



Full wwPDB X-ray Structure Validation Report i

Feb 26, 2014 – 11:41 PM GMT

PDB ID : 1CVA
Title : STRUCTURAL AND FUNCTIONAL IMPORTANCE OF A CONSERVED
HYDROGEN BOND NETWORK IN HUMAN CARBONIC ANHYDRASE
II
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Deposited on : 1993-02-04
Resolution : 2.25 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

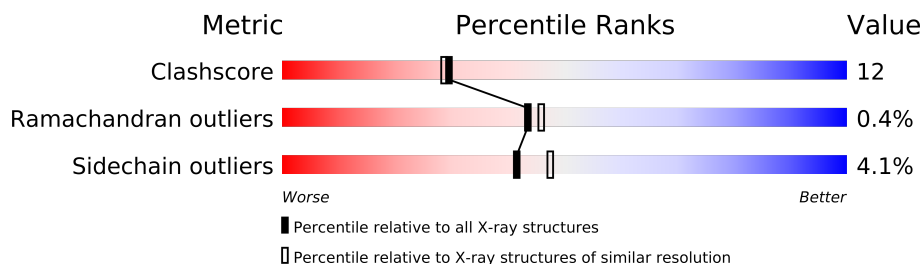
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.25 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	79885	1326 (2.28-2.24)
Ramachandran outliers	78287	1291 (2.28-2.24)
Sidechain outliers	78261	1291 (2.28-2.24)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	259	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2127 atoms, of which 0 are hydrogen and 0 are deuterium.

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	255	Total	C	N	O	S	0	0	0
			2029	1304	347	376	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	199	VAL	THR	CONFLICT	UNP P00918

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is AZIDE ION (three-letter code: AZI) (formula: N₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total N 3 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	94	Total O 94 94	0	0

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.70Å 41.70Å 73.00Å 90.00° 104.60° 90.00°	Depositor
Resolution (Å)	6.50 – 2.25	Depositor
% Data completeness (in resolution range)	(Not available) (6.50-2.25)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.173 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2127	wwPDB-VP
Average B, all atoms (Å ²)	14.0	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: AZI, 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	1.51	14/2089 (0.7%)	1.65	27/2836 (1.0%)

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	0	2

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	14	GLU	CD-OE1	8.64	1.35	1.25
1	A	238	GLU	CD-OE1	8.41	1.34	1.25
1	A	236	GLU	CD-OE2	7.31	1.33	1.25
1	A	129	GLY	N-CA	-6.75	1.35	1.46
1	A	236	GLU	CD-OE1	-6.64	1.18	1.25
1	A	205	GLU	CD-OE2	6.00	1.32	1.25
1	A	238	GLU	CD-OE2	-5.90	1.19	1.25
1	A	192	TRP	CD2-CE2	5.53	1.48	1.41
1	A	95	PHE	CE2-CZ	5.39	1.47	1.37
1	A	226	PHE	CG-CD2	5.34	1.46	1.38
1	A	14	GLU	CD-OE2	-5.33	1.19	1.25
1	A	151	GLY	CA-C	5.31	1.60	1.51
1	A	215	PRO	N-CD	5.19	1.55	1.47
1	A	214	GLU	CD-OE2	-5.10	1.20	1.25

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	246	ARG	NE-CZ-NH1	10.65	125.63	120.30
1	A	89	ARG	NE-CZ-NH1	10.00	125.30	120.30
1	A	85	ASP	CB-CG-OD2	8.42	125.88	118.30
1	A	27	ARG	NE-CZ-NH1	8.07	124.34	120.30
1	A	202	PRO	CA-N-CD	-7.82	100.55	111.50
1	A	51	TYR	CB-CG-CD1	7.82	125.69	121.00
1	A	72	ASP	CB-CG-OD2	7.11	124.70	118.30
1	A	202	PRO	N-CA-CB	7.06	111.77	103.30
1	A	75	ASP	CB-CG-OD1	6.84	124.45	118.30
1	A	58	ARG	NE-CZ-NH1	6.49	123.55	120.30
1	A	201	PRO	CA-C-O	-6.16	105.41	120.20
1	A	30	PRO	CA-N-CD	-6.10	102.96	111.50
1	A	209	TRP	CD1-CG-CD2	6.07	111.15	106.30
1	A	202	PRO	N-CD-CG	6.03	112.24	103.20
1	A	89	ARG	NE-CZ-NH2	-6.00	117.30	120.30
1	A	110	ASP	CB-CG-OD2	5.93	123.63	118.30
1	A	40	TYR	CB-CG-CD1	-5.86	117.49	121.00
1	A	239	GLU	CA-CB-CG	5.64	125.80	113.40
1	A	175	ASP	CB-CG-OD1	5.56	123.31	118.30
1	A	34	ASP	CB-CG-OD2	5.46	123.22	118.30
1	A	139	ASP	CB-CG-OD1	5.24	123.02	118.30
1	A	175	ASP	CB-CA-C	5.22	120.84	110.40
1	A	130	ASP	CB-CG-OD1	5.13	122.92	118.30
1	A	236	GLU	CG-CD-OE2	-5.11	108.09	118.30
1	A	182	ARG	CD-NE-CZ	-5.07	116.50	123.60
1	A	141	LEU	CA-CB-CG	5.06	126.94	115.30
1	A	23	ALA	O-C-N	5.05	130.77	122.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	254	ARG	Sidechain
1	A	58	ARG	Sidechain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2029	0	1984	49	1
2	A	1	0	0	0	0
3	A	3	0	0	2	0
4	A	94	0	0	3	1
All	All	2127	0	1984	49	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

All (49) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:58:ARG:HD2	1:A:69:GLU:OE1	1.46	1.15
1:A:63:GLY:HA3	1:A:170:LYS:HZ3	1.33	0.91
1:A:253:ASN:HD22	1:A:254:ARG:N	1.77	0.82
1:A:165:ASP:HB2	4:A:304:HOH:O	1.86	0.75
1:A:161:VAL:CG1	1:A:225:LYS:HD2	2.17	0.74
1:A:253:ASN:ND2	1:A:254:ARG:N	2.35	0.73
1:A:63:GLY:HA3	1:A:170:LYS:NZ	2.03	0.72
1:A:253:ASN:HD22	1:A:253:ASN:C	1.94	0.70
1:A:161:VAL:HG13	1:A:225:LYS:HD2	1.75	0.67
1:A:213:LYS:HD3	1:A:260:PHE:CZ	2.31	0.66
1:A:250:PRO:HB2	1:A:252:LYS:HG3	1.82	0.61
1:A:236:GLU:HB3	1:A:237:PRO:HD2	1.84	0.60
1:A:62:ASN:O	1:A:170:LYS:NZ	2.33	0.60
1:A:110:ASP:O	1:A:111:LYS:HB2	2.02	0.59
1:A:128:TYR:CZ	1:A:137:GLN:HG3	2.38	0.59
1:A:253:ASN:C	1:A:253:ASN:ND2	2.59	0.56
1:A:128:TYR:CE1	1:A:137:GLN:HG3	2.40	0.56
1:A:249:GLN:HB3	1:A:250:PRO:CD	2.36	0.56
1:A:160:VAL:O	1:A:163:VAL:HG12	2.06	0.56
1:A:45:LYS:O	1:A:82:GLY:HA2	2.08	0.54
1:A:202:PRO:HG2	1:A:204:LEU:HG	1.90	0.54
1:A:159:LYS:HE2	1:A:179:PHE:HD1	1.72	0.53
1:A:103:GLN:NE2	1:A:243:ASP:OD1	2.44	0.51
1:A:201:PRO:HA	1:A:203:LEU:HG	1.93	0.51
1:A:213:LYS:HD3	1:A:260:PHE:CE2	2.46	0.50
1:A:27:ARG:HG3	1:A:205:GLU:HB3	1.94	0.50
1:A:249:GLN:HB3	1:A:250:PRO:HD2	1.94	0.49
1:A:47:LEU:HD11	1:A:210:ILE:HG21	1.94	0.49
1:A:75:ASP:OD1	1:A:89:ARG:NE	2.41	0.47
1:A:180:ASP:HA	1:A:181:PRO:HD2	1.76	0.47
1:A:27:ARG:CG	1:A:205:GLU:HB3	2.45	0.46
1:A:199:VAL:HG22	3:A:357:AZI:N3	2.31	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:243:ASP:HA	1:A:245:TRP:CD1	2.50	0.45
1:A:199:VAL:HG22	3:A:357:AZI:N2	2.31	0.45
1:A:72:ASP:OD2	1:A:123:TRP:NE1	2.42	0.45
1:A:159:LYS:HD2	4:A:308:HOH:O	2.17	0.45
1:A:230:ASN:HB3	1:A:232:ASN:OD1	2.18	0.44
1:A:59:ILE:HA	1:A:67:ASN:O	2.18	0.44
1:A:58:ARG:CD	1:A:69:GLU:OE1	2.39	0.43
1:A:88:TYR:CE2	1:A:124:ASN:HB2	2.53	0.43
1:A:223:VAL:O	1:A:226:PHE:HB2	2.19	0.43
1:A:89:ARG:O	1:A:122:HIS:HA	2.20	0.42
1:A:60:LEU:HD21	1:A:67:ASN:HB2	2.02	0.42
1:A:51:TYR:CD1	1:A:77:ALA:HB1	2.55	0.42
1:A:167:ILE:HG13	1:A:167:ILE:O	2.19	0.41
1:A:144:LEU:HA	1:A:144:LEU:HD23	1.87	0.41
1:A:178:ASN:HB2	4:A:325:HOH:O	2.22	0.40
1:A:146:ILE:HG12	1:A:212:LEU:HD12	2.04	0.40
1:A:5:TRP:CH2	1:A:200:THR:HB	2.55	0.40

All (1) 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	Distance(Å)	Clash(Å)
1:A:162:ASP:OD2	4:A:352:HOH:O[2_445]	2.00	0.20

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	253/259 (98%)	237 (94%)	15 (6%)	1 (0%)	43	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	253	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	220/224 (98%)	211 (96%)	9 (4%)	41 47

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	LYS
1	A	30	PRO
1	A	44	LEU
1	A	58	ARG
1	A	79	LEU
1	A	83	PRO
1	A	127	LYS
1	A	220	SER
1	A	253	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	253	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	AZI	A	357	2	2,2,2	1.92	1 (50%)	0,1,1	0.00	-

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
3	AZI	A	357	2	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	357	AZI	N3-N2	2.17	1.29	1.21

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.