



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:15 PM UTC

PDB ID : 2NX9 / pdb_00002nx9
Title : Crystal structure of the carboxyltransferase domain of the oxaloacetate decarboxylase Na⁺ pump from *Vibrio cholerae*
Authors : Studer, R.; Dimroth, P.
Deposited on : 2006-11-17
Resolution : 1.70 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

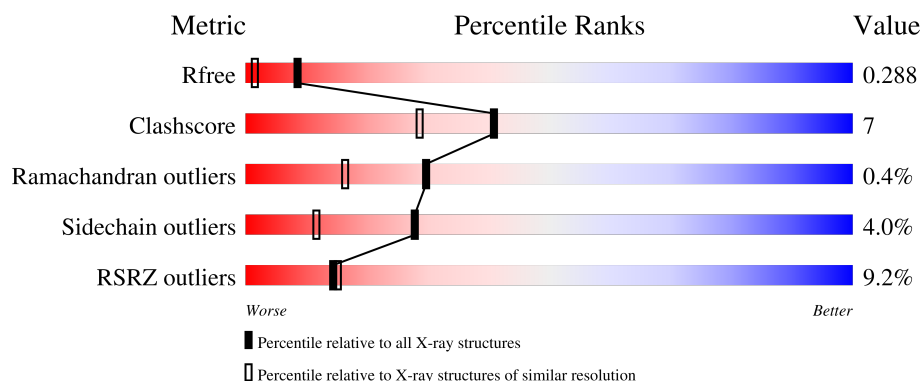
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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 $\leq 5\%$. 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
1	A	464	 6% 79% 16% ..
1	B	464	 11% 80% 17% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7541 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 Oxaloacetate decarboxylase 2, subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	451	Total	C	N	O	S	0	1	0
			3492	2202	608	661	21			
1	B	453	Total	C	N	O	S	0	1	0
			3508	2211	611	665	21			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	457	LEU	-	cloning artifact	UNP Q6A1F6
A	458	GLU	-	cloning artifact	UNP Q6A1F6
A	459	HIS	-	expression tag	UNP Q6A1F6
A	460	HIS	-	expression tag	UNP Q6A1F6
A	461	HIS	-	expression tag	UNP Q6A1F6
A	462	HIS	-	expression tag	UNP Q6A1F6
A	463	HIS	-	expression tag	UNP Q6A1F6
A	464	HIS	-	expression tag	UNP Q6A1F6
B	457	LEU	-	cloning artifact	UNP Q6A1F6
B	458	GLU	-	cloning artifact	UNP Q6A1F6
B	459	HIS	-	expression tag	UNP Q6A1F6
B	460	HIS	-	expression tag	UNP Q6A1F6
B	461	HIS	-	expression tag	UNP Q6A1F6
B	462	HIS	-	expression tag	UNP Q6A1F6
B	463	HIS	-	expression tag	UNP Q6A1F6
B	464	HIS	-	expression tag	UNP Q6A1F6

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	315	Total 315	O 315	0	0
3	B	224	Total 224	O 224	0	0

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.

- Chain A:
-
- 79% 16%
- Chain A: MET THR GLN A4 V10 T11 L15 A18 H19 L22 F23 A24 T25 T29 I35 A36 Q37 Q41 V45 S46 M50 D65 P66 M67 Q68 R69 L70 K74 M77 R87 E107 V110 K111 M112 G113 M123 V126 M129 A132 L133 M308 Q311 L312 N316 A317 L318 L321 L328 G336 F337 L338 V341 T344 I347 V348 G349 T350 V353 V356 V357 E368 P381 T386 A390 L393 A394 G395 L407 A408 A409 E410 M411 P412 T413 D416 R417 V418 L419 A422 Q425 R426

- Chain B:

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	90.83Å 91.66Å 116.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.00 – 1.70 35.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.5 (35.00-1.70) 98.5 (35.00-1.70)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.232 , 0.284 0.238 , 0.288	Depositor DCC
R_{free} test set	5272 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	22.2	Xtriage
Anisotropy	0.422	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.055 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7541	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.53% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.87	1/3551 (0.0%)	1.12	12/4817 (0.2%)
1	B	0.69	1/3567 (0.0%)	0.98	7/4839 (0.1%)
All	All	0.78	2/7118 (0.0%)	1.05	19/9656 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	209	HIS	ND1-CE1	6.78	1.39	1.32
1	B	209	HIS	ND1-CE1	5.05	1.37	1.32

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	10	VAL	N-CA-C	6.71	117.50	108.11
1	A	77	MET	CA-C-N	5.89	125.51	119.56
1	A	77	MET	C-N-CA	5.89	125.51	119.56
1	B	207	HIS	CG-CD2-NE2	5.65	112.85	107.20
1	B	250	VAL	N-CA-C	5.65	116.29	110.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3492	0	3533	51	0
1	B	3508	0	3548	42	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	315	0	0	0	0
3	B	224	0	0	0	0
All	All	7541	0	7081	92	0

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 7.

The worst 5 of 92 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:316:ASN:HB2	1:B:317:ALA:HA	1.19	1.09
1:B:148:CYS:SG	1:B:178:LYS:NZ	2.41	0.94
1:A:246:THR:O	1:A:250:VAL:HG23	1.73	0.89
1:B:316:ASN:HB2	1:B:317:ALA:CA	2.03	0.88
1:B:394:ALA:H	1:B:395:GLY:HA2	1.43	0.84

There are no symmetry-related clashes.

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	Percentiles	
1	A	450/464 (97%)	431 (96%)	16 (4%)	3 (1%)	18	7
1	B	452/464 (97%)	435 (96%)	16 (4%)	1 (0%)	43	28
All	All	902/928 (97%)	866 (96%)	32 (4%)	4 (0%)	30	16

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	394	ALA
1	B	394	ALA
1	A	259	ASP
1	A	316	ASN

5.3.2 Protein sidechains ⓘ

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	374/386 (97%)	357 (96%)	17 (4%)	24	9
1	B	376/386 (97%)	363 (96%)	13 (4%)	32	15
All	All	750/772 (97%)	720 (96%)	30 (4%)	28	12

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	425	GLN
1	B	338	LEU
1	B	2	THR
1	B	397	GLU
1	B	178	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	385	ASN
1	B	346	GLN
1	B	112	ASN
1	B	315	GLN
1	B	90	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

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](#)

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, 95th 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	A	451/464 (97%)	0.45	30 (6%) 24 26	3, 16, 37, 57	1 (0%)
1	B	453/464 (97%)	0.70	53 (11%) 9 9	5, 19, 39, 49	1 (0%)
All	All	904/928 (97%)	0.58	83 (9%) 14 15	3, 17, 38, 57	2 (0%)

The worst 5 of 83 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	394	ALA	8.4
1	B	430	ALA	4.8
1	B	394	ALA	4.5
1	B	386	THR	4.2
1	A	412	PRO	3.8

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 oligosaccharides 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, 95th 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($\text{\AA}^2$)	Q<0.9
2	ZN	A	601	1/1	0.99	0.19	34,34,34,34	0
2	ZN	B	602	1/1	0.99	0.18	36,36,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.