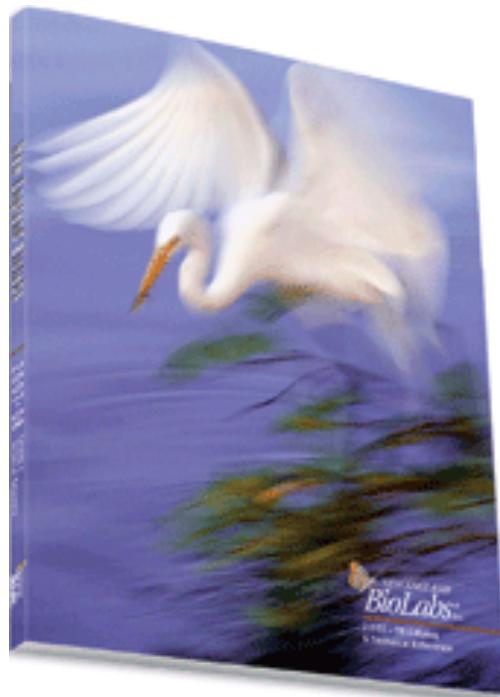
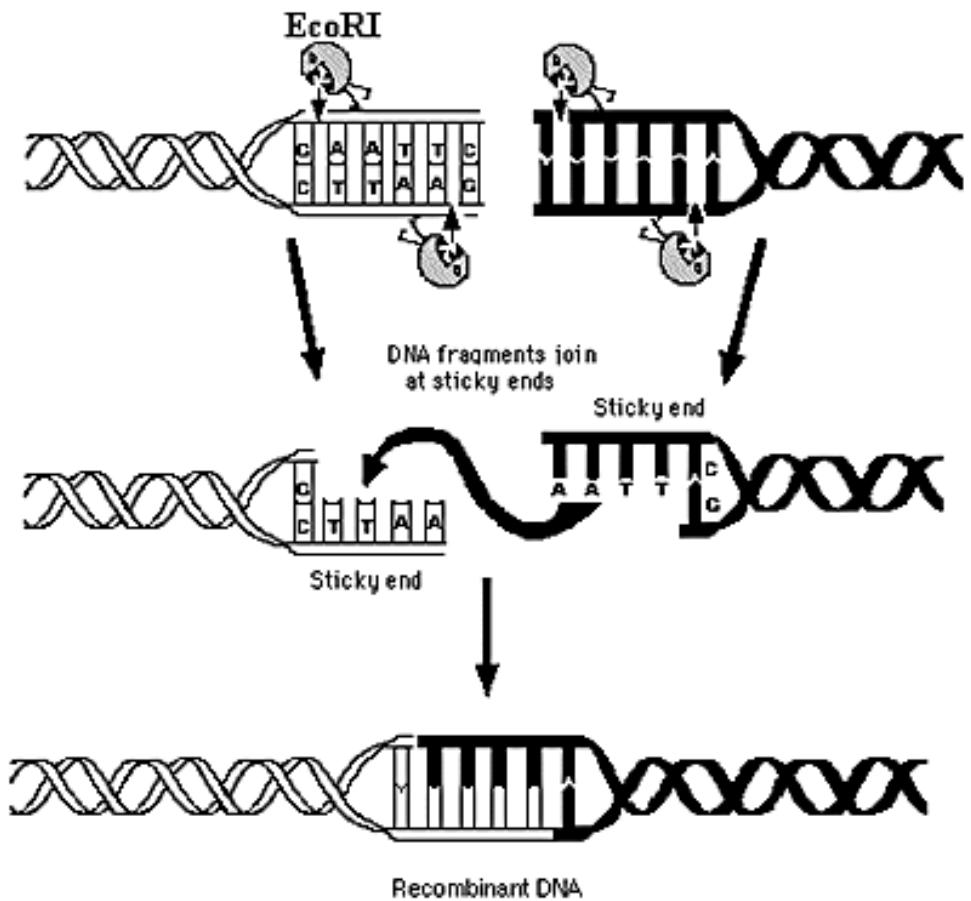


**Writing DNA code = forward
engineering**

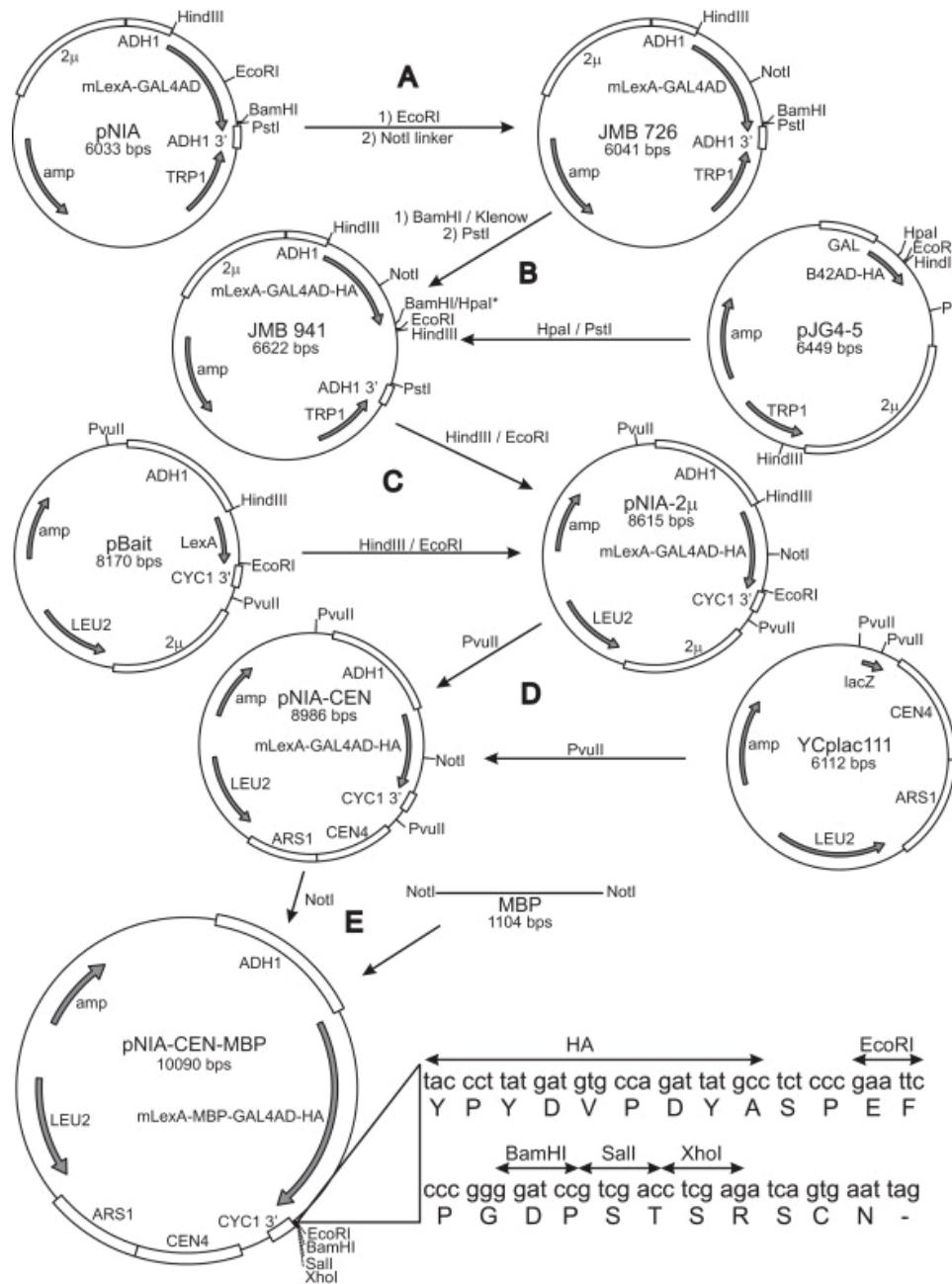
(Synthetic Biology)

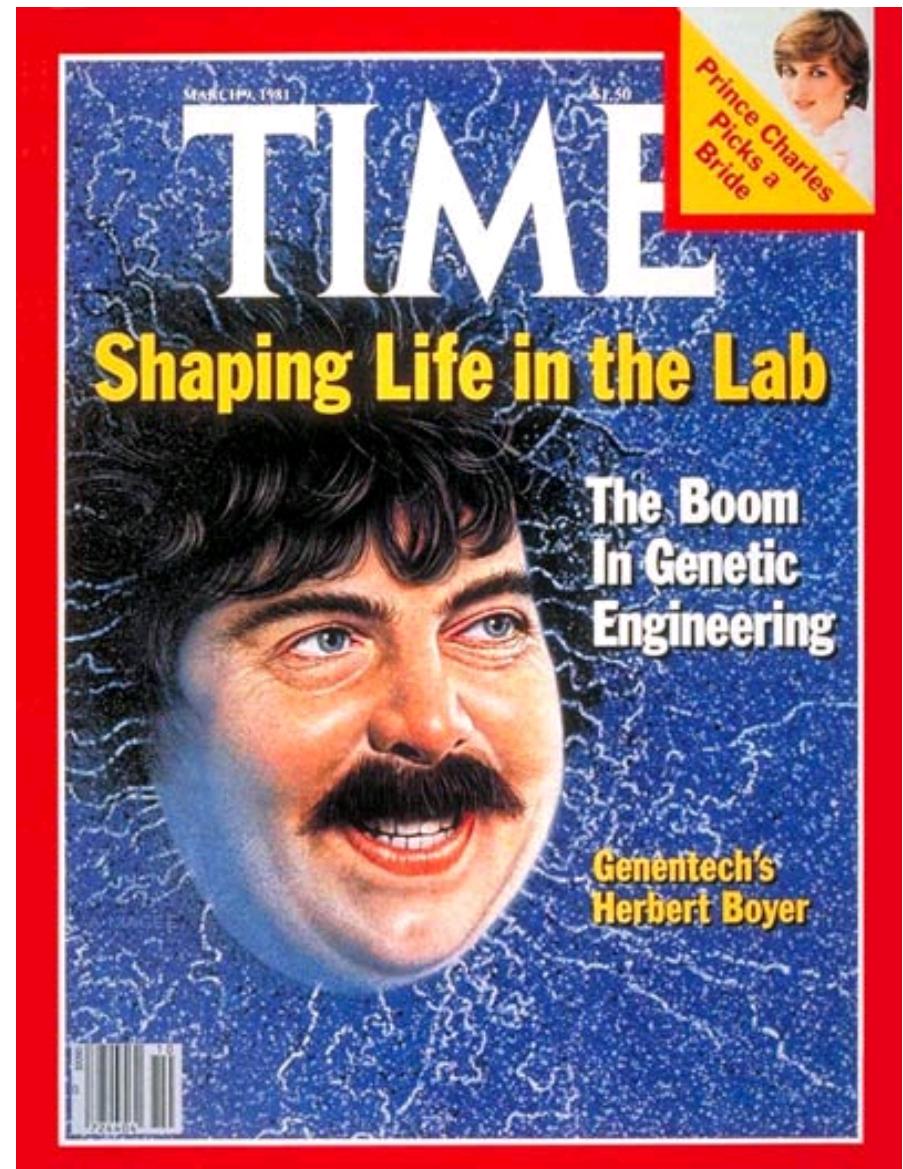
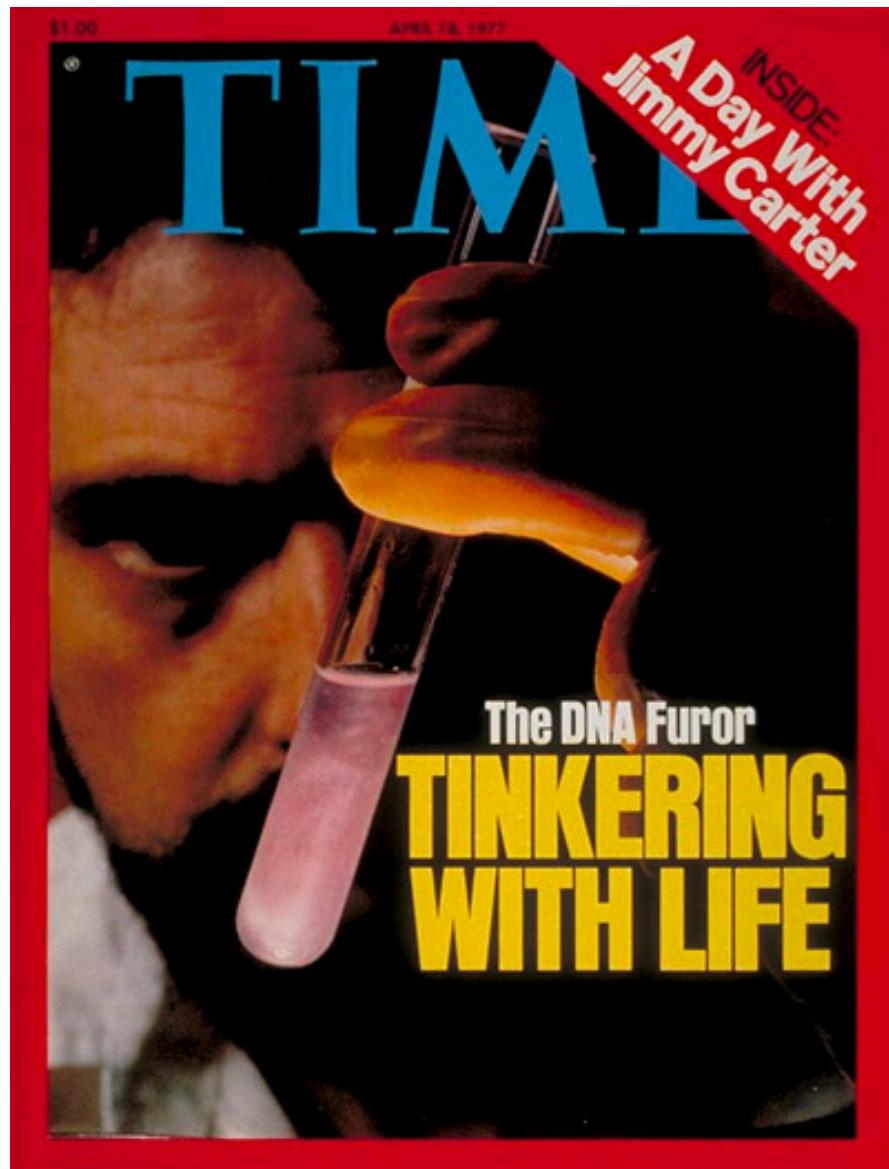


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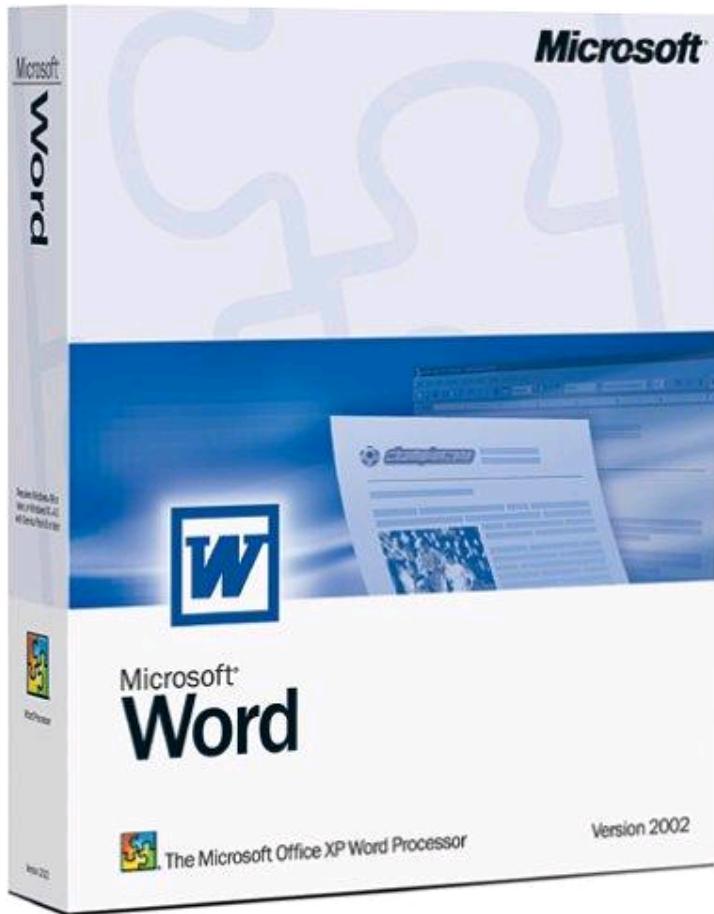
Restriction Enzyme Action of EcoRI







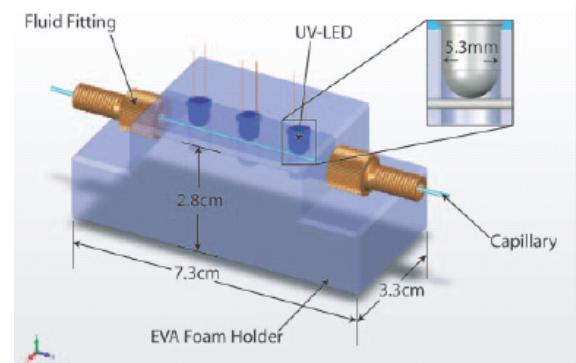
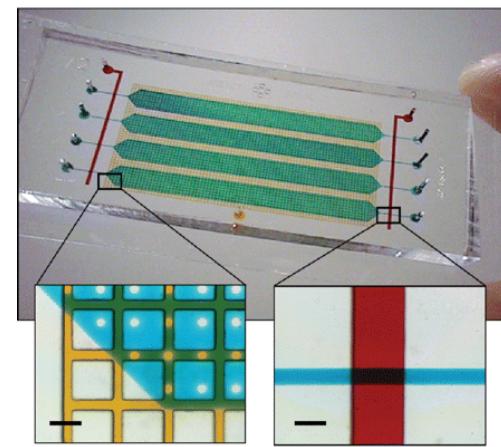
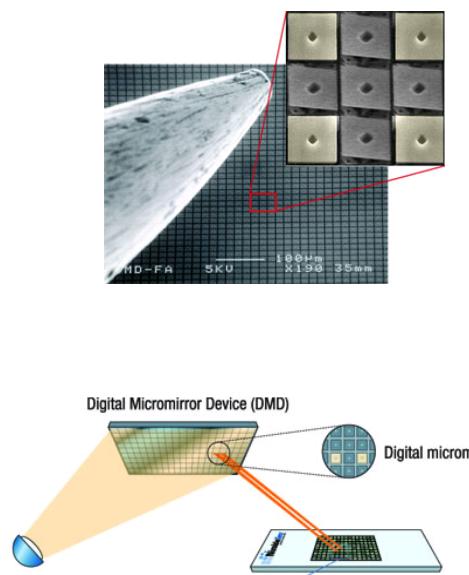
if you can **WRIte** **DNA** ,
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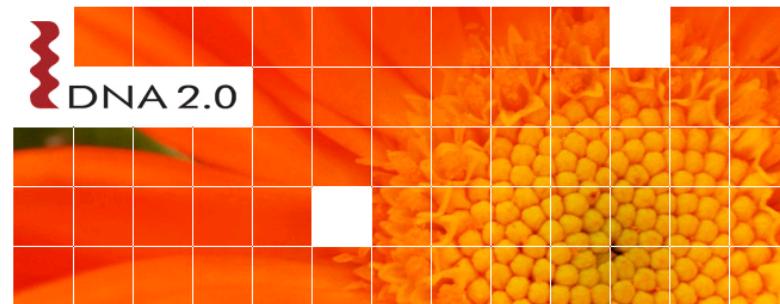
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Cost per Base of DNA Sequencing and Synthesis

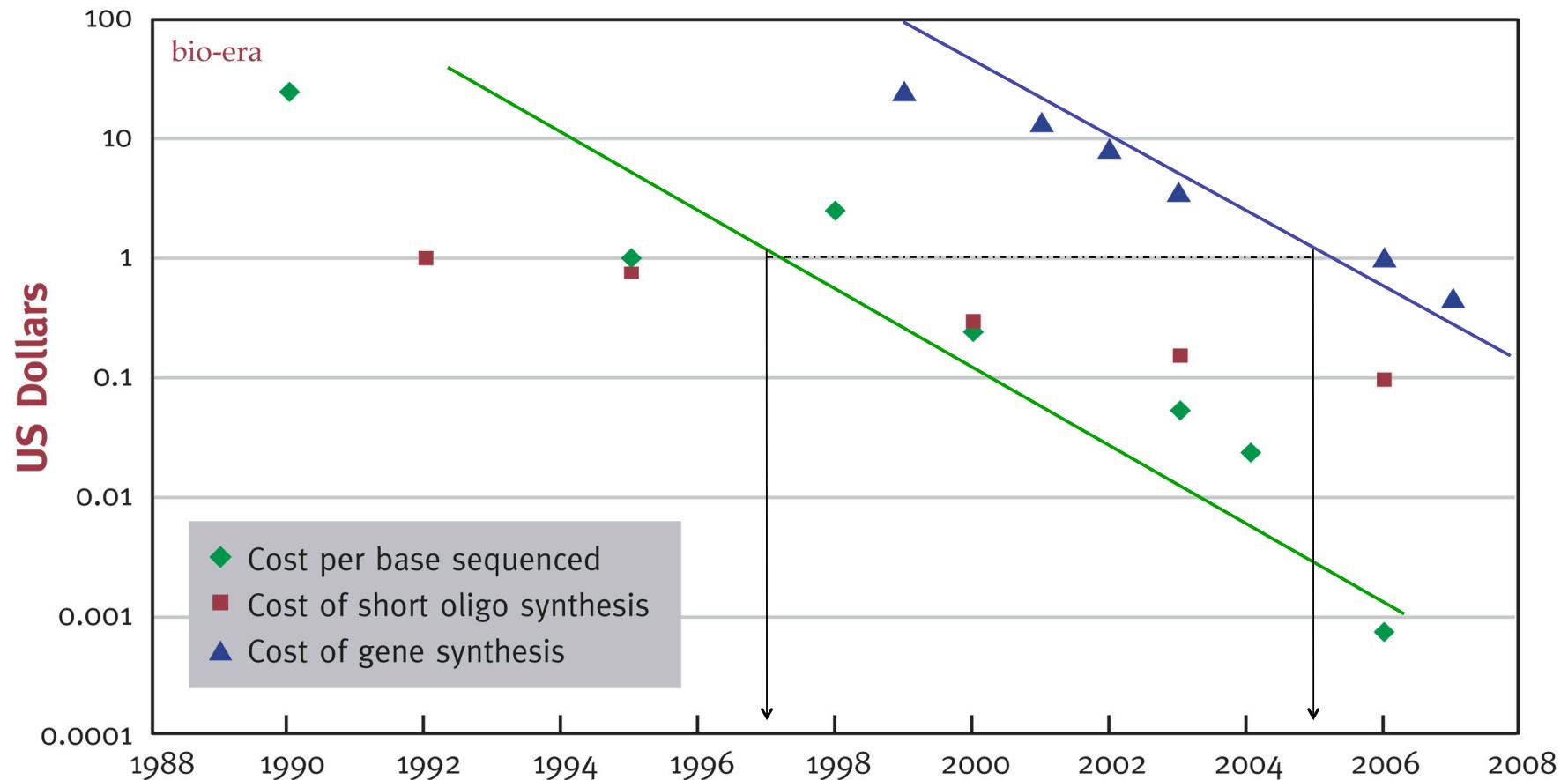
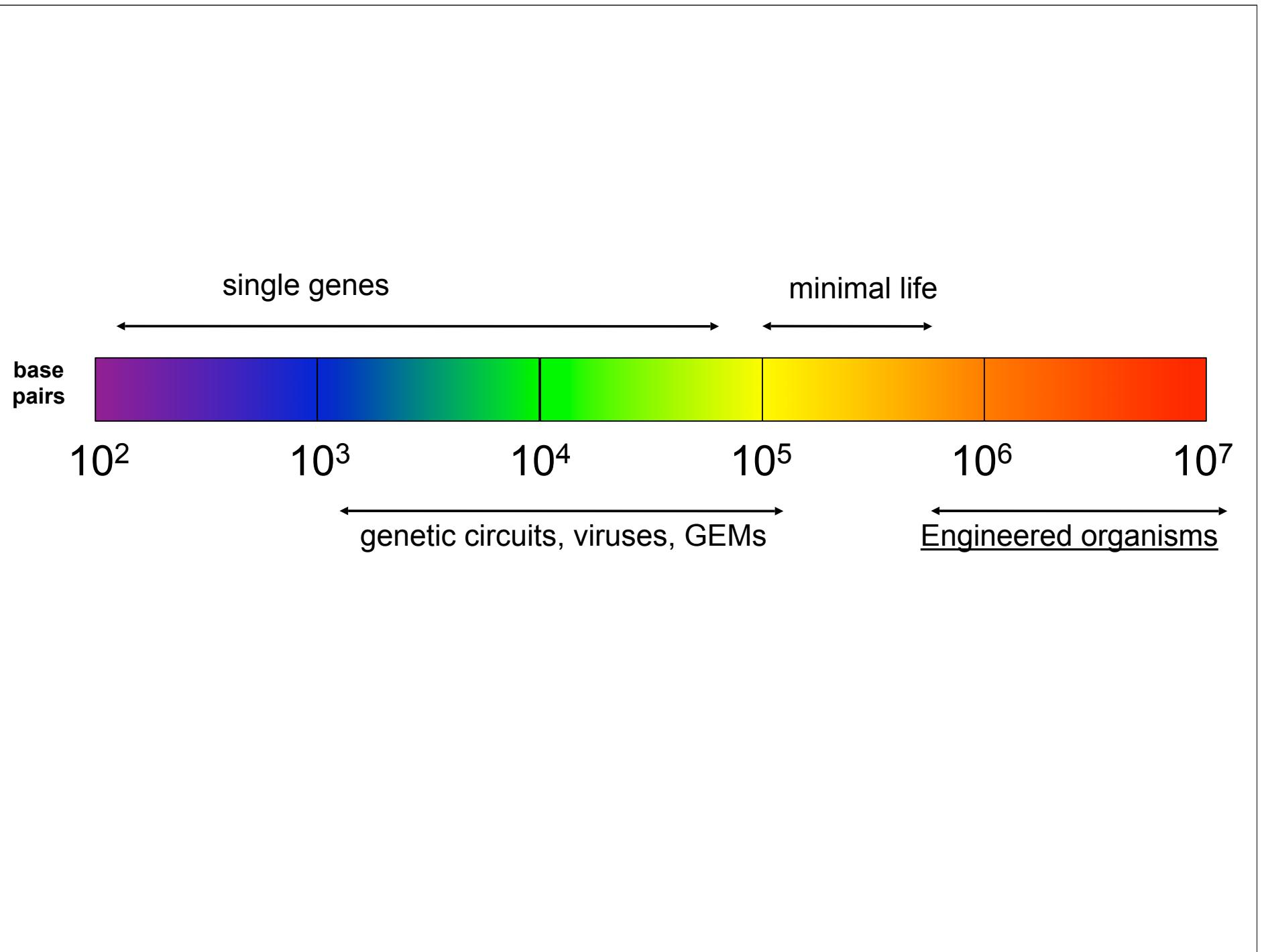


Figure from *Genome Synthesis and Design Futures*, Bio Economic Research Associates, © 2007. www.bio-era.net

Synthetic trend lags by about 8 years

Today, if you can type, you
can do genetic engineering



(CBCD) CENTER FOR BIOLOGICAL CIRCUIT DESIGN

INFORMATION SCIENCE AND TECHNOLOGY



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● CBCD : THE CIRCUITRY OF LIFE

The CBCD is developing new ways to design, build and analyze biological circuits. Biological circuits control information flow in biological systems, and as such are a core area of Information Science and Technology. The study of circuits cuts across vast areas of biology, from biochemistry, biophysics and genetics, to cell and developmental biology, to neurobiology and ecology.

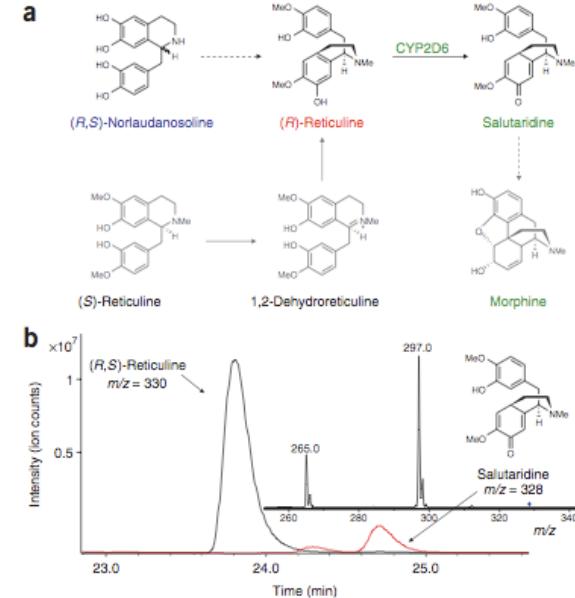
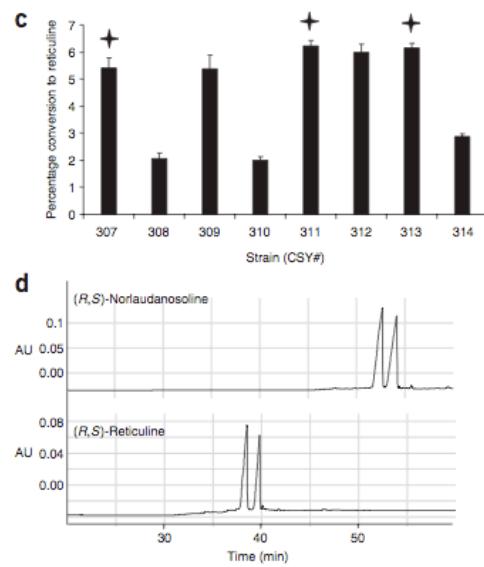
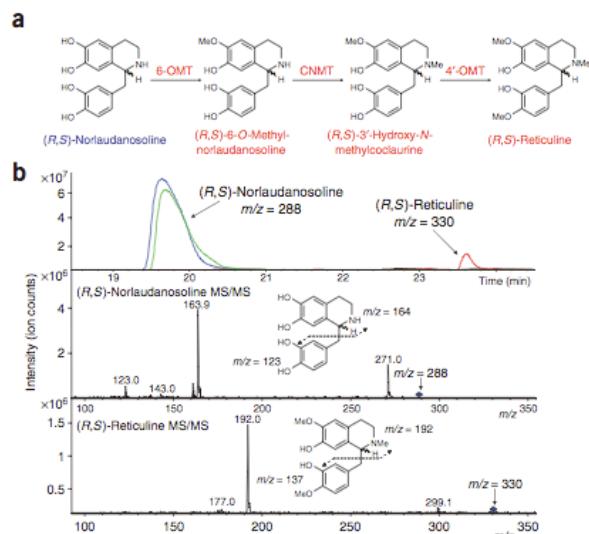
Understanding how to design and build circuits is crucial for the next generation of **bioengineering**. The study of biological circuits also opens up new areas for theory in computation. We combine the experimental biologist's desire to abstract the key principles from the richness and diversity of biological circuits, the physicist's sense of measurement and of simple underlying mechanisms, and the engineer's aesthetic of "to build is to understand." The CBCD is an interdisciplinary group of biologists and engineers from a broad range of engineering and biology disciplines.

Goals: We will deduce simple rules about biological circuits and understand how they act in circuits at the levels of molecules, cells, organisms and ecosystems. We will learn how to model, design, build and analyze biological circuits. We will forge effective interdisciplinary research teams and train interdisciplinary researchers, with fundamental connections between engineering and circuit biology, systems and molecular neuroscience.

Production of benzylisoquinoline alkaloids in *Saccharomyces cerevisiae*

Kristy M Hawkins & Christina D Smolke

The benzylisoquinoline alkaloids (BIAs) are a diverse class of metabolites that exhibit a broad range of pharmacological activities and are synthesized through plant biosynthetic pathways comprised of complex enzyme activities and regulatory strategies. We have engineered yeast to produce the key intermediate reticuline and downstream BIA metabolites from a commercially available substrate. An enzyme tuning strategy was implemented that identified activity differences between variants from different plants and determined optimal expression levels. By synthesizing both stereoisomer forms of reticuline and integrating enzyme activities from three plant sources and humans, we demonstrated the synthesis of metabolites in the sanguinarine/berberine and morphinan branches. We also demonstrated that a human P450 enzyme exhibits a novel activity in the conversion of (*R*)-reticuline to the morphinan alkaloid salutaridine. Our engineered microbial hosts offer access to a rich group of BIA molecules and associated activities that will be further expanded through synthetic chemistry and biology approaches.





CHEMICAL SYNTHESIS OF THE MYCOPLASMA GENITALIUM GENOME

Overview

We have developed methods for assembly of the complete synthetic 582,970 bp *Mycoplasma genitalium* JCVI 1.0 genome. This synthetic genome contains all the genes of wild type *M. genitalium* G37 except MG408, which is disrupted to block pathogenicity. The genome also contains added "watermark" sequences located at intergenic sites known to tolerate transposon insertions, for identification of the genome as synthetic and also antibiotic resistance markers to allow its selection.



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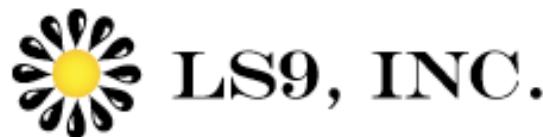
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"Nothing is too wonderful to be true if it be consistent with the laws of nature." - Michael Faraday



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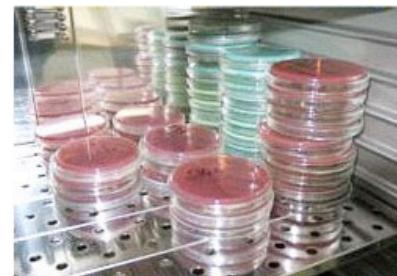
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