



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 07:14 PM GMT

PDB ID : 1EPX
Title : CRYSTAL STRUCTURE ANALYSIS OF ALDOLASE FROM L. MEXI-
CANA
Authors : Chudzik, D.M.; Michels, P.A.; de Walque, S.; Hol, W.G.J.
Deposited on : 2000-03-29
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

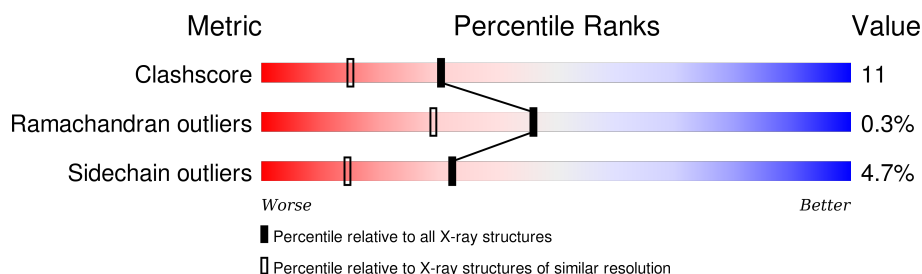
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	370	 74% 19% . . .
1	B	370	 72% 20% . . .
1	C	370	 68% 23% 5% . .
1	D	370	 67% 24% 5% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12131 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 FRUCTOSE-1,6-BISPHOSPHATE ALDOLASE.

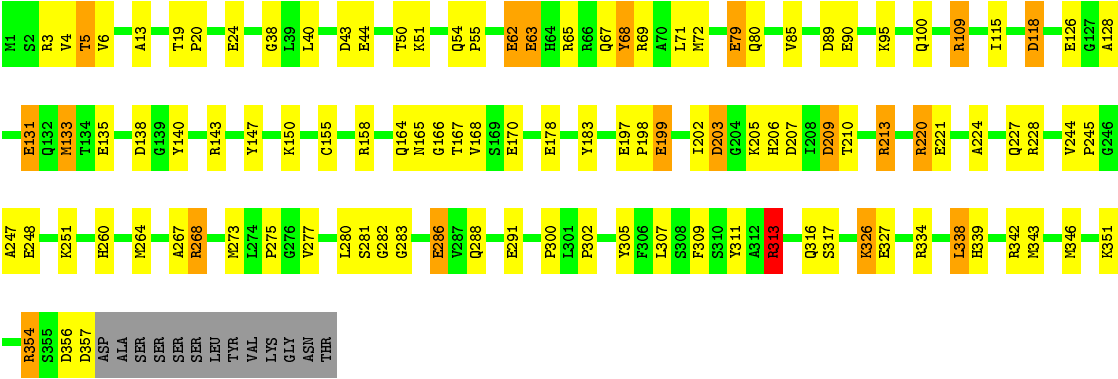
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	0	0	0
			2694	1695	477	504	18			
1	B	357	Total	C	N	O	S	0	0	0
			2694	1695	477	504	18			
1	C	357	Total	C	N	O	S	0	0	0
			2694	1695	477	504	18			
1	D	357	Total	C	N	O	S	0	0	0
			2694	1695	477	504	18			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	329	Total	O	0	0
			329	329		
2	B	291	Total	O	0	0
			291	291		
2	C	376	Total	O	0	0
			376	376		
2	D	359	Total	O	0	0
			359	359		

SER
LEU
TYR
VAL
LYS
GLY
ASN
THR

● Molecule 1: FRUCTOSE-1,6-BISPHOSPHATE ALDOLASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.80 Å 118.10 Å 159.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.80	Depositor
% Data completeness (in resolution range)	92.5 (20.00-1.80)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.161 , 0.213	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12131	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	1.24	17/2749 (0.6%)	1.58	35/3730 (0.9%)
1	B	1.24	17/2749 (0.6%)	1.58	35/3730 (0.9%)
1	C	1.24	16/2749 (0.6%)	1.58	35/3730 (0.9%)
1	D	1.24	17/2749 (0.6%)	1.58	35/3730 (0.9%)
All	All	1.24	67/10996 (0.6%)	1.58	140/14920 (0.9%)

The worst 5 of 67 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	135	GLU	CD-OE1	-8.09	1.16	1.25
1	D	135	GLU	CD-OE1	-8.09	1.16	1.25
1	B	135	GLU	CD-OE1	-8.08	1.16	1.25
1	C	135	GLU	CD-OE1	-8.07	1.16	1.25
1	D	199	GLU	CD-OE2	7.97	1.34	1.25

The worst 5 of 140 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	268	ARG	NE-CZ-NH1	28.54	134.57	120.30
1	A	268	ARG	NE-CZ-NH1	28.52	134.56	120.30
1	C	268	ARG	NE-CZ-NH1	28.52	134.56	120.30
1	D	268	ARG	NE-CZ-NH1	28.48	134.54	120.30
1	B	268	ARG	NE-CZ-NH2	-18.17	111.22	120.30

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	2694	0	2628	53	1
1	B	2694	0	2628	59	1
1	C	2694	0	2628	91	3
1	D	2694	0	2628	96	3
2	A	329	0	0	4	0
2	B	291	0	0	10	0
2	C	376	0	0	36	1
2	D	359	0	0	32	1
All	All	12131	0	10512	233	5

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 11.

The worst 5 of 233 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:D:51:LYS:CB	2:D:1443:HOH:O	1.94	1.16
1:C:353:LYS:HE3	2:C:1042:HOH:O	1.51	1.11
1:D:50:THR:O	2:D:2072:HOH:O	1.72	1.04
1:A:227:GLN:HB3	1:D:220:ARG:HD2	1.47	0.95
1:D:205:LYS:O	2:D:1417:HOH:O	1.86	0.93

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:51:LYS:CB	2:D:1790:HOH:O[4_435]	2.02	0.18
1:A:98:ASN:O	1:D:62:GLU:OE2[1_455]	2.04	0.16
1:B:98:ASN:O	1:C:62:GLU:OE2[1_655]	2.06	0.14
1:C:108:ALA:O	1:D:109:ARG:NH2[2_345]	2.09	0.11
1:D:100:GLN:NE2	2:C:2073:HOH:O[2_344]	2.15	0.05

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	355/370 (96%)	346 (98%)	8 (2%)	1 (0%)	46	29
1	B	355/370 (96%)	346 (98%)	8 (2%)	1 (0%)	46	29
1	C	355/370 (96%)	346 (98%)	8 (2%)	1 (0%)	46	29
1	D	355/370 (96%)	346 (98%)	8 (2%)	1 (0%)	46	29
All	All	1420/1480 (96%)	1384 (98%)	32 (2%)	4 (0%)	46	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	198	PRO
1	B	198	PRO
1	C	198	PRO
1	D	198	PRO

5.3.2 Protein sidechains ⓘ

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	274/303 (90%)	261 (95%)	13 (5%)	32	14
1	B	274/303 (90%)	261 (95%)	13 (5%)	32	14
1	C	274/303 (90%)	261 (95%)	13 (5%)	32	14
1	D	274/303 (90%)	261 (95%)	13 (5%)	32	14
All	All	1096/1212 (90%)	1044 (95%)	52 (5%)	32	14

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	326	LYS
1	C	183	TYR
1	D	317	SER
1	B	338	LEU
1	C	69	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	88	HIS
1	D	339	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.