



Article

Comparison of Carbonic Anhydrases for CO₂ Sequestration

Franziska Steger ¹, Johanna Reich ^{1,2}, Werner Fuchs ¹, Simon K.-M. R. Rittmann ³, Georg M. Gubits ¹,
Doris Ribitsch ^{2,*} and Günther Bochmann ¹

¹ Institute of Environmental Biotechnology, Department for Agrobiotechnology, University of Natural Resources and Life Sciences Vienna, Konrad Lorenz Str. 20, A-3430 Tulln, Austria; franziska.steger@boku.ac.at (F.S.); johanna.reich@boku.ac.at (J.R.); werner.fuchs@boku.ac.at (W.F.); guebitz@boku.ac.at (G.M.G.); guenther.bochmann@boku.ac.at (G.B.)

² ACIB — Austrian Centre of Industrial Biotechnology, Krenngasse 37, 8010 Graz, Austria

³ Archaea Physiology & Biotechnology Group, Department of Functional and Evolutionary Ecology, University of Vienna, Djerassiplatz 1, 1030 Vienna, Austria; simon.rittmann@univie.ac.at

* Correspondence: doris.ribitsch@boku.ac.at

1. Original SDS-PAGE of CAs in Cleared Cell Lysate and After Purification

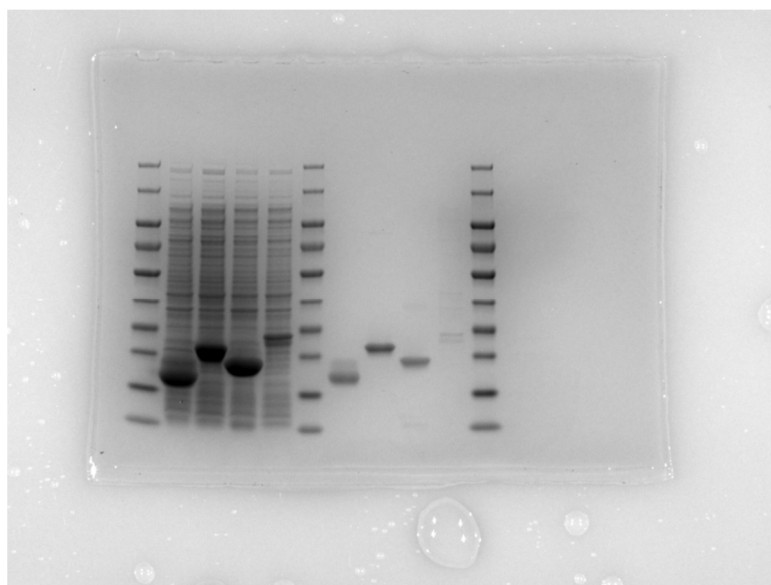


Figure S1. original SDS-PAGE of CAs expressed in *E. coli*. Samples of cleared cell lysate and after purification by affinity chromatography.

2. SDS-PAGEs of Timepoints During Expression and Purification of CAs

2.1. *AwCA*

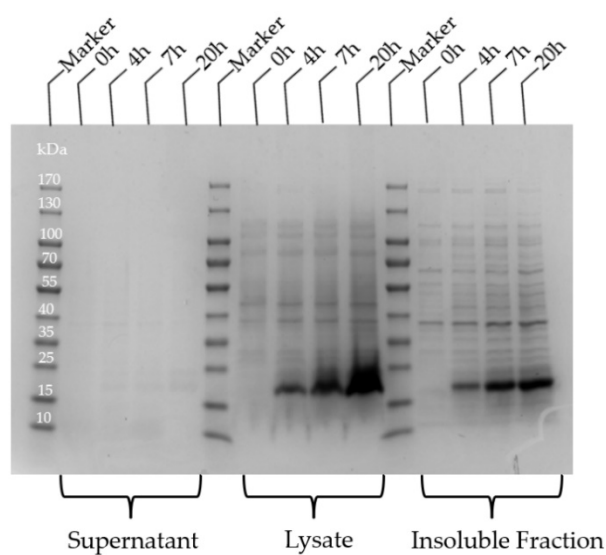


Figure S2. SDS-PAGE of supernatant, lysate and insoluble fraction during expression of AwCA in *E. coli*. Expected molecular weight is 22.0 kDa (AwCA).

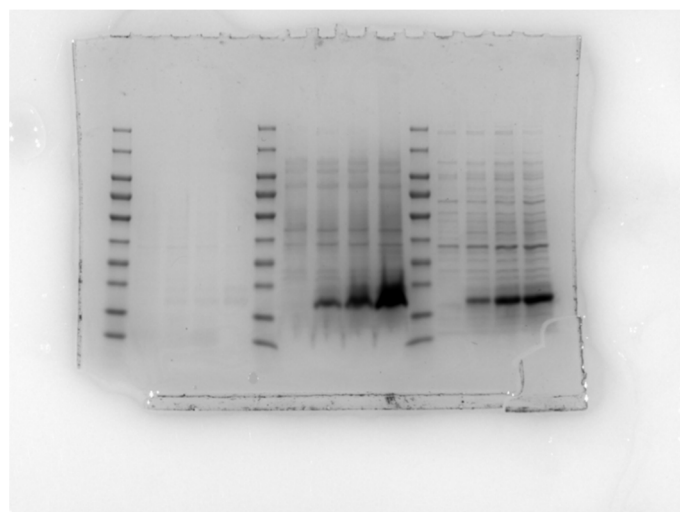


Figure S3. original SDS-PAGE of supernatant, lysate and insoluble fraction during expression of AwCA in *E. coli*.

- 1) Marker
- 2) Lysate
- 3) Flowthrough
- 4) Flowthrough
- 5-14) Elution

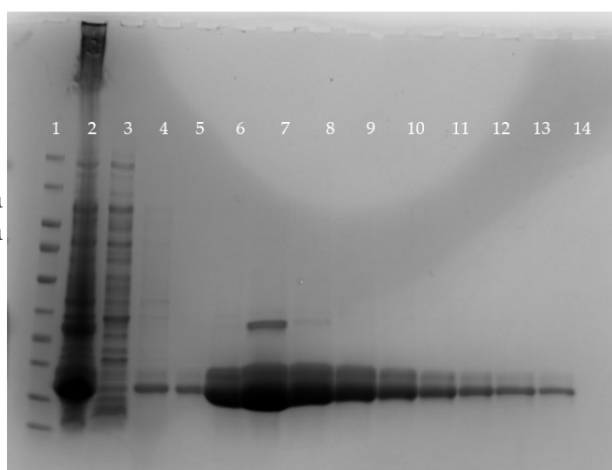


Figure S4. SDS-PAGE of lysate (2), flowthrough (3&4) and elution fractions (5-14) during purification of AwCA by affinity chromatography.

2.2. PmCA

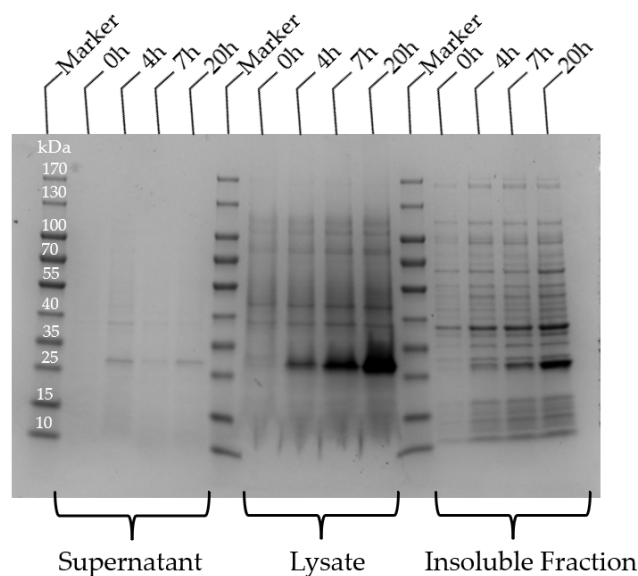


Figure S5. SDS-PAGE of supernatant, lysate and insoluble fraction during expression of PmCA in *E. coli*. Expected molecular weight is 26.9 kDa (PmCA).

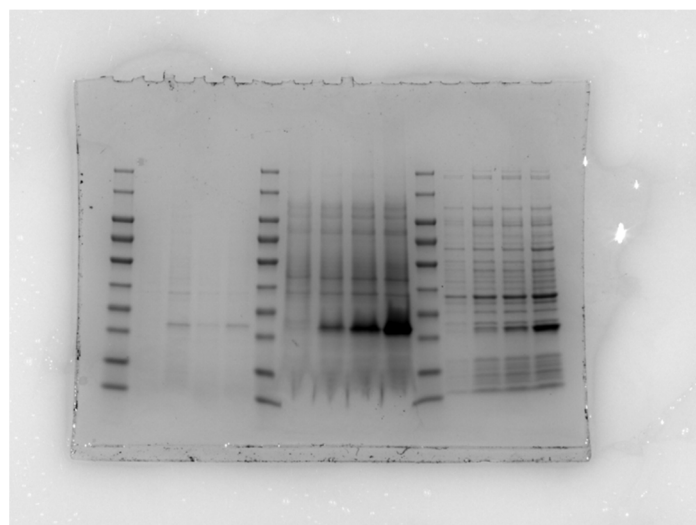


Figure S6. original SDS-PAGE of supernatant, lysate and insoluble fraction during expression of PmCA in *E. coli*.

- 1) Marker
- 2) Lysate
- 3) Flowthrough
- 4-13) Elution

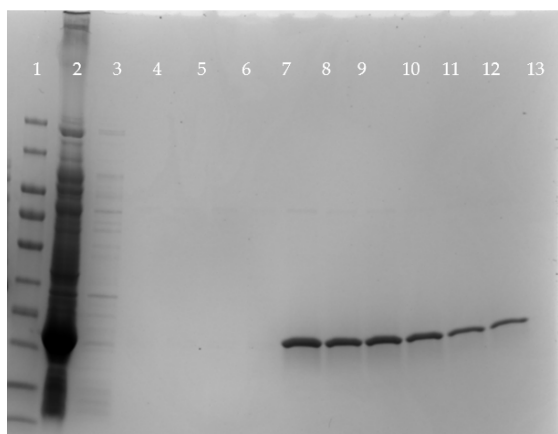


Figure S7. SDS-PAGE of lysate (2), flow through (3) and elution fractions (4-13) during purification of PmCA by affinity chromatography.

2.3. MtaCA

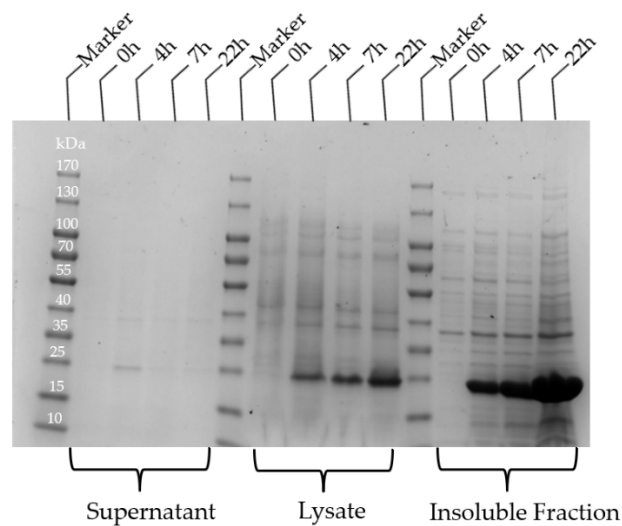


Figure S8. SDS-PAGE of supernatant, lysate and insoluble fraction during expression of MtaCA in *E. coli*. Expected molecular weight is 19.9 kDa (MtCA).

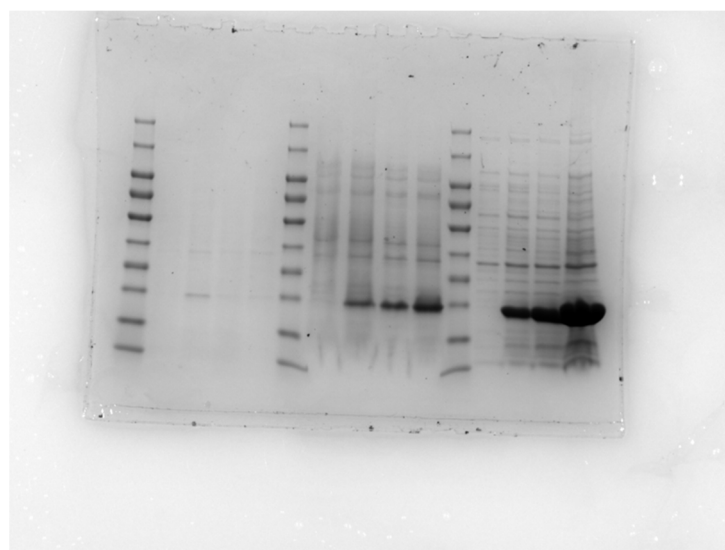


Figure S9. original SDS-PAGE of supernatant, lysate and insoluble fraction during expression of MtaCA in *E. coli*.

- 1) Marker
- 2) Lysate
- 3) Flowthrough
- 4-13) Elution

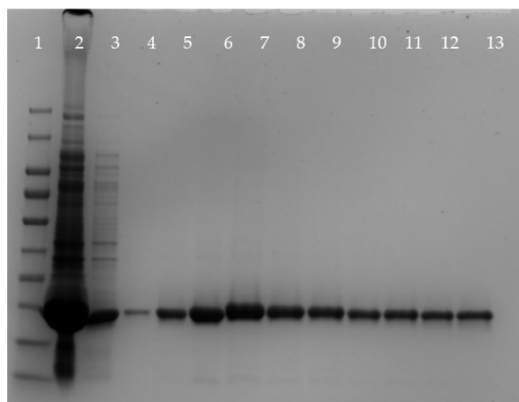


Figure S10. SDS-PAGE of lysate (2), flow through (3) and elution fractions (4-13) during purification of MtaCA by affinity chromatography.

2.4. SspCA

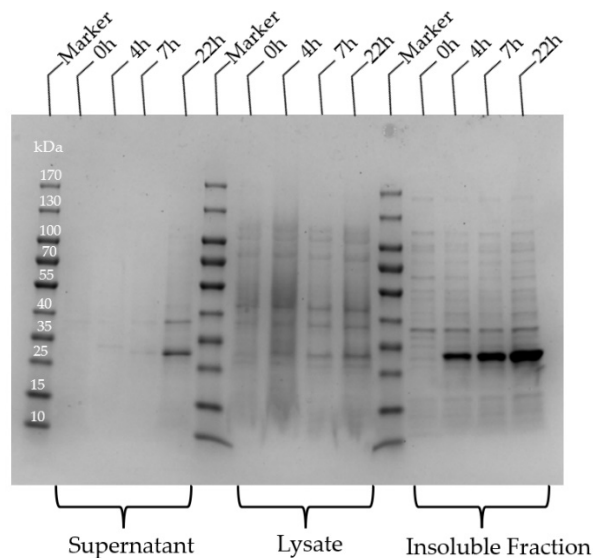


Figure S11. SDS-PAGE of supernatant, lysate and insoluble fraction during expression of SspCA in *E. coli*. Expected molecular weight is 27.5 kDa (SspCA).

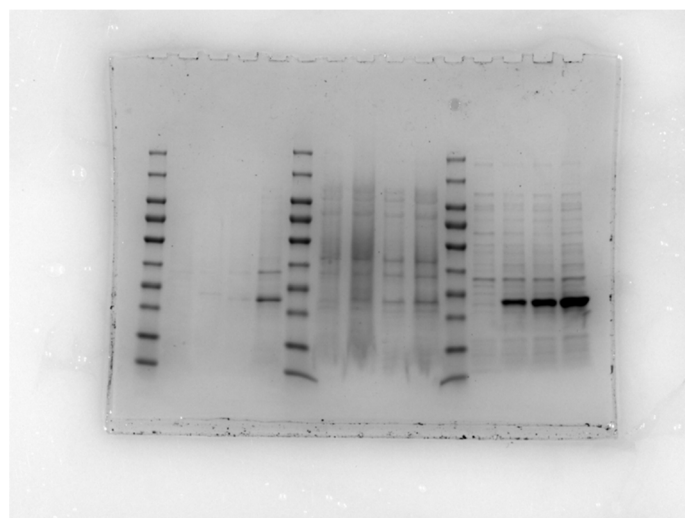


Figure S12. original SDS-PAGE of supernatant, lysate and insoluble fraction during expression of SspCA in *E. coli*.

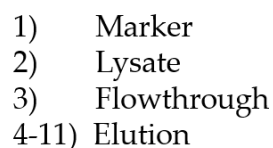


Figure S13. SDS-PAGE of lysate (2), flow through (3) and elution fractions (4-11) during purification of SspCA by affinity chromatography.

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
 10 20 30 40 50
PmCA -----MG GGWSYHGEHG PEHWGDLKDE YIMCKIGKNQ SPVDINR--I
SspCA MWSHPQFEKE HEWSYEGEKG PEHWAQLKPE FFWCKL-KNQ SPINIDKKYK
Consensus WSY GE G PEHW LK E CK KNQ SP I

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
 60 70 80 90 100
PmCA VDAKLKPIKI EYRAG-ATKV LNNGHTIKVS YEPGSYIVVD GIKFELKQFH
SspCA VKANLPKLNLY YKTAKESV VNNGHTIQIN IKEDNTLNYL GEKYQLKQFH
Consensus V A L Y V NNGHTI G K LKQFH

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
 110 120 130 140 150
PmCA FHAPSEHKLK GQHYPFEAHF VHADKHGNLA VIGVFFKEGR ENPILEKIWK
SspCA FHTPSEHTIE KKSYPLEIHf VHKTEDGKIL VVGVMakLGK TNKELDKILN
Consensus FH PSEH YP E HF VH G V GV K G N L KI

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
 160 170 180 190 200
PmCA VMPENAGEEV KLAHKINAED LLPKDRDYR YSGSLITTPPC SEGVRWIVME
SspCA VAPAEEGEKI -LDKNLNLNN LIPKDkRYMT YSGSLITTPPC TEGVRWIVLK
Consensus V P GE L N L PKD Y YSGSLITTPPC EGVRWIV

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
 210 220 230 240
PmCA EEMEMSKEQI EKFRKIMGGD TNRPVQPLNA RMIMEKWShP QFEK
SspCA KPISISKQQL EKLSVMVNP NNRPVQEINS RWIIIEGF--- ----
Consensus SK Q EK M NRpvQ N R I E

Figure S14: ClustalW Multiple Alignment (BioEdit Sequence Alignment Editor v7.0.5) of α -CAs from *Persephonella marina* (PmCA) and *Sulphurihydrogenibium yellowstonense* (SspCA) as expressed in this study. Orange: StrepTag. Grey background highlights the zinc-coordinating histidines, red background indicates the proton shuttle residues and blue background shows the „gate-keeper” residues of α -CAs.

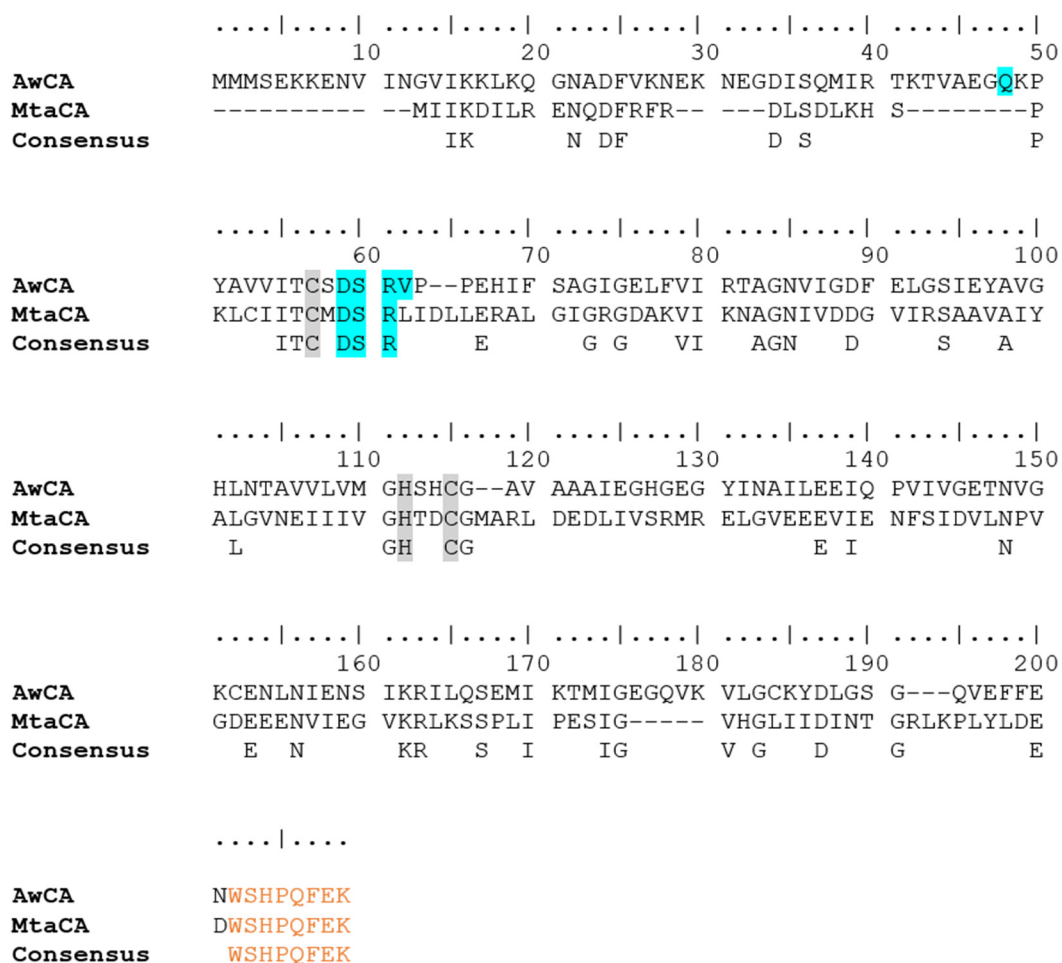


Figure S15: ClustalW Multiple Alignment (BioEdit Sequence Alignment Editor v7.0.5) of β -CAs from *Methanobacterium thermoautotrophicum* (MtaCA) and *Acetobacterium woodii* (AwCA). Orange: StrepTag. Grey background highlights the zinc-coordinating histidines and blue background indicates amino acids which are involved in the catalytic reaction.

4. Codon Optimized CA Gene Sequences

AwCA-StrepTag

3'-CATATG

ATGATGAGCGAGAAGAAGGAGAACGTGATCAACGGTGTGATTAAGAAGCTGAAGCAAGGCAACGCGGACTTTGTG
AAGAACGAGAAAAACGAGGGCGACATCAGCCAGATGATTCGTACCAAGACCGTGGCGGAAGGTCAAAAACCGTAC
GCGGTGGTTATCACCTGCAGCGATAGCCGTGTTCCGCCGAGCACATCTTCAGCGCGGTATTGGCGAACTGTTT
GTGATCCGTACCGCGGCAACGTTATTGGTGACTTCGAGCTGGGCAGCATCGAATACGCGGTGGGTACCTGAAC
ACCGCGGTGGTTCTGGTGATGGGTACAGCCATTGCGGTGCGGTTGCGGCGCGGATTGAGGGTCATGGTGAAGGT
TATATCAACGCGATTCTGGAGGAAATCCAGCCGGTGATTGTTGGCGAAACCAACGTTGGCAAGTGCGAGAACCTG
AACATCGAAAACAGCATCAAGCGTATTCTGCAGAGCGAGATGATCAAAACCATGATTGGCGAAGGTCAAGTGAAG
GTTCTGGGCTGCAAATATGATCTGGGTAGCGGTGAGTTGAGTTCTTTGAAAACCTGGAGCCATCCGCAATTGAA
AAATAA

AAGCTT-5'

PmCA-StrepTag

3`-CATATG

GGCGGCGGTTGGAGCTACACGGCGAGCATGGCCCCGAGCATTGGGGTGACCTGAAGGACGAGTACATTATGTGC
 AAGATCGGCAAGAACCAGAGCCCCGGTGGACATCAACCGTATTGTTGATGCGAAGCTGAAACCGATCAAGATTGAG
 TACCGTGCGGGCGCGACCAAAGTGCTGAACAACGGTCACACCATCAAGGTTAGCTACGAACCGGGCAGCTATATC
 GTGGTTGACGGTATTAAGTTCGAACTGAAACAGTTCCTACTTTCACGCGCCGAGCGAGCACAAGCTGAAAGGCCAA
 CACTATCCGTTTCGAAGCGCACTTTGTGCACGCGGATAAACACGGTAACCTGGCGGTGATTGGCGTTTTCTTTAAG
 GAAGGTCGTGAGAACCCGATCCTGGAAAAGATTTGGAAAGTGATGCCGGAACGCGGGCGAGGAAGTTAAGCTG
 GCGCACAAAATCAACGCGGAGGACCTGCTGCCGAAAGACCGTGATTACTATCGTTATAGCGGCAGCCTGACCACC
 CCGCCGTGCAGCGAGGGTGTGCGTTGGATTGTTATGGAGGAAGAGATGGAAATGAGCAAGGAACAAATCGAGAAG
 TTTTCGTAAAATTATGGGTGGCGATACCAACCGTCCGGTTCAACCGCTGAATGCGCGTATGATTATGGAGAAATGG
 AGCCACCCGCAATTTGAGAAGTAA

AAGCTT-5`

MtaCA-StrepTag

3`-CATATG

CATCAAAGACATCCTGCGTGAGAACCAAGATTTCCGTTTCCGTGACCTGAGCGACCTGAAGCATAGCCCGAAGCT
 GTGCATCATTACCTGCATGGACAGCCGTCTGATCGATCTGCTGGAACGTGCGCTGGGTATTGGCCGTGGTGACGC
 GAAAGTGATTAAAAACGCGGGCAACATCGTGACGATGGTGTTATTCGTAGCGCGGCGGTTGCGATCTATGCGCT
 GGGCGTGAACGAGATCATTATCGTTGGCCACACCGATTGCGGTATGGCGCGTCTGGACGAGGATCTGATCGTGAG
 CCGTATGCGTGAACCTGGGTGTGGAGGAAGAGTTATTGAGAACTTCAGCATCGACGTGCTGAACCCGGTTGGCGA
 TGAAGAGGAAAACGTGATCGAAGGTGTTAAGCGTCTGAAAAGCAGCCCGCTGATTCCGGAGAGCATCGGCGTTCA
 CGGTCTGATTATCGACATTAACACCGGTGCGCTGAAACCGCTGTATCTGGACGAAGACTGGAGCCATCCGCAATT
 TGAGAAGTAA

AAGCTT-5`

StrepTag-SspCA

3`-CATATG

TGGAGCCACCCGCAATTTGAAAAGGAGCATGAGTGGAGCTACGAAGGCGAGAAAGGCCCGGAGCATTGGGCGCAA
 CTGAAGCCGGAGTTTTTCTGGTGCAAACCTGAAGAACCAGAGCCCGATCAACATTGACAAGAAATACAAGGTGAAA
 GCGAACCTGCCGAACTGAACCTGTACTATAAGACCGCGAAAGAGAGCGAAGTGTTAACAACGGCCACACCATC
 CAAATTAACATCAAAGAGGACAACACCCTGAACTACCTGGGTGAAAAATATCAGCTGAAGCAATTCCACTTTCAC
 ACCCCGAGCGAGCACACCATTGAAAAGAAAAGCTATCCGCTGGAGATCCACTTCGTGCACAAAACCGAAGACGGC
 AAGATTCTGGTGGTTGGCGTTATGGCGAAGCTGGGTAAAAACCAACAAGGAGCTGGATAAAATTCTGAACGTGGCG
 CCGGCGGAGGAAGGCGAAAAAATTCTGGACAAGAACCTGAACCTGAACAACCTGATCCCGAAGGATAAACGTTAC
 ATGACCTATAGCGGCAGCCTGACCACCCCGCGTGCACCGAGGGTGTGCGTTGGATTGTTCTGAAGAAACCGATT
 AGCATCAGCAAGCAGCAACTGGAAGAGCTGAAAAGCGTGATGGTTAACCCGAACAACCGTCCGGTTCAGGAGATT
 AATAGCCGTTGGATCATCGAAGGTTTCTAA

AAGCTT-5`

5. Calculated Hydratase Activities for Thermostability Experiments

Table S1. Calculated hydratase activities at 25 °C for AwCA and PmCA after preincubation for thermostability determination in turnover rate per mg enzyme and WAU per mg enzyme.

Temperature	Incubation Time	AwCA			PmCA		
		Total turnover rate $\mu\text{mol s}^{-1} \text{L}^{-1}$	Turnover rate per mg enzyme $\mu\text{mol s}^{-1} \text{mg}^{-1}$	WAU per mg enzyme	Total turnover rate $\mu\text{mol s}^{-1} \text{L}^{-1}$	Turnover rate per mg enzyme $\mu\text{mol s}^{-1} \text{mg}^{-1}$	WAU per mg enzyme
30 °C	96 h	1417 ± 37	2580 ± 75	1400 ± 165	1552 ± 59	3123 ± 120	2079 ± 327
	120 h	1408 ± 63	2349 ± 137	1368 ± 279	1530 ± 36	2837 ± 90	1956 ± 190
	144 h	1414 ± 40	2520 ± 99	1388 ± 185	1548 ± 32	3057 ± 86	2052 ± 175
40 °C	96 h	1289 ± 42	2068 ± 86	873 ± 160	1574 ± 11	3211 ± 26	2193 ± 58
	120 h	1222 ± 35	1606 ± 89	640 ± 118	1495 ± 41	2695 ± 99	1774 ± 208
	144 h	1199 ± 44	1662 ± 105	567 ± 136	1540 ± 8	3024 ± 60	2005 ± 44
50 °C	24 h	1262 ± 31	1944 ± 66	775 ± 111	1485 ± 25	2833 ± 55	1721 ± 124
	48 h	1090 ± 22	1115 ± 54	258 ± 53	1501 ± 31	2757 ± 64	1804 ± 156
	72 h	888 ± 28	489 ± 64	−105 ± 34	1480 ± 12	2859 ± 40	1700 ± 60
60 °C	96 h	868 ± 3	387 ± 17	−128 ± 3	1507 ± 8	2942 ± 23	1833 ± 42
	120 h	833 ± 26	47 ± 75	−159 ± 20	1474 ± 28	2610 ± 78	1667 ± 138
	144 h	813 ± 10	116 ± 61	−175 ± 6	1502 ± 9	2874 ± 60	1810 ± 45
70 °C	24 h	1116 ± 55	1204 ± 110	328 ± 138	1532 ± 28	2868 ± 59	1964 ± 149
	48 h	790 ± 24	−202 ± 64	−188 ± 12	1490 ± 12	2598 ± 49	1746 ± 62
	72 h	n. a.	n. a.	n. a.	1436 ± 9	2757 ± 20	1487 ± 41
80 °C	96 h	n. a.	n. a.	n. a.	1396 ± 2	2477 ± 35	1307 ± 8
	120 h	n. a.	n. a.	n. a.	1524 ± 14	2858 ± 37	1921 ± 71
	144 h	n. a.	n. a.	n. a.	1445 ± 49	2090 ± 105	1532 ± 231
90 °C	24 h	n. a.	n. a.	n. a.	1560 ± 33	3153 ± 68	2114 ± 182
	48 h	n. a.	n. a.	n. a.	1577 ± 17	3030 ± 38	2205 ± 96
	72 h	n. a.	n. a.	n. a.	1469 ± 10	2629 ± 24	1644 ± 51
100 °C	96 h	n. a.	n. a.	n. a.	1477 ± 36	2798 ± 79	1684 ± 176
	120 h	n. a.	n. a.	n. a.	1436 ± 10	2461 ± 57	1488 ± 45
	144 h	n. a.	n. a.	n. a.	1418 ± 26	2535 ± 77	1403 ± 117
110 °C	24 h	n. a.	n. a.	n. a.	1400 ± 27	2486 ± 61	1326 ± 119
	48 h	n. a.	n. a.	n. a.	1377 ± 33	2195 ± 69	1225 ± 140
	72 h	n. a.	n. a.	n. a.	1413 ± 29	2512 ± 59	1385 ± 130
120 °C	96 h	n. a.	n. a.	n. a.	1066 ± 18	979 ± 65	200 ± 41
	120 h	n. a.	n. a.	n. a.	1148 ± 37	1451 ± 79	412 ± 104
	144 h	n. a.	n. a.	n. a.			