



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 17, 2023 – 08:51 PM EDT

PDB ID : 4YGF
Title : Crystal structure of the complex of Helicobacter pylori alpha-Carbonic Anhydrase with acetazolamide
Authors : Roujeinikova, A.; Modak, J.K.
Deposited on : 2015-02-26
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 ⓘ 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

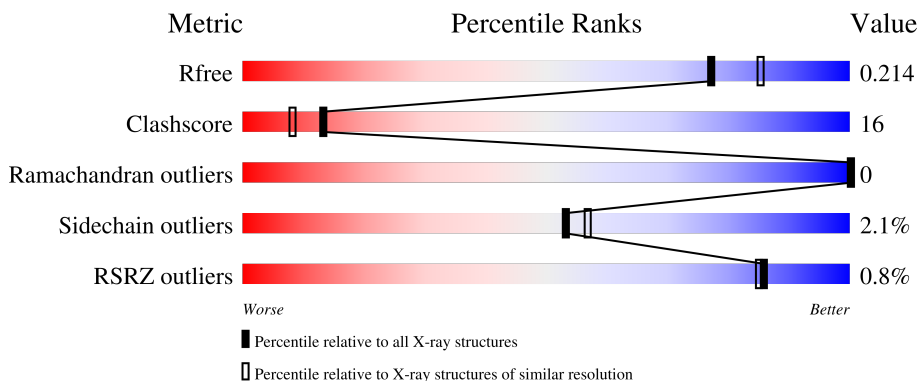
1 Overall quality at a glance i

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))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (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 $\leq 5\%$. 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	234	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 64%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 32%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">64% 32% ..</p>
1	B	234	<div style="display: flex; align-items: center;"> <div style="width: 68%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 26%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">68% 26% . 5%</p>
1	C	234	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 74%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 22%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">74% 22% ..</p>
1	D	234	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 58%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 34%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">2% 58% 34% . .</p>
1	E	234	<div style="display: flex; align-items: center;"> <div style="width: 74%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 23%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">74% 23% .</p>

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Mol	Chain	Length	Quality of chain
1	F	234	 % 63% 33% .
1	G	234	 64% 32% ..
1	H	234	 67% 26% . .

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	CL	B	302	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 15976 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 Alpha-carbonic anhydrase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	226	Total 1866	C 1201	N 325	O 336	S 4	0	4	0
1	B	223	Total 1833	C 1178	N 320	O 331	S 4	0	2	0
1	C	227	Total 1860	C 1192	N 326	O 338	S 4	0	1	0
1	D	224	Total 1836	C 1180	N 323	O 329	S 4	0	1	0
1	E	226	Total 1853	C 1188	N 325	O 336	S 4	0	1	0
1	F	225	Total 1841	C 1180	N 323	O 334	S 4	0	0	0
1	G	228	Total 1877	C 1205	N 328	O 340	S 4	0	3	0
1	H	225	Total 1841	C 1180	N 323	O 334	S 4	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	GLY	-	expression tag	UNP K4NGD4
A	15	ILE	-	expression tag	UNP K4NGD4
A	16	ASP	-	expression tag	UNP K4NGD4
A	17	PRO	-	expression tag	UNP K4NGD4
A	18	PHE	-	expression tag	UNP K4NGD4
A	19	THR	-	expression tag	UNP K4NGD4
B	14	GLY	-	expression tag	UNP K4NGD4
B	15	ILE	-	expression tag	UNP K4NGD4
B	16	ASP	-	expression tag	UNP K4NGD4
B	17	PRO	-	expression tag	UNP K4NGD4
B	18	PHE	-	expression tag	UNP K4NGD4
B	19	THR	-	expression tag	UNP K4NGD4
C	14	GLY	-	expression tag	UNP K4NGD4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	15	ILE	-	expression tag	UNP K4NGD4
C	16	ASP	-	expression tag	UNP K4NGD4
C	17	PRO	-	expression tag	UNP K4NGD4
C	18	PHE	-	expression tag	UNP K4NGD4
C	19	THR	-	expression tag	UNP K4NGD4
D	14	GLY	-	expression tag	UNP K4NGD4
D	15	ILE	-	expression tag	UNP K4NGD4
D	16	ASP	-	expression tag	UNP K4NGD4
D	17	PRO	-	expression tag	UNP K4NGD4
D	18	PHE	-	expression tag	UNP K4NGD4
D	19	THR	-	expression tag	UNP K4NGD4
E	14	GLY	-	expression tag	UNP K4NGD4
E	15	ILE	-	expression tag	UNP K4NGD4
E	16	ASP	-	expression tag	UNP K4NGD4
E	17	PRO	-	expression tag	UNP K4NGD4
E	18	PHE	-	expression tag	UNP K4NGD4
E	19	THR	-	expression tag	UNP K4NGD4
F	14	GLY	-	expression tag	UNP K4NGD4
F	15	ILE	-	expression tag	UNP K4NGD4
F	16	ASP	-	expression tag	UNP K4NGD4
F	17	PRO	-	expression tag	UNP K4NGD4
F	18	PHE	-	expression tag	UNP K4NGD4
F	19	THR	-	expression tag	UNP K4NGD4
G	14	GLY	-	expression tag	UNP K4NGD4
G	15	ILE	-	expression tag	UNP K4NGD4
G	16	ASP	-	expression tag	UNP K4NGD4
G	17	PRO	-	expression tag	UNP K4NGD4
G	18	PHE	-	expression tag	UNP K4NGD4
G	19	THR	-	expression tag	UNP K4NGD4
H	14	GLY	-	expression tag	UNP K4NGD4
H	15	ILE	-	expression tag	UNP K4NGD4
H	16	ASP	-	expression tag	UNP K4NGD4
H	17	PRO	-	expression tag	UNP K4NGD4
H	18	PHE	-	expression tag	UNP K4NGD4
H	19	THR	-	expression tag	UNP K4NGD4

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

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

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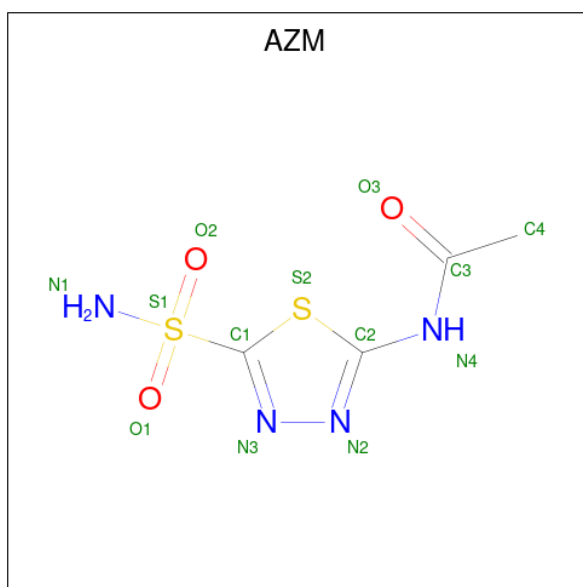
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total 1	Zn 1	0	0
2	D	1	Total 1	Zn 1	0	0
2	E	1	Total 1	Zn 1	0	0
2	F	1	Total 1	Zn 1	0	0
2	G	1	Total 1	Zn 1	0	0
2	H	1	Total 1	Zn 1	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Cl 1	0	0
3	B	1	Total 1	Cl 1	0	0
3	C	1	Total 1	Cl 1	0	0
3	D	1	Total 1	Cl 1	0	0
3	E	1	Total 1	Cl 1	0	0
3	F	1	Total 1	Cl 1	0	0
3	G	1	Total 1	Cl 1	0	0
3	H	1	Total 1	Cl 1	0	0

- Molecule 4 is 5-ACETAMIDO-1,3,4-THIADIAZOLE-2-SULFONAMIDE (three-letter code: AZM) (formula: C₄H₆N₄O₃S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
4	A	1	Total 13	C 4	N 4	O 3	S 2	0	0
4	B	1	Total 13	C 4	N 4	O 3	S 2	0	0
4	C	1	Total 13	C 4	N 4	O 3	S 2	0	0
4	D	1	Total 13	C 4	N 4	O 3	S 2	0	0
4	E	1	Total 13	C 4	N 4	O 3	S 2	0	0
4	F	1	Total 13	C 4	N 4	O 3	S 2	0	0
4	G	1	Total 13	C 4	N 4	O 3	S 2	0	0
4	H	1	Total 13	C 4	N 4	O 3	S 2	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	C	1	Total C O 6 3 3	0	0
5	E	1	Total C O 6 3 3	0	0
5	G	1	Total C O 6 3 3	0	0
5	H	1	Total C O 6 3 3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	90	Total O 90 90	0	0
6	B	134	Total O 134 134	0	0
6	C	210	Total O 210 210	0	0
6	D	68	Total O 68 68	0	0
6	E	237	Total O 237 237	0	0
6	F	69	Total O 69 69	0	0
6	G	92	Total O 92 92	0	0

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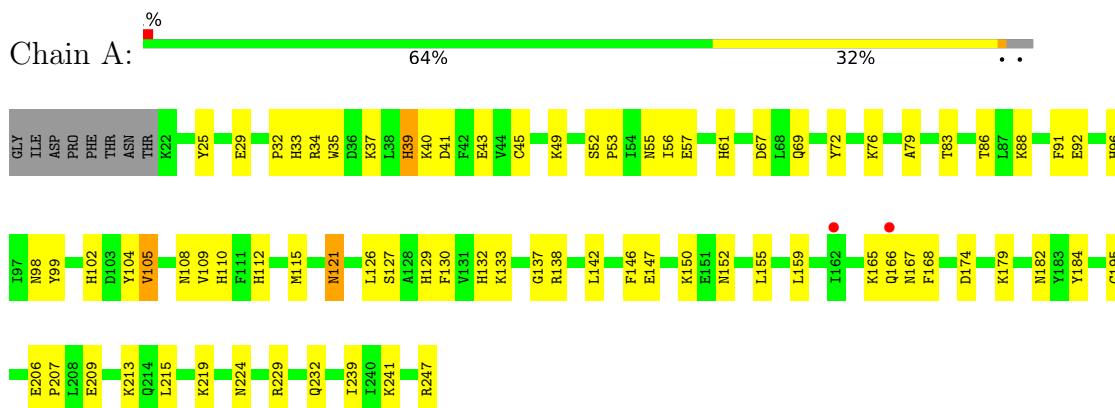
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	119	Total 119	O 119	0	0

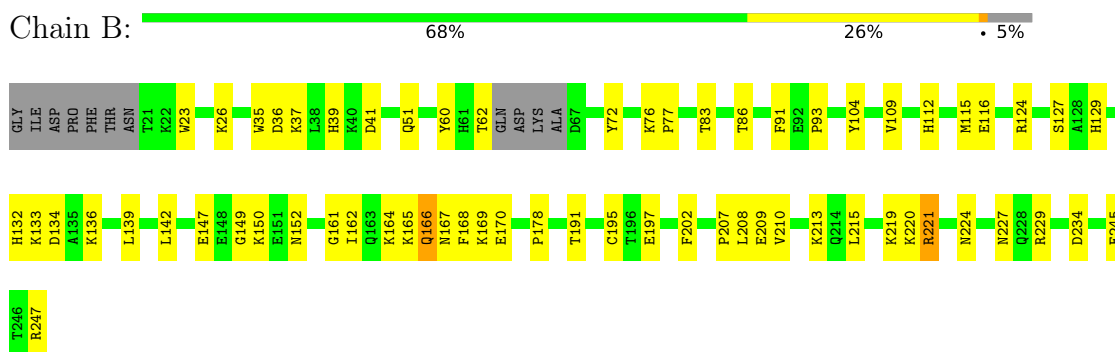
3 Residue-property plots

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 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.

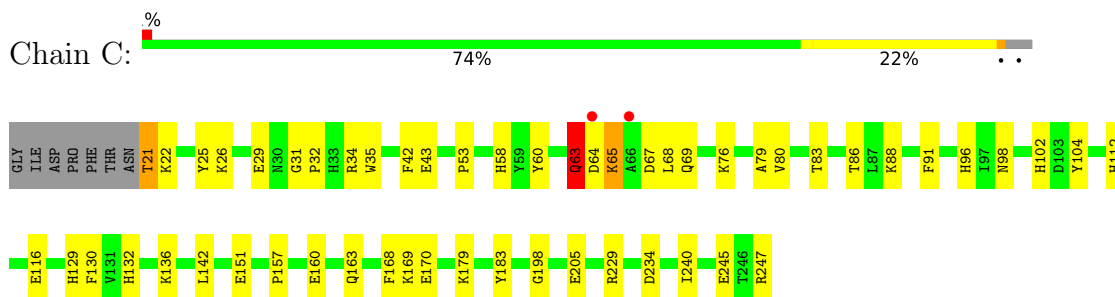
- Molecule 1: Alpha-carbonic anhydrase



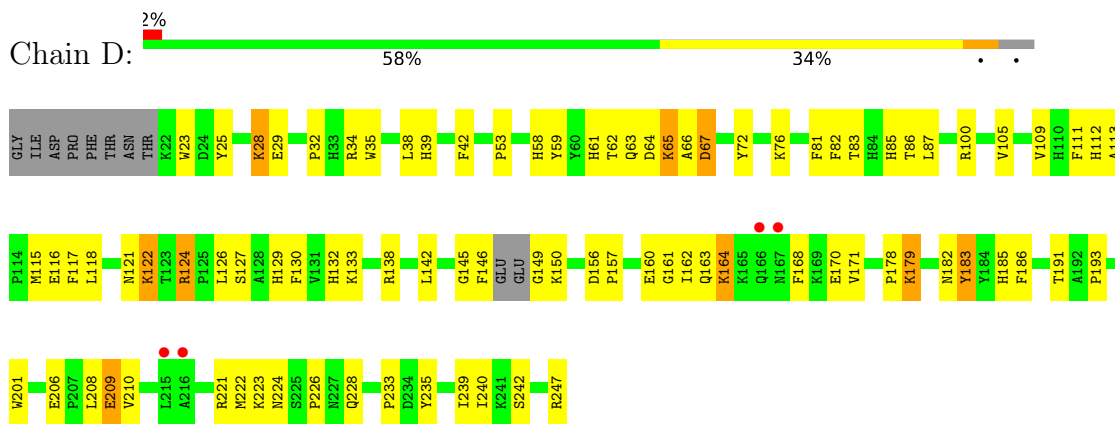
- Molecule 1: Alpha-carbonic anhydrase



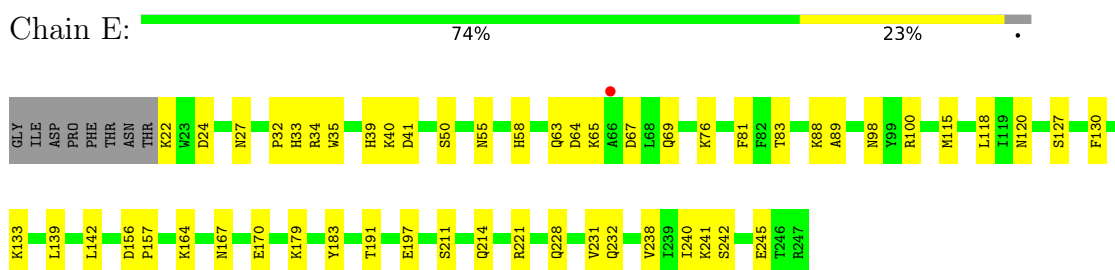
- Molecule 1: Alpha-carbonic anhydrase



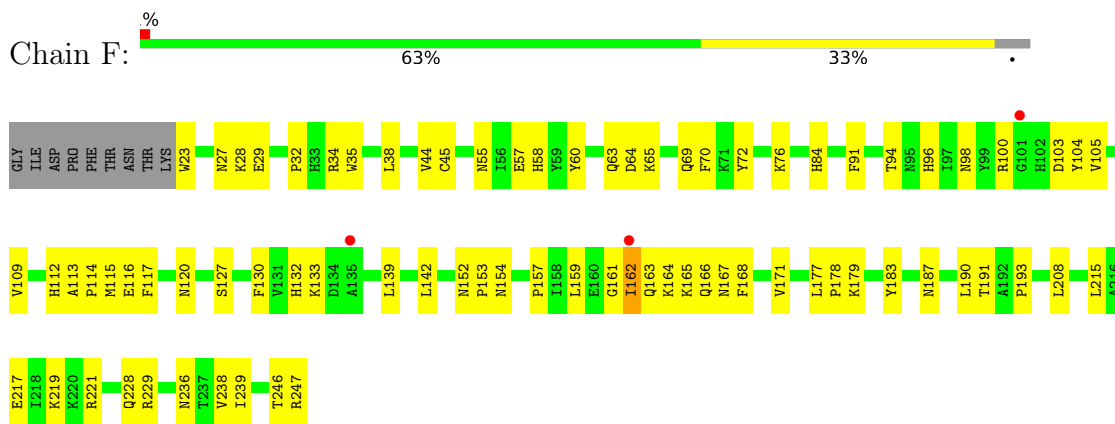
- Molecule 1: Alpha-carbonic anhydrase



- Molecule 1: Alpha-carbonic anhydrase



- Molecule 1: Alpha-carbonic anhydrase

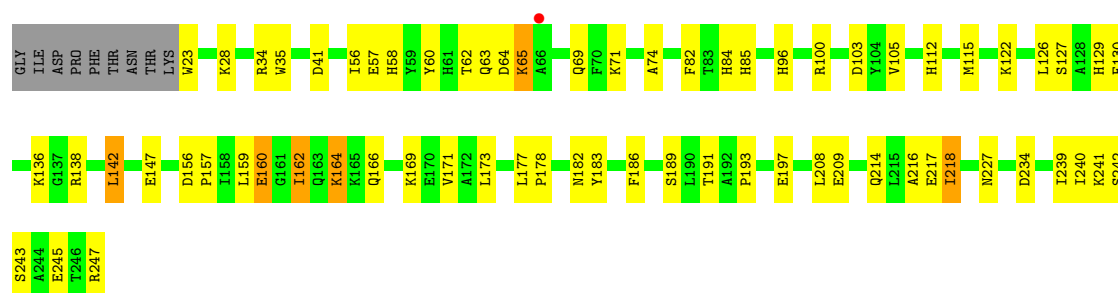


- Molecule 1: Alpha-carbonic anhydrase



- Molecule 1: Alpha-carbonic anhydrase

Chain H:  67% 26%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	41.78Å 133.61Å 166.54Å 90.00° 90.16° 90.00°	Depositor
Resolution (Å)	32.57 – 2.00 32.57 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.4 (32.57-2.00) 96.6 (32.57-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.74 (at 2.00Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.187 , 0.215 0.186 , 0.214	Depositor DCC
R_{free} test set	6010 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	23.7	Xtrriage
Anisotropy	0.310	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.457 for h,-k,-l	Xtrriage
Reported twinning fraction	0.500 for h,-k,-l	Depositor
Outliers	0 of 119787 reflections	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15976	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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, GOL, AZM, CL

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	0.46	0/1933	0.65	0/2615
1	B	0.47	0/1893	0.69	1/2560 (0.0%)
1	C	0.52	0/1918	0.66	0/2594
1	D	0.44	0/1893	0.65	0/2559
1	E	0.51	0/1911	0.64	0/2584
1	F	0.46	0/1896	0.65	0/2565
1	G	0.43	0/1941	0.70	1/2626 (0.0%)
1	H	0.49	0/1896	0.73	2/2565 (0.1%)
All	All	0.47	0/15281	0.67	4/20668 (0.0%)

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	C	0	2
1	D	0	3
All	All	0	5

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	221	ARG	NE-CZ-NH1	-6.72	116.94	120.30
1	H	142	LEU	CA-CB-CG	6.41	130.05	115.30
1	G	142	LEU	CA-CB-CG	5.24	127.35	115.30
1	H	65	LYS	CA-CB-CG	5.03	124.47	113.40

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	63	GLN	Peptide
1	C	65	LYS	Peptide
1	D	64	ASP	Peptide
1	D	65	LYS	Peptide
1	D	66	ALA	Peptide

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	1866	0	1845	65	0
1	B	1833	0	1801	58	1
1	C	1860	0	1823	62	1
1	D	1836	0	1807	71	0
1	E	1853	0	1816	64	0
1	F	1841	0	1798	67	1
1	G	1877	0	1849	64	2
1	H	1841	0	1798	66	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	2	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	1	0
4	A	13	0	6	0	0
4	B	13	0	6	0	0
4	C	13	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	13	0	6	1	0
4	E	13	0	6	1	0
4	F	13	0	6	1	0
4	G	13	0	6	0	0
4	H	13	0	6	2	0
5	A	6	0	8	2	0
5	C	6	0	8	1	0
5	E	6	0	8	1	0
5	G	6	0	8	0	0
5	H	6	0	8	1	0
6	A	90	0	0	10	0
6	B	134	0	0	19	3
6	C	210	0	0	11	5
6	D	68	0	0	16	1
6	E	237	0	0	31	4
6	F	69	0	0	17	0
6	G	92	0	0	8	0
6	H	119	0	0	17	2
All	All	15976	0	14625	478	11

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 16.

The worst 5 of 478 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:C:64:ASP:HB2	1:H:64:ASP:OD2	1.54	1.05
1:E:58:HIS:CD2	1:F:65:LYS:HZ2	1.76	1.03
1:B:164:LYS:HE3	1:B:166:GLN:HG3	1.39	1.02
1:A:195:CYS:SG	6:A:470:HOH:O	2.14	1.01
1:A:166:GLN:HG2	1:A:167:ASN:H	1.27	0.97

The worst 5 of 11 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	Interatomic distance (Å)	Clash overlap (Å)
6:C:499:HOH:O	6:E:530:HOH:O[2_444]	2.08	0.12
6:E:587:HOH:O	6:E:600:HOH:O[1_455]	2.12	0.08
1:B:150:LYS:NZ	1:C:163:GLN:O[2_454]	2.14	0.06
6:C:508:HOH:O	6:D:460:HOH:O[1_655]	2.16	0.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:597:HOH:O	6:H:419:HOH:O[2_554]	2.16	0.04

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	228/234 (97%)	216 (95%)	12 (5%)	0	100	100
1	B	221/234 (94%)	212 (96%)	9 (4%)	0	100	100
1	C	226/234 (97%)	216 (96%)	10 (4%)	0	100	100
1	D	221/234 (94%)	215 (97%)	6 (3%)	0	100	100
1	E	225/234 (96%)	213 (95%)	12 (5%)	0	100	100
1	F	223/234 (95%)	213 (96%)	10 (4%)	0	100	100
1	G	229/234 (98%)	219 (96%)	10 (4%)	0	100	100
1	H	223/234 (95%)	215 (96%)	8 (4%)	0	100	100
All	All	1796/1872 (96%)	1719 (96%)	77 (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	205/208 (99%)	201 (98%)	4 (2%)	55	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	201/208 (97%)	198 (98%)	3 (2%)	65	69
1	C	203/208 (98%)	200 (98%)	3 (2%)	65	69
1	D	200/208 (96%)	190 (95%)	10 (5%)	24	20
1	E	202/208 (97%)	201 (100%)	1 (0%)	88	92
1	F	200/208 (96%)	195 (98%)	5 (2%)	47	49
1	G	206/208 (99%)	203 (98%)	3 (2%)	65	69
1	H	200/208 (96%)	194 (97%)	6 (3%)	41	41
All	All	1617/1664 (97%)	1582 (98%)	35 (2%)	53	55

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	156	ASP
1	H	69	GLN
1	H	162	ILE
1	D	67	ASP
1	D	65	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	96	HIS
1	H	228	GLN
1	H	129	HIS
1	D	163	GLN
1	H	69	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 29 ligands modelled in this entry, 16 are monoatomic - leaving 13 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
4	AZM	A	303	2	8,13,13	3.01	5 (62%)	9,19,19	2.51	4 (44%)
4	AZM	H	303	2	8,13,13	2.91	5 (62%)	9,19,19	2.98	5 (55%)
5	GOL	A	304	-	5,5,5	0.44	0	5,5,5	0.81	0
5	GOL	C	304	-	5,5,5	0.62	0	5,5,5	0.91	0
4	AZM	B	303	2	8,13,13	2.95	5 (62%)	9,19,19	3.06	5 (55%)
5	GOL	E	304	-	5,5,5	0.76	0	5,5,5	0.87	0
5	GOL	H	304	-	5,5,5	0.46	0	5,5,5	0.50	0
4	AZM	F	303	2	8,13,13	3.08	5 (62%)	9,19,19	2.89	5 (55%)
4	AZM	C	303	2	8,13,13	2.85	5 (62%)	9,19,19	2.43	4 (44%)
4	AZM	E	303	2	8,13,13	2.78	4 (50%)	9,19,19	2.37	5 (55%)
4	AZM	D	303	2	8,13,13	3.03	5 (62%)	9,19,19	2.41	4 (44%)
5	GOL	G	304	-	5,5,5	0.38	0	5,5,5	0.58	0
4	AZM	G	303	2	8,13,13	2.94	5 (62%)	9,19,19	2.08	3 (33%)

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
4	AZM	A	303	2	-	0/2/10/10	0/1/1/1
4	AZM	H	303	2	-	0/2/10/10	0/1/1/1
5	GOL	A	304	-	-	2/4/4/4	-
5	GOL	C	304	-	-	3/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	AZM	B	303	2	-	0/2/10/10	0/1/1/1
5	GOL	E	304	-	-	4/4/4/4	-
5	GOL	H	304	-	-	4/4/4/4	-
4	AZM	F	303	2	-	0/2/10/10	0/1/1/1
4	AZM	C	303	2	-	0/2/10/10	0/1/1/1
4	AZM	E	303	2	-	0/2/10/10	0/1/1/1
4	AZM	D	303	2	-	0/2/10/10	0/1/1/1
5	GOL	G	304	-	-	1/4/4/4	-
4	AZM	G	303	2	-	0/2/10/10	0/1/1/1

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	303	AZM	C3-N4	4.56	1.44	1.36
4	F	303	AZM	C3-N4	4.43	1.44	1.36
4	G	303	AZM	C2-N4	4.43	1.44	1.36
4	G	303	AZM	C3-N4	4.36	1.44	1.36
4	A	303	AZM	C3-N4	4.29	1.44	1.36

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	303	AZM	O2-S1-C1	-5.05	102.66	108.59
4	H	303	AZM	O2-S1-O1	-4.99	110.55	118.76
4	F	303	AZM	O2-S1-O1	-4.94	110.63	118.76
4	D	303	AZM	O2-S1-O1	-4.81	110.86	118.76
4	F	303	AZM	O2-S1-C1	-4.68	103.09	108.59

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	304	GOL	O1-C1-C2-C3
5	C	304	GOL	C1-C2-C3-O3
5	E	304	GOL	O1-C1-C2-C3
5	H	304	GOL	C1-C2-C3-O3
5	A	304	GOL	O1-C1-C2-O2

There are no ring outliers.

8 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	303	AZM	2	0
5	A	304	GOL	2	0
5	C	304	GOL	1	0
5	E	304	GOL	1	0
5	H	304	GOL	1	0
4	F	303	AZM	1	0
4	E	303	AZM	1	0
4	D	303	AZM	1	0

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	226/234 (96%)	-0.39	2 (0%) 84 83	15, 30, 43, 60	0
1	B	223/234 (95%)	-0.43	0 100 100	13, 24, 44, 55	0
1	C	227/234 (97%)	-0.60	2 (0%) 84 83	10, 17, 33, 50	0
1	D	224/234 (95%)	-0.04	4 (1%) 68 66	18, 37, 57, 88	0
1	E	226/234 (96%)	-0.59	1 (0%) 92 92	9, 16, 33, 49	0
1	F	225/234 (96%)	-0.14	3 (1%) 77 76	18, 34, 52, 74	0
1	G	228/234 (97%)	-0.35	1 (0%) 92 92	15, 31, 50, 64	0
1	H	225/234 (96%)	-0.48	1 (0%) 92 92	10, 23, 41, 55	0
All	All	1804/1872 (96%)	-0.38	14 (0%) 86 85	9, 26, 50, 88	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	66	ALA	4.1
1	E	66	ALA	3.8
1	G	166	GLN	3.2
1	A	166	GLN	3.0
1	D	167	ASN	3.0

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 monosaccharides 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(Å ²)	Q<0.9
5	GOL	G	304	6/6	0.94	0.16	26,32,35,37	0
5	GOL	C	304	6/6	0.95	0.10	15,17,20,30	0
5	GOL	A	304	6/6	0.95	0.10	18,23,24,30	0
3	CL	F	302	1/1	0.97	0.07	31,31,31,31	0
5	GOL	E	304	6/6	0.97	0.10	14,16,19,19	0
3	CL	D	302	1/1	0.97	0.05	35,35,35,35	0
5	GOL	H	304	6/6	0.97	0.12	18,22,27,33	0
4	AZM	F	303	13/13	0.98	0.11	20,23,31,38	12
4	AZM	G	303	13/13	0.98	0.11	16,21,32,35	2
4	AZM	H	303	13/13	0.98	0.09	14,18,28,28	2
3	CL	B	302	1/1	0.98	0.10	20,20,20,20	0
2	ZN	B	301	1/1	0.98	0.10	19,19,19,19	0
2	ZN	H	301	1/1	0.98	0.10	24,24,24,24	0
4	AZM	B	303	13/13	0.98	0.09	12,18,23,24	0
4	AZM	D	303	13/13	0.98	0.08	19,21,27,31	9
3	CL	A	302	1/1	0.99	0.06	26,26,26,26	0
4	AZM	E	303	13/13	0.99	0.10	9,12,19,20	7
2	ZN	D	301	1/1	0.99	0.07	32,32,32,32	0
2	ZN	F	301	1/1	0.99	0.06	31,31,31,31	0
2	ZN	G	301	1/1	0.99	0.07	24,24,24,24	0
3	CL	G	302	1/1	0.99	0.06	24,24,24,24	0
3	CL	H	302	1/1	0.99	0.11	18,18,18,18	0
4	AZM	A	303	13/13	0.99	0.10	15,18,27,30	0
2	ZN	A	301	1/1	0.99	0.07	21,21,21,21	0
4	AZM	C	303	13/13	0.99	0.09	11,14,21,23	9
2	ZN	C	301	1/1	1.00	0.09	14,14,14,14	0
3	CL	C	302	1/1	1.00	0.09	13,13,13,13	0
2	ZN	E	301	1/1	1.00	0.09	14,14,14,14	0
3	CL	E	302	1/1	1.00	0.08	12,12,12,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.