

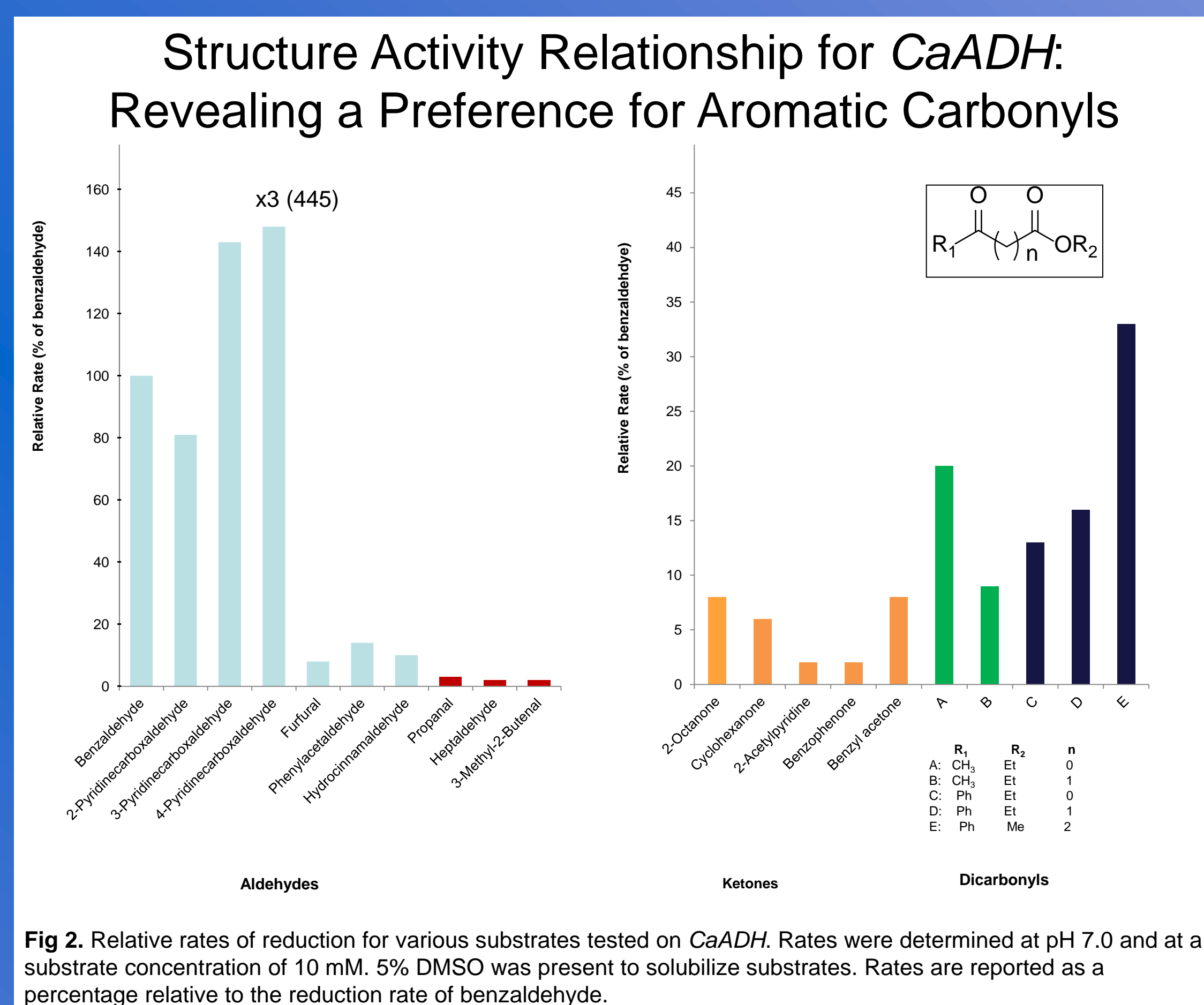
# Expression, Characterization and Use of a New Bacterial Dehydrogenase in Asymmetric Synthesis – Glucose as a “Chiral, Biorenewable Reductant”



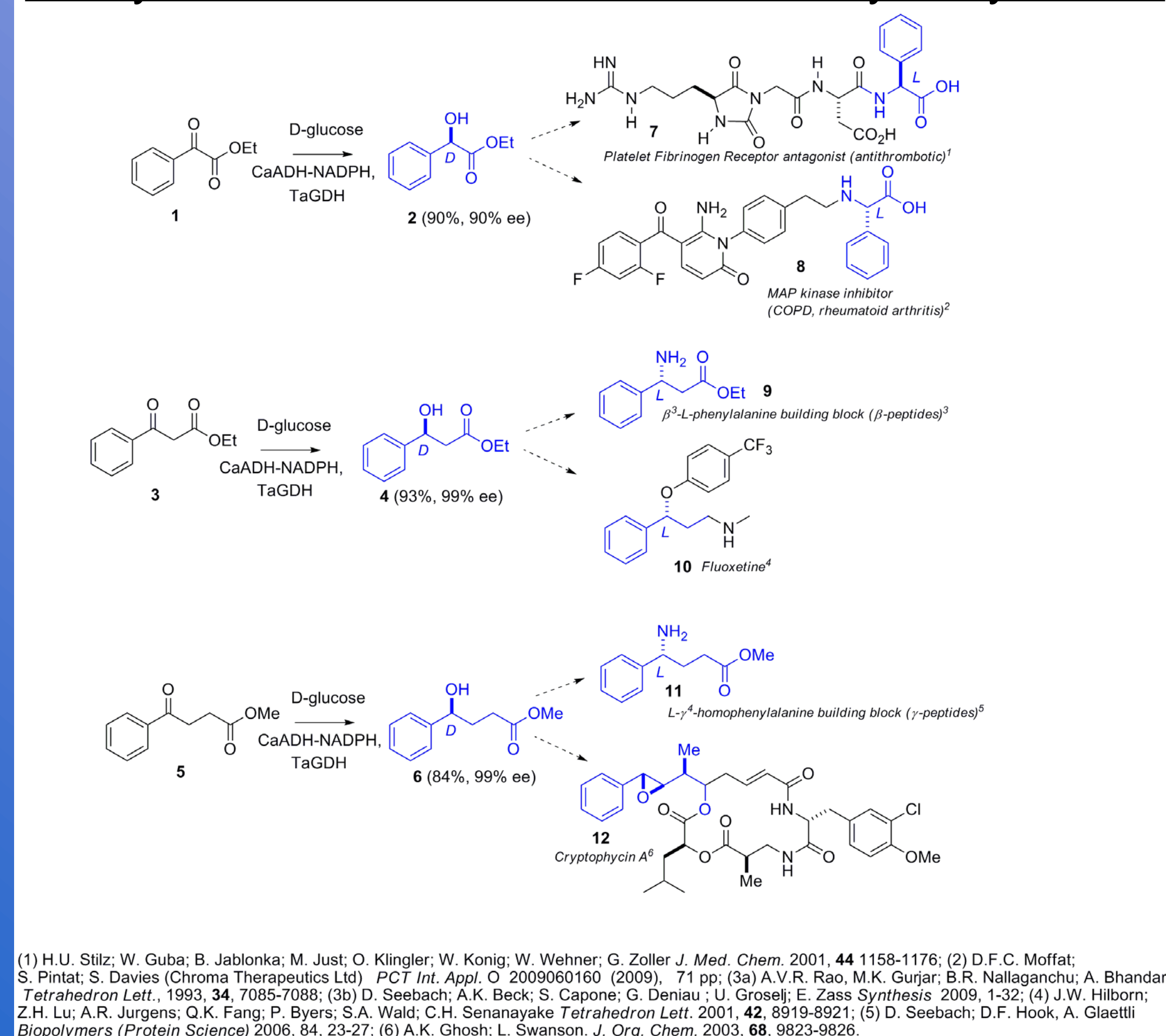
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**Abstract:** This work focuses on the expression of a previously uncharacterized alcohol dehydrogenase (ADH) enzyme and its use in asymmetric carbonyl reduction chemistry. Initially, we describe the expression system and purification of the protein. Homogeneous protein has been examined for substrate specificity across a battery of carbonyl compounds, of variable structures. Finally, we describe the application of the enzyme to asymmetric carbonyl reduction, to produce highly enantiomerically enriched synthetic building blocks of note. For this application, conditions are described in which glucose serves as the terminal reductant, thermodynamically driving the process. In this way, one is harnessing biorenewable redox equivalents for asymmetric synthesis.



## Ability to Reduce $\omega$ -Keto Esters to D-Hydroxy Esters



## Adding a Stereocenter to the $\beta$ -Ketoester Motif: A DYRKR Entry into the Taxoid Sidechain

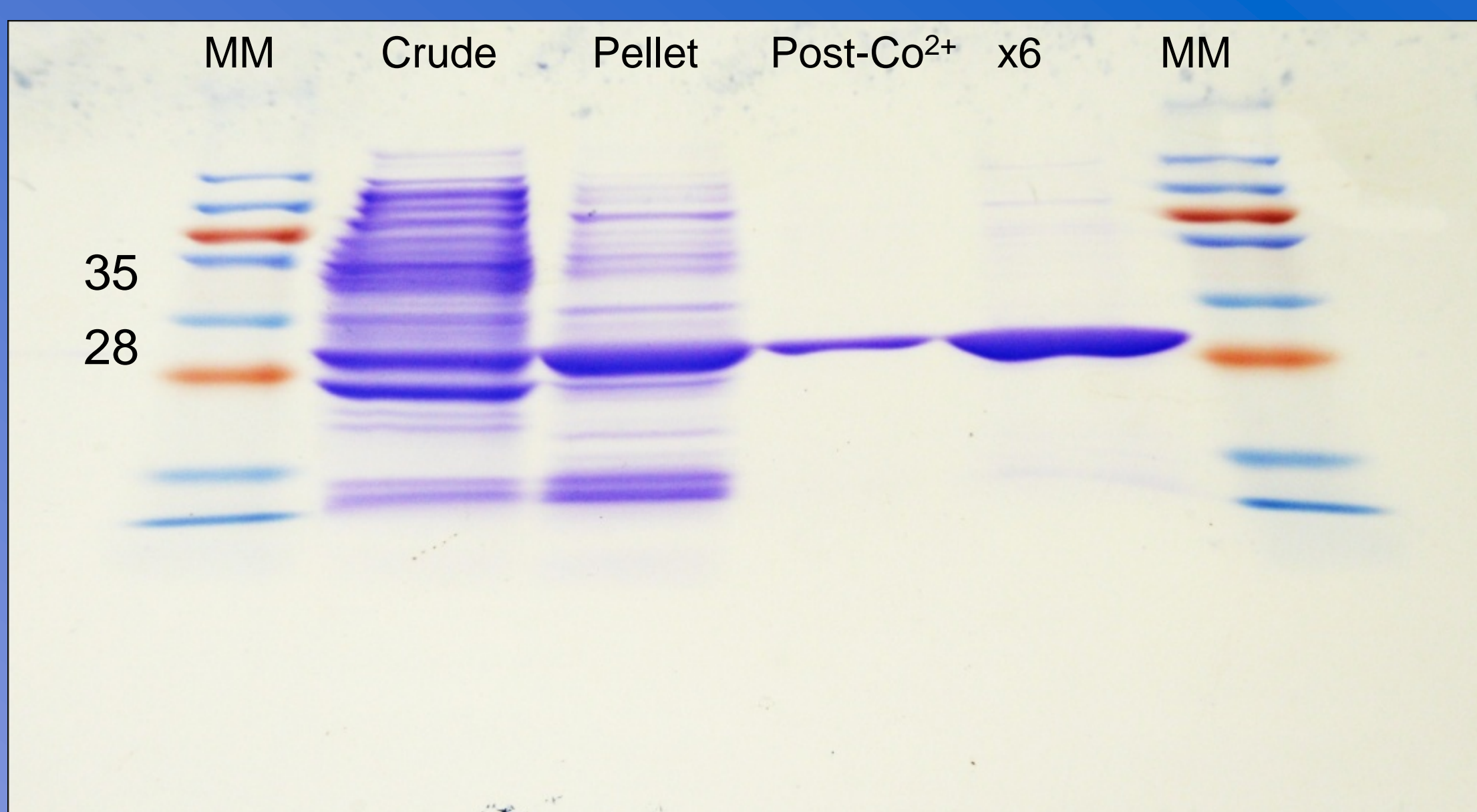
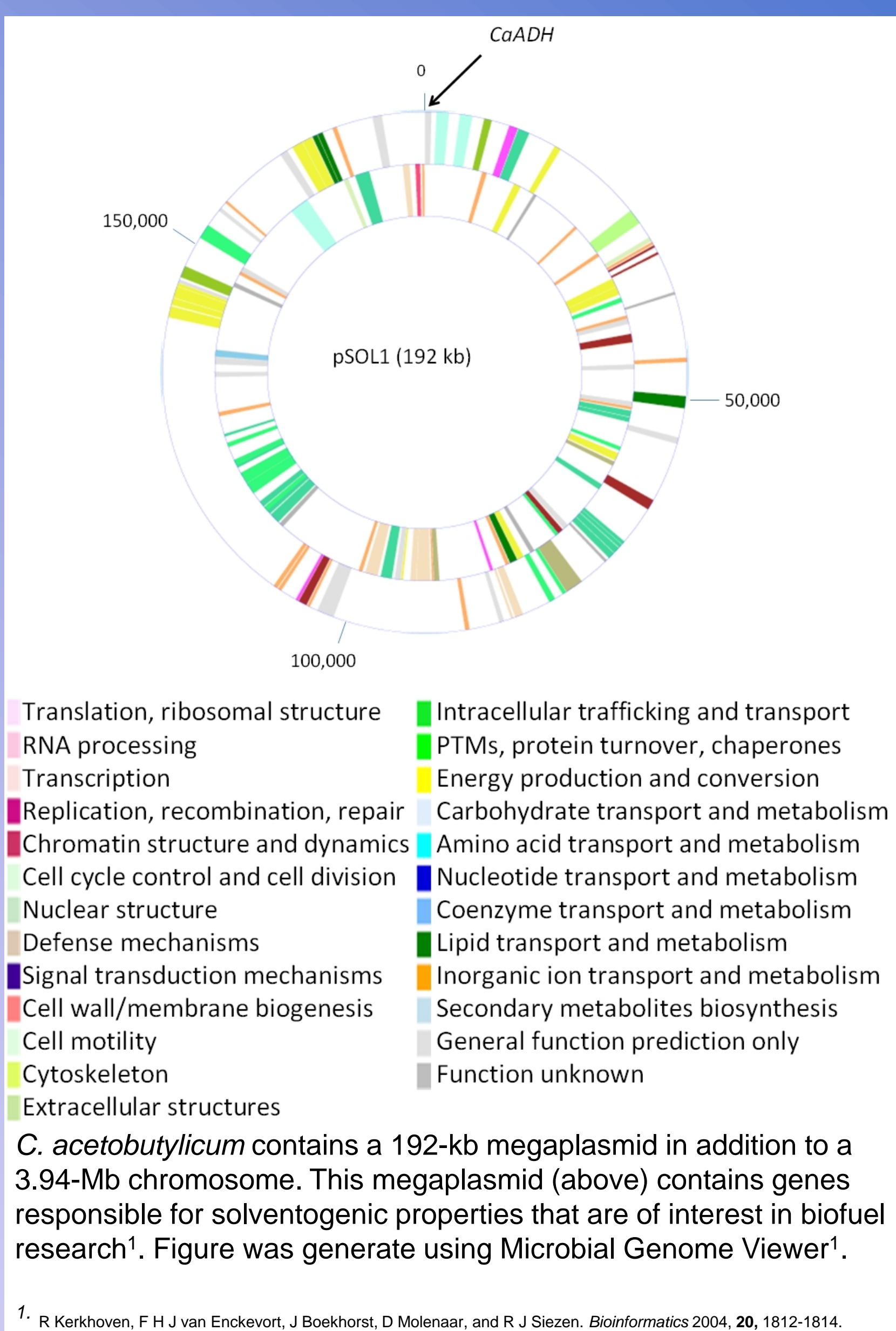
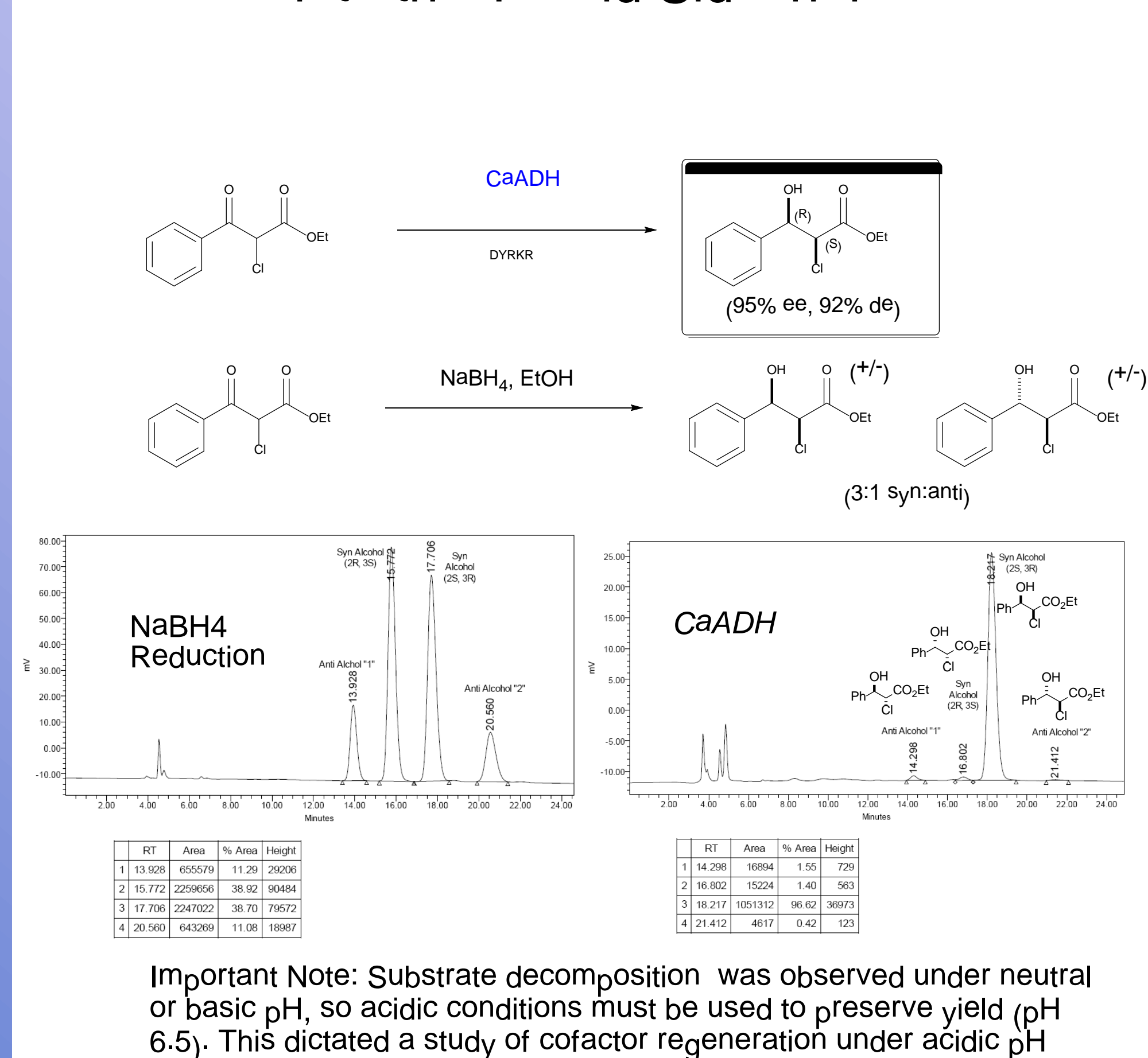


Fig 1. SDS-PAGE (12%) of *CaADH* purification

Fraction	Units/mL*	Total Units	mg/mL	Total mg	Units/mg	Yield	Pur Factor
Crude	38.5	463.1	19.7	236.4	1.95		1
Final	32.1	321.5	0.56	5.6	58.1	70%	30

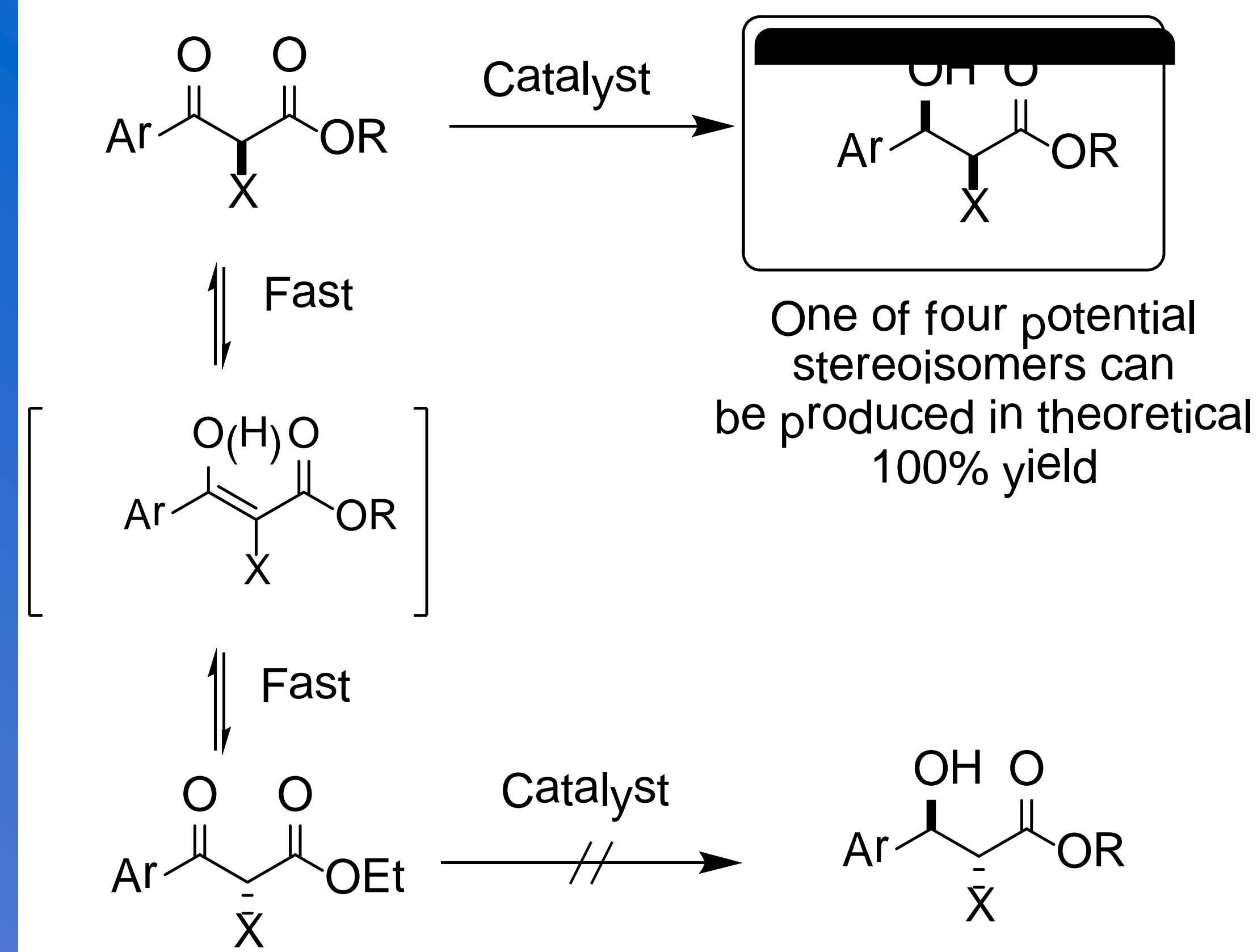
\* Units defined as  $\mu$ moles of benzaldehyde reduced per minute

## Use of *Clostridium acetobutylicum* ADH (*CaADH*) for value added synthesis using cellulose derived terminal reductants

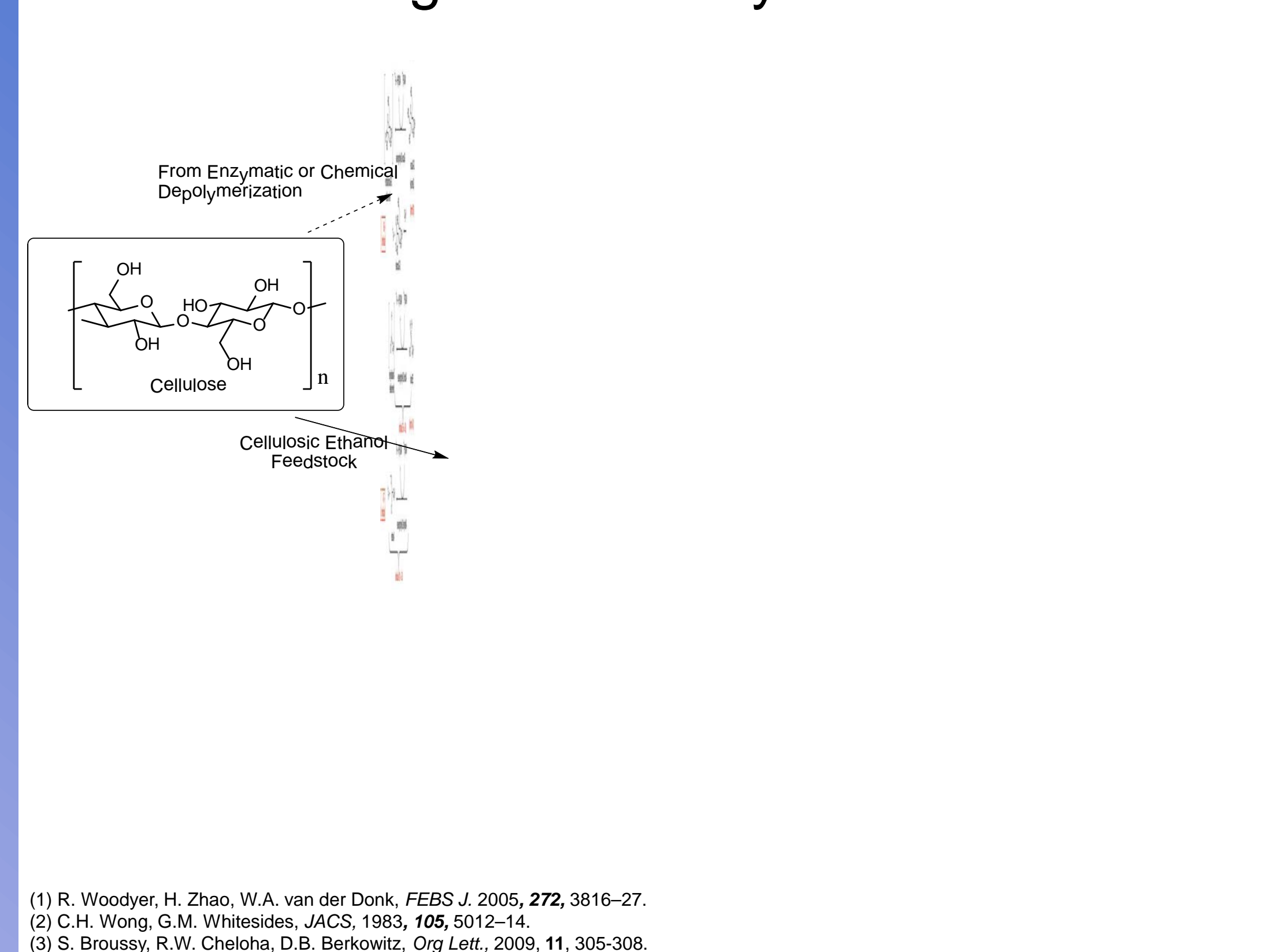
- Biocatalysts are increasingly being used as the asymmetric catalyst of choice for many organic transformations
- Some enzymes (ADH's) require exogenous cofactor (NAD(P)H) addition for activity
- Cofactor is too expensive to be used in stoichiometric amounts as terminal reductant
- Through coupling reactions, other economical, biological molecules can be used as terminal reductants (see biomass, ethanol, and glucose)

J.C. Moore, D. J. Pollard, B. Kosjek, P. N. Devine, *Acc. Chem. Res.*, 2007, **40**, 1412-1419

## Mechanism of DYRKR

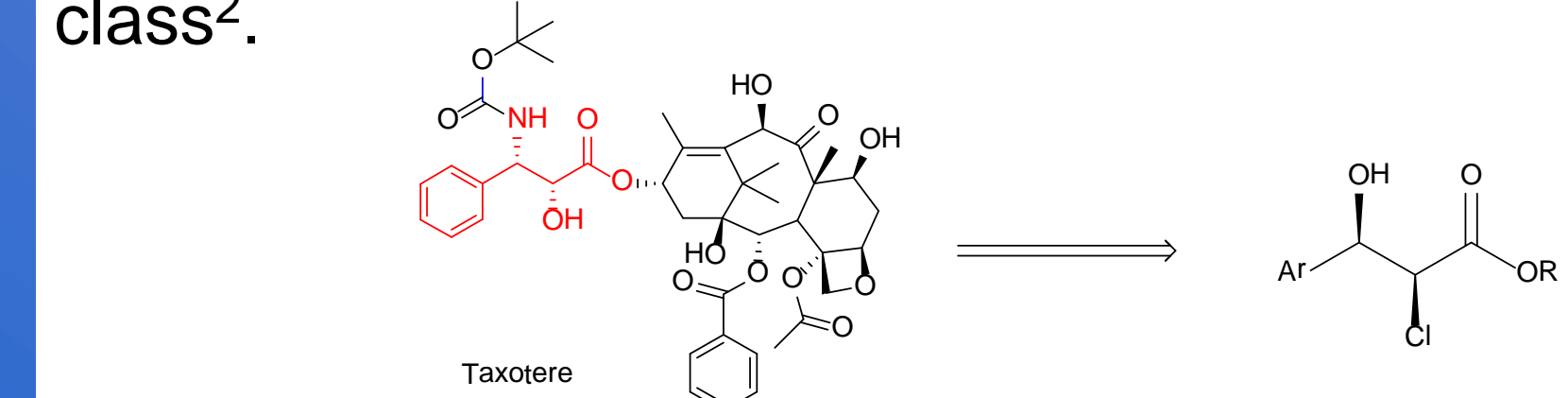


## Potential Bio-Cellulosic Feeding into Cofactor Regeneration Systems



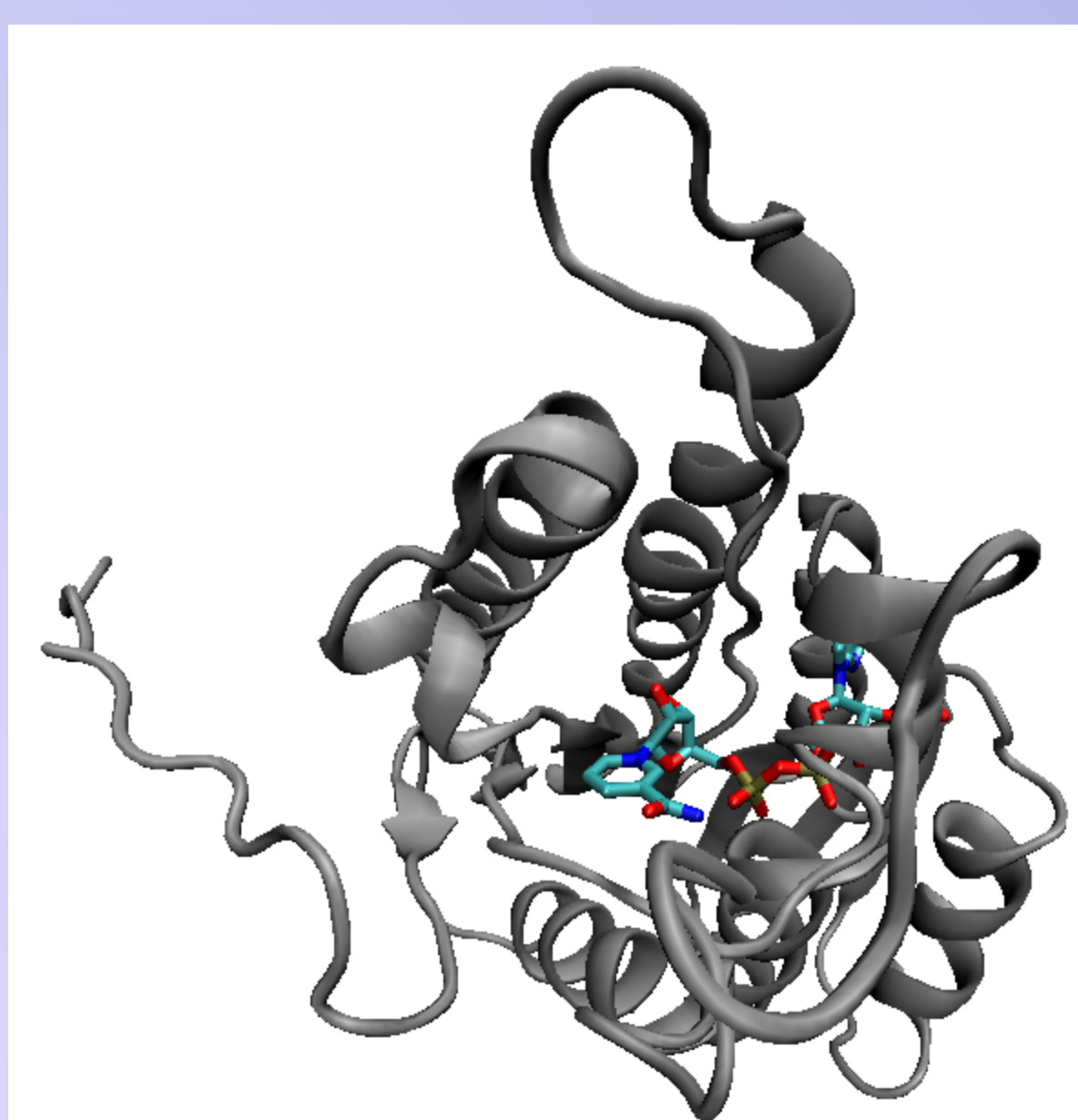
## Taxane Targets

Taxanes are a class of therapeutics that display anti-mitotic activity. Taxol, an extract from the Pacific Yew, has the longest running history of Taxane therapeutics. Due to the detrimental effects of bark extraction, semi-synthetic routes to Taxol analogs were employed. Taxotere utilizes the 10-deacetylbaccatin core from the leaves and needles of the Yew family – a process both renewable and readily available<sup>1</sup>. The described *CaADH* has the ability to reduce an  $\alpha$ -chloro- $\beta$ -ketoester to the corresponding hydroxyester (above left). This reduced product can be converted and installed as the phenylisoserine side chain of the taxane class<sup>2</sup>.



1. J. N. Denis, A. E. Greene, D. Guenard, F. Guertler-Voegel, L. Mangat, P. Potier, *JACS*, 1988, **110**, 5917-5919.  
2. B. Feske, I. Kaluzna, J. D. Stewart, *JOC*, 2005, **70**, 9654-9657.

**Conclusions:** A new ADH enzyme from *Clostridium acetobutylicum* (*CaADH*) was expressed, purified and characterized. In addition to displaying high activity for aromatic aldehyde reduction, *CaADH*, showed a general ability to reduce  $\omega$ -keto esters, bearing that same aryl moiety. A general preference for formation of D-hydroxy esters was seen, leading to valuable  $\alpha$ -,  $\beta$ - and  $\gamma$ -hydroxy ester building blocks in 90-99% ee. Expanding on this trend, successful DYRKR entry into the syn  $\alpha$ -chloro-D- $\beta$ -hydroxy ester building block for Taxol and Taxotere was achieved (95% de; 99% ee). When coupled with a biomass derived cofactor regeneration system (e.g. glucose), these transformations represent a highly value added application of biorenewable reducing equivalents. **Support from the NSF (CHE-0911732), NCESR and ACS (SURF award to RWC) is acknowledged.**



Homology model of *CaADH*<sup>1</sup>. Model is based off of 1XG5 (Human Putative DH, 2NWQ (*P. aeruginosa* DH), and 2NPF (*A. aquifex* DH).

(1) N. Eswar, M. A. Mari-Renom, B. Webb, M. S. Madhusudan, D. Eramian, M. Shen, U. Pieper, A. Sali, *Curr. Protocols in Bioinformatics*, John Wiley & Sons, Inc., Supplement 15, 5.6.1-5.6.30, 2006.