

Full wwPDB X-ray Structure Validation Report (i)

Jan 17, 2023 – 05:35 AM EST

:	1VLY
:	Crystal structure of a putative aminomethyltransferase (ygfz) from escherichia
	coli at 1.30 A resolution
:	Joint Center for Structural Genomics (JCSG)
	2004-08-20
:	1.30 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:

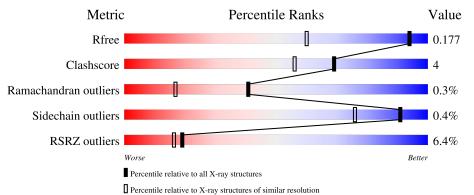
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.30 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	1058 (1.30-1.30)
Clashscore	141614	1101 (1.30-1.30)
Ramachandran outliers	138981	1058 (1.30-1.30)
Sidechain outliers	138945	1058 (1.30-1.30)
RSRZ outliers	127900	1029 (1.30-1.30)

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 <=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		
			6%		
1	А	338	89%	7%	•



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3020 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 Unknown protein from 2D-page.

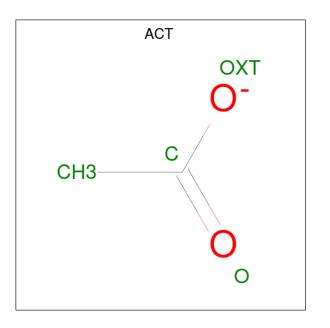
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	А	323	Total 2524	C 1603	N 435	O 472	${ m S} { m 3}$	Se 11	0	15	0

Chain	Residue	Modelled	Actual	Comment	Reference
А	-11	MSE	-	expression tag	UNP P39179
А	-10	GLY	-	expression tag	UNP P39179
А	-9	SER	-	expression tag	UNP P39179
А	-8	ASP	-	expression tag	UNP P39179
A	-7	LYS	-	expression tag	UNP P39179
А	-6	ILE	-	expression tag	UNP P39179
А	-5	HIS	-	expression tag	UNP P39179
A	-4	HIS	-	expression tag	UNP P39179
А	-3	HIS	-	expression tag	UNP P39179
A	-2	HIS	-	expression tag	UNP P39179
А	-1	HIS	-	expression tag	UNP P39179
A	0	HIS	-	expression tag	UNP P39179
А	1	MSE	-	expression tag	UNP P39179
А	22	MSE	MET	modified residue	UNP P39179
А	41	MSE	MET	modified residue	UNP P39179
А	52	MSE	MET	modified residue	UNP P39179
А	69	MSE	MET	modified residue	UNP P39179
А	172	MSE	MET	modified residue	UNP P39179
А	234	MSE	MET	modified residue	UNP P39179
А	269	MSE	MET	modified residue	UNP P39179
А	296	MSE	MET	modified residue	UNP P39179
А	300	MSE	MET	modified residue	UNP P39179

There are 22 discrepancies between the modelled and reference sequences:

• Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	А	1	Total 4	$\begin{array}{c} \mathrm{C} \\ \mathrm{2} \end{array}$	O 2	0	0

• Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

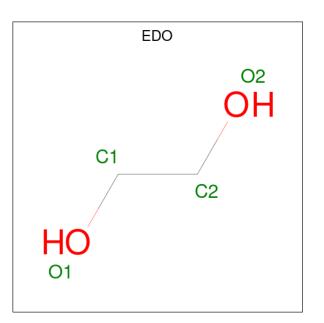
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total Ca 1 1	0	0

• Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total Cl 1 1	0	0

• Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 5 2 3 \end{array}$	0	1

• Molecule 6 is water.

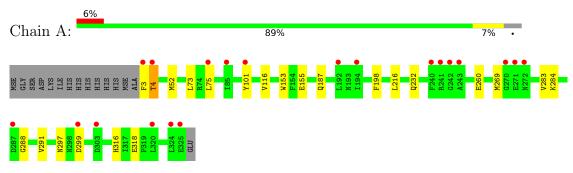
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	А	477	Total 477	O 477	0	0



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: Unknown protein from 2D-page





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants	44.81Å 50.08Å 52.01Å	Denegitor
a, b, c, α , β , γ	94.68° 115.29° 116.46°	Depositor
Resolution (Å)	26.45 - 1.30	Depositor
Resolution (A)	26.45 - 1.30	EDS
% Data completeness	89.3 (26.45-1.30)	Depositor
(in resolution range)	$89.3\ (26.45\text{-}1.30)$	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	0.04	Depositor
$< I/\sigma(I) > 1$	$2.67 (at 1.30 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D D.	0.134 , 0.168	Depositor
R, R_{free}	0.147 , 0.177	DCC
R_{free} test set	3802 reflections $(5.02%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	13.0	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34, 47.8	EDS
L-test for twinning ²	$< L > = 0.49, < L^2 > = 0.32$	Xtriage
	0.017 for h,-h-k,-h-l	
Estimated twinning fraction	0.012 for -h,-l,-k	Xtriage
	0.014 for -h,h+l,h+k	
F_o, F_c correlation	0.97	EDS
Total number of atoms	3020	wwPDB-VP
Average B, all atoms $(Å^2)$	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.10% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities 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: EDO, CL, CA, ACT

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	Bo	nd lengths	Bond	angles
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.56	2/2622~(0.1%)	0.73	0/3540

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
1	А	52[A]	MSE	SE-CE	-6.47	1.57	1.95
1	А	52[B]	MSE	SE-CE	-6.47	1.57	1.95

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

CLOSE-CONTACTS INFOmissingINFO

5.2 Torsion angles (i)

5.2.1 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	А	335/338~(99%)	330~(98%)	4 (1%)	1 (0%)	41 17

All (1) Ramachandran outliers are listed below:



Mol	Chain	Res	Type	
1	А	4	THR	

5.2.2 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	А	265/265~(100%)	264 (100%)	1 (0%)	91 76

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	269	MSE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.2.3 RNA (i)

There are no RNA molecules in this entry.

5.3 Non-standard residues in protein, DNA, RNA chains (i)

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

5.4 Carbohydrates (i)

There are no monosaccharides in this entry.

5.5 Ligand geometry (i)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	Turne	Chain	Res	Link	B	ond leng	gths	B	ond ang	gles
NIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	EDO	А	503[B]	-	$3,\!3,\!3$	0.76	0	2,2,2	1.56	1 (50%)
5	EDO	А	502	-	$3,\!3,\!3$	0.40	0	2,2,2	0.66	0
5	EDO	А	503[A]	-	$3,\!3,\!3$	0.73	0	2,2,2	1.88	1 (50%)
2	ACT	А	504	-	3,3,3	0.79	0	3,3,3	0.69	0
5	EDO	А	501	-	$3,\!3,\!3$	0.69	0	$2,\!2,\!2$	0.29	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
5	EDO	А	503[A]	-	-	0/1/1/1	-
5	EDO	А	503[B]	-	-	1/1/1/1	-
5	EDO	А	502	-	-	0/1/1/1	-
5	EDO	А	501	-	-	0/1/1/1	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Ι	Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
	5	А	503[A]	EDO	O1-C1-C2	-2.65	92.83	111.91
	5	А	503[B]	EDO	O1-C1-C2	-2.20	96.07	111.91

There are no chirality outliers.

All (1) torsion outliers are listed below:

M	bl	Chain			
5		A	503[B]	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 6 short contacts:

5 A 503[B] EDO 2 1	shes	Symm-Clash	Clashes	Type	Res	Chain	Mol
		1	2	EDO	503[B]	А	5

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	А	503[A]	EDO	2	1
5	А	501	EDO	1	0

5.6 Other polymers (i)

There are no such residues in this entry.

5.7 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	Chain	Analysed	<RSRZ $>$	#RSRZ>2		$OWAB(Å^2)$	Q<0.9
1	А	314/338~(92%)	0.22	20 (6%) 19	16	9, 14, 27, 45	1 (0%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	3	PHE	5.5
1	А	240	PHE	5.4
1	А	241	ARG	5.3
1	А	242	GLY	4.3
1	А	325	GLU	4.1
1	А	270	GLY	3.7
1	А	4	THR	3.4
1	А	271	GLU	3.1
1	А	243	ALA	2.8
1	А	272	ASN	2.6
1	А	303	ASP	2.6
1	А	320	LEU	2.6
1	А	75[A]	LEU	2.5
1	А	299	ASP	2.4
1	А	287	ASP	2.2
1	А	101	TYR	2.1
1	А	192	LEU	2.1
1	А	85	ILE	2.1
1	А	194	ILE	2.1
1	А	324	LEU	2.0

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 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	B-factors(Å ²)	Q < 0.9
5	EDO	А	503[A]	4/4	0.79	0.23	19,21,23,35	1
5	EDO	А	503[B]	4/4	0.79	0.23	17,19,23,35	1
5	EDO	А	501	4/4	0.85	0.19	21,25,29,35	0
5	EDO	А	502	4/4	0.95	0.09	15,16,18,21	0
2	ACT	А	504	4/4	0.98	0.09	11,13,14,14	0
4	CL	А	506	1/1	0.99	0.03	21,21,21,21	0
3	CA	А	505	1/1	1.00	0.08	20,20,20,20	0

6.5 Other polymers (i)

There are no such residues in this entry.

