43
1:A:136:HTI:HAI	2:A:372:PO4:P	2.42	0.43
1:A:336:ARG:NH1	1:A:338:LEU:HD23	2.35	0.42
1:A:136:HTI:OAO	1:A:270:ARG:NH2	2.49	0.42
1:A:97:ASP:HB3	1:A:132:VAL:HG13	2.03	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	352/371 (95%)	339 (96%)	11 (3%)	2 (1%)	25 18

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type		
1	A	112	LEU		
1	A	101	ALA		

#### 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	296/304 (97%)	290 (98%)	6 (2%)	55 59	

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	137	THR
1	A	234	LEU
1	A	270	ARG
1	A	321	PRO
1	A	340	MET

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	3	ASN
1	A	23	GLN
1	A	80	ASN
1	A	135	ASN
1	A	163	GLN
1	A	310	ASN
1	A	353	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)

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		
IVIOI					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	HTI	A	136	1	8,13,14	0.88	0	8,16,18	0.87	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
1	HTI	A	136	1	-	2/11/15/17	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Iol   Chain   Res		Type	Atoms		
1	A	136	HTI	CAH-CAJ-CAK-NAL		
1	A	136	HTI	CAH-CAJ-CAK-CAM		

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain			Clashes	Symm-Clashes	
1	A	136	HTI	3	0	

#### 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	Type	Chain	Dec	Res Link	Bond lengths			Bond angles		
IVIOI			nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
2	PO4	A	373	-	4,4,4	1.41	1 (25%)	6,6,6	0.85	0
2	PO4	A	372	-	4,4,4	1.52	1 (25%)	6,6,6	0.84	0

All (2) bond length outliers are listed below:

	Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\text{\AA})$
Ī	2	A	372	PO4	P-O1	2.52	1.56	1.50
Ī	2	A	373	PO4	P-O1	2.43	1.56	1.50

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:

$\mathbf{Mol}$	Chain	Res	Type	Clashes	Symm-Clashes
2	A	372	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)

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,  $95^{th}$  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	Tol Chain Analysed		<RSRZ $>$	# RSRZ > 2		$OWAB(A^2)$	Q<0.9
1	A	356/371 (95%)	0.34	20 (5%) 24	33	13, 31, 58, 74	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res Type		RSRZ	
1	A	289	LEU	3.2	
1	A	55	LEU	2.8	
1	A	118	HIS	2.7	
1	A	259	ASP	2.7	
1	A	296	GLN	2.6	
1	A	153	LEU	2.6	
1	A	92	ASP	2.6	
1	A	287	LYS	2.6	
1	A	84	PRO	2.6	
1	A	258	SER	2.5	
1	A	248	TYR	2.4	
1	A	156	TRP	2.4	
1	A	288	ASP	2.3	
1	A	88	ALA	2.2	
1	A	291	LEU	2.1	
1	A	235	LEU	2.1	
1	A	124	LEU	2.0	
1	A	292	GLU	2.0	
1	A	148	LEU	2.0	
1	A	285	LEU	2.0	

## 6.2 Non-standard residues in protein, DNA, RNA chains (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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	HTI	A	136	14/15	0.91	0.16	23,32,35,37	0

### 6.3 Carbohydrates (i)

There are no monosaccharides 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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	PO4	A	373	5/5	0.89	0.19	65,66,66,67	0
2	PO4	A	372	5/5	0.97	0.13	31,32,33,35	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

