Full wwPDB X-ray Structure Validation Report ⓘ

Dec 3, 2023 – 07:03 am GMT

PDB ID	:	1E5F
Title	:	METHIONINE GAMMA-LYASE (MGL) FROM TRICHOMONAS VAGINALIS
Authors	:	Goodall, G.; Mottram, J.C.; Coombs, G.H.; Lapthorn, A.J.
Deposited on	:	2000-07-25
Resolution	:	2.18 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 ⓘ 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.18 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.

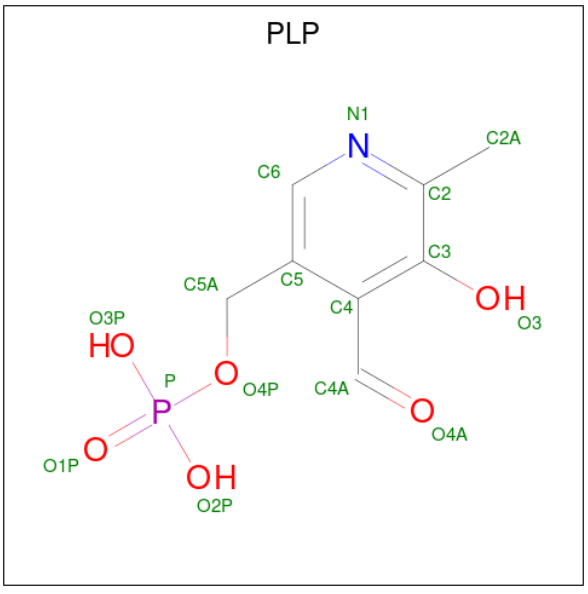
- Molecule 1 is a protein called METHIONINE GAMMA-LYASE.

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

There are 4 discrepancies between the modelled and reference sequences:

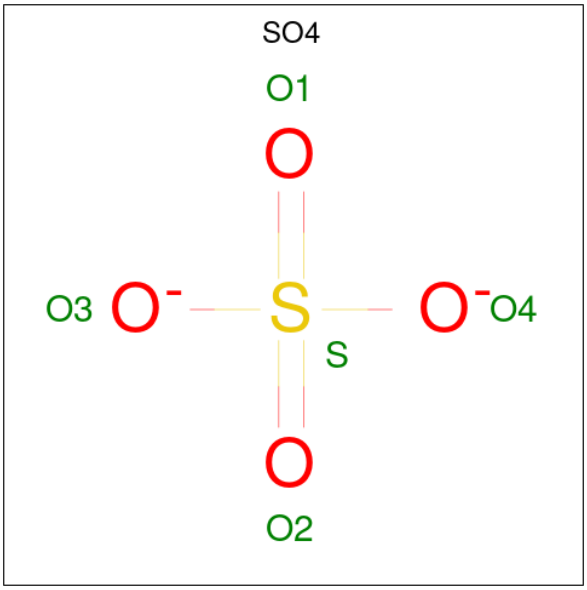
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	SER	cloning artifact	UNP O15564
A	308	TYR	SER	cloning artifact	UNP O15564
B	2	ALA	SER	cloning artifact	UNP O15564
B	308	TYR	SER	cloning artifact	UNP O15564

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



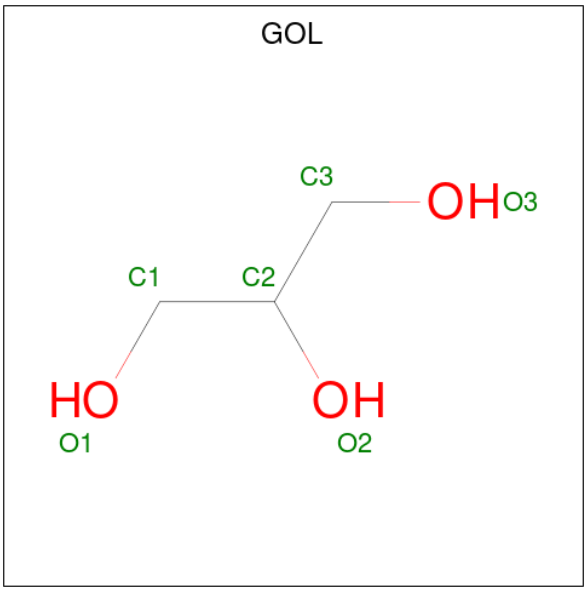
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O P 15 8 1 5 1	0	0
2	B	1	Total C N O P 15 8 1 5 1	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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 (i)

Xtriage (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.	Xtriage
Total number of atoms	6649	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

4 Model quality

4.1 Standard geometry

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

4.2 Too-close contacts

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

4.3 Torsion angles

4.3.1 Protein backbone

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

4.3.2 Protein sidechains

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

4.3.3 RNA

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

4.4 Non-standard residues in protein, DNA, RNA chains

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

4.5 Carbohydrates

There are no monosaccharides in this entry.

4.6 Ligand geometry

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	A	409	-	4,4,4	0.71	0	6,6,6	0.67	0
2	PLP	A	405	-	15,15,16	1.79	3 (20%)	20,22,23	3.46	8 (40%)
3	SO4	B	410	-	4,4,4	0.93	0	6,6,6	0.50	0
3	SO4	A	407	-	4,4,4	0.85	0	6,6,6	1.46	0
3	SO4	B	406	-	4,4,4	0.80	0	6,6,6	1.31	1 (16%)
2	PLP	B	405	-	15,15,16	1.57	2 (13%)	20,22,23	2.05	8 (40%)
3	SO4	A	408	-	4,4,4	0.53	0	6,6,6	0.61	0
4	GOL	A	412	-	5,5,5	1.03	0	5,5,5	1.54	1 (20%)
3	SO4	B	411	-	4,4,4	0.88	0	6,6,6	1.10	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
4	GOL	A	412	-	-	1/4/4/4	-
2	PLP	B	405	-	-	1/6/6/8	0/1/1/1
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	-4.70	1.35	1.40
2	B	405	PLP	C5-C4	-4.42	1.35	1.40
2	A	405	PLP	C4A-C4	3.54	1.59	1.51
2	B	405	PLP	C4A-C4	3.09	1.58	1.51
2	A	405	PLP	P-O2P	-2.01	1.47	1.54

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	405	PLP	C3-C2-N1	-8.57	109.70	120.77
2	A	405	PLP	C4A-C4-C5	6.41	127.53	120.94
2	A	405	PLP	C2A-C2-N1	6.38	130.13	117.67
2	A	405	PLP	C4A-C4-C3	-5.44	111.27	120.50
2	B	405	PLP	C3-C2-N1	-4.57	114.87	120.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	405	PLP	C2A-C2-C3	-3.62	116.42	120.89
2	A	405	PLP	C5-C6-N1	-3.32	118.28	123.82
2	B	405	PLP	C2A-C2-C3	3.30	124.96	120.89
2	B	405	PLP	C6-N1-C2	3.28	125.25	119.17
2	B	405	PLP	O4P-C5A-C5	-3.01	103.62	109.35
2	A	405	PLP	C4-C3-C2	2.87	124.32	120.07
4	A	412	GOL	O3-C3-C2	-2.81	96.72	110.20
2	B	405	PLP	C5A-C5-C6	-2.67	114.97	119.37
2	B	405	PLP	O2P-P-O1P	2.64	121.03	110.68
3	B	406	SO4	O3-S-O1	-2.30	97.30	109.31
2	B	405	PLP	C5-C6-N1	-2.21	120.13	123.82
2	A	405	PLP	O2P-P-O4P	-2.20	100.89	106.73
2	B	405	PLP	C4A-C4-C3	-2.02	117.08	120.50

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

5.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

5.3 Carbohydrates

EDS was not executed - this section is therefore empty.

5.4 Ligands

EDS was not executed - this section is therefore empty.

5.5 Other polymers

EDS was not executed - this section is therefore empty.