

wwPDB X-ray Structure Validation Summary Report (i)

Dec 8, 2023 - 06:19 am GMT

PDB ID : 10CL

Title : THE CRYSTAL STRUCTURE OF MALONAMIDASE E2 COMPLEXED

WITH MALONATE FROM BRADYRHIZOBIUM JAPONICUM

Authors: Shin, S.; Ha, N.-C.; Lee, T.-H.; Oh, B.-H.

Deposited on : 2003-02-08

Resolution : 2.00 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 (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 (i)) were used in the production of this report:

Mol Probity : 4.02b-467

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)

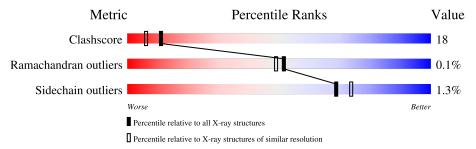
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.00 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	A	412	78%	22%	
1	В	412	79%	20%	



2 Entry composition (i)

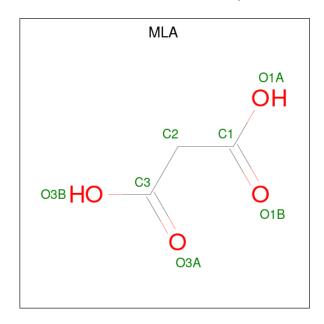
There are 3 unique types of molecules in this entry. The entry contains 6651 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 MALONAMIDASE E2.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	412	Total	С	N	О	S	0	0	0
1	A	412	3062	1919	562	568	13		U	0
1	B	412	Total	С	N	О	S	0	0	0
1	ъ	412	3062	1919	562	568	13			

• Molecule 2 is MALONIC ACID (three-letter code: MLA) (formula: $C_3H_4O_4$).



Mo	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 7 3 4	0	0
2	В	1	Total C O 7 3 4	0	0

• Molecule 3 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	283	Total O 283 283	0	0
3	В	230	Total O 230 230	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. 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. 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.

Note EDS was not executed.

• Molecule 1: MALONAMIDASE E2





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 21 21 2	Depositor	
Cell constants	103.82Å 94.94Å 74.78Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	20.00 - 2.00	Depositor	
% Data completeness	96.4 (20.00-2.00)	Depositor	
(in resolution range)	30.4 (20.00-2.00)		
R_{merge}	(Not available)	Depositor	
R_{sym}	0.06	Depositor	
Refinement program	CNS 1.1	Depositor	
R, R_{free}	0.196 , 0.243	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	6651	wwPDB-VP	
Average B, all atoms (Å ²)	20.0	wwPDB-VP	



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: MLA

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	Mol Chain		lengths	Bond angles	
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.29	0/3126	0.59	0/4247
1	В	0.29	0/3126	0.59	0/4247
All	All	0.29	0/6252	0.59	0/8494

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3062	0	3073	144	0
1	В	3062	0	3073	79	0
2	A	7	0	2	0	0
2	В	7	0	2	0	0
3	A	283	0	0	84	4
3	В	230	0	0	5	0
All	All	6651	0	6150	221	4

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 18.

The worst 5 of 221 close contacts within the same asymmetric unit are listed below, sorted by



their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:395:ASN:HB3	3:A:2270:HOH:O	1.33	1.25
1:A:223:ARG:HB2	3:A:2235:HOH:O	1.35	1.23
1:A:398:HIS:CE1	3:A:2276:HOH:O	1.92	1.22
1:A:337:ASP:CG	3:A:2234:HOH:O	1.78	1.19
1:A:395:ASN:CB	3:A:2270:HOH:O	1.79	1.16

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{(Å)} \end{aligned}$	Clash overlap (Å)
3:A:2265:HOH:O	3:A:2265:HOH:O[2_555]	1.24	0.96
3:A:2142:HOH:O	3:A:2146:HOH:O[2_555]	1.52	0.68
3:A:2047:HOH:O	3:A:2145:HOH:O[2_555]	1.68	0.52
3:A:2218:HOH:O	3:A:2223:HOH:O[2_555]	2.11	0.09

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	Percent	tiles
1	A	410/412 (100%)	393 (96%)	16 (4%)	1 (0%)	47	44
1	В	410/412 (100%)	393 (96%)	17 (4%)	0	100	100
All	All	820/824 (100%)	786 (96%)	33 (4%)	1 (0%)	51	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	63	ASP



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	305/305 (100%)	303 (99%)	2 (1%)	84	88	
1	В	305/305 (100%)	299 (98%)	6 (2%)	55	58	
All	All	610/610 (100%)	602 (99%)	8 (1%)	69	74	

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	406	LEU
1	В	378	LEU
1	В	202	ARG
1	В	30	GLU
1	В	283	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	395	ASN
1	В	362	ASN
1	A	398	HIS
1	В	388	GLN
1	В	83	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	Trino	Chain	Res	Link Bond lengths			В	ond ang	gles	
IVIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
2	MLA	A	1413	-	6,6,6	2.31	2 (33%)	7,7,7	2.01	2 (28%)
2	MLA	В	1413	-	6,6,6	2.26	2 (33%)	7,7,7	1.94	2 (28%)

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	MLA	A	1413	-	-	2/4/4/4	-
2	MLA	В	1413	-	-	0/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
2	В	1413	MLA	O1B-C1	3.97	1.35	1.22
2	A	1413	MLA	O1B-C1	3.74	1.34	1.22
2	A	1413	MLA	O1A-C1	-3.45	1.19	1.30
2	В	1413	MLA	O1A-C1	-3.23	1.19	1.30

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	A	1413	MLA	O1A-C1-C2	3.56	125.90	114.54
2	A	1413	MLA	O1B-C1-C2	-3.52	111.78	122.08

Continued on next page...



Continued from previous page...

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	1413	MLA	O1B-C1-C2	-3.47	111.93	122.08
2	В	1413	MLA	O1A-C1-C2	3.39	125.37	114.54

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1413	MLA	C1-C2-C3-O3A
2	A	1413	MLA	C1-C2-C3-O3B

There are no ring outliers.

No monomer is involved in short contacts.

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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

