



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:48 PM GMT

PDB ID : 1HED
Title : STRUCTURAL CONSEQUENCES OF HYDROPHILIC AMINO-ACID
SUBSTITUTIONS IN THE HYDROPHOBIC POCKET OF HUMAN CAR-
BONIC ANHYDRASE II
Authors : Nair, S.K.; Christianson, D.W.
Deposited on : 1992-07-16
Resolution : 2.00 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

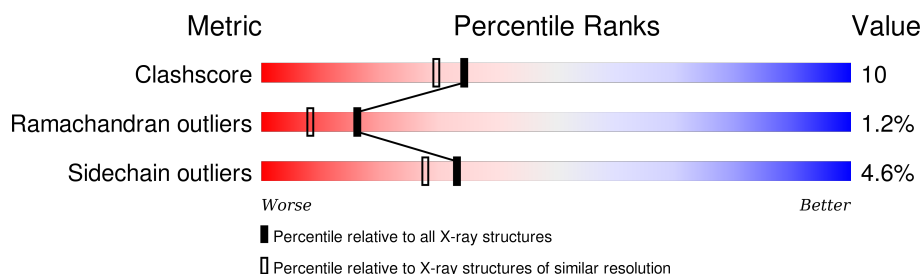
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	260	 70% 23% . . .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2136 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	255	Total	C	N	O	S	0	0	0
			2026	1300	347	377	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	198	ALA	LEU	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 MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Hg	0	0
			2	2		

- Molecule 4 is water.

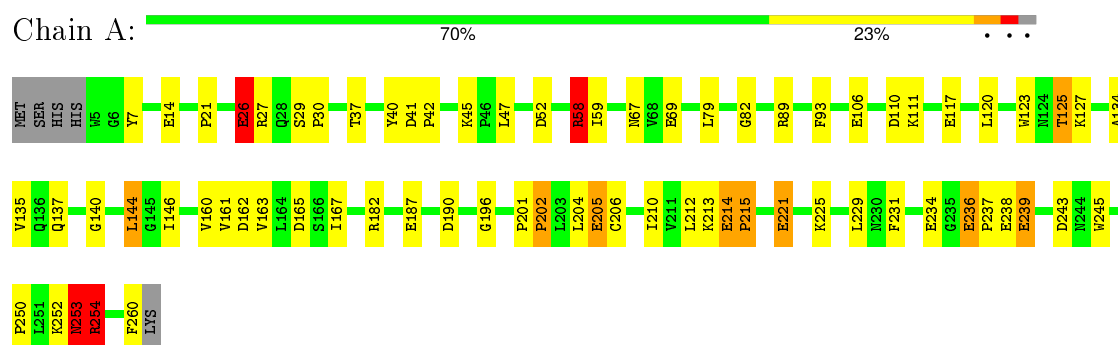
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	107	Total	O	0	0
			107	107		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

• Molecule 1: CARBONIC ANHYDRASE II



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	42.70 Å 41.70 Å 73.00 Å 90.00° 104.60° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.186 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2136	wwPDB-VP
Average B, all atoms (Å ²)	10.0	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: ZN, HG

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	1.64	16/2086 (0.8%)	1.62	24/2832 (0.8%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	125	THR	C-N	28.39	1.99	1.34
1	A	239	GLU	CD-OE2	9.83	1.36	1.25
1	A	205	GLU	CD-OE2	8.49	1.34	1.25
1	A	236	GLU	CD-OE2	7.87	1.34	1.25
1	A	14	GLU	CD-OE1	7.65	1.34	1.25
1	A	221	GLU	CD-OE1	6.53	1.32	1.25
1	A	214	GLU	CD-OE1	5.88	1.32	1.25
1	A	238	GLU	CD-OE2	-5.88	1.19	1.25
1	A	187	GLU	CD-OE1	5.78	1.32	1.25
1	A	239	GLU	CD-OE1	-5.59	1.19	1.25
1	A	106	GLU	CB-CG	5.53	1.62	1.52
1	A	234	GLU	CD-OE1	5.29	1.31	1.25
1	A	215	PRO	N-CD	5.25	1.55	1.47
1	A	26	GLU	CD-OE2	5.23	1.31	1.25
1	A	117	GLU	CD-OE1	-5.22	1.20	1.25
1	A	196	GLY	N-CA	5.19	1.53	1.46

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	ARG	NE-CZ-NH2	-11.12	114.74	120.30
1	A	89	ARG	NE-CZ-NH1	9.55	125.08	120.30
1	A	30	PRO	CA-N-CD	-9.39	98.35	111.50
1	A	201	PRO	O-C-N	9.05	138.30	121.10
1	A	165	ASP	CB-CG-OD1	8.67	126.11	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	202	PRO	CA-N-CD	-8.49	99.61	111.50
1	A	162	ASP	CB-CG-OD1	8.49	125.94	118.30
1	A	202	PRO	N-CD-CG	8.45	115.87	103.20
1	A	201	PRO	CA-C-O	-8.42	100.00	120.20
1	A	29	SER	CA-C-O	-8.21	102.87	120.10
1	A	30	PRO	N-CD-CG	7.91	115.07	103.20
1	A	29	SER	O-C-N	7.86	136.04	121.10
1	A	30	PRO	N-CA-CB	7.63	112.46	103.30
1	A	239	GLU	CA-CB-CG	7.52	129.95	113.40
1	A	125	THR	C-N-CA	-6.77	104.77	121.70
1	A	202	PRO	N-CA-CB	6.69	111.33	103.30
1	A	254	ARG	NE-CZ-NH2	6.16	123.38	120.30
1	A	93	PHE	CB-CG-CD2	-6.00	116.60	120.80
1	A	182	ARG	NE-CZ-NH1	-5.98	117.31	120.30
1	A	7	TYR	CB-CG-CD1	-5.97	117.42	121.00
1	A	236	GLU	CA-CB-CG	5.70	125.94	113.40
1	A	221	GLU	CG-CD-OE2	5.38	129.07	118.30
1	A	41	ASP	CB-CG-OD2	5.29	123.06	118.30
1	A	58	ARG	CD-NE-CZ	5.12	130.76	123.60

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	2026	0	1974	40	0
2	A	1	0	0	0	0
3	A	2	0	0	0	0
4	A	107	0	0	2	0
All	All	2136	0	1974	40	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 10.

All (40) 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:125:THR:C	1:A:127:LYS:N	1.99	1.14
1:A:58:ARG:HD2	1:A:69:GLU:OE1	1.57	1.03
1:A:213:LYS:HD3	1:A:260:PHE:CZ	2.11	0.86
1:A:253:ASN:HD22	1:A:254:ARG:N	1.85	0.75
1:A:253:ASN:ND2	1:A:254:ARG:N	2.41	0.69
1:A:26:GLU:OE1	1:A:205:GLU:OE1	2.09	0.69
1:A:253:ASN:HD22	1:A:253:ASN:C	1.96	0.68
1:A:58:ARG:CD	1:A:69:GLU:OE1	2.40	0.65
1:A:236:GLU:HB3	1:A:237:PRO:HD2	1.77	0.65
1:A:144:LEU:HD22	1:A:212:LEU:HD21	1.82	0.61
1:A:45:LYS:O	1:A:82:GLY:HA2	2.00	0.60
1:A:146:ILE:HG12	1:A:212:LEU:HD23	1.82	0.60
1:A:231:PHE:HD2	1:A:239:GLU:HG2	1.67	0.59
1:A:252:LYS:O	1:A:253:ASN:CG	2.42	0.57
1:A:58:ARG:HD2	1:A:69:GLU:CD	2.25	0.56
1:A:253:ASN:C	1:A:253:ASN:ND2	2.60	0.54
1:A:110:ASP:O	1:A:111:LYS:HB2	2.06	0.54
1:A:236:GLU:HB3	1:A:237:PRO:CD	2.38	0.54
1:A:125:THR:C	1:A:127:LYS:CA	2.76	0.53
1:A:213:LYS:HD3	1:A:260:PHE:CE1	2.42	0.52
1:A:144:LEU:HD22	1:A:212:LEU:CD2	2.41	0.50
1:A:134:ALA:O	1:A:140:GLY:HA3	2.12	0.50
1:A:161:VAL:HG13	1:A:225:LYS:HD2	1.95	0.48
1:A:190:ASP:HB3	1:A:260:PHE:CD2	2.49	0.48
1:A:59:ILE:HA	1:A:67:ASN:O	2.13	0.48
1:A:146:ILE:CG1	1:A:212:LEU:HD23	2.44	0.47
1:A:59:ILE:HG12	1:A:167:ILE:HD13	1.96	0.46
1:A:202:PRO:HG2	1:A:204:LEU:HG	1.99	0.45
1:A:239:GLU:HB2	4:A:370:HOH:O	2.17	0.44
1:A:160:VAL:O	1:A:163:VAL:HG12	2.18	0.44
1:A:26:GLU:CD	1:A:26:GLU:H	2.19	0.43
1:A:214:GLU:HA	1:A:215:PRO:HD3	1.75	0.43
1:A:123:TRP:CZ3	1:A:125:THR:HA	2.54	0.43
1:A:243:ASP:HA	1:A:245:TRP:CD1	2.53	0.43
1:A:137:GLN:O	1:A:206:CYS:HB3	2.19	0.42
1:A:250:PRO:HB2	1:A:252:LYS:HG3	2.01	0.42
1:A:27:ARG:CG	1:A:205:GLU:HB3	2.50	0.41
1:A:40:TYR:CE2	1:A:42:PRO:HG3	2.55	0.41
1:A:21:PRO:HD2	4:A:272:HOH:O	2.22	0.40
1:A:47:LEU:HD11	1:A:210:ILE:HG21	2.02	0.40

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	253/260 (97%)	240 (95%)	10 (4%)	3 (1%)	16 8

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	253	ASN
1	A	254	ARG
1	A	135	VAL

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	219/224 (98%)	209 (95%)	10 (5%)	33 28

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	GLU
1	A	37	THR
1	A	52	ASP
1	A	58	ARG
1	A	79	LEU
1	A	120	LEU
1	A	144	LEU
1	A	221	GLU

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Mol	Chain	Res	Type
1	A	229	LEU
1	A	253	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	136	GLN
1	A	137	GLN
1	A	253	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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 ⓘ

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.