



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:31 PM UTC

PDB ID : 1CAY / pdb_00001cay
Title : WILD-TYPE AND E106Q MUTANT CARBONIC ANHYDRASE COM-
PLEXED WITH ACETATE
Authors : Hakansson, K.; Briand, C.; Zaitsev, V.; Xue, Y.; Liljas, A.
Deposited on : 1993-02-26
Resolution : 2.10 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (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

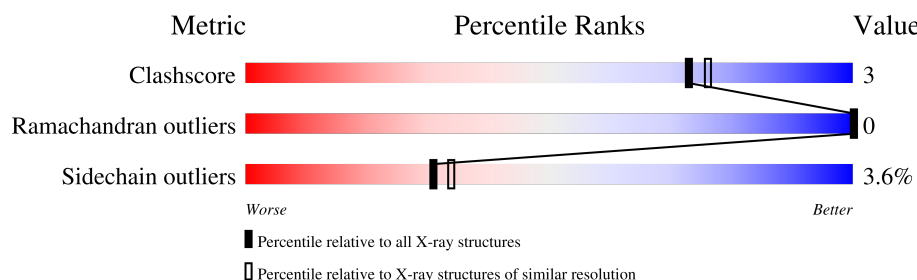
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	259	 71% 25% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ACY	A	500	-	X	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2301 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.

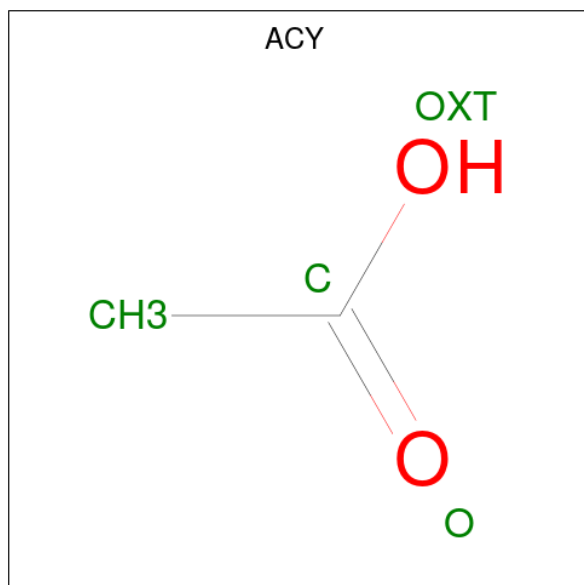
- Molecule 1 is a protein called CARBONIC ANHYDRASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	4	0
			2079	1333	360	384	2			

- 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		

- Molecule 3 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	217	Total 217	O 217	0	0

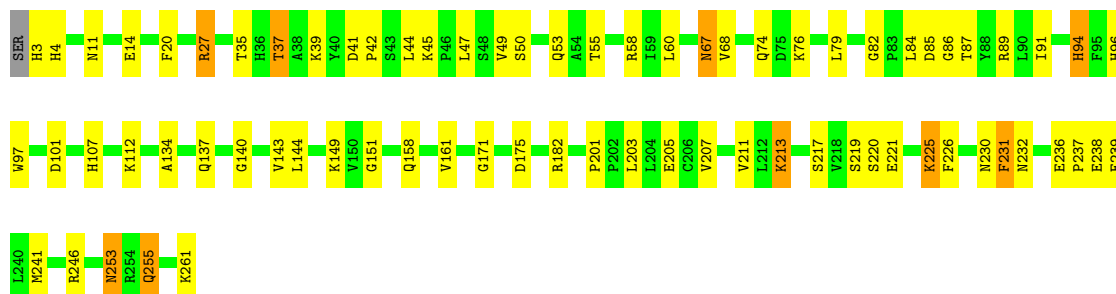
3 Residue-property plots

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: CARBONIC ANHYDRASE II

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.70 Å 41.70 Å 73.00 Å 90.00° 104.60° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROFFT	Depositor
R, R_{free}	0.141 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2301	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACY, 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	1.45	6/2161 (0.3%)	2.06	74/2931 (2.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	2	0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	94	HIS	CD2-NE2	-7.96	1.29	1.37
1	A	86	GLY	N-CA	6.97	1.52	1.45
1	A	144	LEU	C-N	-6.28	1.29	1.33
1	A	253	ASN	C-O	5.83	1.31	1.24
1	A	87	THR	CA-CB	5.31	1.61	1.53
1	A	253	ASN	N-CA	5.12	1.52	1.46

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	230	ASN	CA-CB-CG	10.48	123.08	112.60
1	A	85	ASP	CA-CB-CG	8.97	121.57	112.60
1	A	158	GLN	OE1-CD-NE2	-8.93	113.67	122.60
1	A	58	ARG	N-CA-CB	-8.64	98.17	111.56
1	A	182	ARG	NE-CZ-NH1	7.61	129.10	121.50
1	A	221	GLU	CG-CD-OE1	7.61	135.89	118.40
1	A	3	HIS	CA-CB-CG	7.44	121.24	113.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	220	SER	CA-CB-OG	-7.26	96.58	111.10
1	A	87	THR	CA-CB-OG1	-7.20	98.80	109.60
1	A	53	GLN	CG-CD-NE2	-7.14	105.70	116.40
1	A	101	ASP	CA-CB-CG	7.00	119.60	112.60
1	A	68	VAL	CA-C-O	-6.96	113.00	120.59
1	A	226	PHE	CA-CB-CG	6.94	120.74	113.80
1	A	89	ARG	NE-CZ-NH2	-6.86	113.03	119.20
1	A	219	SER	CA-C-O	6.83	129.78	121.72
1	A	97	TRP	CA-C-N	-6.62	114.76	122.77
1	A	97	TRP	C-N-CA	-6.62	114.76	122.77
1	A	85	ASP	CA-C-N	-6.44	112.72	122.06
1	A	85	ASP	C-N-CA	-6.44	112.72	122.06
1	A	94	HIS	CA-CB-CG	-6.39	107.41	113.80
1	A	207	VAL	N-CA-C	6.25	117.59	108.53
1	A	137	GLN	O-C-N	6.13	127.52	121.57
1	A	231	PHE	CA-CB-CG	6.07	119.87	113.80
1	A	42	PRO	CB-CA-C	6.05	119.41	110.88
1	A	14[A]	GLU	CA-C-O	6.03	126.80	119.38
1	A	14[B]	GLU	CA-C-O	6.03	126.80	119.38
1	A	94	HIS	CE1-NE2-CD2	5.99	114.99	109.00
1	A	236	GLU	CB-CG-CD	5.99	122.78	112.60
1	A	84	LEU	O-C-N	5.97	129.75	123.06
1	A	237	PRO	CB-CA-C	5.96	119.14	111.46
1	A	37	THR	CA-CB-CG2	5.90	120.54	110.50
1	A	27	ARG	CA-CB-CG	5.85	125.79	114.10
1	A	96	HIS	CA-CB-CG	-5.83	107.97	113.80
1	A	225	LYS	CA-CB-CG	-5.82	102.46	114.10
1	A	171	GLY	CA-C-O	-5.78	113.08	119.27
1	A	217	SER	CA-CB-OG	-5.73	99.63	111.10
1	A	182	ARG	CA-CB-CG	-5.71	102.68	114.10
1	A	41	ASP	CB-CA-C	5.68	118.08	110.13
1	A	35	THR	N-CA-C	5.64	118.37	111.82
1	A	53	GLN	OE1-CD-NE2	5.63	128.23	122.60
1	A	67	ASN	CA-C-O	-5.61	114.77	120.71
1	A	49	VAL	CA-C-O	-5.61	114.10	120.66
1	A	236	GLU	N-CA-C	-5.58	102.02	110.50
1	A	41	ASP	CA-C-O	5.53	124.81	119.62
1	A	11	ASN	O-C-N	5.51	129.65	122.15
1	A	255	GLN	OE1-CD-NE2	5.46	128.06	122.60
1	A	246	ARG	CA-C-O	5.45	124.77	120.19
1	A	68	VAL	N-CA-C	-5.41	100.09	107.99
1	A	3	HIS	CA-C-O	-5.40	111.61	120.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	211	VAL	CA-C-O	-5.39	114.76	120.53
1	A	261	LYS	N-CA-CB	5.38	119.64	110.50
1	A	44	LEU	O-C-N	5.37	129.35	123.01
1	A	107	HIS	CA-CB-CG	-5.36	108.44	113.80
1	A	253	ASN	CA-C-O	-5.36	112.84	120.51
1	A	230	ASN	CB-CG-ND2	5.36	124.43	116.40
1	A	255	GLN	CA-C-O	-5.35	115.04	120.71
1	A	37	THR	CA-CB-OG1	-5.33	101.61	109.60
1	A	87	THR	O-C-N	5.33	129.42	123.19
1	A	151	GLY	N-CA-C	-5.31	100.58	113.18
1	A	60	LEU	N-CA-CB	-5.30	101.65	111.13
1	A	236	GLU	CA-CB-CG	5.28	124.66	114.10
1	A	144	LEU	CA-C-O	-5.27	114.53	120.43
1	A	74	GLN	O-C-N	5.21	129.09	123.10
1	A	175	ASP	N-CA-C	-5.20	102.69	110.23
1	A	213	LYS	CB-CG-CD	5.13	123.11	111.30
1	A	11	ASN	OD1-CG-ND2	-5.13	117.47	122.60
1	A	20	PHE	O-C-N	5.13	125.99	121.37
1	A	107	HIS	N-CA-CB	5.11	117.52	110.17
1	A	4[A]	HIS	CA-CB-CG	-5.09	108.71	113.80
1	A	4[B]	HIS	CA-CB-CG	-5.09	108.71	113.80
1	A	232	ASN	CA-C-O	5.06	127.74	121.87
1	A	91	ILE	CA-CB-CG2	5.04	119.07	110.50
1	A	238	GLU	CG-CD-OE2	5.04	130.00	118.40
1	A	96	HIS	CA-C-O	-5.02	114.74	120.32

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	4[A]	HIS	CA
1	A	4[B]	HIS	CA

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	2079	0	2021	13	0
2	A	1	0	0	0	0
3	A	4	0	3	2	0
4	A	217	0	0	2	0
All	All	2301	0	2024	13	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 3.

All (13) 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:A:201:PRO:HA	1:A:203:LEU:HG	1.88	0.55
1:A:143:VAL:HG21	3:A:500:ACY:CH3	2.38	0.54
1:A:47:LEU:HD22	1:A:79:LEU:HD11	1.90	0.52
1:A:112:LYS:NZ	4:A:423:HOH:O	2.45	0.50
1:A:161:VAL:CG1	1:A:225:LYS:HD2	2.42	0.50
1:A:27:ARG:HG3	1:A:205:GLU:HB3	1.93	0.48
1:A:55:THR:OG1	1:A:76:LYS:HE2	2.16	0.46
1:A:45:LYS:O	1:A:82:GLY:HA2	2.17	0.44
1:A:27:ARG:HD3	4:A:294:HOH:O	2.17	0.43
1:A:67:ASN:HD22	1:A:94:HIS:HB3	1.83	0.43
1:A:143:VAL:HG21	3:A:500:ACY:H1	2.01	0.41
1:A:134:ALA:O	1:A:140:GLY:HA3	2.20	0.40
1:A:231:PHE:CE1	1:A:241:MET:HG3	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	260/259 (100%)	250 (96%)	10 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	227/224 (101%)	219 (96%)	8 (4%)	32 35

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	THR
1	A	39	LYS
1	A	50	SER
1	A	149	LYS
1	A	213	LYS
1	A	239	GLU
1	A	253	ASN
1	A	255	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	ACY	A	500	2	3,3,3	1.49	1 (33%)	3,3,3	2.45	2 (66%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	ACY	CH3-C	2.01	1.57	1.49

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	500	ACY	O-C-CH3	3.42	136.55	122.53
3	A	500	ACY	OXT-C-CH3	-2.21	105.78	115.05

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	500	ACY	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.