



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2023 – 05:57 PM EDT

PDB ID : 4OTC  
Title : 4-OXALOCROTONATE TAUTOMERASE OBSERVED AS AN OCTODE-CAMER, TRIGONAL CRYSTAL FORM  
Authors : Taylor, A.B.; Whitman, C.P.; Hackert, M.L.  
Deposited on : 1998-10-15  
Resolution : 2.28 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](mailto: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>.

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

MolProbity : **FAILED**  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (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) : 2.35.1

# 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 2.28 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

There are 3 unique types of molecules in this entry. The entry contains 4245 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 4-OXALOCROTONATE TAUTOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	60	Total 455	C 284	N 81	O 89	S 1	0	0	0
1	B	60	Total 455	C 284	N 81	O 89	S 1	0	0	0
1	C	60	Total 455	C 284	N 81	O 89	S 1	0	0	0
1	D	60	Total 455	C 284	N 81	O 89	S 1	0	0	0
1	E	60	Total 455	C 284	N 81	O 89	S 1	0	0	0
1	F	60	Total 455	C 284	N 81	O 89	S 1	0	0	0
1	G	60	Total 455	C 284	N 81	O 89	S 1	0	0	0
1	H	60	Total 455	C 284	N 81	O 89	S 1	0	0	0
1	I	60	Total 455	C 284	N 81	O 89	S 1	0	0	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	H	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		
2	I	1	Total	O	S	0	0
			5	4	1		
2	I	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		
3	B	7	Total	O	0	0
			7	7		
3	C	6	Total	O	0	0
			6	6		
3	D	10	Total	O	0	0
			10	10		
3	E	6	Total	O	0	0
			6	6		
3	F	4	Total	O	0	0
			4	4		
3	G	7	Total	O	0	0
			7	7		
3	H	7	Total	O	0	0
			7	7		
3	I	7	Total	O	0	0
			7	7		

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 3 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.00Å 88.00Å 124.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.28	Depositor
% Data completeness (in resolution range)	95.8 (20.00-2.28)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.234 , 0.265	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	4245	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	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 monosaccharides in this entry.

### 4.6 Ligand geometry [i](#)

18 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	C	105	-	4,4,4	0.66	0	6,6,6	0.59	0
2	SO4	I	118	-	4,4,4	0.76	0	6,6,6	0.44	0
2	SO4	G	114	-	4,4,4	0.75	0	6,6,6	0.49	0
2	SO4	H	117	-	4,4,4	0.68	0	6,6,6	0.62	0
2	SO4	G	111	-	4,4,4	0.68	0	6,6,6	0.56	0
2	SO4	F	112	-	4,4,4	0.78	0	6,6,6	0.58	0
2	SO4	B	104	-	4,4,4	0.79	0	6,6,6	0.53	0
2	SO4	D	108	-	4,4,4	0.88	0	6,6,6	0.48	0
2	SO4	B	103	-	4,4,4	0.76	0	6,6,6	0.50	0
2	SO4	A	102	-	4,4,4	0.84	0	6,6,6	0.41	0
2	SO4	G	113	-	4,4,4	0.73	0	6,6,6	0.57	0
2	SO4	A	101	-	4,4,4	0.85	0	6,6,6	0.51	0
2	SO4	E	107	-	4,4,4	0.87	0	6,6,6	0.49	0
2	SO4	I	115	-	4,4,4	0.89	0	6,6,6	0.49	0
2	SO4	C	106	-	4,4,4	0.71	0	6,6,6	0.46	0
2	SO4	E	110	-	4,4,4	0.79	0	6,6,6	0.55	0
2	SO4	H	116	-	4,4,4	0.86	0	6,6,6	0.49	0
2	SO4	D	109	-	4,4,4	0.95	0	6,6,6	0.62	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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.