

Team member: M.Sc. Zhen Chen, M.Sc. Doinita Frank, Dr. Sugima Rappert

Supervisor: Prof. Dr. An-Ping Zeng

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Description:

The future of industrial biotechnology requires efficient development of highly productive and robust strains of microorganisms. Present praxis of strain development cannot adequately fulfill this requirement, primarily owing to the inability to precisely control reactions at a molecular level or to reliably predict the behavior of cells upon perturbation. This project aims to combine the latest advances of structural biology and synthetic biology to provide new tools to precisely design and assemble controllable elements (e.g. enzymes) and modules (pathways) for re-programming cellular metabolism (Fig.1).

Within this novel approach, we are developing new computational and experimental approaches to targeted reengineering the enzyme allostery, enzyme/coenzyme specificity, novel genetic circuit, etc from atomic level. These predictly designed modules are combined together to produce a minimally mutated industrial strain for amino acid (e.g lysine) production with high production rate and yield (Fig.2).

References

Chen, Z., Rappert, S., Sun, J.B., Zeng, A.P. (2011) **Integrating molecular dynamics and co-evolutionary analysis for reliable target prediction and deregulation of the allosteric inhibition of aspartokinase for amino acid production.** J. Biotechnol. Accepted

Chen, Z., Meyer, W.Q., Rappert, S., Sun, J.B., Zeng, A.P. (2011) **Co-evolutionary analysis enables rational deregulation of allosteric enzyme inhibition in *Corynebacterium glutamicum* for lysine production.** Appl. Environ. Microbiol. doi:10.1128/AEM.02912-10.

Chen, Z., Wilmanns, M., Zeng, A.P. (2010) **Structural synthetic biotechnology: from molecular structure to predictable design for industrial strain development.** Trends Biotechnol. 28, 534-542.

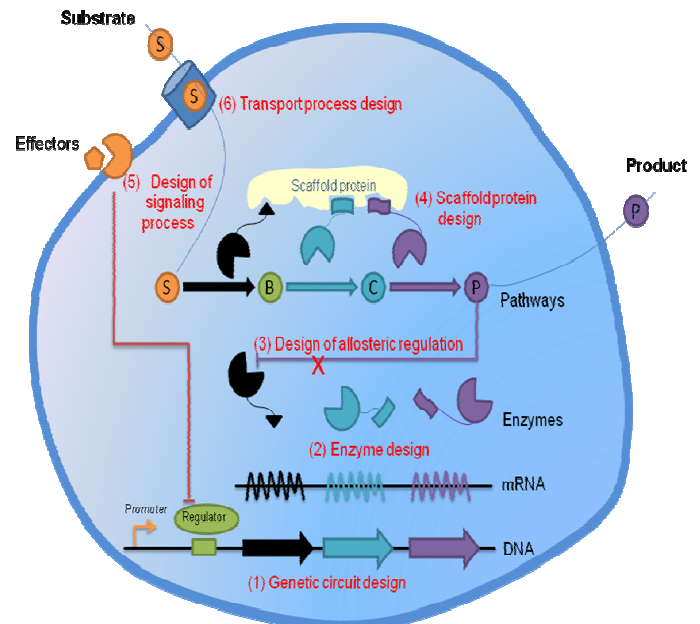


Fig. 1: Framework of structural synthetic biology for strain development

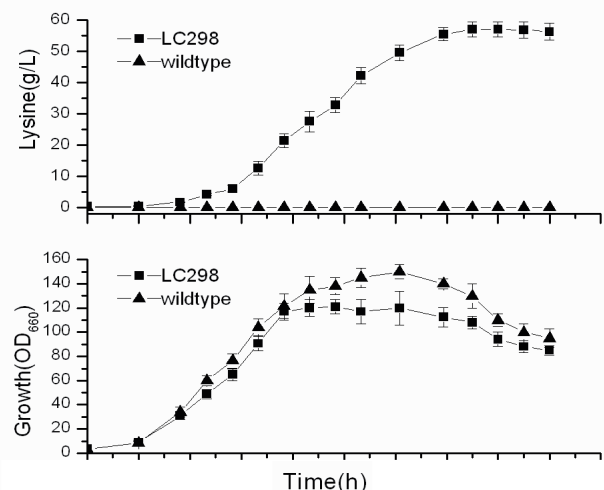


Fig. 2: Lysine production by a *Corynebacterium glutamicum* strain with a single mutation for feedback-insensitive aspartokinase.

Contact: Prof. Dr. An-Ping Zeng

Institute of Bioprocess and Biosystems Engineering, Technical University Hamburg-Harburg.

Denickestrasse 15, D-21073 Hamburg, Germany.

Phone: +49-40-42878-4183 Email: aze@tu-harburg.de Web: www.tu-harburg.de/ibb