

An attempt in mitigating global warming through carbonic anhydrase mediated carbon sequestration



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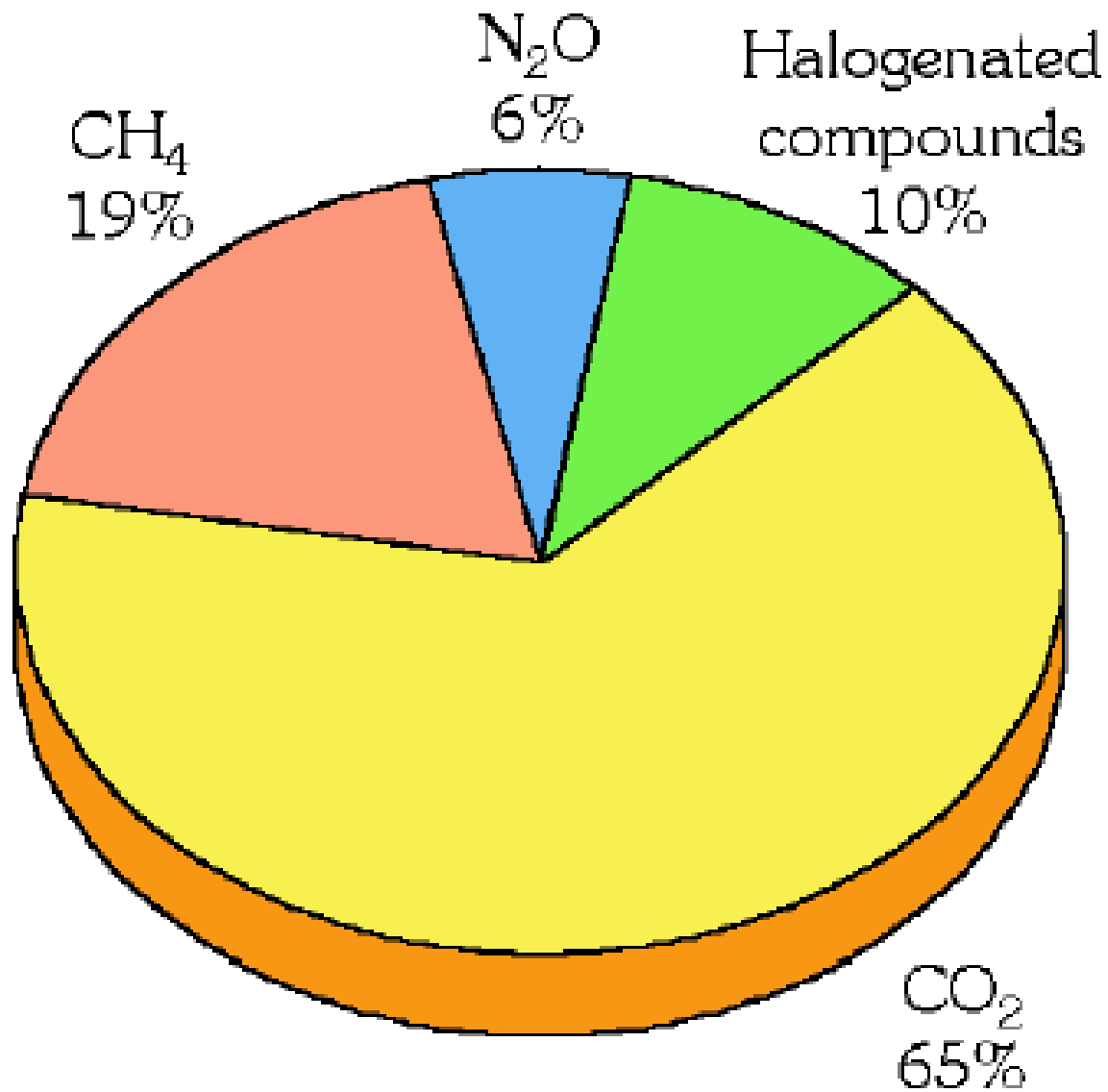
GLOBAL WARMING

**Increase in the average temperature of Earth's
near-surface air and oceans**

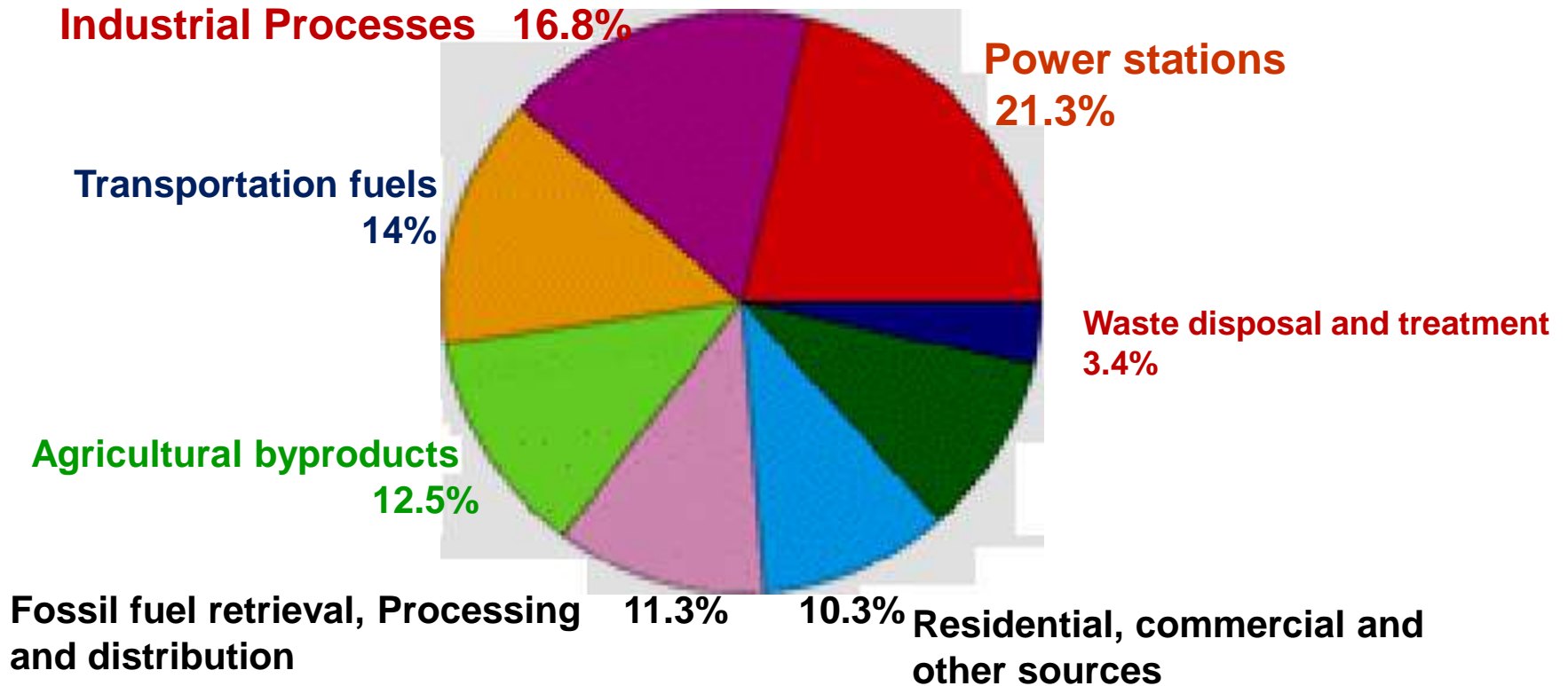
Global surface temperature has increased by 0.74 ± 0.18 °C in 20th century

This may rise further to 1 – 6.4 °C in 21st century, if not checked.

CONTRIBUTION TO GLOBAL WARMING



Annual Greenhouse Gas Emissions



**Annual Release of CO₂ into the atmosphere:
22 billion tonnes**

Global Warming: The Current Scenario

- In the past 100 years, global temperatures are the warmest at present.
- Atmospheric CO₂ has increased by 31% from pre-industrial levels.
- Ice is disappearing from the Arctic Ocean and Greenland.
- If the Antarctic and the Arctic ice melts, sea levels would rise by almost 11 meters.

Global Warming: The Consequences

Some anticipated effects include:

- **Sea level rise of 110 to 770 mm by 2100**
- **Repercussions to agriculture**
- **Possible slowing of the thermo-haline circulation**
- **Reductions in the ozone layer**
- **Increased intensity and frequency of hurricanes and extreme weather events**
- **Lowering of ocean pH**
- **The spread of diseases such as malaria and dengue fever**
- **Mass extinction events**
- **Physiological effects involving reduction in the pH value of the blood serum (acidosis)**
- **Reduction in rains**

Combating Global Warming

- Reduction of energy use (per person)
- Shifting from carbon-based fossil fuels to alternative energy sources
- Carbon capture and storage; Geo-engineering including carbon sequestration
- Population control

Mineralization of CO₂

CO₂ reacts with available metal oxides, which in turn produces stable carbonates. This process occurs naturally over many years and is responsible for a large amount of surface limestones.



Advantage of the process

- ❖ Mineral carbonation is thermodynamically favourable and occurs naturally
- ❖ Raw materials such as mineral silicates and industrial wastes rich in MgO and CaO are abundant
- ❖ Produced carbonates are stable
- ❖ The process can be made economical by utilizing carbonates

Uses of mineral carbonates

- Can be used for synthesis of industrially valuable and useful by-products such as chemicals, cements and construction materials, white pigment in paints, a therapeutic source in antacids and calcium supplements, and tableting excipient as well as remediation of waste feed stocks
- Mineralization process parameters can be optimized to produce high purity valuable metals, silica and carbonate mineral powders

The conventional carbonation pathways are, however, very slow under ambient temperature and pressure.

Carbon sequestration

Carbon sequestration or CCS (carbon capture and storage) can be defined as the capture and secure storage of carbon that would otherwise be emitted to or remain in the atmosphere

Methods of carbon sequestration

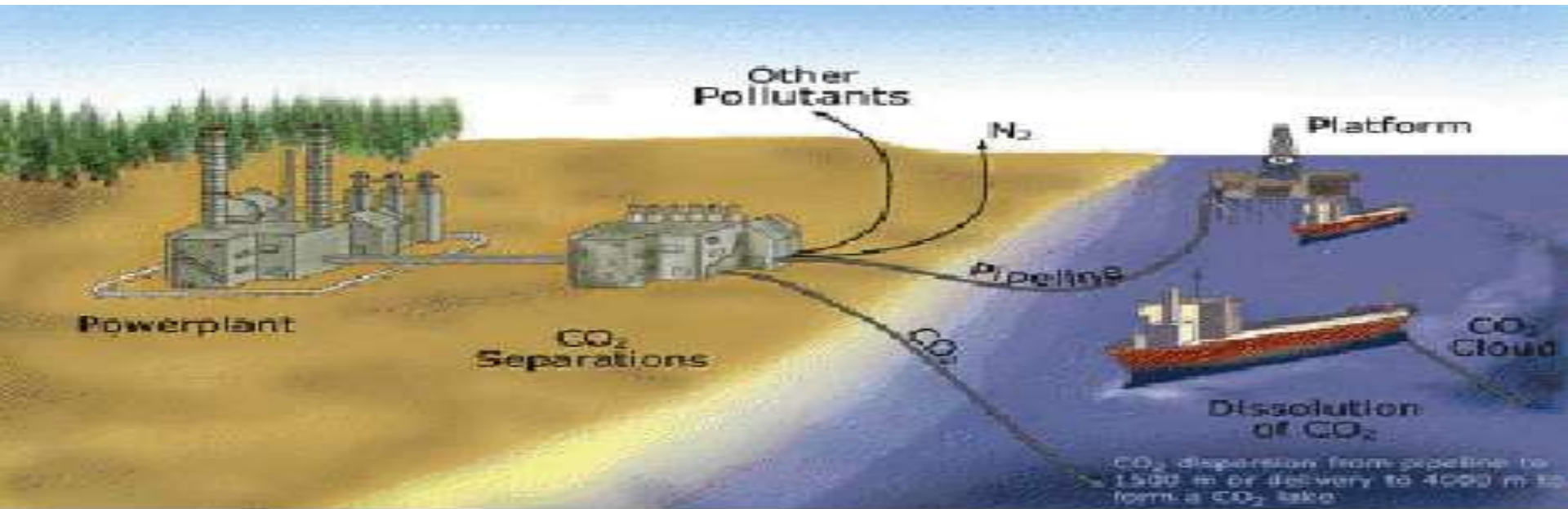
1. Terrestrial sequestration in plants and soil

2. Geological sequestration

- ❖ Underground structures eg. Unminable coal seam
- ❖ CO₂ is sometimes injected into declining oil fields to increase oil recovery
- ❖ CO₂ can also be sequestered in deep saline aquifers where it displaces brine and some of it would get partially dissolved

3. Ocean sequestration

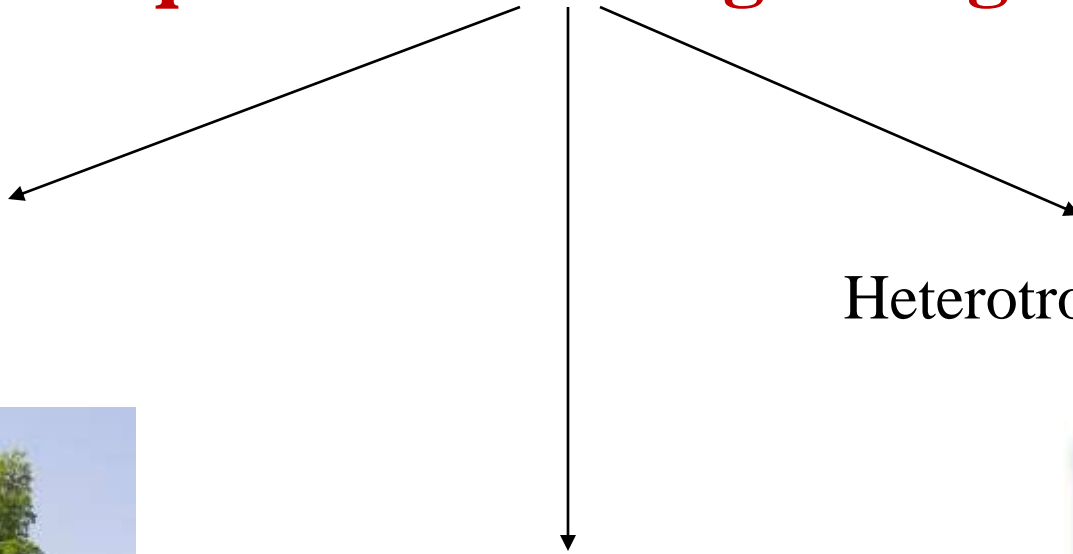
Carbon sequestration by direct injection into the deep ocean involves the capture, separation, concentration, transport, and injection of CO₂ from land or tankers



Drawbacks associated with ocean and geological storage of carbon dioxide

- ❖ Future risk of leakage from the site of injection and could cause local ecological damage.
- ❖ Separation, concentration and transportation increases the cost of the process

Carbon sequestration using biological systems



Heterotrophic microbes



Algal cultivation



Carbonic anhydrase

Carbonic anhydrases (CA) are one of the fastest known (K_{cat} ranging from 10^5 to 10^7 s^{-1}) and ubiquitously present zinc containing metalloenzymes that catalyzes the interconversion of CO_2 and water to bicarbonate and protons.



CA can speed up the process of calcification by catalyzing the rate-determining step (step 2a) in the conversion of CO_2 to CaCO_3 .

Mechanism of action of CA



Types of carbonic anhydrases (CA)

There are at least six distinct CA families (α , β , γ , δ , ζ and η).

These families have no significant amino acid sequence similarity and are an excellent example of convergent evolution.

Desirable characteristics for an ideal CA to be useful for CO₂ mineralization

- ❖ Thermostability**
- ❖ Alkalistability**

Carbonic anhydrase assay methods

Wilbur Anderson assay

Its an electrometric assay in which the time required (in seconds) for a saturated CO₂ solution to drop the pH of 0.02 M Tris·HCl buffer from 8.3 to 7.3 at 0°C is determined. The time without enzyme is recorded at T₀; with enzyme, T.

(pH meter: Metrohm, Switzerland with biotrode electrode)

WA Unit = $T_0 - T/T$

1 WA unit is defined as the amount of enzyme that causes the pH of a 20 mM Tris buffer to drop from pH 8.3 to 7.3 per minute at 0 °C.

CHEMIST'S PRAYER

Lord I fall upon my knees
And pray that all my syntheses
May no longer be inferior
To those conducted by bacteria

OBJECTIVES

1. Selection of a potent carbonic anhydrase (CA) producing bacterial strain
2. Optimization of native CA production
3. Purification and characterization of native CA
4. Cloning, purification and characterization of CA produced heterologously in *E. coli* and *Pichia pastoris*
5. Application of CA in biomimetic carbon sequestration
6. Immobilization of CA and its utility in carbon sequestration

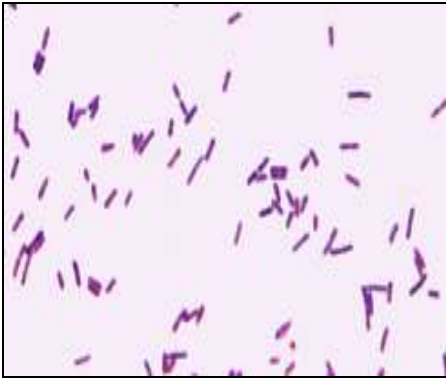
Screening of a potent carbonic anhydrase producing strain*

Strain	Location	U/ml	U/g dry biomass (gdbm)	SEA (U/mg)
<i>Bacillus halodurans</i> (TSLV1)	Extracellular	-	-	-
	Intracellular		6,300 ± 430	4.3
<i>Geobacillus thermoleovorans</i> (NP33)	Extracellular	-		
	Intracellular		-	
<i>G. thermodenitrificans</i> (C360)	Extracellular	-		
	Intracellular		-	
<i>Sporosarcina pasteurii</i>	Extracellular	0.33		0.043
	Intracellular		26 ± 2.0	0.63

*By Wilbur-Anderson assay

Identification of the selected bacterium

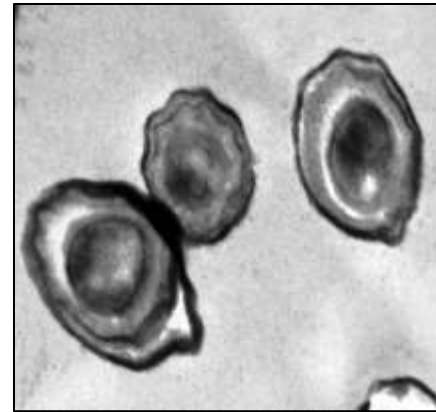
Bacillus halodurans (TSLVI)



Gram's staining



Endospore staining

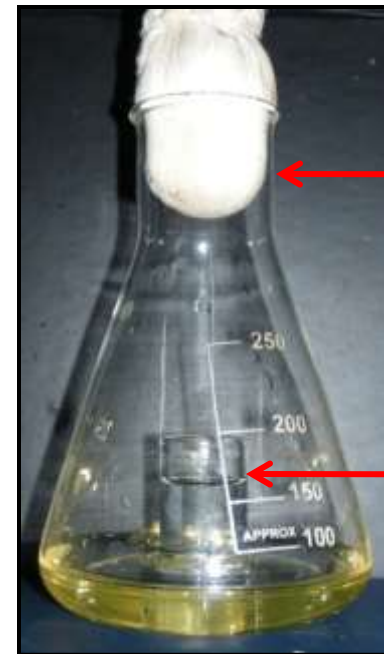


**Endospore under
TEM**

Bacillus halodurans is a rod-shaped, Gram positive, motile and spore forming bacterium isolated from the alkaline sediments of Lonar Lake.

Effect of elevated levels of CO₂ on growth and CA production by *Bacillus halodurans*

CO ₂ concentration (%)	U/ gdbm
0	6,344 ± 320
0.03	6,456 ± 385
5.0	5,822 ± 452
10.0	5,004 ± 765



Cotton plug containing zeolite

5M KOH

**Optimization of carbonic anhydrase
production by *B. halodurans* TSLV1**

Enzyme preparation

Cells harvested and washed with saline and resuspended in 10 mL, 20 mM Tris buffer pH 8.3



Sonication at 50% amplitude (3s pulse on 3s off)



Cell debris removed by centrifugation.



Supernatant served as crude enzyme

Optimal variables for carbonic anhydrase production by *B. halodurans*

Culture variables that significantly affected carbonic anhydrase production identified by one-variable-at-a-time approach

Component	%
Starch	0.5
Peptone	0.5
KH ₂ PO ₄	0.1
MgSO ₄	0.05
pH	8.5
Temperature (°C)	45.0
Agitation	200 rpm
Inoculum age	8 h
Inoculum size	2(%)1.5x10 ⁶ cfu ml ⁻¹

Approach	CA production (U / gdbm)	Fold increase in production	Specific activity (U/mg protein)
Unoptimized medium	6,300 ± 580	1	4.3
Optimized medium (One-variable-at-a-time approach)	25,000 ± 800	3.97	12

Optimization of CA production by Statistical methods

S.no.	Starch (%)	MgSO ₄ (%)	Inoculum size (%)	Predicted values	Observed values
1	2.5	0.12	2.49	30,278.8	31,120±985
2	2.13	0.10	3.71	29,573.5	28,203±1,024
3	2.92	0.08	2.99	34,353.2	35,920±1,105
4	3.34	0.07	3.54	30,672.9	29,728±1,000

Approach	CA production (U / gdbm)	Fold increase in production
Unoptimized medium	6,300 ± 350	1
Optimized medium (Statistical approach)	35,920 ± 1105	5.7

Component	%
Starch	2.5
Peptone	0.5
KH ₂ PO ₄	0.1
MgSO ₄	0.1
pH	8.5
Temperature (°C)	45.0
Agitation	200 rpm
Inoculum age	8 h
Inoculum size	3(%)

Optimized culture variables

Purification of CA from
B. halodurans TSLV1

Steps involved in the purification process

Crude lysate



Acetone precipitation(0-50%, 50-70%)



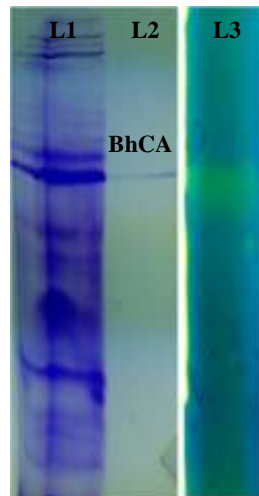
Anion exchange using (Hicapto™)



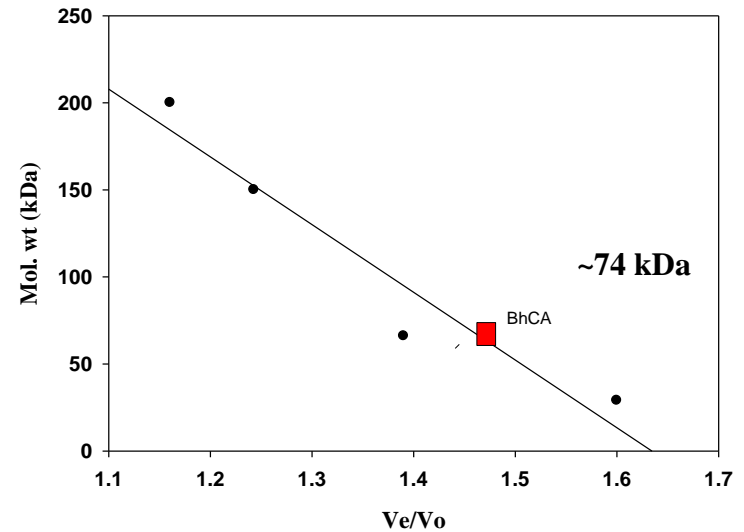
pAMBS affinity chromatography

Purification profile

Purification step	Activity (WA U/mL)	Total activity (WA U)	Protein (mg/mL)	Specific activity (U/mg)	Yield (%)	Fold purification
Crude protein	329.0	21155.0	7.6	43.29	100	1.0
Acetone precipitation	2311	12666	27.18	85	59.8	1.97
Anion exchange using (Hicapo Q™)	4798.0	9076.1	2.5	1912.2	42.9	44.17
pAMBS affinity chromatography	625.88	8136.44	0.05	3,425	38.46	79.11

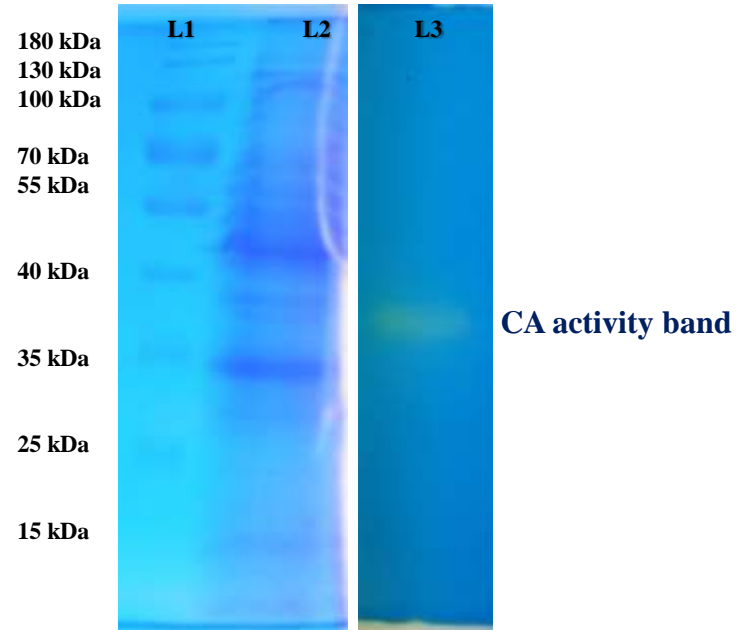


. Figure Native PAGE of purified BhCA along with zymogram. *Lane 1:* Crude lysate, *Lane 2:* Purified BhCA, *Lane 3:* Zymogram of BhCA



Molecular weight markers used with purified BhCA (1) β-Amylase (200); (2) Alcohol dehydrogenase (150); (3) Albumin (66); (4) Carbonic anhydrase (29kDa); (5) Cytochrome C (12.4kDa).

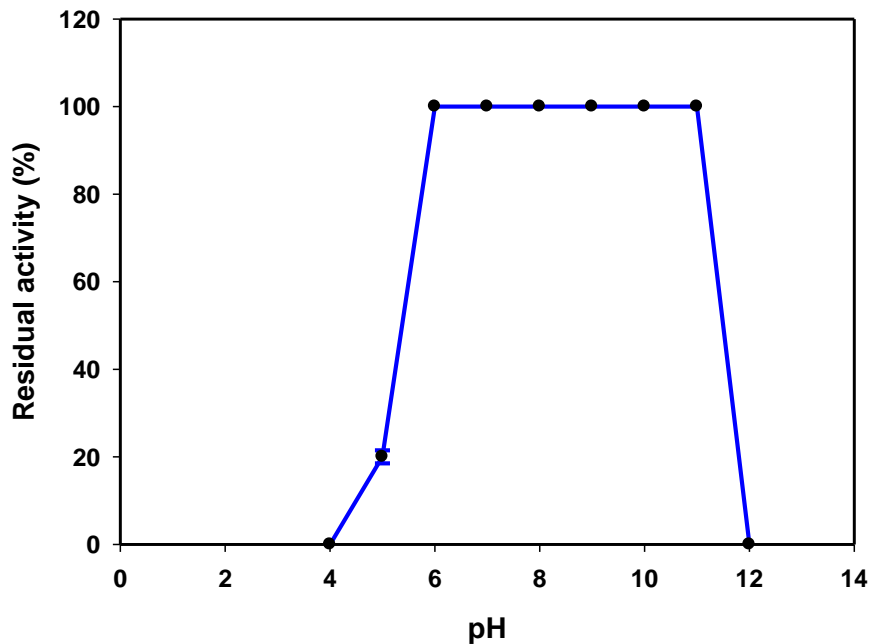
Zymogram of crude lysate of *B. halodurans*



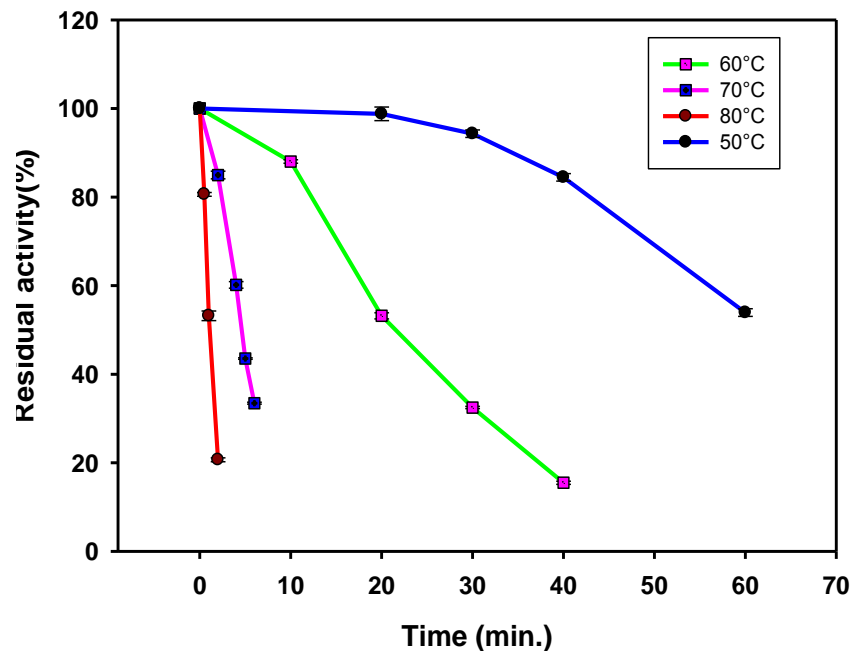
SDS PAGE of crude lysate of *B. halodurans*: L1: Protein molecular weight marker, L2: Crude lysate, L3: Zymogram of CA activity

Characterization of BhCA

Effect of different pH and temperature on the stability of BhC



Effect of different pH on BhCA stability:
BhCA is stable in pH 6.0-11.0 for 24 h retaining 100 % activity



Effect of different temperatures on BhCA stability:
 $T_{1/2}$ is 65 ± 1 , 25 ± 1 , 4.7 ± 0.5 and 1.2 ± 0.2 min at 50, 60, 70 and 80° respectively

Effect of CA specific inhibitors on the activity of BhCA

Inhibitor	AZA	EZA	MZA	SA	BSA	SNA	AS
IC₅₀ (μM)	0.22	0.33	1.03	8580	4.58	76.2	168.36

***AZA- Acetazolamide**
EZA- Ethazolamide
MZA- Methazolamide
SA- Sulfamic acid
BSA- Benzenesulfonamide
SNA- Sulfanilamide
SA- Sulfamic acid

Effect of different metal ions and anions on enzyme activity

Metal ions	Concentration	Residual activity (%)
Mg ²⁺	1 mM	100±0.30
	5 mM	100±1.04
Zn ²⁺	500 µM	100±1.00
	1 mM	55.47±1.21
Hg ²⁺	500 µM	31.83±0.31
	1 mM	23.37±0.26
	5 mM	0±0.5
Co ²⁺	1 mM	40.43±0.27
	5 mM	27.41±0.46
Cu ²⁺	500 µM	44.60±1.19
	1 mM	36.66±0.38
	5 mM	0±1
Mn ²⁺	1 mM	99.57±1.24
	5 mM	100.±0.95
Ca ²⁺	1 mM	99.43±1.30
	5 mM	100.08±0.73
Ni ²⁺	1 mM	22.65±0.30
	5 mM	18.97±0.14
Fe ³⁺	1 mM	21.36±0.27
	5 mM	0±0.5
Fe ²⁺	1 mM	27.72±1.17
	5 mM	0.64±1.24
Al ³⁺	1 mM	100 ±0.82
	5 mM	100.01±0.61
Ag ²⁺	1 mM	100±0.27
	5 mM	100.±0.61
Sn ²⁺	1 mM	124.71±3.91
	5 mM	148.16±1.28
Pb ²⁺	1 mM	100±0.27
	5 mM	68.92±1.79
Ba ²⁺	1 mM	100.92±1.50
	5 mM	100±0
NH ₄ ⁺	1 mM	99.5±1.25
	5 Mm	100±0.5
Na ⁺	1 M	100.87 ±0.29
	2 M	73.27 ±1.64

Stimulators:

Sn²⁺, SO₄²⁻

No observable effect of SO₃²⁻

Anions	Concentration	Residual activity(%)
SO ₄ ⁻	1 M	167.8 ±2.76
	0.125 M	100 ±2.44
SO ₃ ²⁻	1.0 M	100.66 ±0.86
	1.25 M	100 ±0
NO ₃ ⁻	0.5 M	100 ±2.08
	1 M	83.01 ±1.66
	1.5 M	75.12 ±2.64
HCO ₃ ⁻	0.1 M	100 ±0
	0.75 M	30.25±1.42
CO ₃ ²⁻	0.01 M	100 ±0.12
	0.05 M	75.63 ±0.66
Cl ⁻	0.1 M	60.05 ±1.08
	0.5 M	100.27 ±1.71
I ⁻	1 M	100.8 ±1.53
	1 mM	100.6 ±1.78
F ⁻	5 mM	99.8 ±1.29
	1 mM	100±1.5
Br ⁻	5 mM	100±1.0
	1 mM	100±0.5
	5 mM	100±0.76

Effect of different modulators (inhibitors, ionic and non ionic detergents) on enzyme activity

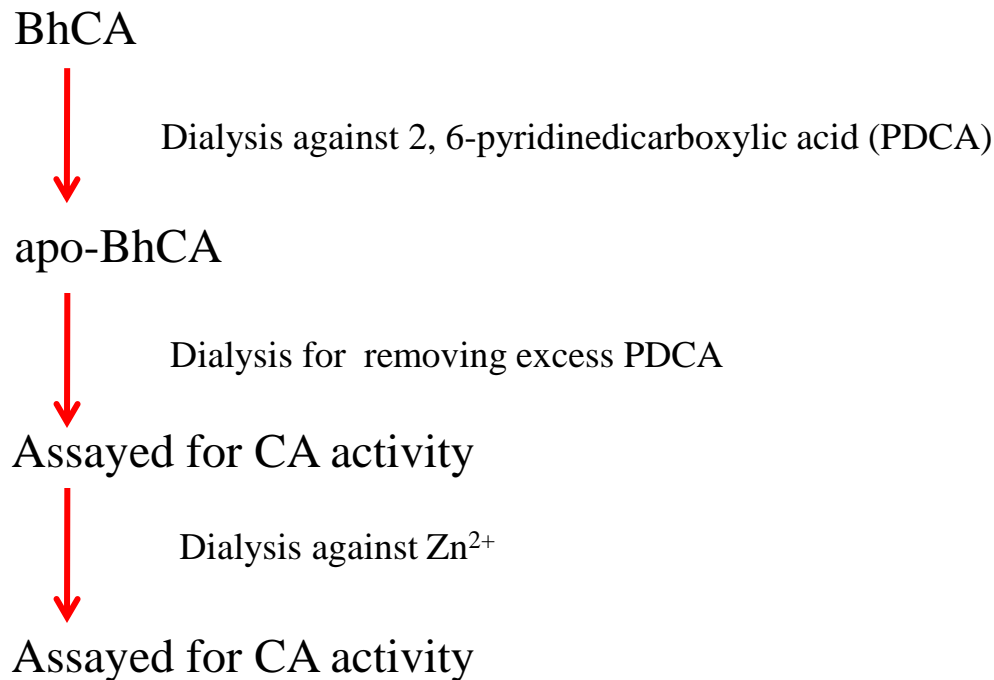
Modulator	Concentration	Residual activity (%)
WRK	1 Mm	96 ±3.7
	5 mM	0 ±0.55
NBS	1 mM	6.0±1.21
	5 mM	0 ±0.53
NEM	1 mM	95.3 ±2.57
	5 mM	0 ±0.41
DEPC	1 mM	76±1.5
	5 mM	0.85±1
PMSF	1 mM	36.06±1.42
	5 mM	27.44±1.76
DTT	1 mM	93.8 ±2.93
	5 mM	43.2 ±3.89
IAA	1 mM	50.3 ±2.36
	5 mM	0 ±0.63
β-ME	1 mM	100±1.02
	5 mM	80.88
TRITON X100	0.1%	84.5 ±1.54
	0.2%	83.22 ±1.5
TWEEN 80	0.1%	100.2 ±1.67
	0.2%	101.5 ±2.07
SDS	1%	99.24
	5%	86.22
EDTA	50 mM	100 ±0.2
	1 M	100.58±0.66

No observable effect of EDTA

DTT- dithiothreitol
 β-ME - β-mercaptoethanol
 WRK - Woodward's reagent K
 IAA - Iodo acetamide
 PMSF- phenyl methyl sulfonyl fluoride
 NBS - N-bromosuccinimide
 NEM - N-ethylmaleimide
 DEPC - Diethylpyrocarbonate
 EDTA –ethylenediaminetetraacetic

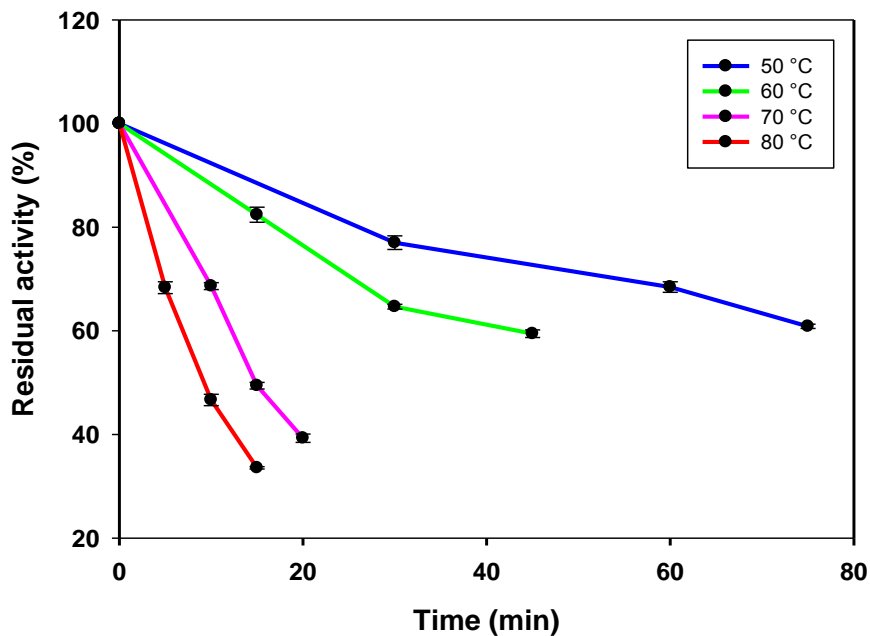
BhCA is a zinc containing metalloenzyme

2, 6-pyridinedicarboxylic acid (PDCA) – specific chelator of zinc ion



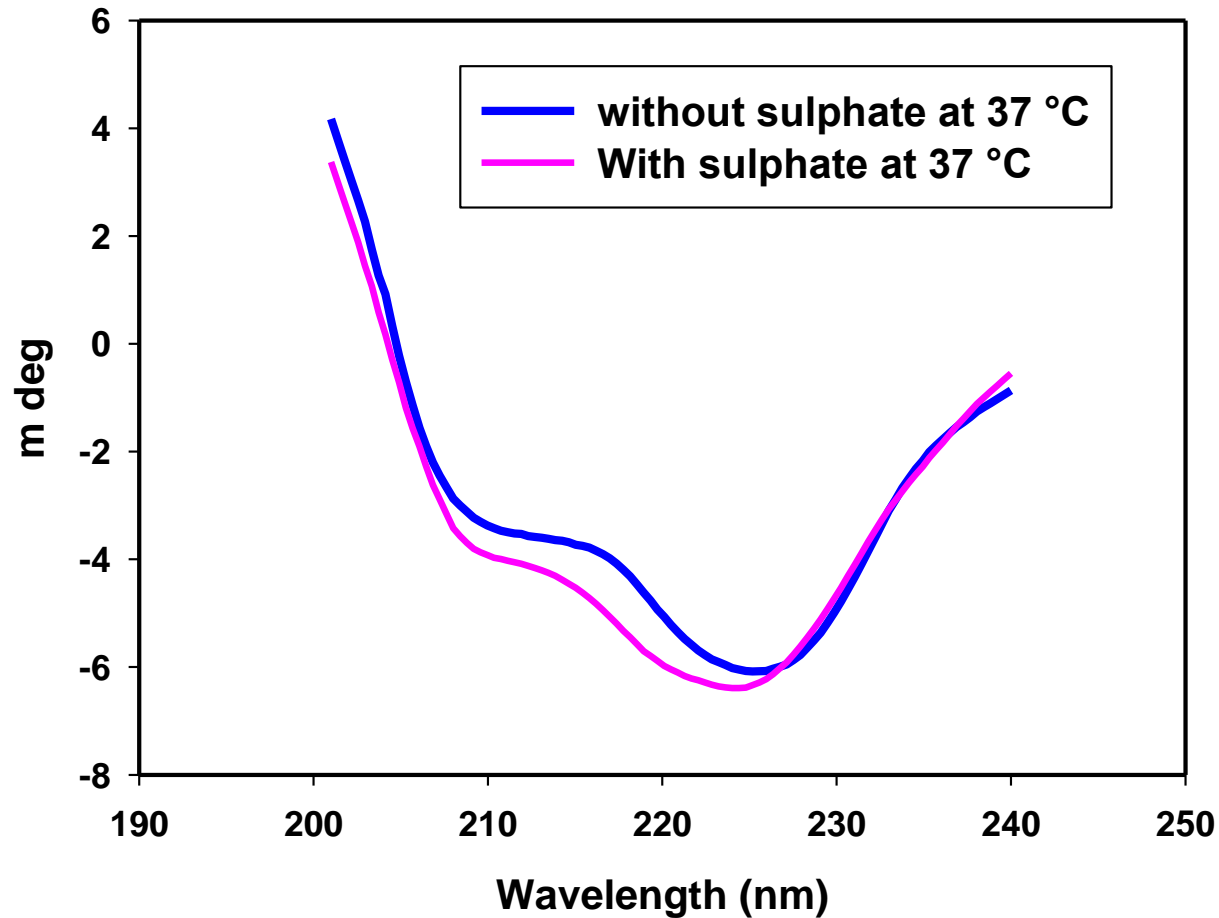
BhCA lost activity upon dialysis against PDCA , and the activity was restored upon dialysis against Zn²⁺ confirmed BhCA to be a zinc metalloenzyme.

Temperature stability of BhCA in presence of sulphate

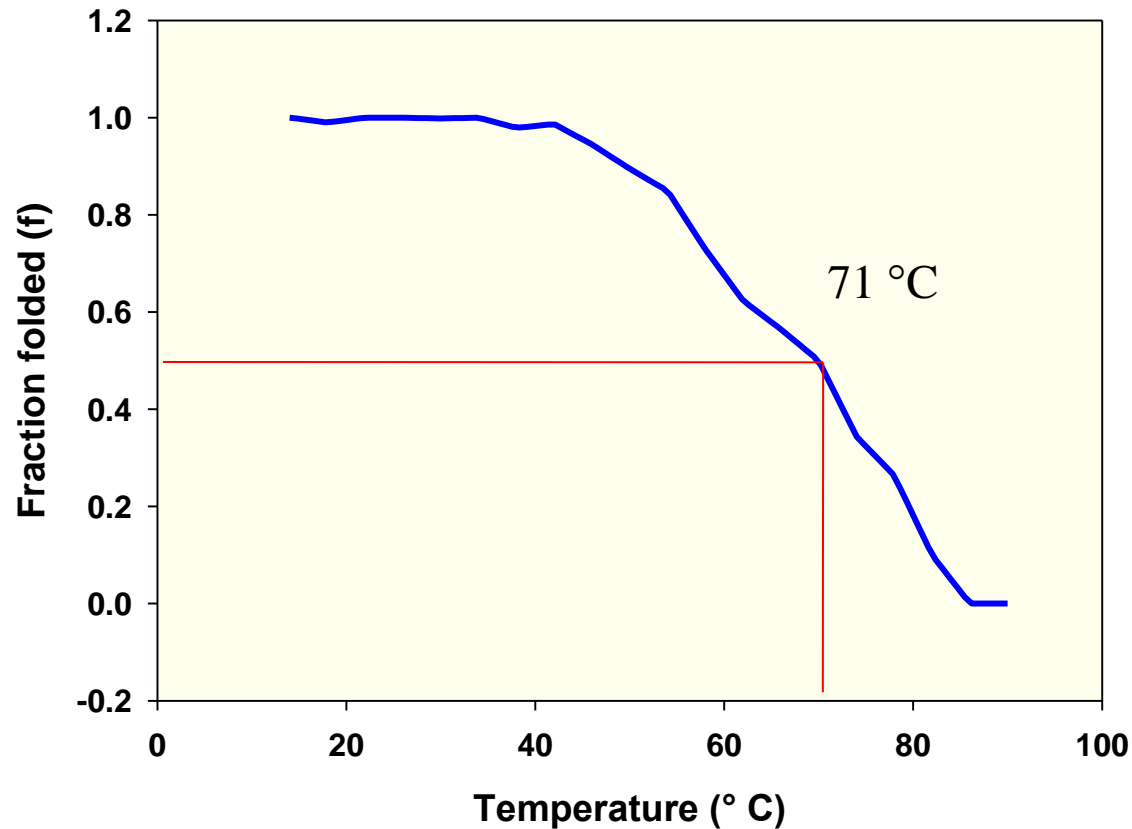


Temperature °C	$T_{1/2}$ min
50	95 ± 1.0
60	54 ± 0.5
70	15 ± 1.0
80	19 ± 1.0

Far-UV CD spectra of BhCA in presence and absence of sulphate



Melting Temperature (T_m) of BhCA



Thermal unfolding curve for BhCA

Shelf life of BhCA

	Residual activity (%)	
Duration	4 °C	Room temperature
6 months	100	100
12 months	100	100
18 months	100	94
24 months	100	85

Application of BhCA in biomineralization of CO₂

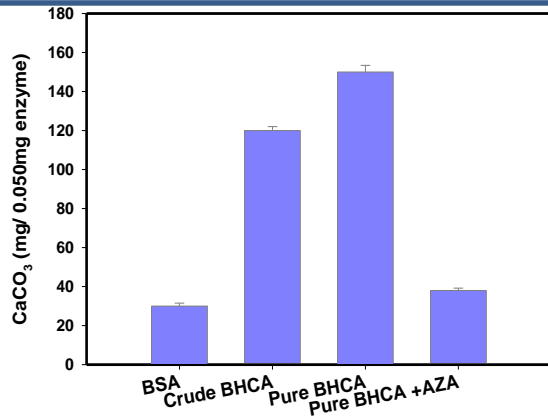
Turbidometric experiment to study the effect of CA enzymes on acceleration of CaCO_3 precipitation

Sample	BSA	BhCA	BCA
Time (s)	130 ± 2.5	8 ± 0.5	38 ± 2.0

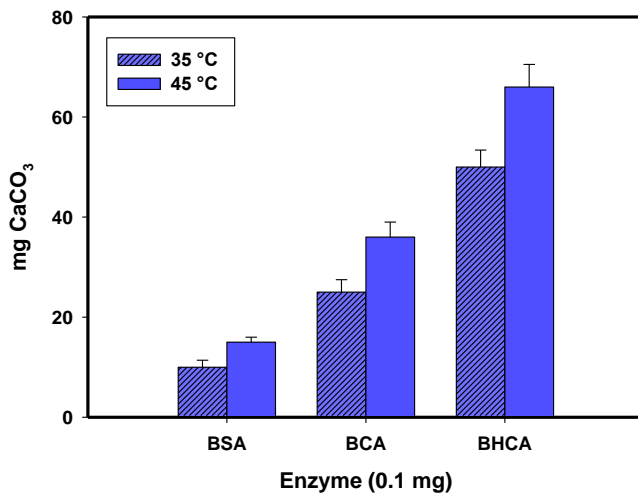
*BSA= Bovine serum albumin

BCA= Bovine carbonic anhydrase

Application of BhCA in mineralization based CO₂ sequestration



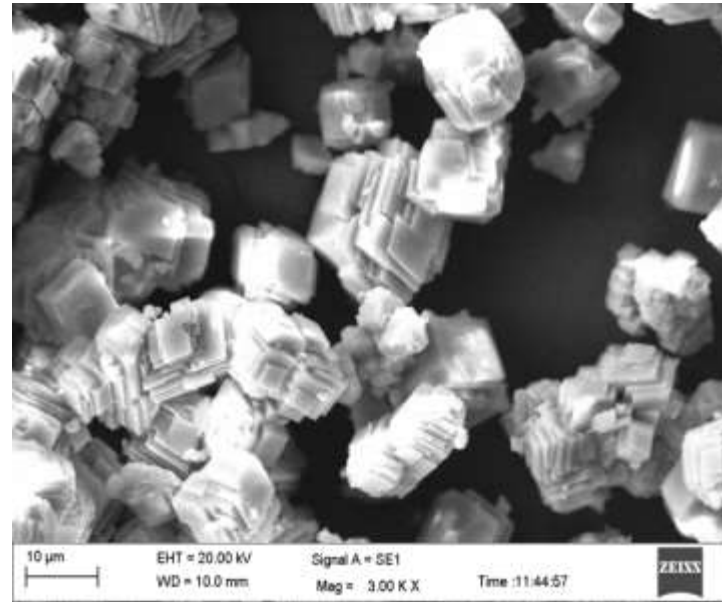
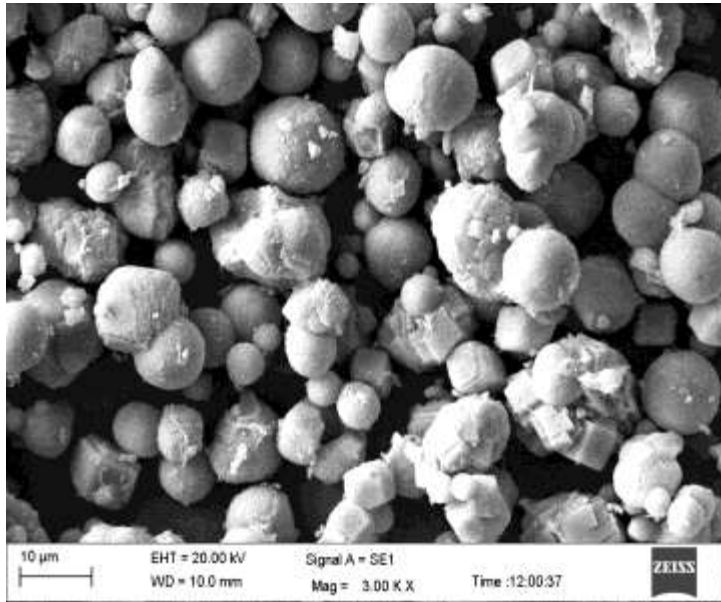
Analysis of carbonate precipitation catalyzed by crude and pure preparations of BhCA. BSA served as a negative control. Specific inhibition of purified BhCA by AZA led to decline in carbonate precipitation



Mineralization of exhaust gas CO₂ using BhCA and Ca²⁺

Comparison of sequestration efficiencies of BCA and BhCA at 37 and 45 °C in presence of SO₄²⁻ and NO₃⁻ in terms of carbonate precipitation. BSA served as a negative control

SEM images of CaCO_3 precipitate obtained after mineralization of CO_2



(a) Vaterite form of CaCO_3 formed in absence of rBhCA; (b) Calcite form of CaCO_3 formed in the presence of BhCA

Cloning of α CA in *E. coli*

Cloning of α -CA from *B. halodurans*

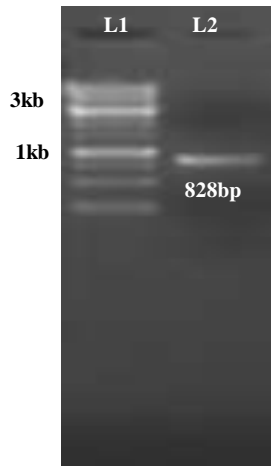
α -CA (828bp)

ATGAAAAATATTTATGGGGAAAAACGTGTTTAGTTGTATCATTAAAGTGTGCATGGTGACCGCATGCTCTTCTGCACCTTCCACAGAACCA
 GTCGATGAGCCGAGCGAGACACATGAGGAAACGAGCGGTGGCGCACACGAGGTTTCATTGGTCTTACACTGGAGACACTGGTCCAGAGC
 ATTGGGCAGAGTTGGATTCCGAATATGGTGCTTGCCTCAAGGAGAAGAGCAGTCACCGATCAACTTAGACAAAGCGGAGGCCGTTGAT
 ACCGATACCGAAATCCAAGTTCATTATGAGCCGAGCGCGTTTACGATTAATAAATAATGGTCACACGATTCAAGCAGAGACTACCTCAGA
 TGGGAACACGATTGAAATCGATGGAAAAGAATACACACTCGTTCAATTCCACTTCCATATTCTTCCGAGCATGAAATGGAAGGAAAGA
 ATTTAGATATGGAGCTACATTTTGTCCATAAAAATGAAAACGACGAGCTCGCCGTA CTGGGGTCTTAATGAAGGCCGGCGAAGAGAAC
 GAAGAGCTAGCGAAGCTATGGTCTGAAGCTACCAGCAGAAGAAACAGAAGAAAATATTTCTGTTAGATGAGTCAATTGATTTGAACGCGCT
 CTTACCAGAAAGCAAAGAAGGATTCCATTACAACGGTTCCTTAACGACGCCTCCTTGCTCAGAAGGGGTAAAGTGGACCGTGCTATCTGA
 ACCGATTACTGTTTCACAAGAGCAAATCGACGCGTTTGCTGAGATCTTCCAGACAATCACCGACCAGTCCAACCTTGGAACGACCGTGA
 TGTCTATGACGTGATCACTGAATAG

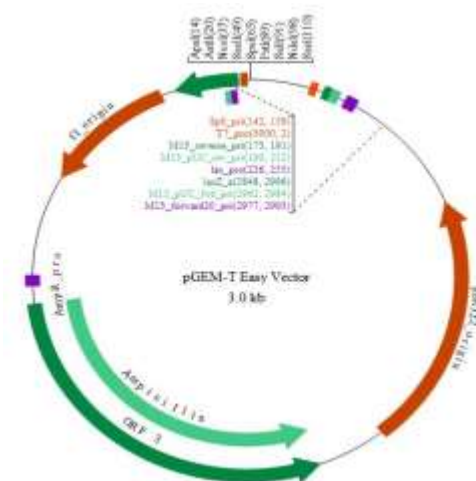
Full length primers:

FP: CCCCCGAATTCATGAAAAATATTTATGGGGAAAAACGTG

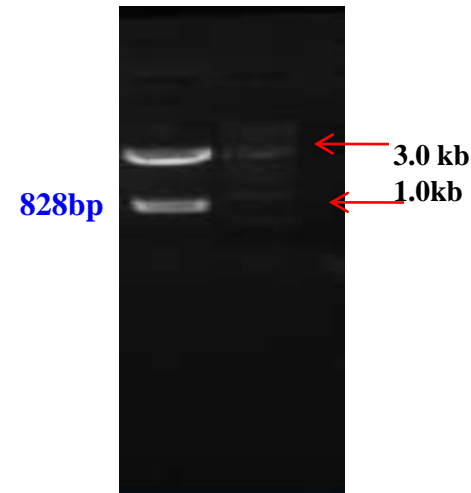
RP: CCCCCGCGCCGCTTTCAGTGATCACGTCATAGACATCAC



PCR amplification of BhCA



pGEMT-Easy vector



pGEMT fall out

Deduced amino acid sequence of α -CA (275 amino acids)

MKKYLWGKTCLVVSL SVMVTACSSAPSTEPVDEPSETHEETS GGAHEVHWSYTGDTGPEHWAELDSEYGAC
AQGEEQSPINLDKTEAIDTDTEIHVHYEPSSFTIKNNG **H**TIQAETTSDKNTIEIDGKEYTLV **Q****F****H****F**HIP**S****E**HEMEG
KNLDMEL **H**FVHKNNENDELAVLGVLMKAGEENEELAQLWSKLPAAETEENISLDESIDLNVLLPESKEGFHYNG
SL **T**TPPCSEGVKWTVLSEPIVSQEQIDAFAEIFPDNHRPVQPWNDRDVYDVITE

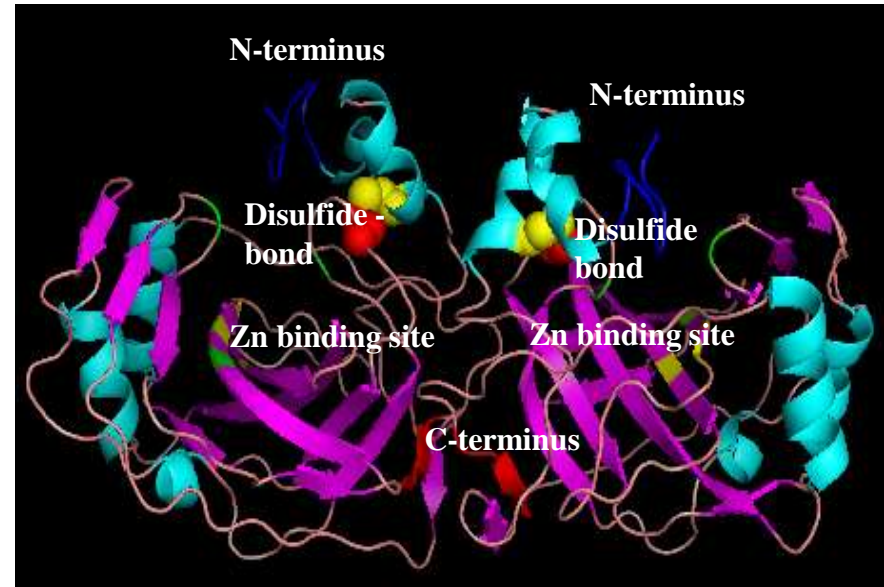
Catalytically important amino acids

His 136, His 138, His 155 – involved in zinc binding

Theoretical mol. mass= 31 kDa

Active site : 110-223

Signal peptide : 1-25



Proposed 3D structure of acidic α -CA from *B. halodurans*. The template α -CA of *Sulfurihydrogenebium azorense* (PDB ID 4x5s.1) shared 43.88% identity with α -CA of *B. halodurans*.

Total number of **negatively** charged residues (Asp + Glu): **56**

Total number of **positively** charged residues (Arg + Lys): **15**

Multiple sequence alignment of α -CA from *B. halodurans* with α -CAs of other microbes

Bacillus halodurans TSLV1
B. halodurans C-125
B. marmarensis
B. pseudofirmus
P. mucilaginosus
Paenibacillus polymyxa
Paenibacillus riograndensis
Thermovibro ammonificans

Bacillus halodurans TSLV1
B. halodurans C-125
B. marmarensis
B. pseudofirmus
Paenibacillus mucilaginosus
Paenibacillus polymyxa
Paenibacillus riograndensis
Thermovibro ammonificans

Bacillus halodurans TSLV1
B. halodurans C-125
B. marmarensis
B. pseudofirmus
Paenibacillus mucilaginosus
Paenibacillus polymyxa
Paenibacillus riograndensis
Thermovibro ammonificans

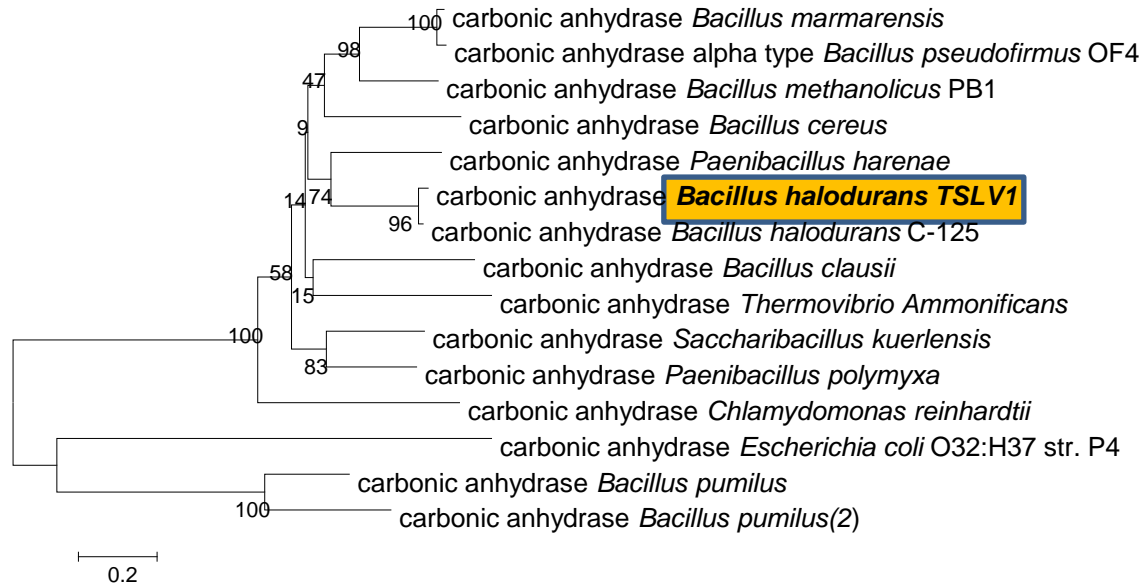
Bacillus halodurans TSLV1
B. halodurans C-125
B. marmarensis
B. pseudofirmus
Paenibacillus mucilaginosus
Paenibacillus polymyxa
Paenibacillus riograndensis
Thermovibro ammonificans

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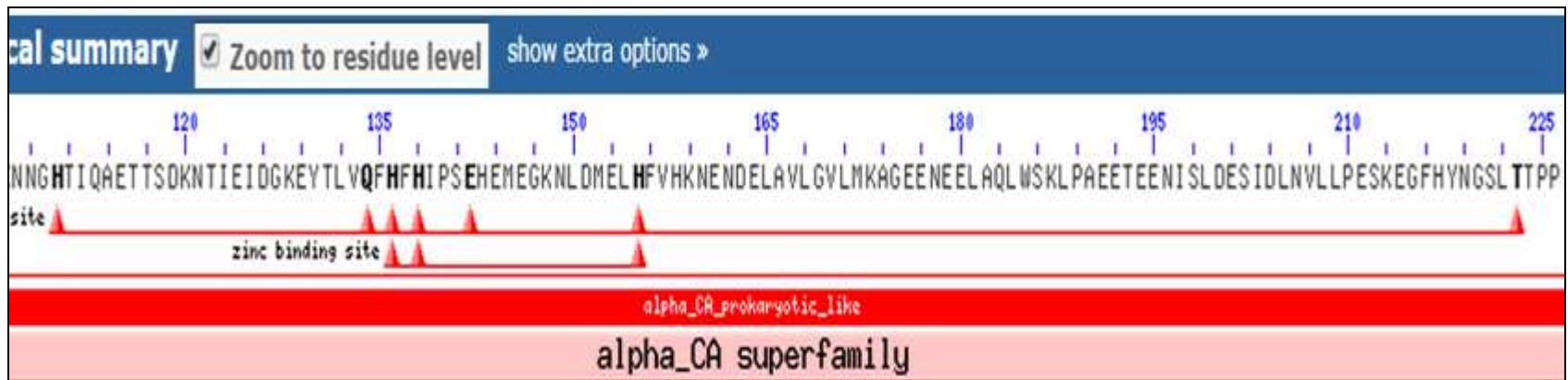
53  TGDTGPEHWAELDSEYGACAQGEEQSPINLDKTEAID--TDTEIHVHYEPSSFTIKNNGH
53  TGDTGPEHWAELDSEYGACAQGEEQSPINLDKAEAVD--TDTEIQVHYEPSAFTIKNNGH
59  DGESGPEHWGHLHASYSACVDGSEQSPINIDLAEMEASQQIEEINIQYEPASFSLVNNGH
71  -----ASYSACVDGSEQSPINIDLAEMEANQQIEEIDIQYEPASFSLVNNGH
59  EGNTGPAHWAELDQTFAACANGTEQSPVDIELTQTKVDKTAVQVELHYQPSAFTLMNNGH
57  EGDEGPEHWGELEKDFVACGNGQEQSPINIEHSHLEASHTQQPLQVHYS'TTKVSILNNGH
71  -----KVKDEGSLSPVVVEYSPSPVAVINNGH
29  SGSIGPEHWGDLSPEYLMCKIGKNQSPIDIN-SADAVKACLAPVSVYYVSDAKYVVNNGH
                                     : : * . : ****
111 TIQAETTS-DKNTIEIDGKEYTLVQFHFHIPSEHEMEGKNLDMELHFVHKNENDELAVLG
111 TIQAETTS-DGNTIEIDGKEYTLVQFHFHIPSEHEMEGKNLDMELHFVHKNENDELAVLG
119 TIQKNAVD-ENNAITLDGQEYQLVQFHFHTPSEHQFNGEHFDMELHLVHQDINGNLAVLG
118 TIQKNAVD-ENNAITLDGQEYQLVQFHFHTPSEHQFNGEHYDMELHLVHQDINGNLAVLG
119 TIQANAAGNGNTITVDGTDYTLAQMHFHHPSENQINGKNFEMEGHLVHKNKDGGLAVVG
117 TVQVNAAS-PSNDIVVDGTKFTLKQFHFHPSEHQIDGKNAEMELHFVHQSDTGSTAVLG
98  TIQVNLKN-QKNRITVEGKTYTLQQFHFHLPSEHEVDGKHADMELHFVHKNEEGQLAVLS
88  TIKVVMGG--RGYVVVDGKRFYLKQFHFHAPSEHTVNGKHYPFEAHFVHLDKNGNITVLG
*:: . : ::* : * *::** *:: :* *::* . . :*:.
170 VLMKAGENEELAQLWSKLPAEETEENISLDESIDLNVLLPESKEGFHYNGSLTTPPCSE
170 VLMKAGENEELAKLWSKLPAEETEENISLDESIDLNALLPESKEGFHYNGSLTTPPCSE
178 VMIEEGAENEELAPAWGELPEEETENDITLEEPINLQNLLPEDQSSFHYNGSLTTPPCTE
177 VMIEEGAENEELAPAWGELPEEETENEVALEEPINLQNLLPDDQSSFHYNGSLTTPPCTE
179 FLMTAGKENKPLAEMWSKLPKQETKEDVKLEQPVDLPGLVPSTAHAFRYEGSLTTPPCSE
176 VLIQSGKENKAFNRIWSKLP-KDISQEAVLDEDVNLAALLPKDLHSVRYNGSLTTPPCTE
157 VLITKGTENAGLNKLWSVLPGEESEEEVPVNGDFDMNKLLPADLHSFRYQGSLTTPPCTE
146 VFFKVGKENPELEKVWRVMP-EEPGQKRHLTARIDPEKLLPENRDYRYSGSLTTPPCSE
.:: * ** : * :* :. : .: *:* :* .*****:*
230 GVKWTVLSEPITVSQEQIDAFAEIF-PDNHRPVQPWNDRDVYDVITE
230 GVKWTVLSEPITVSQEQIDAFAEIF-PDNHRPVQPWNDRDVYDVITE
238 EVKWIVFKEPIQKSAVQIQVFQEIY-EENHRPVQPLNERG-----
237 EVKWIVFKEPIQKSAEQIQAFQEIY-EENHRPVQPLNERG-----
239 HVKWIVLADPIEVSKEQIEAFAAIF-PDNHRPVQPLNQRTVVSN---
135 HVNWTVLEQPIEMSADQIKQFAAIF-PDNHRPVQQLGTRELKADK--
217 GVQWIVLEHPVQSGEQINQFAAIF-PHDNRPVQALGSREVESDE--
205 GVRWIVFKEPVEMSREQLEKFRKVMGFDNNRPVQPLNARKVMK----
*.* *: .*: * *:. * : .:***** . *

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Neighbour joining tree for rBhCA

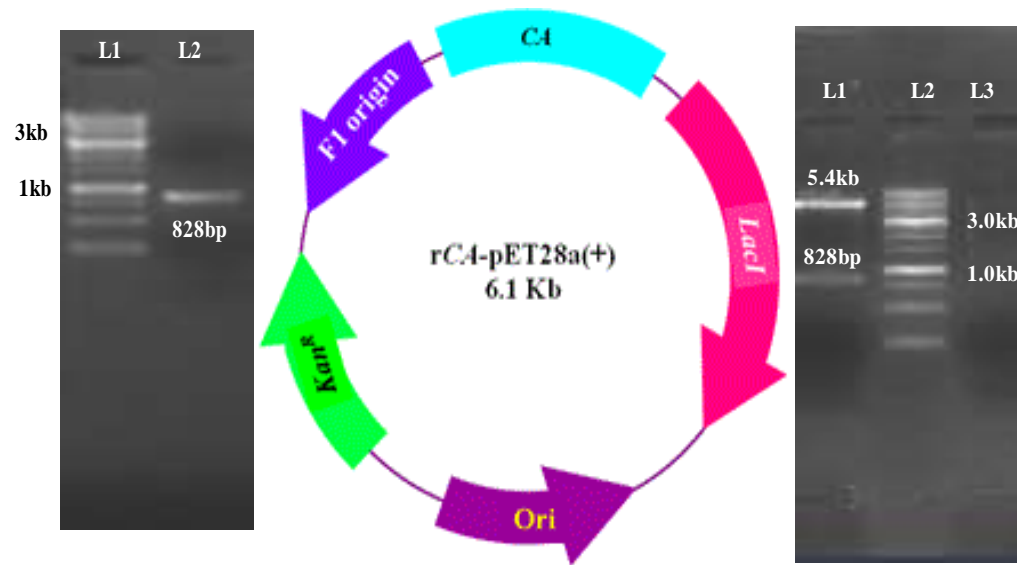


Phylogenetic tree of recombinant α -CA: rBhCA shows highest homology with *Bacillus halodurans* C-125

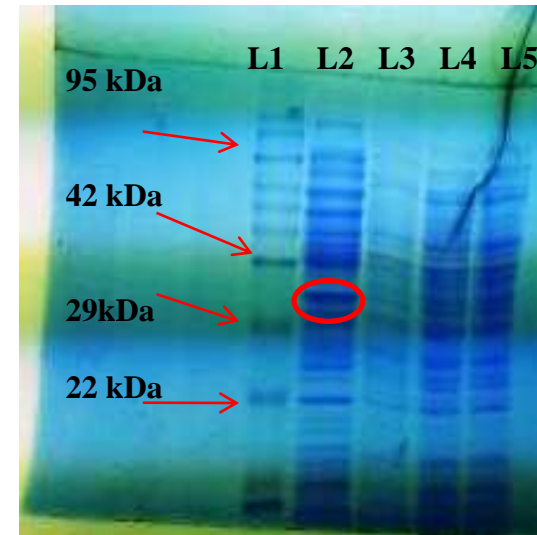


The α -CA encoding gene sequence has been deposited at GenBank database (accession no. KR347171)

Cloning of *BhCA* in pET28a vector & expression analysis after transformation in *E.coli* BL21(DE3)



Construction of the recombinant vector *rBhCA-pET28a*



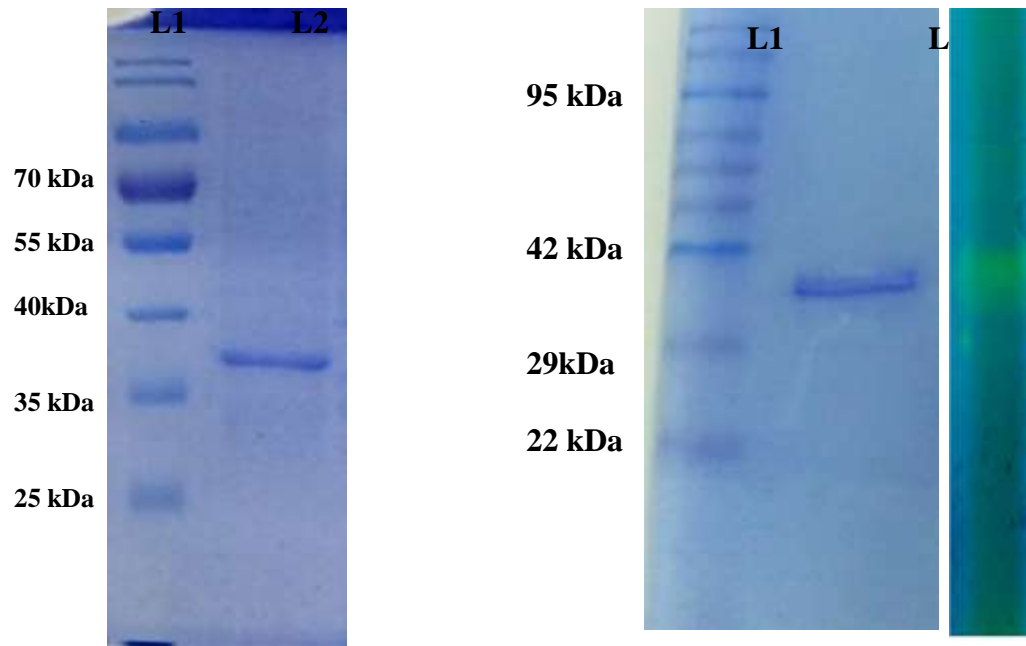
L1 : Marker, L2: Induced soluble fraction,
L2:Uninduced soluble fraction,
L3: Uninduced inclusion bodies ,
L4:Induced inclusion bodies ,

CA production was measured using Wilbur
Anderson assay

$7,85,000 \pm 1000$ U/gdbm

Purification of rBhCA

rBhCA was purified from *E. coli* by using Ni-NTA affinity chromatography. rBhCA was eluted using 300 mM imidazole



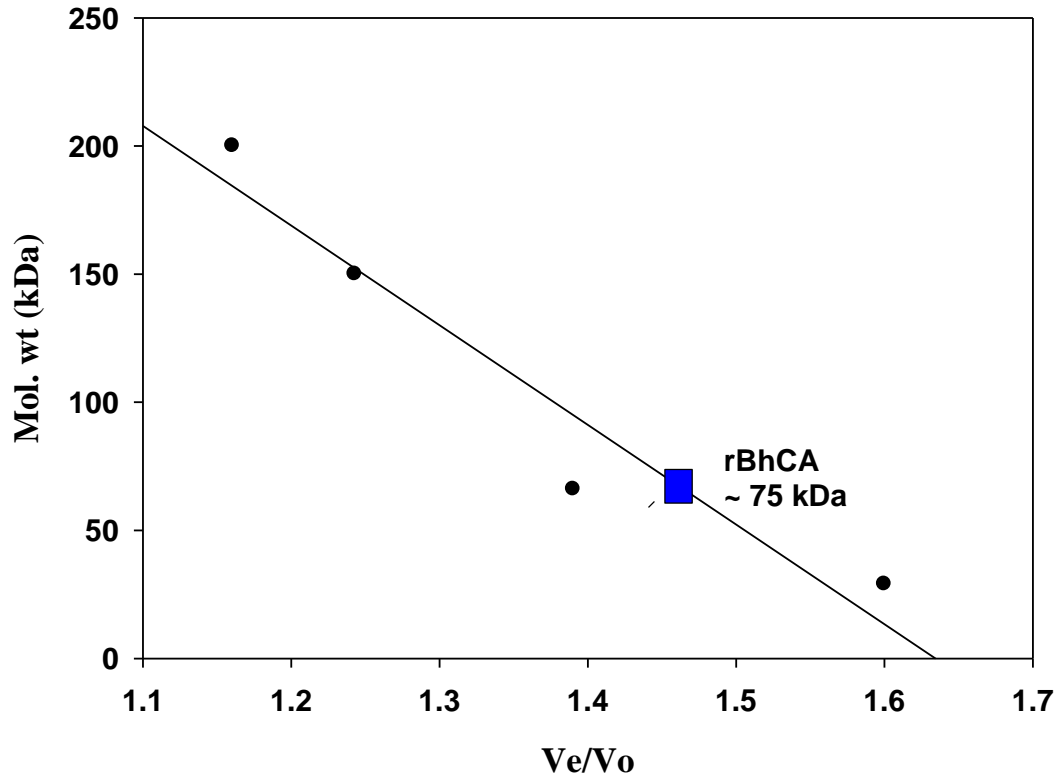
L1 : Marker, L2: Purified rBhCA

L1 : Marker, L2; Purified rBhCA, L3: Zymogram of CA

	EA (U/ml)	Volume (ml)	Total EA	Protein (mg/ml)	Specific activity (u/mg)	Yield	Fold Purificati on
Sample loaded	2019.5	5	10,097.5	2.10	961.66	100%	1
Eluate	804.8	8	7,855.6	0.09	8942.2	77.7%	9.2

Characterization of rBhCA

Native molecular weight determination

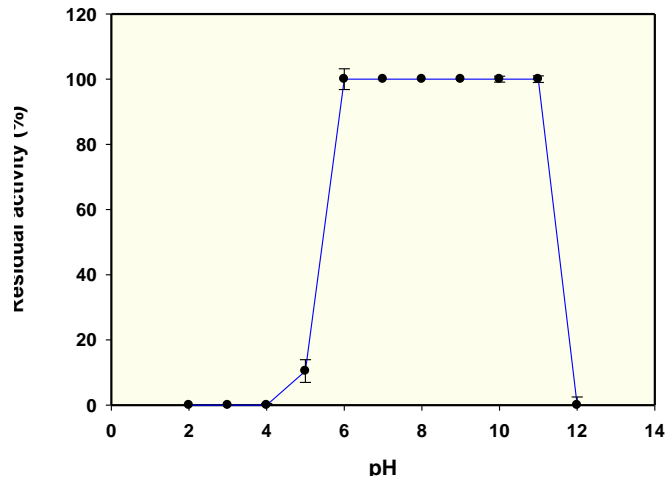


**rBhCA mol.
wt. ~ 75 kDa**

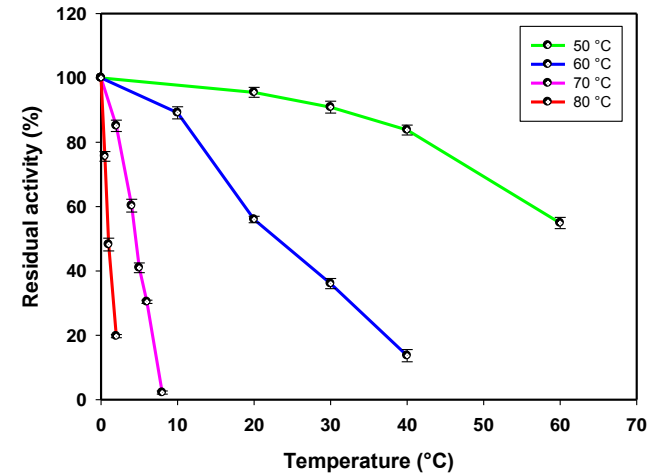
Plot of V_e/V_o against molecular weight of proteins on Sephacryl™ S-200 high resolution column (16/60). Molecular weight markers (kDa) used with purified rBhCA. Cytochrome c (12.4kDa), carbonic anhydrase (29kDa), bovine serum albumin (66kDa), yeast alcohol dehydrogenase (150kDa) and sweet potato β -amylase (200kDa)

Effect of different pH and temperature on the stability of rBhCA

Recombinant pH stability



Effect of different pH on rBhCA stability



Effect of different temperatures on BhCA stability

$T_{1/2}$ is 64.5 ± 1 , 24 ± 1 , 4.4 ± 0.5 and 1.0 ± 0.2 min at 50, 60, 70 and 80 °C respectively

Effect of CA specific inhibitors on the activity of rBhCA

Inhibitor	AZA	EZA	MZA	SA	BSA	SNA	AS
IC ₅₀ (μM)	0.25	0.35	1.0	8610	4.0	76.9	166.5

* Acetazolamide (5-acetamido-1-thia-3, 4-diazole-2-sulphonamide, AAZ), methazolamide (MZA), Ethoxzolamide (EZA), Sulfanilamide (4-amino benzene sulphonamide, SNA), sulfamic acid (SA), Benzenesulfonamide (BSA) and Ammonium sulfamate (AS)

*IC50 = Half maximal inhibitory concentration

Effect of different metal ions, anions on enzyme activity

Metal ions	Concentration	Residual activity (%)
Mg ²⁺	1 mM	100±0.30
	5 mM	100±1.5
Zn²⁺	500 µM	100±0
	1 mM	50.5±1.5
Hg²⁺	500 µM	33.83±1.41
	1 mM	22.08±1.26
	5 mM	0±1.5
Co²⁺	1 mM	43.44±1.8
	5 mM	25.80±2.6
Cu²⁺	500 µM	46.60±1.9
	1 mM	34.56±1.58
	5 mM	0±1.6
Mn ²⁺	1 mM	100±0.5
	5 mM	100±1.5
Ca ²⁺	1 mM	100±1.60
	5 mM	100±0
Ni²⁺	1 mM	20±2.50
	5 mM	15.8±1.54
Fe³⁺	1 mM	24.36±1.87
	5 mM	0±0.9
Fe²⁺	1 mM	25.88±2.1
	5 mM	0±.5
Al ³⁺	1 mM	100 ±1
	5 mM	100±1.8
Ag ²⁺	1 mM	100±1
	5 mM	100±2.88
Sn²⁺	1 mM	126.44±2.55
	5 mM	143.16±3.54
Pb²⁺	1 mM	100±0
	5 mM	70.06±2.76
Ba ²⁺	1 mM	100±0
	5 mM	100±1.5
NH ₄ ⁺	1 mM	100±0.25
	5 mM	100±0.5
Na ⁺	1 M	1100 ±0.29
	2 M	75.5 ±2.8

Stimulators:

Sn²⁺, SO₄²⁻

No effect of SO₃²⁻

Anions	Concentration	Residual activity(%)
SO₄⁻	1 M	170 ±2.5
	0.125 M	100 ±0
SO₃²⁻	1.0 M	100.±0.5
	1.25 M	100 ±0
NO₃⁻	0.5 M	100 ±1.5
	1 M	85.16 ±1.5
	1.5 M	77.44±1.88
HCO₃⁻	0.1 M	100 ±0
	0.75 M	32.55±2.5
CO₃²⁻	0.01 M	100 ±0
	0.05 M	73.63 ±1.74
	0.1 M	62.54 ±2.45
Cl ⁻	0.5 M	100 ±1.8
	1 M	100.±1
I ⁻	1 mM	100.±1.5
	5 mM	99.8 ±1
F ⁻	1 mM	100±1.5
	5 mM	100±1.0
Br ⁻	1 mM	100±0
	5 mM	100±0

Effect of different additives (inhibitors, ionic and non ionic detergents) on enzyme activity

Modulator	Concentration	Residual activity (%)
WRK	1 Mm	92 ±1.5
	5 mM	0 ±0
NBS	1 mM	8.0±1.5
	5 mM	0 ±0.5
NEM	1 mM	97 ±2.6
	5 mM	0 ±0.5
DEPC	1 mM	74±2.0
	5 mM	0.5±1
PMSF	1 mM	38.06±2.6
	5 mM	23.54±0.76
DTT	1 mM	95 ±2.5
	5 mM	45 ±2.8
IAA	1 mM	52.22 ±1.54
	5 mM	0 ±0.5
β-ME	1 mM	100±0
	5 mM	83.4±2.5
TRITON X100	0.1%	87.5 ±2.0
	0.2%	85.22 ±1.8
TWEEN 80	0.1%	100 ±1.5
	0.2%	100. ±0.5
SDS	1%	100±0
	5%	88.5±1.66
EDTA	50 mM	100 ±0.5
	1 M	100±0
2, 6-pyridinedicarboxylic acid	3.34 mM	0

No effect of EDTA

Conserved residues in active site and outside

Trp185, 233

Glu142, 153

Asp117, 204

Cys227

Ser141

H110, H 137, H139, H156

DTT- dithiothreitol

β-ME - β-mercaptoethanol

WRK - Woodward's reagent K

IAA - Iodo acetamide

PMSF- phenyl methyl sulfonyl fluoride

NBS - N-bromosuccinimide

NEM - N-ethylmaleimide

DEPC - Diethylpyrocarbonate

EDTA –ethylenediaminetetraacetic

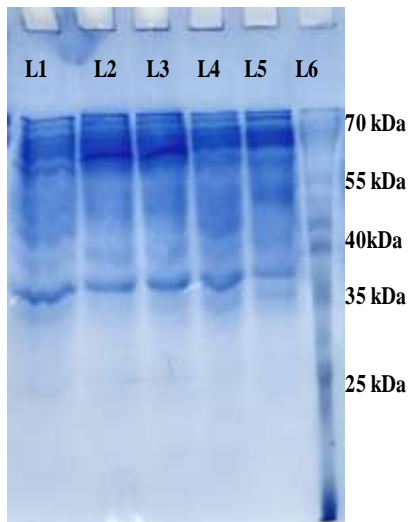
Site directed mutagenesis for confirming the catalytic residues

H₁₃₇-Y CAForward Primer: CCACTCGTTCAATTCTACTTCCATATTCCTTCCGAG
H₁₃₇-Y CARReverse Primer: CTCGGAAGGAATATGGAAGTAGAATTGAACGAGTGTG

H₁₃₉-Y CAForward Primer: CCACTCGTTCAATTCTACTTCCATATTCCTTCCGAG
H₁₉₈-Y CARReverse Primer: CTCGGAAGGAATATGGAAGTAGAATTGAACGAGTGTG

H₁₅₆-Y CAForward Primer: AATTTAGATATGGAGCTTTATTTTGTCCATAAGAATG
H₁₅₆-Y CARReverse Primer: CATTCTTATGGACAAAATAAAGCTCCATATCTAAATT

H₁₁₀-Y CAForward Primer: ACGATTAAAATAATGGTGCTACGATTCAAGCAGAGAC
H₁₁₀-Y CARReverse Primer: GTCTCTGCTTGAATCGTAGCACCATTTTAAATCGT



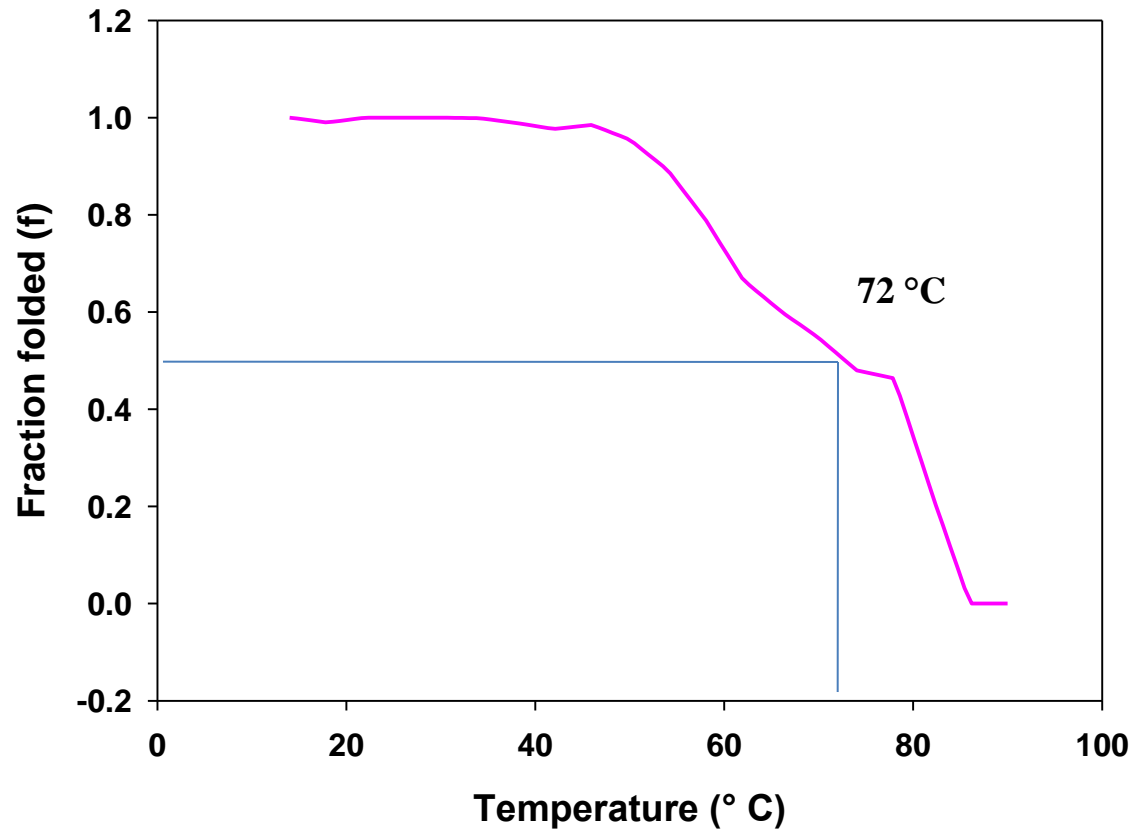
Complete loss of activity occurred with all substitutions

H137Y; H139Y; H156Y

(Y=tyrosine)

SDS PAGE showing expression of muteins. L1-L4: Crude lysates of the muteins H110, H137, H139, H156; L2: Uninduced crude lysate; L6- Protein Markers

Melting Temperature (T_m) of rBhCA



Thermal unfolding curve for rBhCA

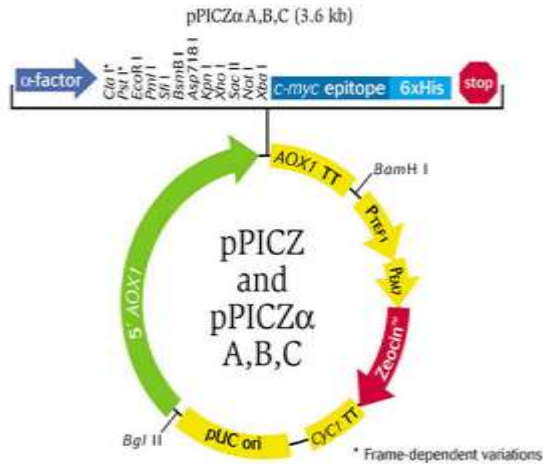
Comparison of wild type and recombinant CA

Properties	Native CA	Recombinant
Production (U/gdbm)	35,000 ± 800	7,85,000 ± 1,105
pH stability	6-11	6-11
Thermal stability ($T_{1/2}$ at 50°C)	65 ± 1min	64.5 ± 1 min
T _m	71 °C	72 °C
Mol. mass	~74 kDa	~75 kDa
Specific activity (U/mg protein)	3,425 ± 95	8,942 ± 112

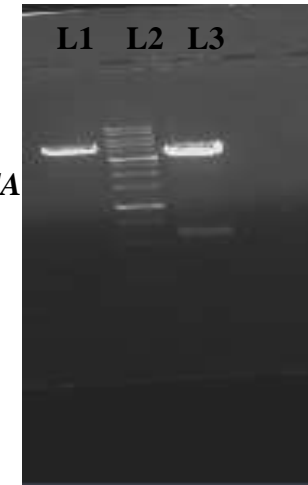
Fold improvement in CA production=22.4

Cloning of *BhCA* in *Pichia pastoris*

Cloning and expression of *BhCA* under AOX1 promoter



Linearized
pPicZα+ *αCA*
construct



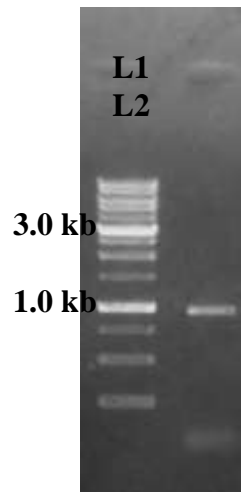
Vector
backbone 3.1kb
828bp *αCA*

Clone confirmation by digesting the construct
with L1: *EcoRI* ; L3: *EcoRI* and *XbaI*

CA production- 1 U/mL



Genomic DNA isolation from
the *Pichia*-pPICZ- *αCA* clone



Amplification of *αCA* from the genome of
Pichia pPICZαCA construct . L1: *αCA*
(828bp)
L2: DNA Ladder

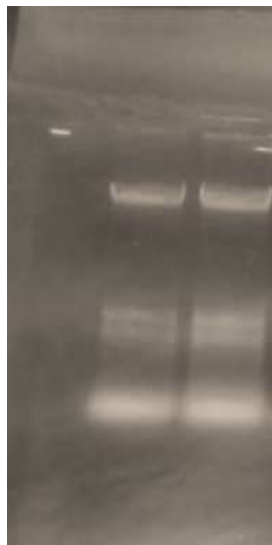
Cloning and expression of *BhCA* under GAP promoter using pGAPZ α vector

L1 L2



Confirmation of pGAPZ- *BhCA* construction by double digestion. L1: α CA fall out after digestion with EcoRI and XbaI, L2: DNA Ladder

L1 L2



Genomic DNA isolation from the *Pichia*- pGAP Z-*BhCA* clone

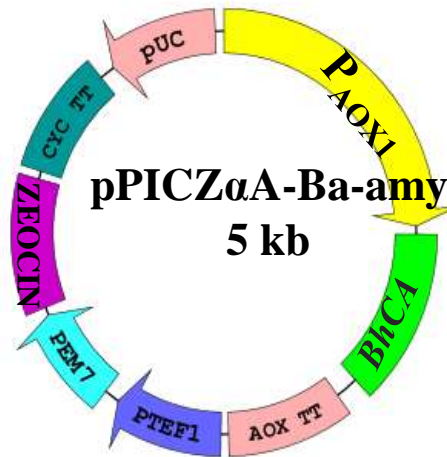
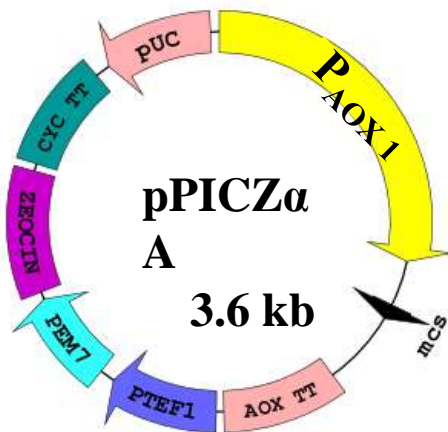
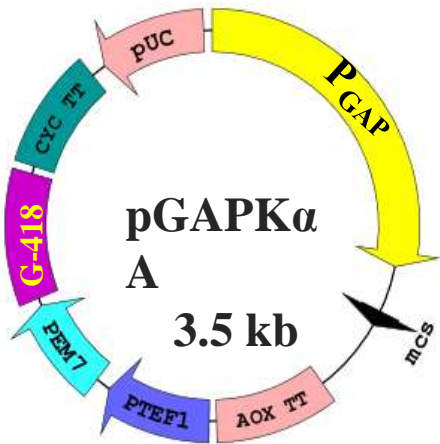
L1 L2 L3

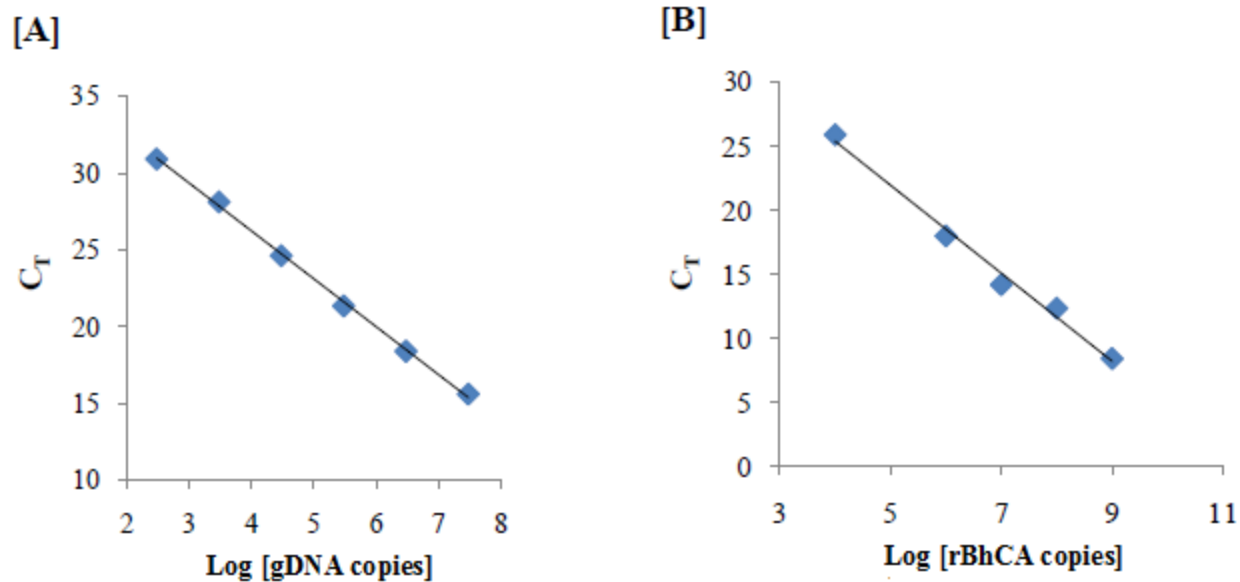


Amplification of α -CA from the genome of *Pichia* pGAP Z-*BhCA* clone . L1: *BhCA* (850bp)
L3: DNA Ladder

After OVAT 25 ± 2 U/mL of r*BhCA* production was attained.

Strategy for construction of *pGAPK α A-BhCA* construct



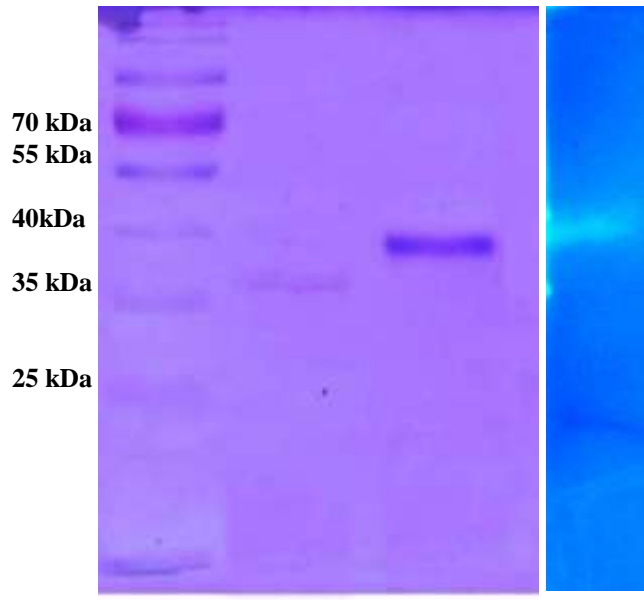
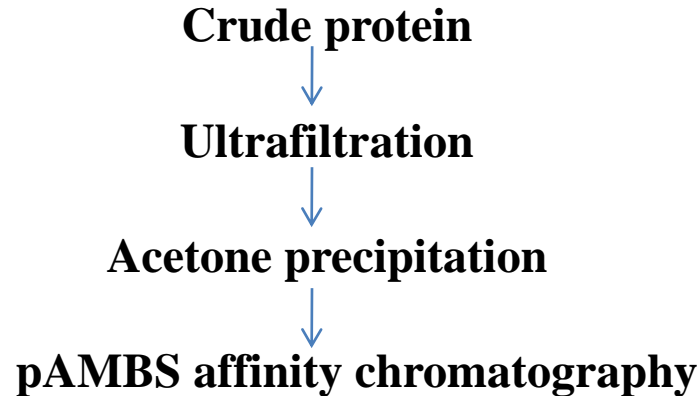


qPCR standard curves. [A] qPCR standard curve for *GAP* gene;
 [B] qPCR standard curve for rBhCA

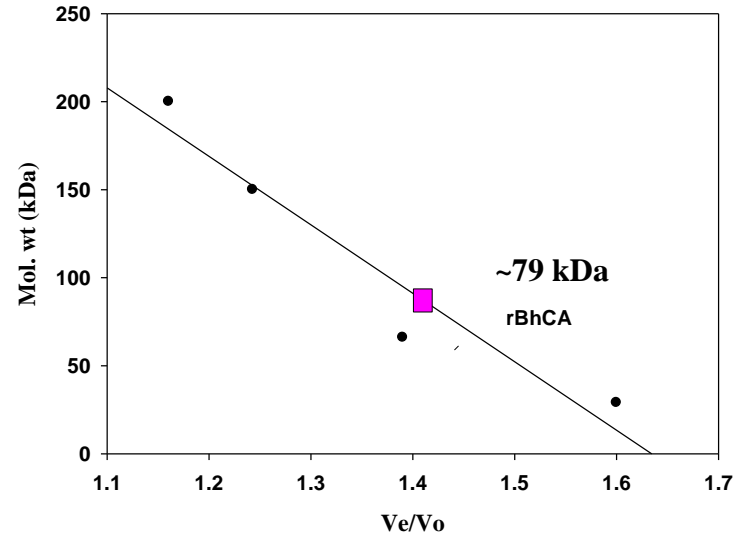
Number of copies of *BhCA* gene in the recombinant: 2

Recombinant BhCA production: 48 U ml⁻¹

Purification of rBhCA from *Pichia pastoris*



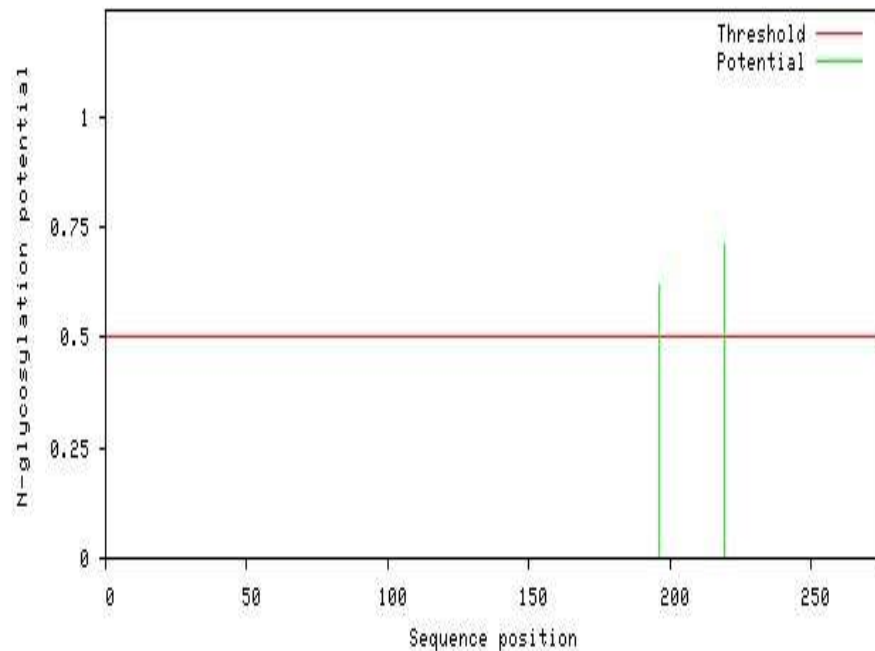
L1 : Marker, L2: Purified rBhCA from *E. coli*, L3, Purified rBhCA from *Pichia*



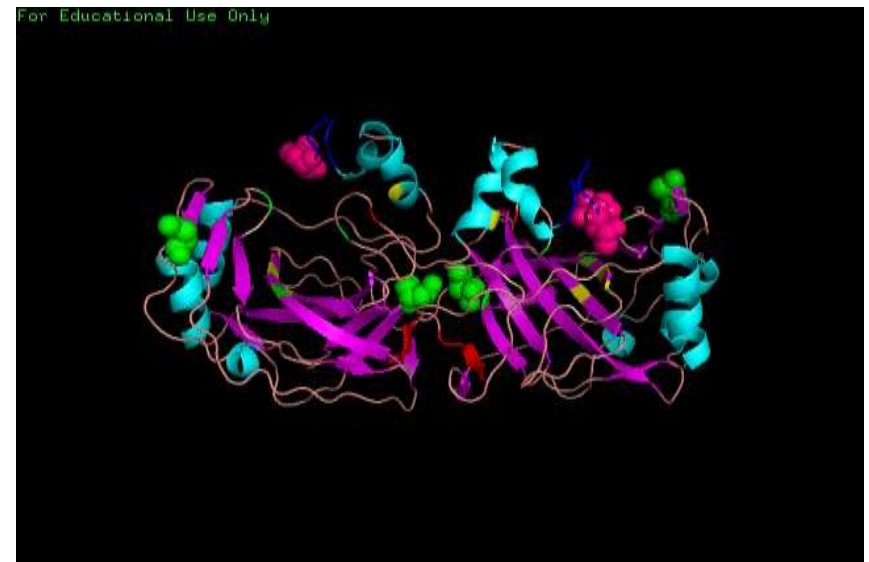
Plot of V_e/V_o against molecular weight of proteins on Sephacryl™ S-200 high resolution column (16/60). Molecular weight markers (kDa) used with purified rBhCA. Cytochrome c (12.4kDa), carbonic anhydrase (29kDa), bovine serum albumin (66kDa), yeast alcohol dehydrogenase (150kDa) and sweet potato β -amylase (200kDa)

In silico analysis of glycosylation sites using NetNGlyc 1.0 server

NetNGlyc 1.0: predicted N-glycosylation sites in Sequence

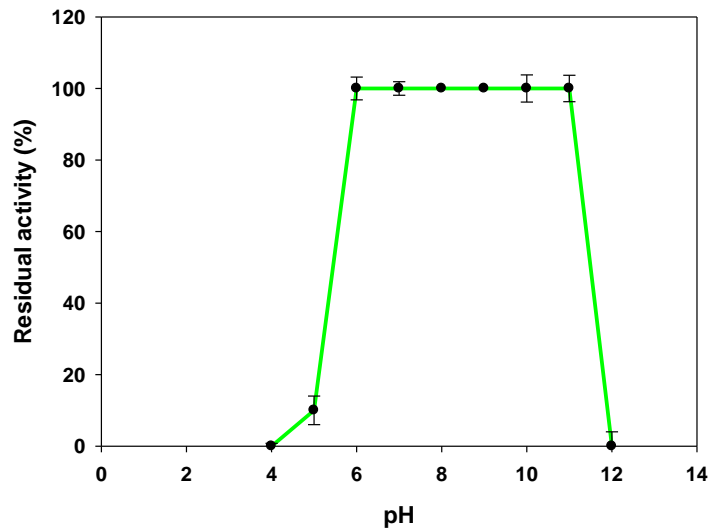


N-glycosylation sites predicted by NetGlyc 1.0 Server

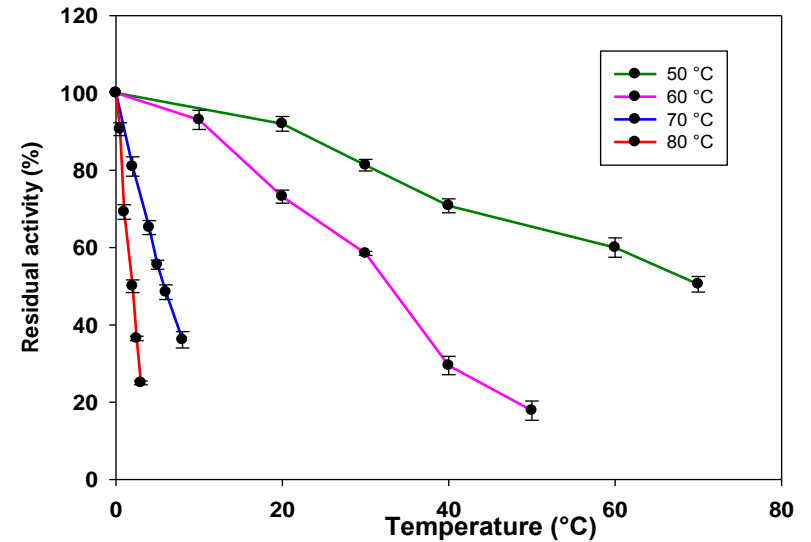


3D model of rBhCA showing distribution of the N-glycosylated residues (green spheres) O-glycosylated residues (magenta spheres)

Characterization of rBhCA expressed in *P. pastoris*



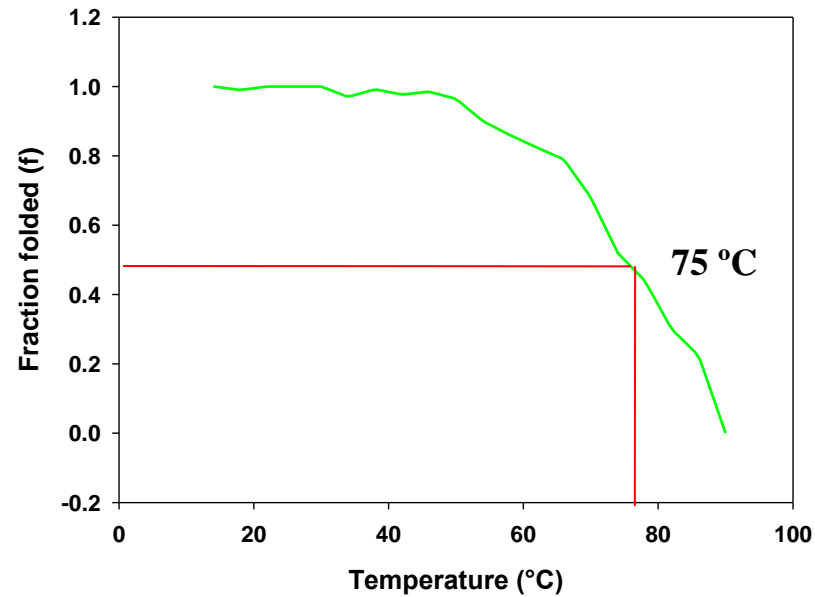
Effect of different pH values on rBhCA stability



Effect of different temperatures on pichBhCA stability

$T_{1/2}$ is 72 ± 1.1 , 32 ± 1 , 7.0 ± 0.5 and 2.0 ± 0.15 min at 50, 60, 70 and 80° respectively

Melting Temperature (T_m) of rBhCA



Thermal unfolding curve for pichBhCA

Comparison of rBhCA expressed in *E. coli* and *Pichia*

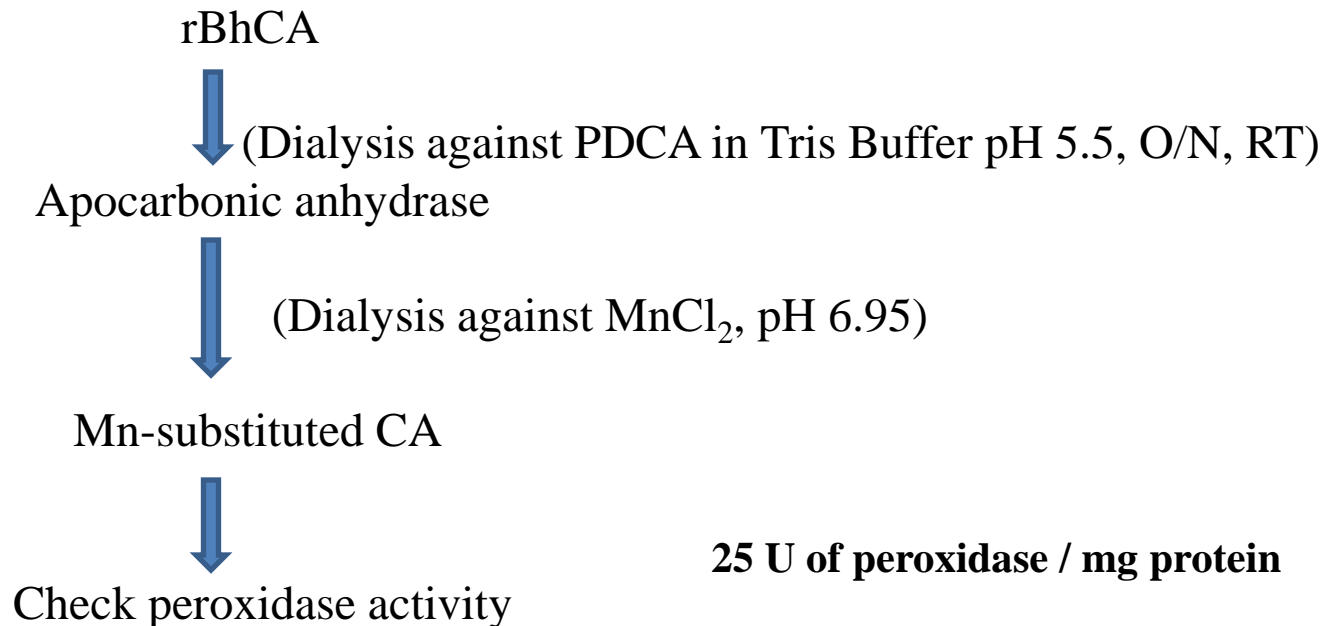
Properties	rBhCA in <i>E. coli</i>	rBhCA in <i>Pichia</i>
Production (UL ⁻¹)	2,53,231 ± 2,875	48, 000 ± 200
pH stability	6-11	6-11
Thermal stability (T _{1/2} at 50°C)	64.5 ± 1 min	72 ± 1 min
T _m	72 °C	75 °C
Mol. Wt.	~ 75 kDa	~ 79 kDa

BhCA as virtual peroxidase

Disadvantages of natural heme based peroxidases

- Rapid inactivation
- yield aldehyde side products
- show low enantioselectivity

rBhCA as peroxidase



Immobilization of rBhCA

Immobilization of CA on montmorillonite K10 by physical adsorption

Montmorillonite K 10 + deionized water



vigorously stirred for 6 h

Filtered, dried at 120 °C for 12 h and calcined at 350 °C for 12 h.



Mixed with equal volumes Tris buffer solution (pH 8.3) and enzyme solution



Shaken for 1 h in a water bath shaker at room temperature.



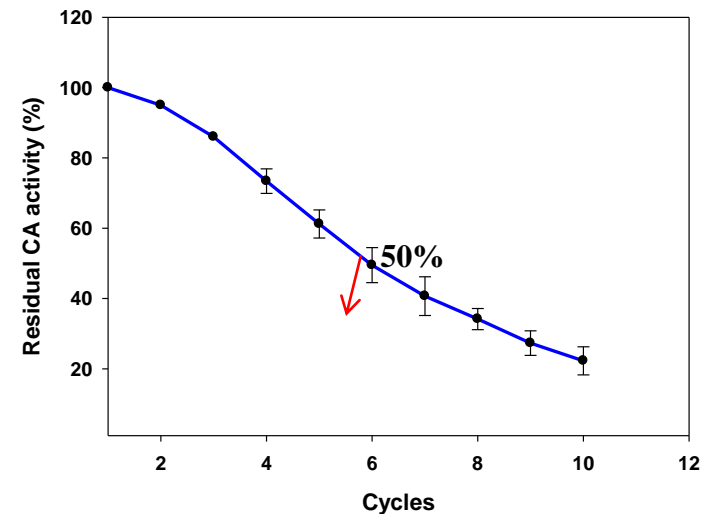
Centrifuged for 1 h



Washed several times



Enzyme assay



CA immobilization on montmorillonite

Immobilization of CA on montmorillonite K10 by covalent attachment

Calcined montmorillonite K 10 +10% (v/v) solution of 3-amino propyl triethoxy silane in acetone

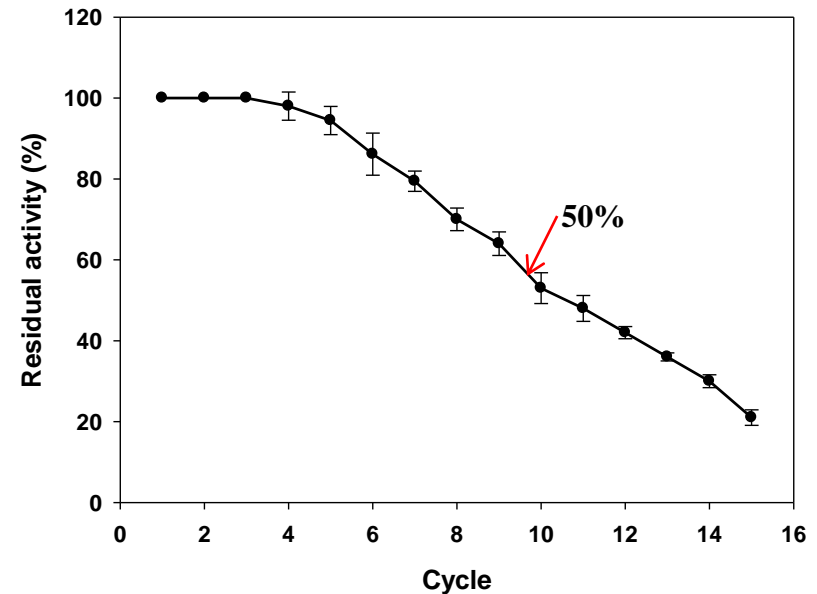
vigorously stirred for 3 h at RT

Filtered, washed several times with acetone until the washings became colourless, dried at 80 °C for 12 h

Silanized clay +10% aqueous solution (v/v) of glutaraldehyde and stirred vigorously for 3 h

Filtered, washed free of excess glutaraldehyde and dried at 60 °C for 12 h

This functionalized clay was used for CA immobilization



Immobilization of CA on magnetized aniline nanofibers

Magnetite iron oxide nanoparticles were prepared by coprecipitation of Fe^{2+} and Fe^{3+} with NH_4OH using the method described by Mahdavi et al. 2013.

0.1% APS + 5 ml of an aniline monomer solution in 1 M HCl

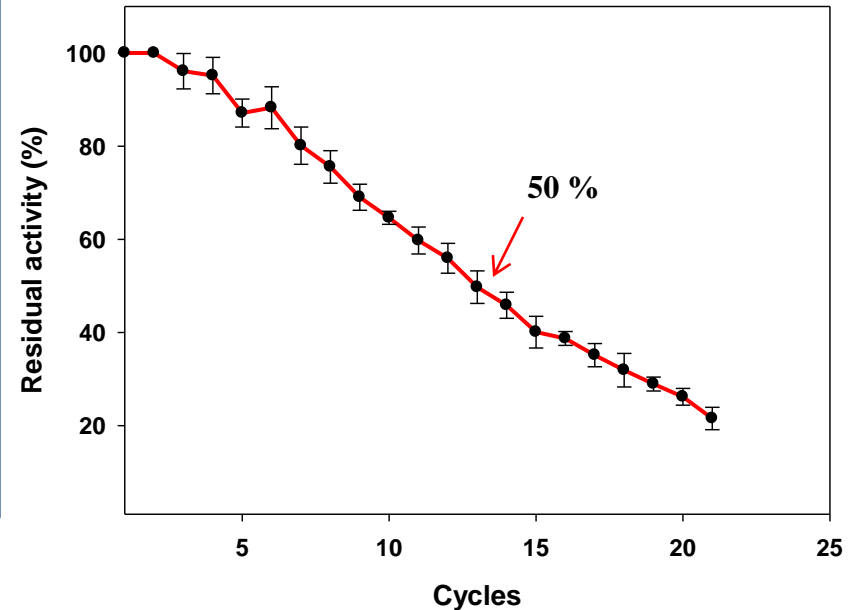


Rapid mixing



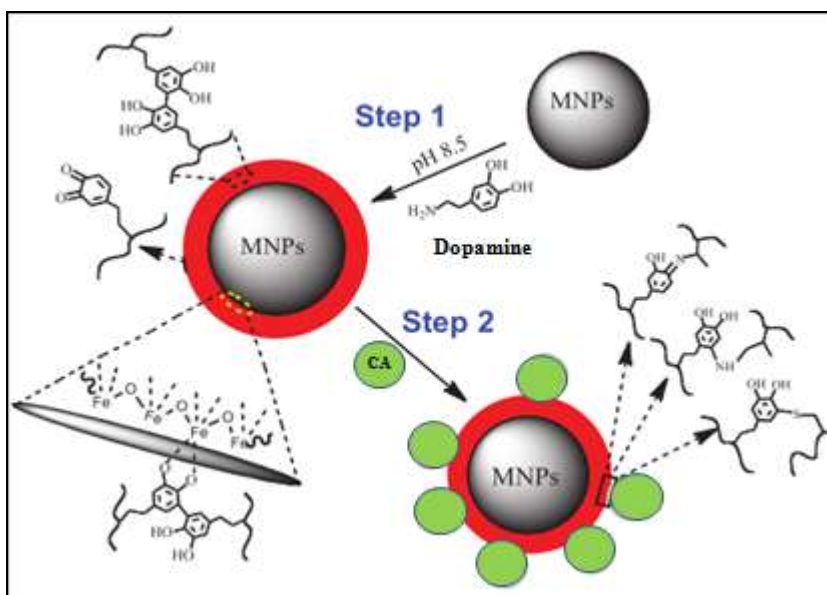
+ 10% (w/v) of iron oxide
(nanoparticle)

Wash to remove remaining HCl

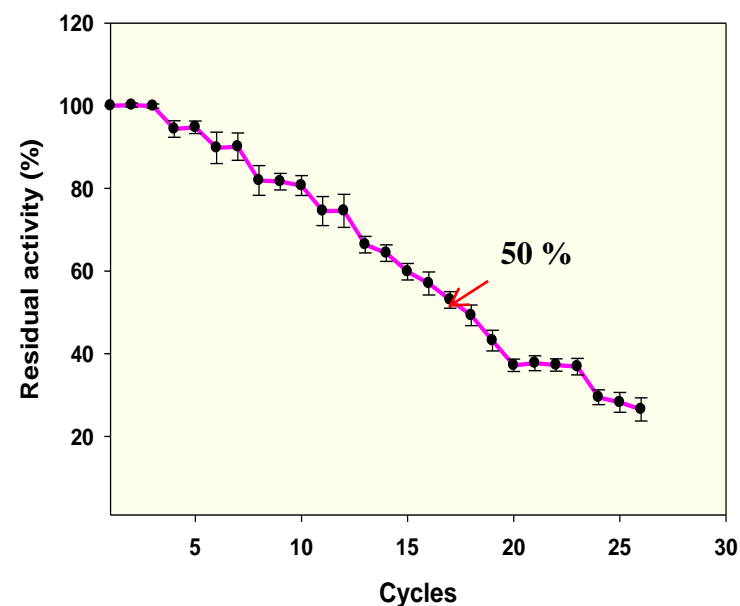


Reusability of CA immobilized on MNPs

Immobilization of CA on dopamine coated iron MNPs

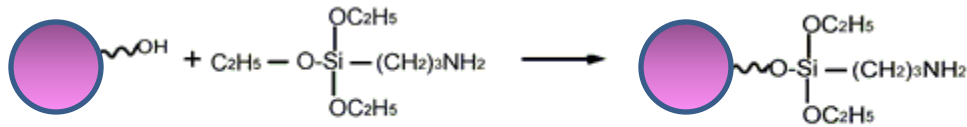


Surface modification of MNPs with polydopamine

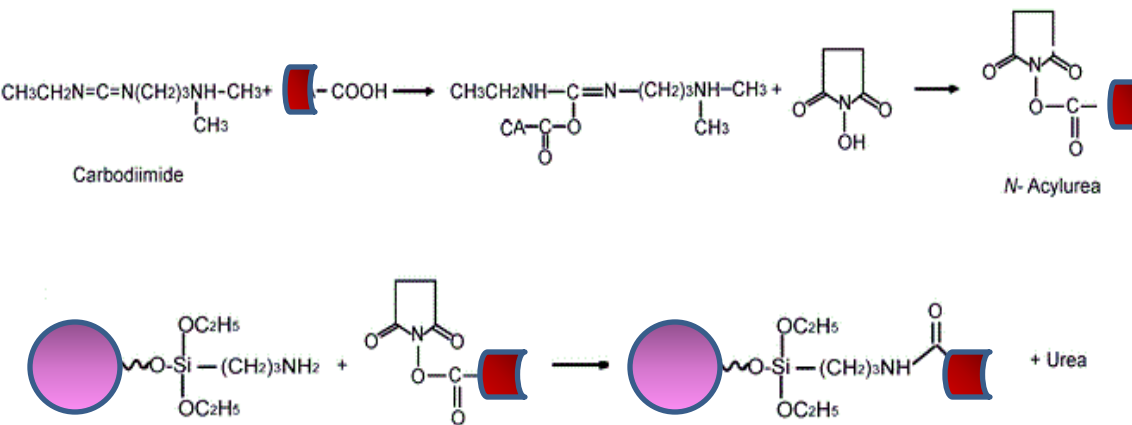


Reusability of CA immobilized on dopamine coated MNPs

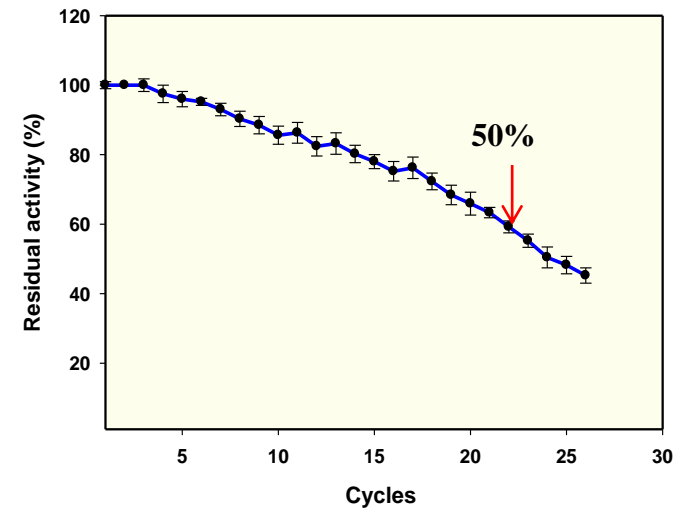
Immobilization of CA on silanized iron MNPs



Silanization of MNPs with APTES

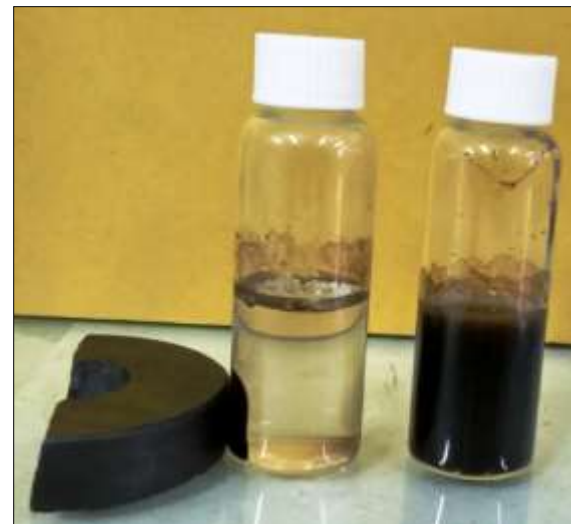
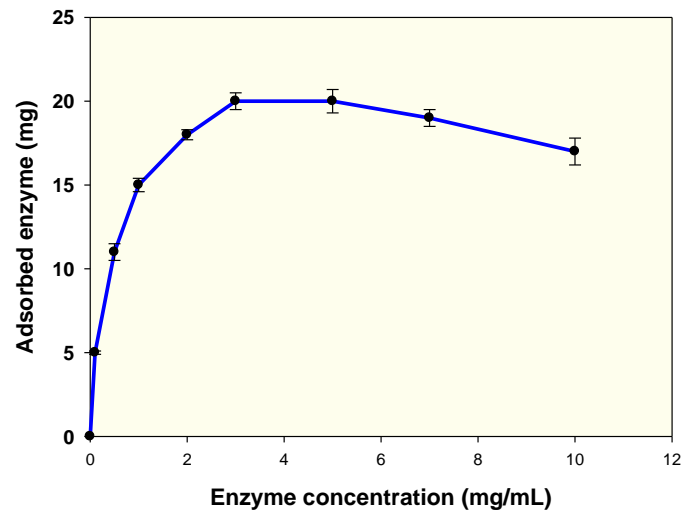


EDC (1-Ethyl-3-(3-dimethylaminopropyl)-carbodiimide) activation of carboxyl groups of CA



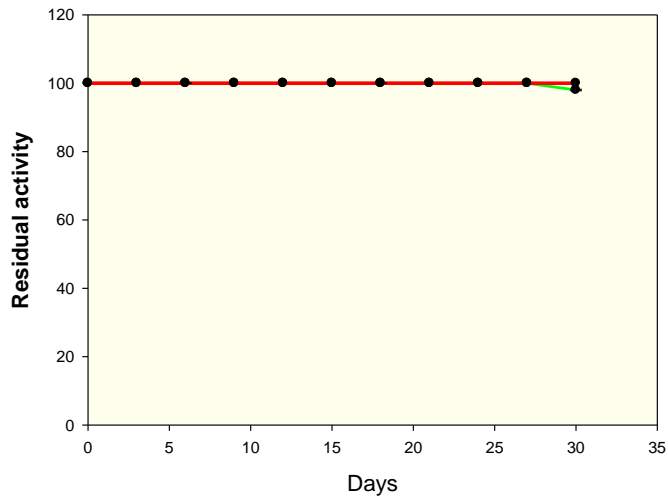
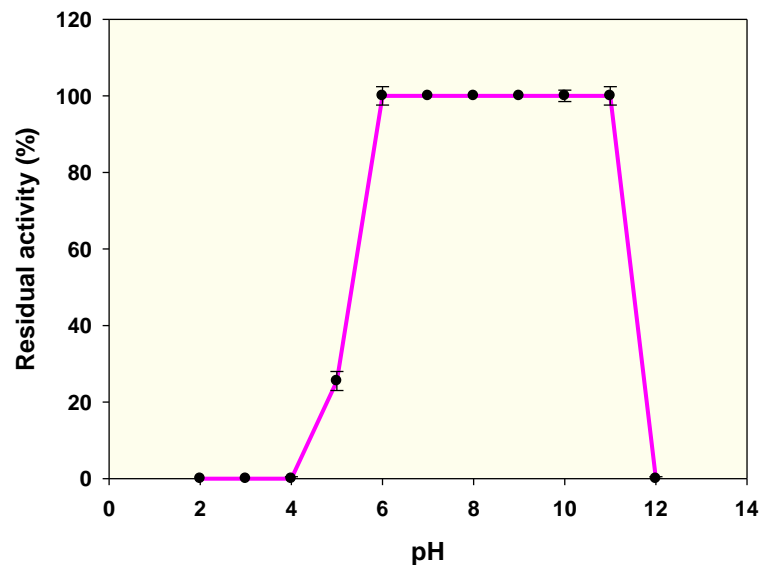
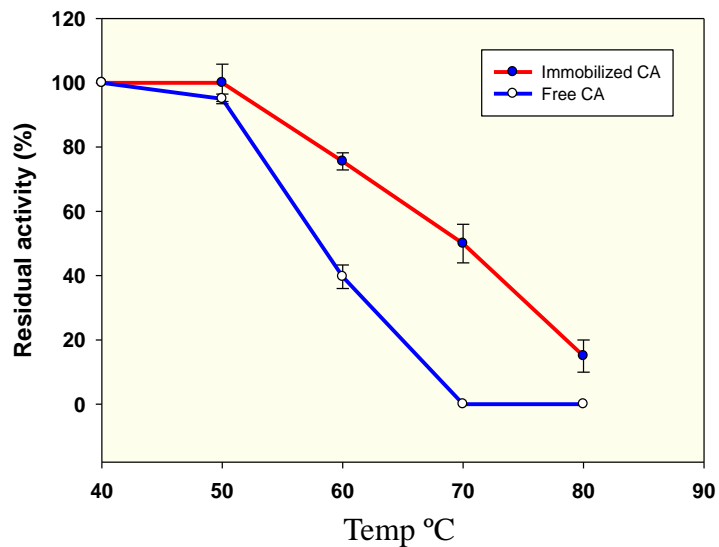
Reusability of CA immobilized on silanized iron MNPs

Effect of enzyme concentration on immobilization of CA on Si-MNPs



CA-Si-MNPs aqueous suspension after and before magnetic separation

Characterization of CA immobilized on iron MNPs



Effect of anions and metal ions on the immobilized rBhCA

Anion	Concentration	Residual activity (%)
SO_4^-	1.0 M	100±0
	1.25M	172 ±3.0
SO_3^{2-}	1.0 M	100.±0.5
	1.25M	100 ±0
NO_3^-	0.5 M	100 ±1.5
	1.0 M	85.1 ±1.5
	1.5 M	77.4±1.8
Pb^{2+}	1.0 mM	100±0
	5.0 mM	85.0±3.0
Hg^{2+}	500 μM	20±2.0
	1.0 mM	0±2.8

Conclusions

Conclusions

- *B. halodurans* produces alkalistable and moderately thermostable intracellular α -CA (BhCA) which is tolerant to SO_x and NO_x present in flue gas.
- The gene encoding BhCA was cloned and heterologously expressed in *E. coli* and *P. pastoris*. Recombinant BhCA displays similar characteristics like the native CA
- Site directed mutagenesis confirmed the identity of catalytically important amino acid residues (H110, H 137 and H 139, H156) of BhCA.
- Application of BhCA in mineralizing CO₂ from flue gas has been confirmed.
- rBhCA has been successfully immobilized on iron MNPs.

PUBLICATIONS

- ❖ **S. Faridi, T. Satyanarayana**, Novel alkalistable α -carbonic anhydrase from the polyextremophilic bacterium *Bacillus halodurans*: characteristics and applicability in flue gas CO₂ sequestration, *Environmental Science and Pollution Research* (2016) 23: 15236-15249 [DOI 10.1007/s11356-016-6642-0].
- ❖ **S. Faridi, H. Bose and T. Satyanarayana**, Characteristics of recombinant α -carbonic anhydrase of *Bacillus halodurans* TSLV1. *International Journal of Biological Macromolecules* (2016). 89: 659-668 [DOI : 10.1016/j.ijbiomac.2016.05.026].
- ❖ **S. Faridi, T. Satyanarayana**, Thermo-alkali-stable α -carbonic anhydrase of *Bacillus halodurans*: Heterologous expression in *Pichia pastoris* and applicability in carbon sequestration, *Environmental Science and Pollution Research* (2017) 25: 6838 – 6849 (DOI: [10.1007/s11356-017-0820-6](https://doi.org/10.1007/s11356-017-0820-6)).



Dr. Shazia Faridi

A close-up photograph of a field of bright red tulips. The flowers are in various stages of bloom, with some fully open and others as buds. The background is a soft, out-of-focus green, suggesting a grassy field. The overall lighting is bright and natural, highlighting the texture of the petals.

Thank You