

Electronic Supplementary Material

Table S1. Identified homologous sequences of CALB.

Source (Organism)	GenBank accession number	Sequence identity	Number of amino acids ^a
<i>Ustilago hordei</i>	CCF54401.1	75.6%	324
<i>Sporisorium reilianum</i> SRZ2	CBQ70828.1	73.5%	322
<i>Sporisorium scitamineum</i>	CDS01539.1	72.8%	321
<i>Kalmanozyma brasiliensis</i> GHG001	XP_016291004.1	70.6%	323
<i>Ustilago maydis</i> 521	XP_011387292.1	69.5%	317
<i>Pseudozyma hubeiensis</i> SY62	XP_012190404.1	65.0%	321

^a: The mature sequences of lipases.

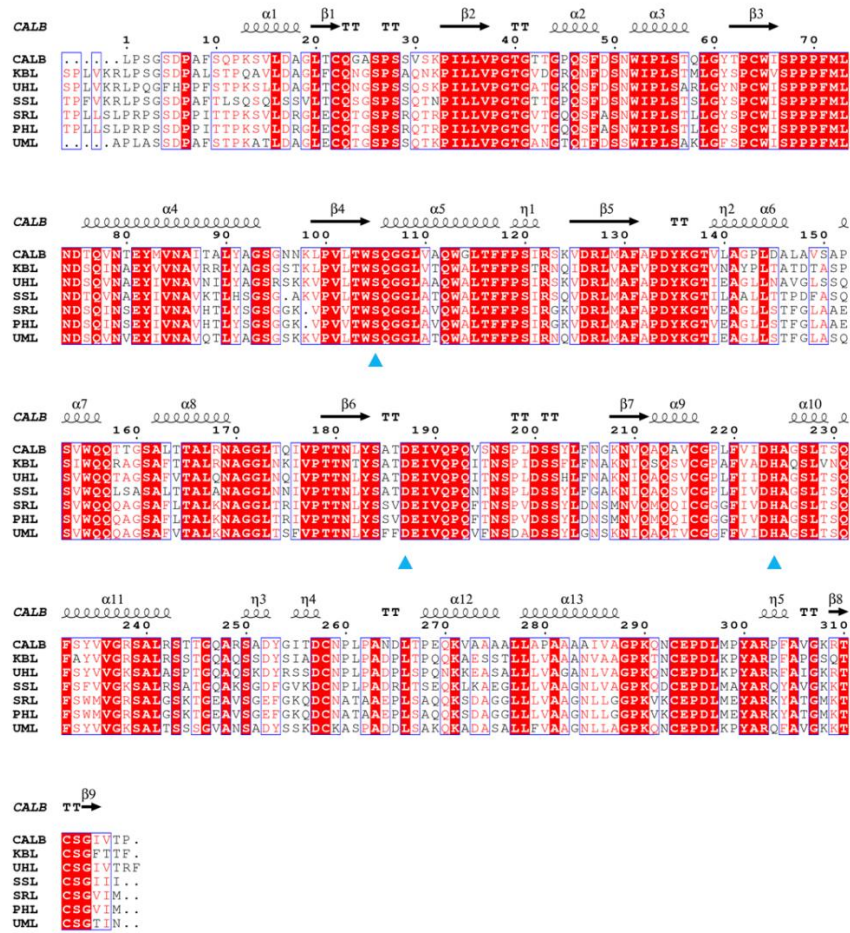


Fig S1. Multiple alignments of amino acid sequences of lipases from *Candida antarctica* lipase B (CALB); *Kalmanozyma brasiliensis* GHG001 (KBL, GenBank accession no. XP_016291004.1); *Ustilago hordei* (UHL, GenBank accession no. CCF54401.1); *Sporisorium scitamineum* (SSL, GenBank accession no. CDS01539.1); *Sporisorium reilianum* SRZ2 (SRL, GenBank accession no. CBQ70828.1); *Pseudozyma hubeiensis* SY62 (PHL, GenBank accession no. XP_012190404.1); *Ustilago maydis* 521 (UML, GenBank accession no. XP_011387292.1). The amino acid residues that are conserved in all sequences are all labeled in red. The blue triangles indicate the catalytic triad. The representations of secondary structures appear above the relevant regions of the sequence: arrows indicate β -strands, squiggles indicate helices and TT indicate turns.

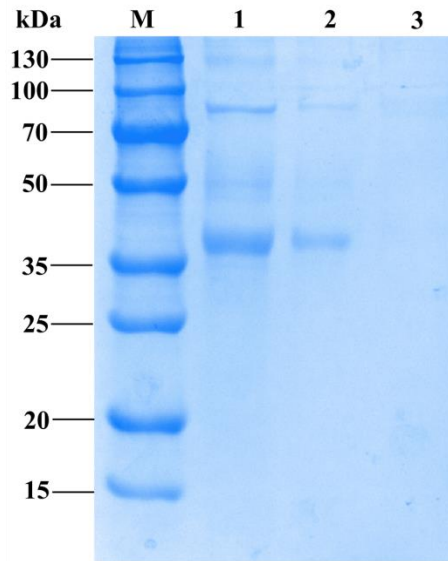


Fig S2. SDS-PAGE analysis of protein concentration in the immobilization course. Line M: protein molecular weight marker; Line 1: crude enzyme solution; Line 2: mixture of buffer solution and crude enzyme solution; Line 3: supernatant after immobilization.