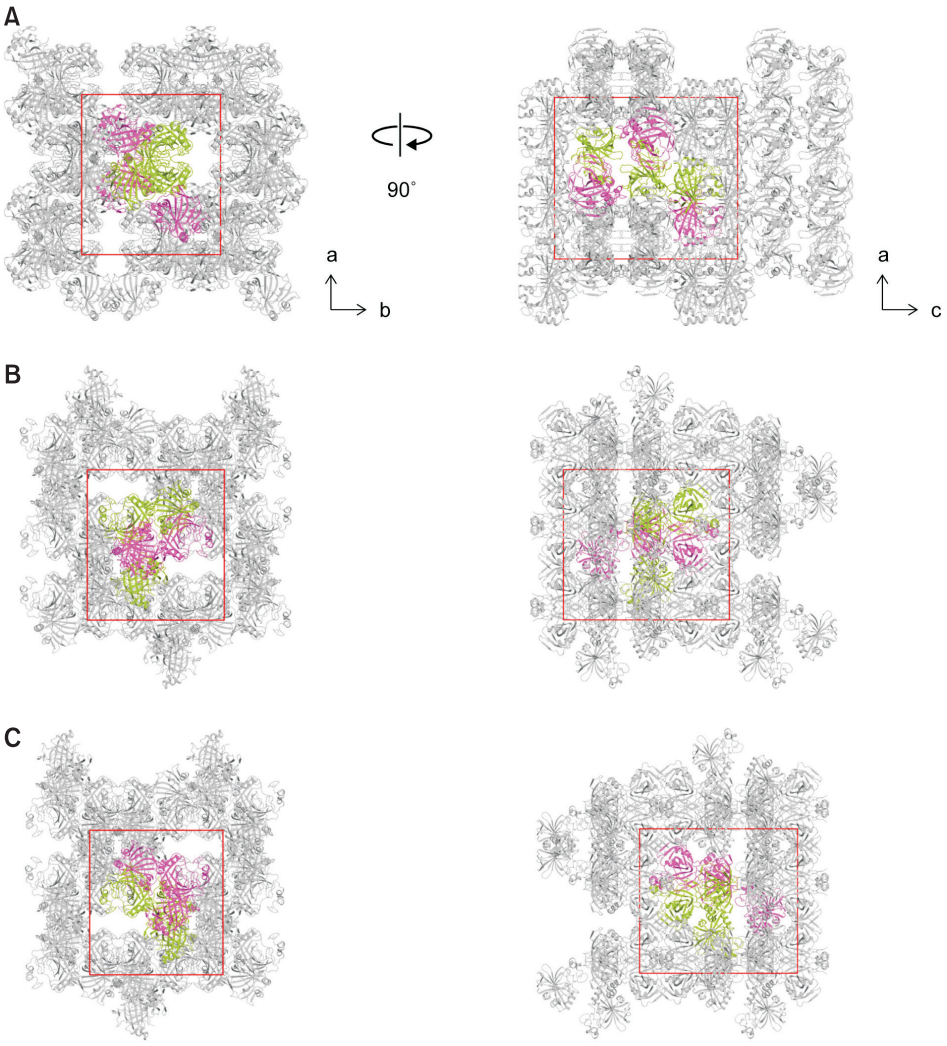
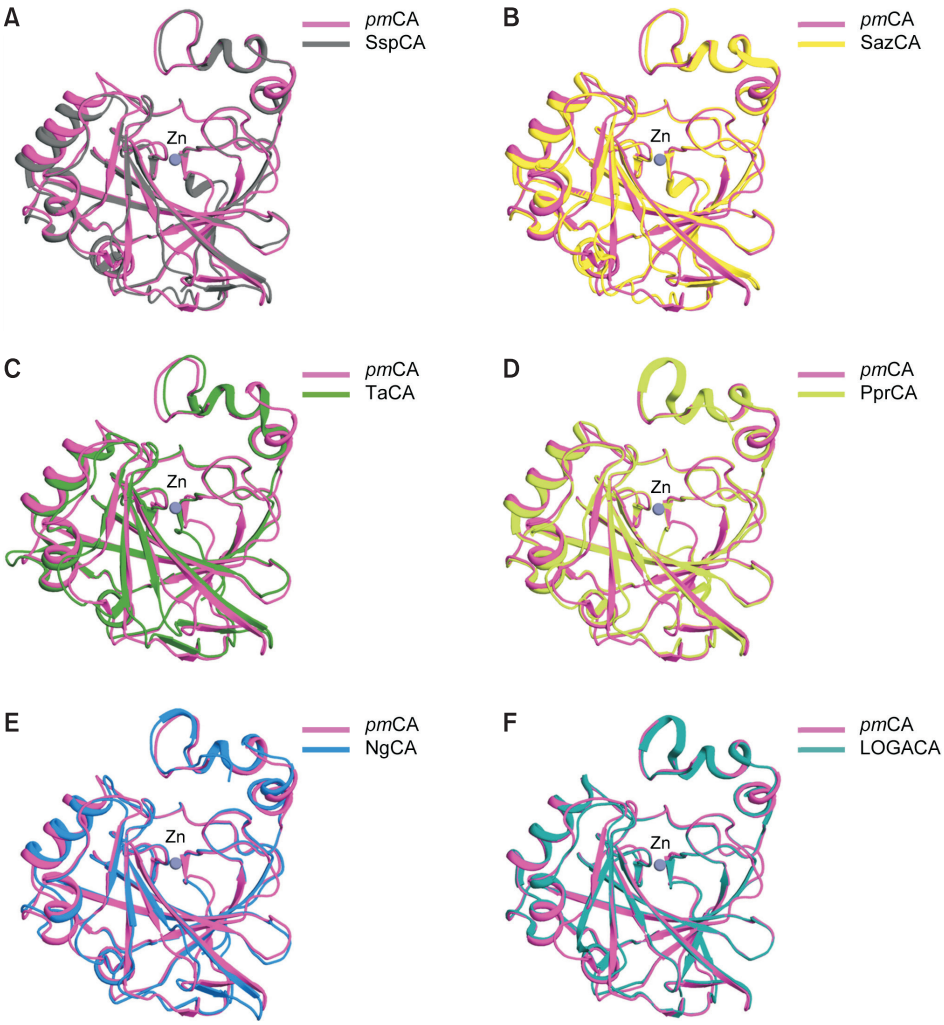
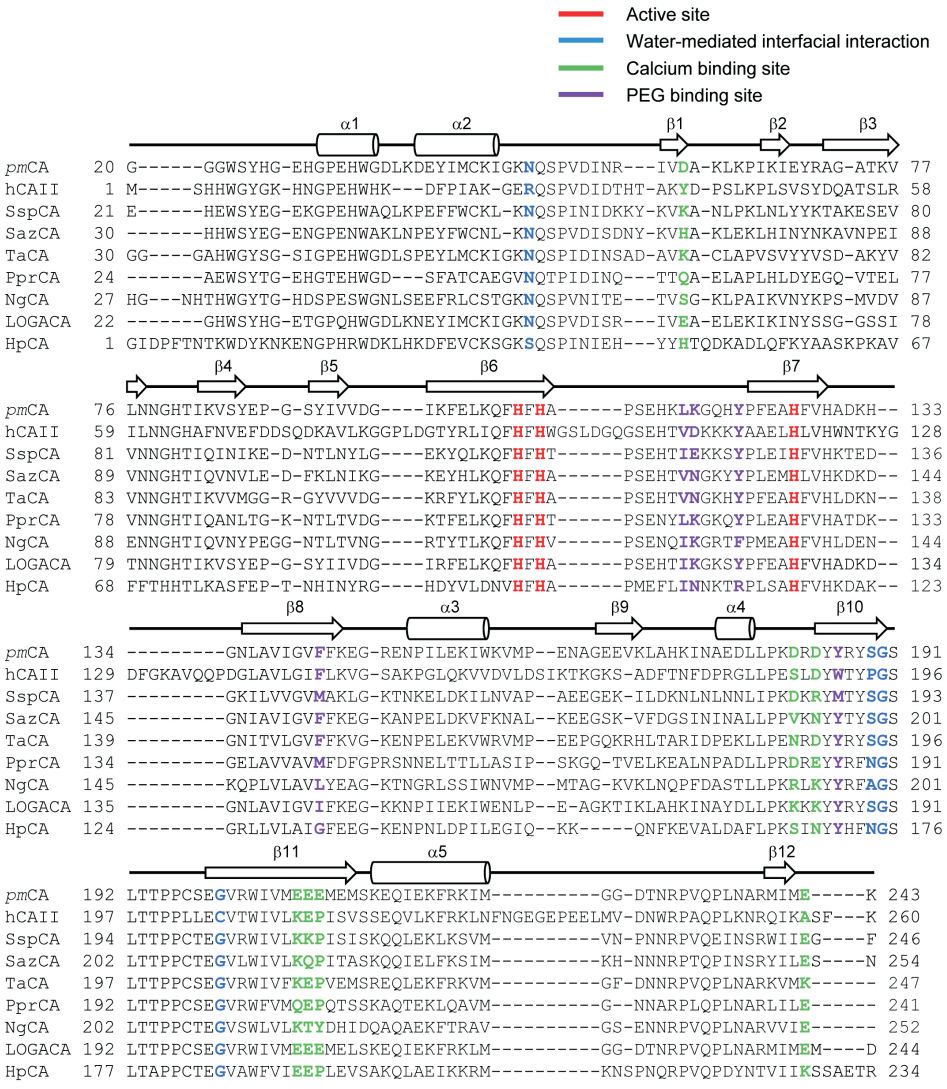


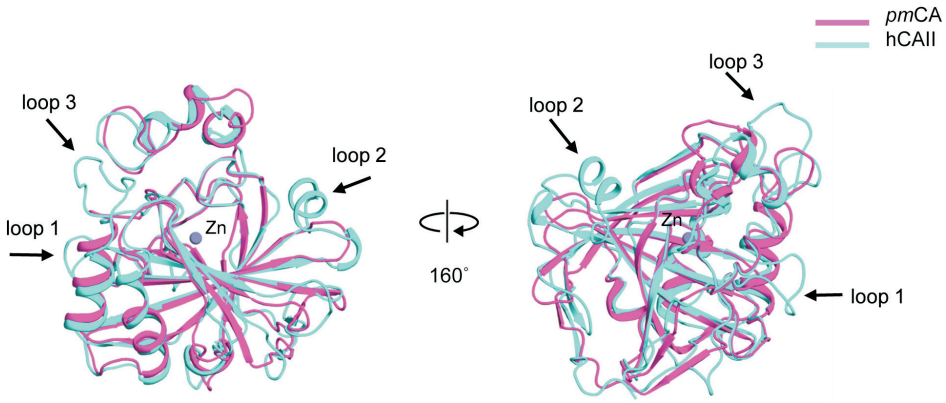
Supplementary Fig. S1. Crystal packing of *pm*CA dimers in the asymmetric unit with and without acetazolamide. (A) Bicarbonate-bound *pm*CA (Crystal form 1), water-bound *pm*CA (Crystal form 2), and acetazolamide-bound *pm*CA (Crystal form 3). Crystal packing is shown along crystallographic axes c (left) and b (right). Unit cells are shown as red boxes. Monomers of the *pm*CA dimer are colored magenta and green, respectively.



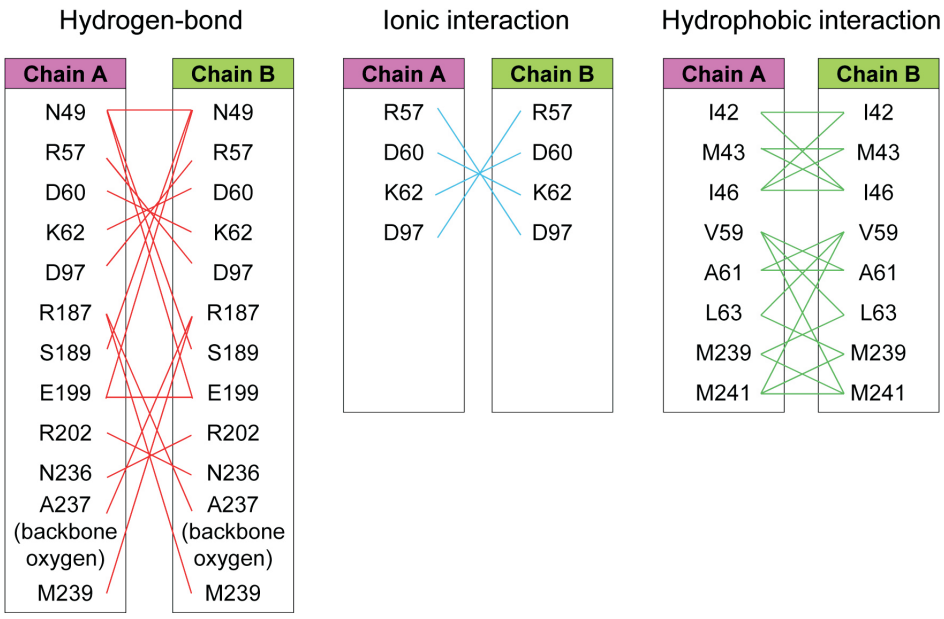
Supplementary Fig. S2. Structural comparison of *pm*CA with other bacterial α-CAs. Superposition of the *pm*CA monomer with SspCA (A, PDB ID 4G7A), SazCA (B, PDB ID 4X5S), TaCA (C, PDB ID 4COQ), PprCA (D, PDB ID 5HPJ), NgCA (E, PDB ID 1KOP), and LOGACA (F, PDB ID 6EKI).



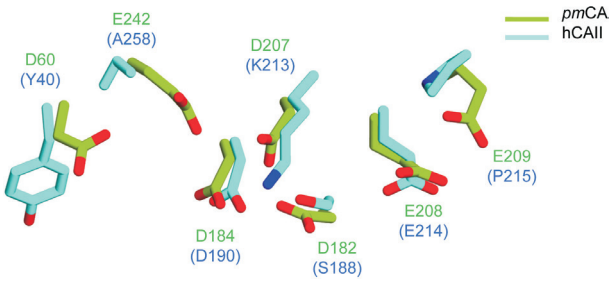
Supplementary Fig. S3. Structure-based sequence alignment of *pm*CA with other α-CAs. *pm*CA, hCAII, SspCA, SazCA, TaCa, PprCA, NgCA, LOGACA, and HpCA amino acid sequences are aligned based on their structures. Conserved catalytic histidine residues, residues involved in water-mediated interactions between monomers, and residues involved in coordination of calcium ions and PEG molecules are colored red, blue, green, and purple, respectively. The positions of α-helices and β-strands are indicated by cylinders and arrows above the sequences, and are numbered accordingly.



Supplementary Fig. S4. Structural differences between *pm*CA and hCAII. The *pm*CA structure is superimposed with that of hCAII (PDB ID 1CA2). Substantial structural differences include deletion of surface loops in *pm*CA (indicated by arrows). Zinc ions are shown as gray spheres.



Supplementary Fig. S5. Schematic diagram of interfacial interactions in the *pm*CA dimer. Interacting residues in the *pm*CA dimer interface are indicated. Hydrogen bonds are represented by red lines. Ionic and hydrophobic interactions are shown as cyan and green lines, respectively.



Supplementary Fig. S6. Comparison of the structures of the calcium binding site of *pm*CA and hCAII. The side chains of residues that differ significantly are shown. Amino acids in parentheses represent the corresponding residues in hCAII (PDB ID 1CA2).

Supplementary Table S1. Data collection and refinement statistics

	Form 1 (PDB ID 6IM0)	Form 2 (PDB ID 6IM1)	Form 3 (PDB ID 6IM3)
Data collection			
Space group	C2	$P2_12_12$	$P2_12_12$
Cell dimensions			
a, b, c (Å)	124.8, 109.0, 123.1	118.9, 120.0, 124.0	119.0, 120.8, 123.9
α, β, γ (°)	90.0, 90.0, 90.0	90.0, 90.0, 90.0	90.0, 90.0, 90.0
Resolution (Å)	50.0-2.6 (2.69-2.60)	50.0-2.0 (2.07-2.00)	50.0-2.0 (2.07-2.00)
R_{pim}	0.08 (0.31)	0.02 (0.33)	0.03 (0.44)
$I/\sigma I$	9.8 (2.0)	48.1 (3.7)	42.4 (2.1)
CC1/2	0.9 (0.7)	0.9 (0.8)	0.9 (0.7)
Completeness (%)	97.9 (98.7)	99.7 (99.8)	99.2 (98.8)
Redundancy	3.4 (3.3)	9.4 (9.5)	9.2 (9.5)
Refinement			
Resolution (Å)	50.0-2.6	50.0-2.0	50.0-2.0
No. reflections (work/test)	47255/2478	113414/5670	113905/5968
R_{work} / R_{free}	18.9/22.7	20.3/23.5	20.9/23.9
No. atoms			
Protein	10824	10824	10824
Zinc	6	6	6
Bicarbonate	24	-	-
Acetazolamide	-	-	78
PEG400	65	52	26
Calcium	15	15	16
Water	249	500	472
B factors (Å^2)			
Protein	43.7	48.3	55.3
Zinc	33.3	43.0	44.8
Bicarbonate	46.5	-	-
Acetazolamide	-	-	66.3
PEG	65.0	71.2	77.3
Calcium	50.7	61.5	68.3
Water	30.2	43.9	49.6
R.m.s. deviations			
Bond lengths (Å)	0.013	0.021	0.019
Bond angles (°)	1.814	1.089	2.167
Ramachandran plot (%)			
Most favored	89.5	91.1	92.0
Allowed	10.0	8.4	7.5
Generously allowed	0.5	0.5	0.5
Disallowed	0	0	0

*Numbers in parentheses were calculated with data in the highest resolution shell.