

Sulfonamide inhibition studies of the β -carbonic anhydrase from the newly discovered bacterium *Enterobacter* sp. B13



Ayşenur Eminoğlu^a, Daniela Vullo^b, Ayca Aşık^c, Dilşat Nigar Çolak^d, Sabriye Çanakçı^e, Ali Osman Beldüz^{e,*}, Claudiu T. Supuran^{b,f,*}

^a Recep Tayyip Erdogan University, Faculty of Art and Science, Department of Biology, Molecular Biology Research Laboratories, Rize, Turkey

^b Università degli Studi di Firenze, Dipartimento di Chimica, Via della Lastruccia 3, 50019 Sesto Fiorentino (Firenze), Italy

^c Selçuk University, Faculty of Medicine, Medical Biology Department, Konya, Turkey

^d Giresun University, Bulancak School of Applied Sciences, Giresun, Turkey

^e Karadeniz Technical University, Faculty of Science, Department of Biology, Trabzon, Turkey

^f Università degli Studi di Firenze, Dipartimento Neurofarba, Sezione di Scienze Farmaceutiche e Nutraceutiche, Via U. Schiff 6, 50019 Sesto Fiorentino, Florence, Italy

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ABSTRACT

The genome of the newly identified bacterium *Enterobacter* sp. B13 encodes for a β -class carbonic anhydrases (CAs, EC 4.2.1.1), EspCA. This enzyme was recently cloned, and characterized kinetically by this group (*J. Enzyme Inhib. Med. Chem.* **2016**, 31). Here we report an inhibition study with sulfonamides and sulfamates of this enzyme. The best EspCA inhibitors were some sulfanylated sulfonamides with elongated molecules, metanilamide, 4-aminoalkyl-benzenesulfonamides, acetazolamide, and deacetylated methazolamide (K_i s in the range of 58.7–96.5 nM). Clinically used agents such as methazolamide, ethoxzolamide, dorzolamide, brinzolamide, benzolamide, zonisamide, sulthiame, sulpiride, topiramate and valdecoxib were slightly less effective inhibitors (K_i s in the range of 103–138 nM). Saccharin, celecoxib, dichlorophenamide and many simple benzenesulfonamides were even less effective as EspCA inhibitors, with K_i s in the range of 384–938 nM. Identification of effective inhibitors of this bacterial enzyme may lead to pharmacological tools useful for understanding the physiological role(s) of the β -class CAs in bacterial pathogenicity/virulence.

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The upsurge of antimicrobial resistance to commonly used antibiotics is a phenomenon which reached dramatic levels all over the world.^{1–3} The current antibiotics were developed decades ago and lost effectiveness due to resistance phenomena and their inappropriate use, whereas few new such drugs reached the market ultimately.^{1–4} Especially Gram-negative pathogens, among which *Enterococcus faecium*, *Klebsiella pneumonia*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp., and the Gram-positive *Staphylococcus aureus* (the so-called ESKAPE pathogens)⁴ are poorly responsive to most clinically used antibiotics. Furthermore, some of these bacteria are able to produce biofilms which are non-responsive to therapy. All of them are common pathogens, also provoking nosocomial infections difficult to eradicate, and representing thus a major threat to the public health worldwide.⁴

Annotation of the genomes of many Gram-positive and Gram-negative pathogenic bacteria gives the opportunity to discover

diverse pathways for inhibiting their vital functions and/or to block their virulence.⁴ In recent years, some metabolically important enzymes became an interesting research topic for the discovery of alternative, druggable anti-infective targets. Among them, the metalloenzyme carbonic anhydrase (CA, EC 4.2.1.1)^{5–7} revealed to be an interesting novel drug target in fighting infections provoked by pathogenic protozoa,⁸ fungi⁹ and some bacteria.¹⁰ This is due to the essential role that CAs play in carbon dioxide hydration to bicarbonate and protons (the physiologic reaction that they catalyze), which is used by the pathogens in essential functions such as pH regulation, chemosensing, or biosynthetic reactions.^{11,12}

The CAs are present in many pathogenic bacteria, suggesting a pivotal role in microbial virulence.^{6,10} These enzymes were classified into several classes, which include the α -, β -, γ -, δ -, ζ - and η -CAs, of which only α -, β -, and γ -ones are present in bacteria. The metal ion from the enzyme active site is crucial in the catalytic process, being coordinated by three His residues in the α -, γ - and δ -classes, by one His, and two Cys residues in β - and ζ -CAs or by two His and one Gln residues in η -class with the fourth ligand being a water molecule/hydroxide ion acting as nucleophile in

* Corresponding authors. Tel./fax: +90 4623772522 (A.O.B.), +39 055 4573729 (C.T.S.).

E-mail addresses: belduz@ktu.edu.tr (A.O. Beldüz), claudiu.supuran@unifi.it (C.T. Supuran).

the enzyme catalytic cycle.^{5–8} The distribution pattern of these enzymes in bacteria is very intriguing as some of them encode CAs belonging just to one class (either α - or β), others from two (α - and β -CAs) whereas there are bacteria which contain all three different genetic classes identified in these organisms so far.^{6,10} Furthermore, there are several species which seem not to encode for CAs, such as the Gram-negative bacteria belonging the genera *Buchnera* and *Rickettsia*,^{6e} but it is not improbable that they may contain CAs from a yet unidentified novel genetic family.

Investigations of CA in the bacteria domain may undoubtedly reveal novel aspects of microbial virulence. For example, bacteria lacking the bicarbonate transporter system, such as *Vibrio cholerae*, a Gram-negative bacterium responsible of the human disease cholera, can increase cytosolic bicarbonate levels through the action of CAs, which convert into bicarbonate the metabolic CO₂ and/or atmospheric CO₂ entered into the cell by simple diffusion.¹⁰ Furthermore, the sulfonamide ethoxzolamide, a potent CA inhibitor (CAI, see later in the text), with a low nanomolar affinity for the CAs from this bacterium,^{10f,13} inhibits the bicarbonate-mediated virulence, suggesting that conversion of CO₂ into bicarbonate by the *V. cholerae* CAs plays a role in virulence induction, and that inhibition of these enzymes may modulate infectivity.^{10,13} In the gastric pathogen *Helicobacter pylori*, which encodes CAs belonging to the α - and β -classes investigated in some detail,¹⁴ it has been demonstrated that inhibition of the two bacterial enzymes with sulfonamides such as acetazolamide, a low-nanomolar *H. pylori* CA inhibitor, is lethal for the pathogen,^{14,15} which explains why sulfonamide CAIs (acetazolamide and ethoxzolamide) were clinically efficient as anti-ulcer drugs.^{15b} Thus, the proposal of bacterial CA inhibitors as anti-infective agents,^{5a,10} eventually in combination with other drug classes, is an idea supported by preclinical and clinical data,^{10,14,15} and prompts us to investigate such proteins in various pathogenic species, as well as to screen various classes of CAIs^{16–18} for their in vitro and in vivo effects against such bacteria.

Recently, our group cloned and purified a recombinant β -CA from a newly identified bacterium belonging to the genus *Enterobacter*, more precisely *Enterobacter* spp. B13, which appeared to be similar to *Enterobacter asburiae*.¹⁹ The new enzyme, denominated from now on as EspCA, was shown to possess a good catalytic activity for the reaction that converts CO₂ to bicarbonate and protons, with a k_{cat} of $4.8 \times 10^5 \text{ s}^{-1}$ and a k_{cat}/K_m of $5.6 \times 10^7 \text{ M}^{-1} \times \text{s}^{-1}$, at pH 8.3 and 20 °C.¹⁹ No inhibition studies were reported so far for this enzyme belonging to the pathogenic CAs from the ESKAPE group of bacteria mentioned above.^{4,19} Identification of potent and possibly selective EspCA inhibitors may lead to pharmacological tools useful for understanding the physiological role(s) of these under-investigated enzymes in pathogenic bacteria. Here we report the first inhibition study of EspCA with a series of sulfonamides and one sulfamate, the main class of CAIs.

Although few pathogenic β -CAs were characterized so far by means of X-ray crystallography (among them are those from *Escherichia coli*,²⁰ *Mycobacterium tuberculosis*,²¹ *Haemophilus influenzae*²² and *V. cholerae*)¹³ it appears that sulfonamides/sulfamates possess the same inhibition mechanism against these enzymes as for the α -CAs, that is, the inhibitor coordinates to the catalytically crucial metal ion, impairing catalysis by substituting the metal-bound nucleophile.⁷ This is the reason why such classical CAIs were included in this study. A library of 40 compounds, comprising 39 sulfonamides and one sulfamate were assayed for EspCA inhibition.²³ Derivatives 1–24 and AAZ–HCT are either simple aromatic/heterocyclic sulfonamides widely used as building blocks for obtaining new families of such pharmacologic agents, or they are clinically used agents, among which acetazolamide AAZ, methazolamide MZA, ethoxzolamide EZA and dichlorophenamide DCP, are the classical, systemically acting antiglaucoma

CAIs.²⁴ Dorzolamide DZA and brinzolamide BRZ are topically-acting antiglaucoma agents,⁵ benzolamide BZA is an orphan drug belonging to this class of pharmacological agents, whereas topiramate TPM, zonisamide ZNS and sulthiame SLT are antiepileptic drugs.²⁵ Sulpiride SLP and indisulam IND were also shown to belong to this class of pharmacological agents, together with the COX2 ‘selective’ inhibitors celecoxib CLX and valdecoxib VLX.⁵ Saccharin and the diuretic hydrochlorothiazide HCT are also known to act as CAIs.⁵

Data of Table 1 show the inhibition data of EspCA with the 40 derivatives mentioned above, as obtained by a stopped-flow CO₂ hydrase assay monitoring the physiologic reaction catalyzed by CAs.²³ Inhibition data of the human (h), possibly off-target isoforms hCA I and II, and of the β -CA (VchCA β) from another bacterial pathogen, *V. cholerae*, recently crystallized and investigated by us,¹³ are also presented in Table 1, for comparison reasons (Chart 1).

The following structure–activity relationship (SAR) can be drawn from the inhibition data of Table 1:

- (i) Weak EspCA inhibition was observed for three sulfonamides investigated here, 10–12 which were micromolar inhibitors: 10 and 11 with K_i s of 8.42–8.95 μM , and 12 with a K_i of $>10 \mu\text{M}$. It should be noted that 11 and 12 are the only benzene-1,3-disulfonamide derivatives (together with DCP,

Table 1
Inhibition data of hCA I, hCA II, VchCA β and EspCA with compounds 1–HCT²³

Compound	hCA I	hCA II K_i (nM) ^a	VchCA β	EspCA
1	45,400	295	463	73.9
2	25,000	240	447	583
3	28,000	300	785	812
4	78,500	320	>10,000	384
5	25,000	170	>10,000	93.6
6	21,000	160	463	90.2
7	8300	60	>10,000	700
8	9800	110	9120	879
9	6500	40	>10,000	87.8
10	6000	70	>10,000	8420
11	5800	63	879	8950
12	8400	75	4450	>10,000
13	8600	60	68.1	523
14	9300	19	82.3	83.7
15	6	2	349	720
16	164	46	304	88.1
17	185	50	3530	674
18	109	33	515	856
19	95	30	2218	775
20	690	12	859	453
21	55	80	4430	647
22	21,000	125	757	485
23	23,000	133	817	96.5
24	24,000	125	361	58.7
AAZ	250	12	4512	78.9
MZA	50	14	6260	137
EZA	25	8	6450	132
DCP	1200	38	2352	938
DZA	50,000	9	4728	103
BRZ	45,000	3	845	107
BZA	15	9	846	120
TPM	250	10	874	131
ZNS	56	35	8570	128
SLP	1200	40	6245	132
IND	31	15	7700	513
VLX	54,000	43	8200	133
CLX	50,000	21	4165	788
SLT	374	9	455	138
SAC	18,540	5959	275	801
HCT	328	290	87.0	133

^a Mean from 3 different assay. Errors in the range of $\pm 10\%$ of the reported values (data not shown).

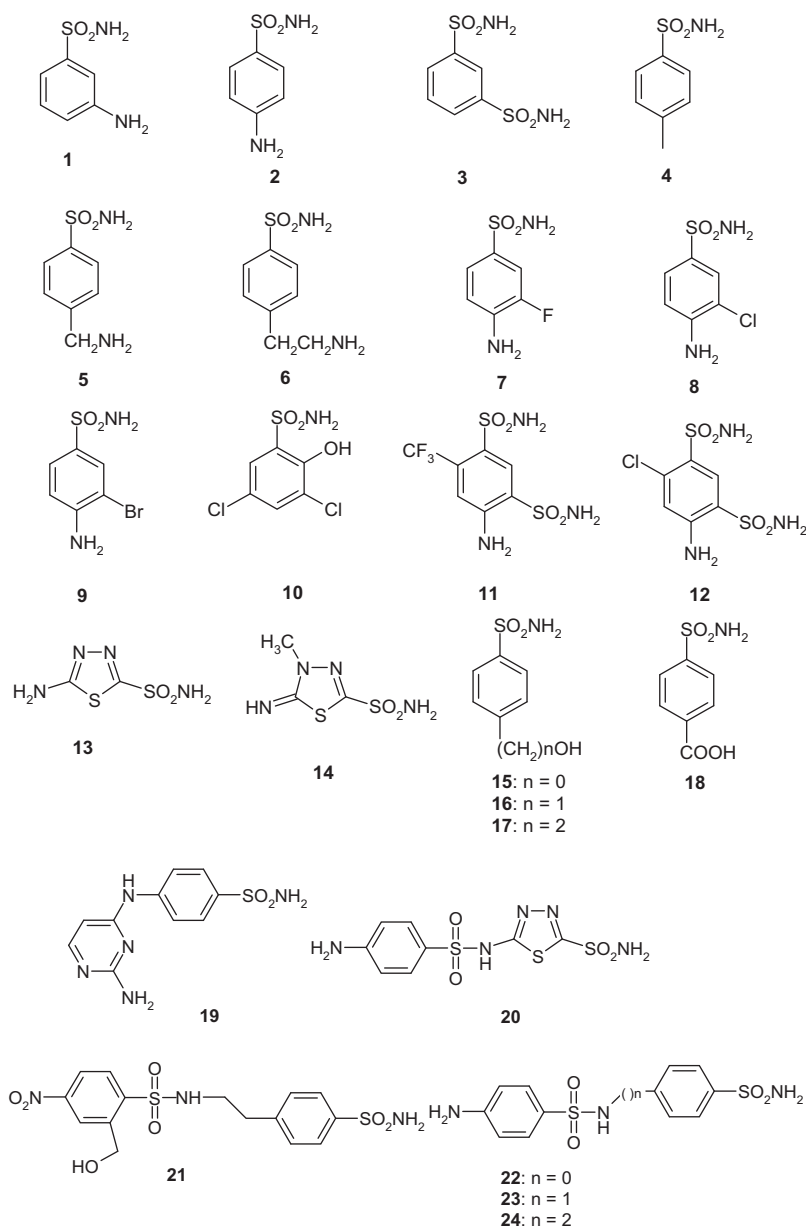


Chart 1. Structure of sulfonamides/sulfamates investigated in the Letter.

which is also not a quite effective inhibitor, with a K_i of 938 nM) investigated here, whereas **10** is also one of the few tetra-substituted benzene derivatives in the series. This prompts us to conclude that bulky, poly-substituted compounds at the aromatic ring are associated with poor inhibitory activity against this enzyme (Table 1).

- (ii) Many of the simple, aromatic sulfonamides with one or two different substituents at the benzene ring, such as **2–4**, **7**, **8**, **17–22**, the clinically used agents with a more complex scaffold based on the benzenesulfonamide motif **DCP**, **IND**, **CLX** and the heterocyclic sulfonamide **13** (deacetylated acetazolamide **AAZ**), were weak–medium potency EspCA inhibitors with K_i s in the range of 384–938 nM (Table 1). Again the SAR is rather obvious, as these compounds are mono- or disubstituted benzenesulfonamides possessing compact moieties in the *meta*- or *para*-positions with respect to the sulfonamide group (**2–4**, **17**, **18**) or they incorporate bulkier moieties in the 4-position, as in the case of **19**, **21** and **22**.

Compound **20** is a benzamide (**BZA**) derivative, and **BZA** itself is a rather effective inhibitor (K_i of 120 nM). The additional 4-amino moiety present in **20** leads to a four-fold loss of activity compared to the parent compound. Another type of compounds in this category is represented by some halogenated sulfanilamides, such as **7** and **8**. However the replacement of the F or Cl atoms from **7** and **8** by a Br (in **9**) leads to a 10-time increase in the inhibitory power, with the bromo-derivative **9** being an effective EspCA inhibitor (K_i of 87.8 nM). Thus minimal variations in the structure lead to dramatic changes in the enzyme inhibitory power of these sulfonamides.

- (iii) Many of the clinically used sulfonamide/sulfamate drugs, such as **MZA**, **EZA**, **DZA**, **BRZ**, **TPM**, **ZNS**, **SLP**, **V LX**, **SLT** and **HCT** showed rather efficient EspCA inhibitory properties, with K_i s in the range of 103–138 nM (Table 1). Although these compounds possess quite diverse scaffolds (mono- or bicyclic aromatic/heterocyclic moieties; protected sugar

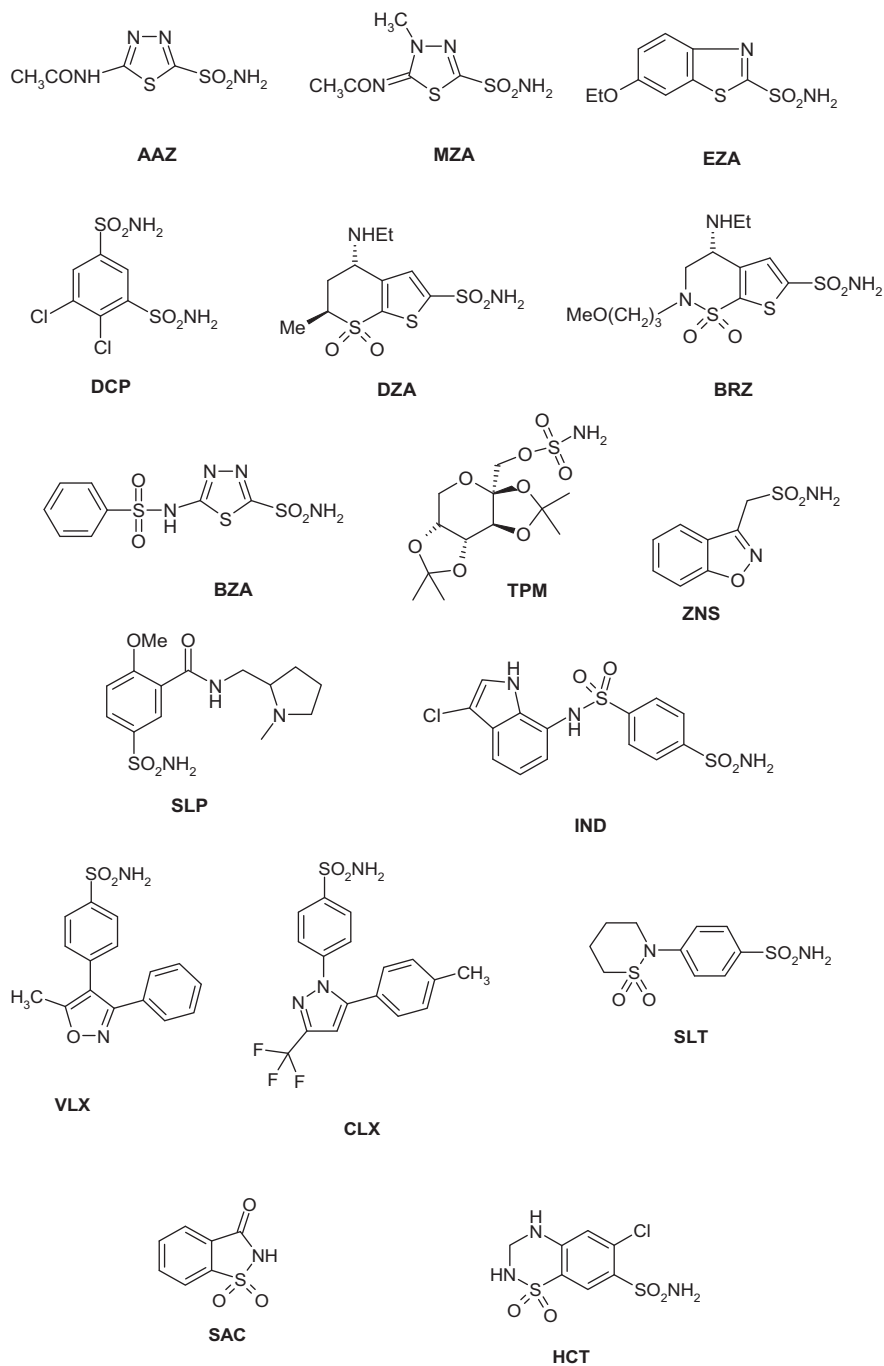


Chart 1. (continued)

moiety with the sulfamate zinc-binding group in **TPM**, aliphatic sulfonamide with a heterocyclic ring attached to it in **ZNS**, etc.), their inhibition profiles against this enzyme are quite similar, proving thus that a rather large number of diverse chemotypes belonging to the sulfonamide/sulfamate classes can effectively bind within the enzyme active site.

- (iv) The most effective EspCA inhibitors were **1**, **5**, **6**, **9**, **14**, **16**, **23**, **24** and **AAZ**, which had K_i s in the range of 58.7–96.5 nM (Table 1). They include the simple benzenesulfonamides with *meta* (metanilamide **1**) or *para* (**5**, **6** and **15**) groups, of the amino, aminoalkyl or hydroxyalkyl type. It is interesting to note again that small structural changes (e.g., the

position of the amino moiety in **1** and **2**) lead to drastic changes of activity. Metanilamide **1** is 7.96 times a better EspCA inhibitor compared to its isomer, sulfanilamide **2**. Comparing the aminoalkyl series (compounds **2**, **5**, **6**, considering the linker of 0 carbon atoms for **2**) with the hydroxyalkyl one (derivatives **15**–**17**), the differences of inhibitory profiles are again quite different. For the aminoalkyl series the inhibitory activity increased with the length of the linker between the sulfamoyl-phenyl ring and the amino moiety (from 0 to 2) whereas for the hydroxyalkyl series, the behavior was quite irregular, with **15** ($n = 0$) and **17** ($n = 2$) behaving as weak inhibitors and **16** ($n = 1$) as a potent one (K_i of 88.1 nM)—Table 1. Comparing the aminoethyl derivative **6**

with the corresponding hydroxyethyl one **17**, again the difference of inhibitory power is important, with **6** being 7.5-times a better inhibitor compared to **17**. Another effective chemotype as EspCA inhibitor is represented by the imino derivative **14** (de-acetylated methazolamide) which is a better inhibitor compared to **MZA** and especially compared to the structurally related de-acetylated **AAZ**, **13**, which is 6.2 times a weaker inhibitor compared to **14**. For the sulfanilyl-sulfonamides subseries (**22–24**) activity increased with the length of the linker from 0 to 2, with **22** behaving as a weak inhibitor, whereas **23** and **24** as effective ones. In fact **24** was the most effective EspCA inhibitors discovered so far.

- (v) The inhibition profile of EspCA is quite different from that of the β -class enzyme from *V. cholerae*, VchCA β or the human isoforms I and II (belonging to the α -class). This is an interesting observation as it prompts us to hypothesize that it might be possible to design EspCA-selective CAIs.

In conclusion, we investigated the inhibition with sulfonamides of the newly identified CA from the bacterium *Enterobacter* sp. B13, EspCA. The best EspCA inhibitors were some sulfanylated sulfonamides with elongated molecules, metanilamide, 4-amino-alkyl-benzenesulfonamides, acetazolamide, and deacetylated methazolamide (K_i s in the range of 58.7–96.5 nM), whereas the clinically used agents such as methazolamide, ethoxzolamide, dorzolamide, brinzolamide, benzolamide, zonisamide, sulthiame, sulpiride, topiramate and valdecoxib were slightly less effective (K_i s in the range of 103–138 nM). Saccharin, celecoxib, dichlorophenamide and many simple benzenesulfonamides were less effective as EspCA inhibitors, with K_i s in the range of 384–938 nM. Identification of effective inhibitors of this bacterial enzyme may lead to pharmacological tools useful for understanding the physiological role(s) of the β -class CAs in bacterial pathogenicity/virulence.

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23. Khalifah, R. G. *J. Biol. Chem.* **1971**, *246*, 2561. A stopped-flow CO₂ hydration assay with an applied photophysics instrument has been used for measuring catalytic activity and inhibition of the enzymes investigated here. Phenol red (at a concentration of 0.2 mM) has been used as indicator, working at the absorbance maximum of 557 nm, with 20 mM Tris (pH 8.3) as buffers, and 20 mM NaClO₄ (for maintaining constant the ionic strength). The initial rates of the CA-catalyzed CO₂ hydration reaction were followed for a period of 10–100 s. The concentrations of substrate (CO₂) ranged from 1.7 to 17 mM for the determination of the kinetic parameters and inhibition constants, with at least six traces of the initial 5–10% of the reaction being used for determining the initial velocity, for each inhibitor. The uncatalyzed rates were subtracted from the total observed rates. Stock solutions of inhibitors (10 mM) were prepared in distilled-deionized water and dilutions up to 0.01 nM were done with the assay buffer. Enzyme and inhibitor solutions were pre-incubated for 15 min (at room temperature) prior to assay, in order to allow for the formation of the E–I complex. The inhibition constants were obtained by non-linear least-squares methods using PRISM 3 and the Cheng–Prusoff equation as reported earlier by our groups.^{24,25} The kinetic parameters for the uninhibited enzymes were derived from Lineweaver–Burk plots, as reported earlier,^{24,25} and represent the mean from at least three different determinations. EspCA was obtained as described in Ref. 19 and its concentration in the assay system was of 14.6 nM.
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