



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 09:47 AM UTC

PDB ID : 4GMF / pdb_00004gmf
Title : Apo Structure of a ThiazolinyI Imine Reductase from Yersinia enterocolitica (Irp3)
Authors : Lamb, A.L.; Meneely, K.M.
Deposited on : 2012-08-15
Resolution : 1.85 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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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

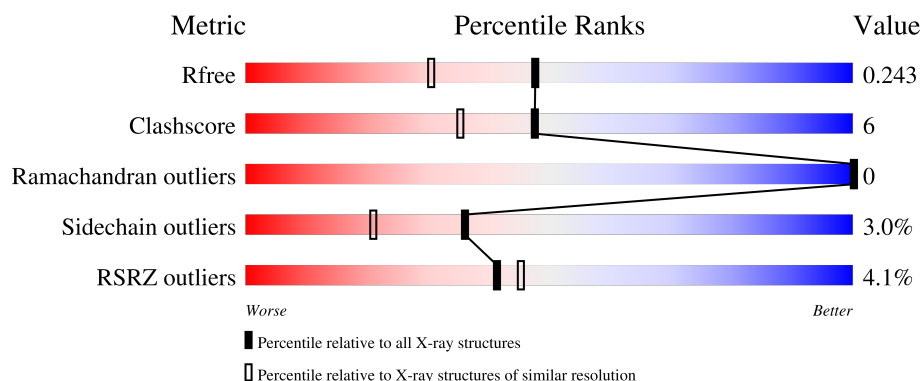
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	372	5% 74% 13% • 10%
1	B	372	4% 78% 9% • 12%
1	C	372	3% 72% 15% • 11%
1	D	372	3% 74% 13% • 11%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10938 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 Yersiniabactin biosynthetic protein YbtU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total	C	N	O	S	0	0	0
			2628	1675	475	463	15			
1	B	329	Total	C	N	O	S	0	0	0
			2576	1643	464	454	15			
1	C	330	Total	C	N	O	S	0	0	0
			2589	1651	467	456	15			
1	D	332	Total	C	N	O	S	0	0	0
			2604	1660	469	460	15			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	366	GLU	-	expression tag	UNP A1JTG0
A	367	HIS	-	expression tag	UNP A1JTG0
A	368	HIS	-	expression tag	UNP A1JTG0
A	369	HIS	-	expression tag	UNP A1JTG0
A	370	HIS	-	expression tag	UNP A1JTG0
A	371	HIS	-	expression tag	UNP A1JTG0
A	372	HIS	-	expression tag	UNP A1JTG0
B	366	GLU	-	expression tag	UNP A1JTG0
B	367	HIS	-	expression tag	UNP A1JTG0
B	368	HIS	-	expression tag	UNP A1JTG0
B	369	HIS	-	expression tag	UNP A1JTG0
B	370	HIS	-	expression tag	UNP A1JTG0
B	371	HIS	-	expression tag	UNP A1JTG0
B	372	HIS	-	expression tag	UNP A1JTG0
C	366	GLU	-	expression tag	UNP A1JTG0
C	367	HIS	-	expression tag	UNP A1JTG0
C	368	HIS	-	expression tag	UNP A1JTG0
C	369	HIS	-	expression tag	UNP A1JTG0
C	370	HIS	-	expression tag	UNP A1JTG0
C	371	HIS	-	expression tag	UNP A1JTG0
C	372	HIS	-	expression tag	UNP A1JTG0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	366	GLU	-	expression tag	UNP A1JTG0
D	367	HIS	-	expression tag	UNP A1JTG0
D	368	HIS	-	expression tag	UNP A1JTG0
D	369	HIS	-	expression tag	UNP A1JTG0
D	370	HIS	-	expression tag	UNP A1JTG0
D	371	HIS	-	expression tag	UNP A1JTG0
D	372	HIS	-	expression tag	UNP A1JTG0

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



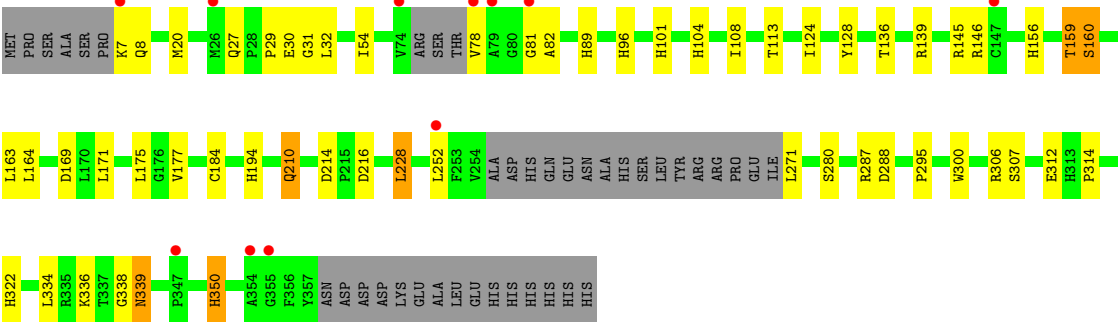
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	D	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	105	Total 105	O 105	0	0
5	B	108	Total 108	O 108	0	0
5	C	125	Total 125	O 125	0	0
5	D	160	Total 160	O 160	0	0



● Molecule 1: Yersiniabactin biosynthetic protein YbtU



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.87Å 93.90Å 181.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.97 – 1.85 40.97 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.6 (40.97-1.85) 99.6 (40.97-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.40	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.88 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.196 , 0.242 0.195 , 0.243	Depositor DCC
R_{free} test set	6153 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	24.9	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10938	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 39.44 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.1708e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: EPE, SO4, EDO

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	1.41	11/2699 (0.4%)	1.20	5/3678 (0.1%)
1	B	1.48	11/2644 (0.4%)	1.23	4/3602 (0.1%)
1	C	1.39	8/2657 (0.3%)	1.23	13/3618 (0.4%)
1	D	1.49	17/2675 (0.6%)	1.23	9/3646 (0.2%)
All	All	1.44	47/10675 (0.4%)	1.22	31/14544 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

The worst 5 of 47 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	101	HIS	ND1-CE1	9.67	1.42	1.32
1	D	169	ASP	N-CA	7.65	1.55	1.46
1	A	130	HIS	CE1-NE2	7.43	1.40	1.32
1	D	81	GLY	N-CA	7.04	1.53	1.45
1	C	104	HIS	CG-CD2	6.80	1.43	1.35

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	346	THR	CA-C-N	-9.26	112.90	119.66
1	B	346	THR	C-N-CA	-9.26	112.90	119.66
1	C	200	TRP	CA-C-N	-7.82	111.58	119.56
1	C	200	TRP	C-N-CA	-7.82	111.58	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	26	MET	N-CA-C	-7.61	103.10	112.38

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	13	VAL	Peptide
1	A	14	GLY	Peptide

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	2628	0	2607	38	0
1	B	2576	0	2552	24	0
1	C	2589	0	2568	32	0
1	D	2604	0	2578	29	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	1	0
2	D	5	0	0	0	0
3	B	4	0	6	0	0
3	D	4	0	6	2	0
4	D	15	0	18	3	0
5	A	105	0	0	4	0
5	B	108	0	0	2	0
5	C	125	0	0	3	0
5	D	160	0	0	5	0
All	All	10938	0	10335	116	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 6.

The worst 5 of 116 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:172:LEU:HD23	1:A:179:THR:HG23	1.36	1.01
1:A:75:ARG:N	1:A:75:ARG:HE	1.61	0.98
1:A:124:ILE:H	1:A:323:GLN:HE22	1.10	0.97
1:A:75:ARG:HE	1:A:75:ARG:H	0.95	0.89
1:D:145:ARG:HH12	3:D:403:EDO:H22	1.40	0.87

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	329/372 (88%)	323 (98%)	6 (2%)	0	100	100
1	B	321/372 (86%)	313 (98%)	8 (2%)	0	100	100
1	C	322/372 (87%)	314 (98%)	8 (2%)	0	100	100
1	D	326/372 (88%)	318 (98%)	8 (2%)	0	100	100
All	All	1298/1488 (87%)	1268 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	281/315 (89%)	271 (96%)	10 (4%)	31	16
1	B	275/315 (87%)	268 (98%)	7 (2%)	42	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	277/315 (88%)	266 (96%)	11 (4%)	28	13
1	D	279/315 (89%)	274 (98%)	5 (2%)	51	40
All	All	1112/1260 (88%)	1079 (97%)	33 (3%)	36	21

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	30	GLU
1	D	163	LEU
1	D	295	PRO
1	B	109	SER
1	B	74	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	319	GLN
1	D	339	ASN
1	B	323	GLN
1	B	304	GLN
1	D	349	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

7 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	D	401	-	4,4,4	0.50	0	6,6,6	0.36	0
3	EDO	B	402	-	3,3,3	0.29	0	2,2,2	1.95	1 (50%)
3	EDO	D	403	-	3,3,3	0.66	0	2,2,2	0.37	0
2	SO4	C	401	-	4,4,4	0.30	0	6,6,6	0.87	0
2	SO4	A	401	-	4,4,4	0.41	0	6,6,6	0.78	0
4	EPE	D	402	-	15,15,15	2.12	2 (13%)	19,20,20	2.77	9 (47%)
2	SO4	B	401	-	4,4,4	0.42	0	6,6,6	0.32	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	EDO	B	402	-	-	0/1/1/1	-
3	EDO	D	403	-	-	1/1/1/1	-
4	EPE	D	402	-	-	3/9/19/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	402	EPE	C10-S	-6.11	1.69	1.77
4	D	402	EPE	O3S-S	3.98	1.62	1.47

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	402	EPE	O2S-S-C10	7.28	117.72	106.73
4	D	402	EPE	C9-N1-C6	4.26	122.58	111.24
4	D	402	EPE	C2-C3-N4	-4.03	102.52	110.65
4	D	402	EPE	C9-N1-C2	-3.08	103.03	111.24
4	D	402	EPE	C6-N1-C2	2.94	115.18	108.84

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	402	EPE	C10-C9-N1-C6
3	D	403	EDO	O1-C1-C2-O2
4	D	402	EPE	N4-C7-C8-O8
4	D	402	EPE	S-C10-C9-N1

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	403	EDO	2	0
2	C	401	SO4	1	0
4	D	402	EPE	3	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, 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	335/372 (90%)	0.23	17 (5%) 33 36	14, 27, 49, 65	0
1	B	329/372 (88%)	0.17	14 (4%) 40 43	14, 26, 46, 57	0
1	C	330/372 (88%)	0.05	12 (3%) 46 50	16, 25, 46, 76	0
1	D	332/372 (89%)	-0.03	11 (3%) 49 53	12, 24, 44, 62	0
All	All	1326/1488 (89%)	0.10	54 (4%) 41 45	12, 26, 46, 76	0

The worst 5 of 54 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	270	ILE	6.5
1	C	270	ILE	5.4
1	A	202	GLU	4.2
1	B	255	ALA	4.2
1	A	28	PRO	4.0

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($\text{\AA}^2$)	Q<0.9
3	EDO	B	402	4/4	0.83	0.13	33,35,35,39	0
3	EDO	D	403	4/4	0.85	0.12	37,37,41,42	0
2	SO4	A	401	5/5	0.88	0.11	53,54,61,64	0
4	EPE	D	402	15/15	0.89	0.13	27,41,50,53	0
2	SO4	B	401	5/5	0.95	0.09	49,50,58,59	0
2	SO4	C	401	5/5	0.95	0.07	47,47,51,56	0
2	SO4	D	401	5/5	0.95	0.07	53,54,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.