



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 15, 2026 – 11:02 AM UTC

PDB ID : 1E5F / pdb_00001e5f
Title : METHIONINE GAMMA-LYASE (MGL) FROM TRICHOMONAS VAGINALIS
Authors : Goodall, G.; Mottram, J.C.; Coombs, G.H.; Laphorn, A.J.
Deposited on : 2000-07-25
Resolution : 2.18 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

<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 : **FAILED**
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
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 2.18 Å.

There are no overall percentile quality scores available for this entry.

MolProbity failed to run properly; EDS was not executed - the sequence quality summary graphics cannot be shown.

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6649 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.

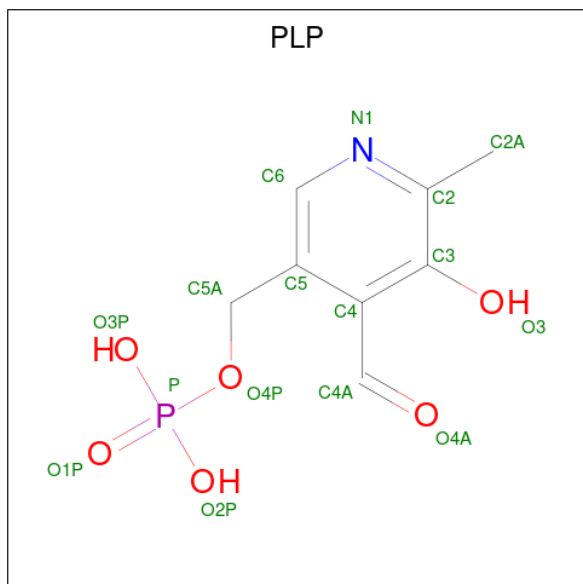
- Molecule 1 is a protein called METHIONINE GAMMA-LYASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	393	2969	1882	501	562	24	0	5	0
1	B	393	2969	1877	505	563	24	0	4	0

There are 4 discrepancies between the modelled and reference sequences:

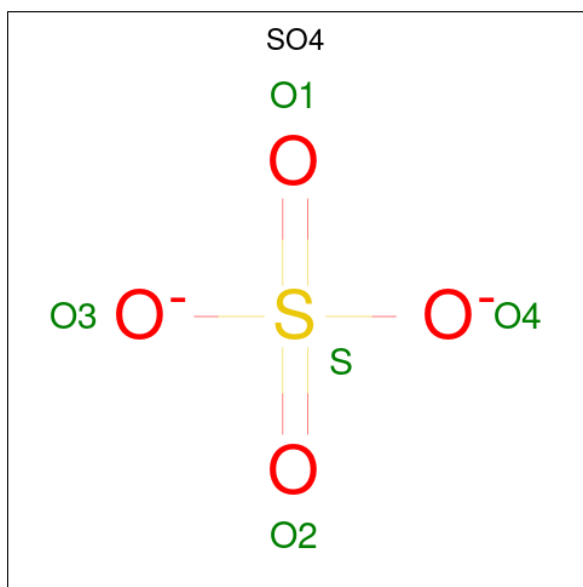
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	SER	cloning artifact	UNP O15564
A	308	TYR	SER	cloning artifact	UNP O15564
B	2	ALA	SER	cloning artifact	UNP O15564
B	308	TYR	SER	cloning artifact	UNP O15564

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: $C_8H_{10}NO_6P$).



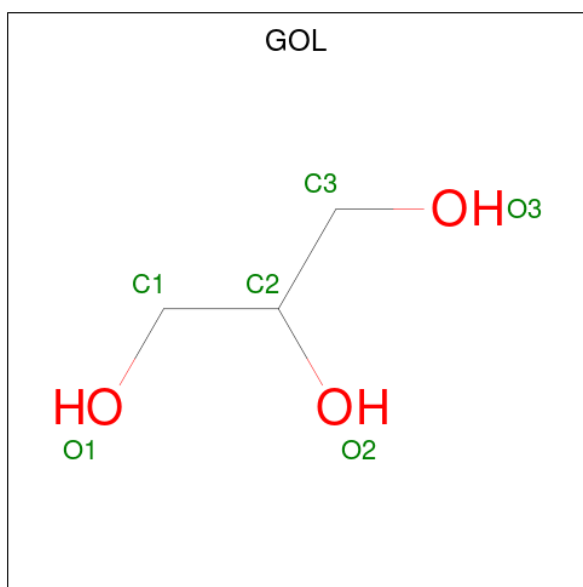
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	O S	0	0
			5	4 1		
3	A	1	Total	O S	0	0
			5	4 1		
3	A	1	Total	O S	0	0
			5	4 1		
3	B	1	Total	O S	0	0
			5	4 1		
3	B	1	Total	O S	0	0
			5	4 1		
3	B	1	Total	O S	0	0
			5	4 1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	329	Total O 329 329	0	0
5	B	316	Total O 316 316	0	0

MolProbity failed to run properly; EDS was not executed - this section is therefore empty.

3 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 31 1 2	Depositor
Cell constants a, b, c, α , β , γ	88.26Å 88.26Å 217.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.00 – 2.18	Depositor
% Data completeness (in resolution range)	98.6 (25.00-2.18)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.162 , 0.212	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	6649	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

9 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
3	SO4	B	406	-	4,4,4	0.86	0	6,6,6	1.30	1 (16%)
2	PLP	B	405	-	15,15,16	1.59	2 (13%)	21,22,23	2.12	9 (42%)
3	SO4	A	408	-	4,4,4	0.60	0	6,6,6	0.58	0
3	SO4	A	409	-	4,4,4	0.77	0	6,6,6	0.69	0
2	PLP	A	405	-	15,15,16	1.82	3 (20%)	21,22,23	3.46	8 (38%)
3	SO4	B	411	-	4,4,4	0.93	0	6,6,6	0.99	0
3	SO4	A	407	-	4,4,4	0.87	0	6,6,6	1.45	0
3	SO4	B	410	-	4,4,4	0.99	0	6,6,6	0.45	0
4	GOL	A	412	-	5,5,5	1.08	0	5,5,5	1.65	1 (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
2	PLP	B	405	-	-	1/6/6/8	0/1/1/1
4	GOL	A	412	-	-	1/4/4/4	-
2	PLP	A	405	-	-	0/6/6/8	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	405	PLP	C5-C4	-4.65	1.35	1.40
2	B	405	PLP	C5-C4	-4.38	1.35	1.40
2	A	405	PLP	C4A-C4	3.71	1.59	1.51
2	B	405	PLP	C4A-C4	3.23	1.58	1.51
2	A	405	PLP	P-O2P	-2.07	1.47	1.54

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	405	PLP	C3-C2-N1	-8.93	109.70	120.96
2	A	405	PLP	C2A-C2-N1	6.63	130.13	117.64
2	A	405	PLP	C4A-C4-C5	6.40	127.53	120.94
2	A	405	PLP	C4A-C4-C3	-5.55	111.27	120.52
2	B	405	PLP	C3-C2-N1	-4.83	114.87	120.96

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	412	GOL	O1-C1-C2-C3
2	B	405	PLP	C4-C5-C5A-O4P

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data [i](#)

5.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

5.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

5.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

5.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.