TAMPERE UNIVERSITY OF TECHNOLOGY

Focused proteomic analysis of cell factories (proChassis)

Academy of Finland: 2013-2017

Consortium:

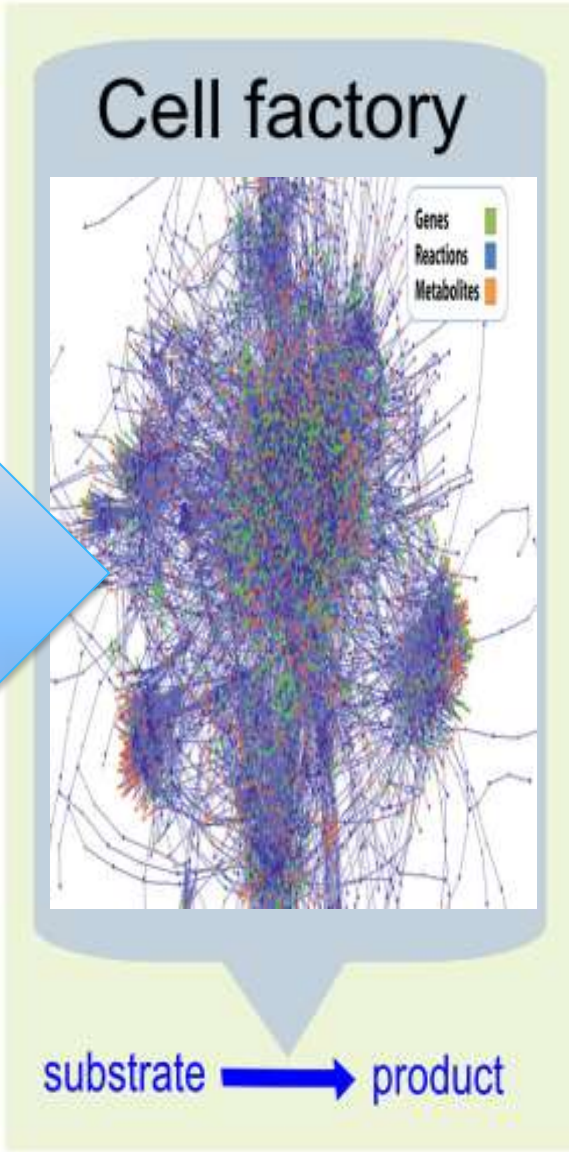
Matti Karp (Tampere University of Technology, TUT)
Urpo Lamminmäki (University of Turku)
Tommi Aho (TUT)

Ville Santala (TUT), FinSynBio opening seminar, 23.1. 2014

Synthetic biology

…engineering principles to biology…

Abstraction
Modularity
Standardization
Designing and Modeling



”The central premise: standardization of reusable biological components is the most efficient and effective way to engineering biology”

Gardner & Hawkins, 2013

Biological components

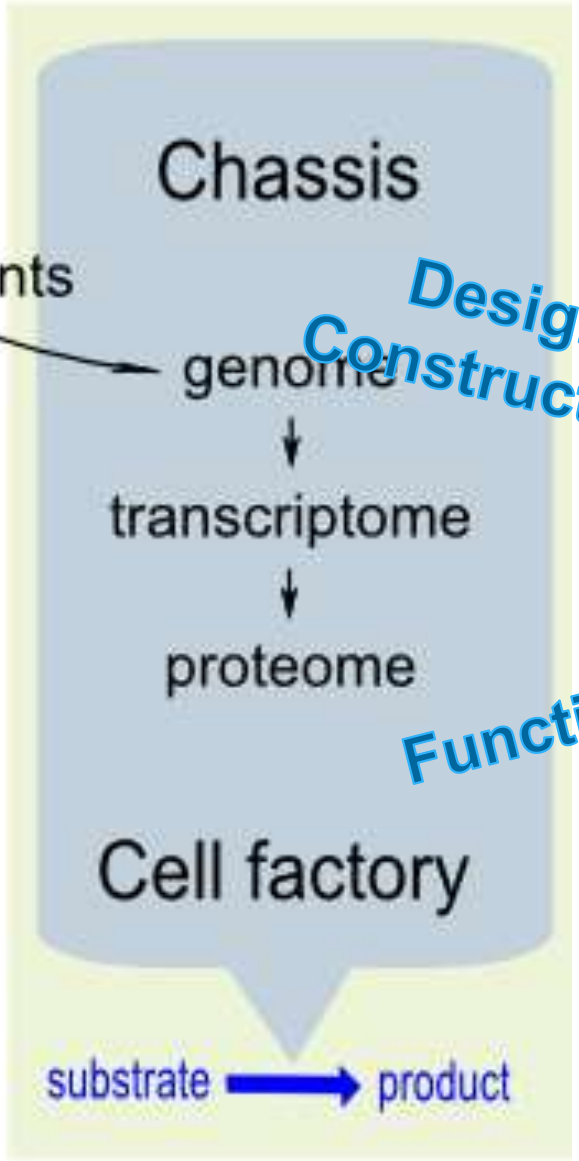
DNA components

Much research effort has been put on the characterization of individual components.

⇒ Standardization

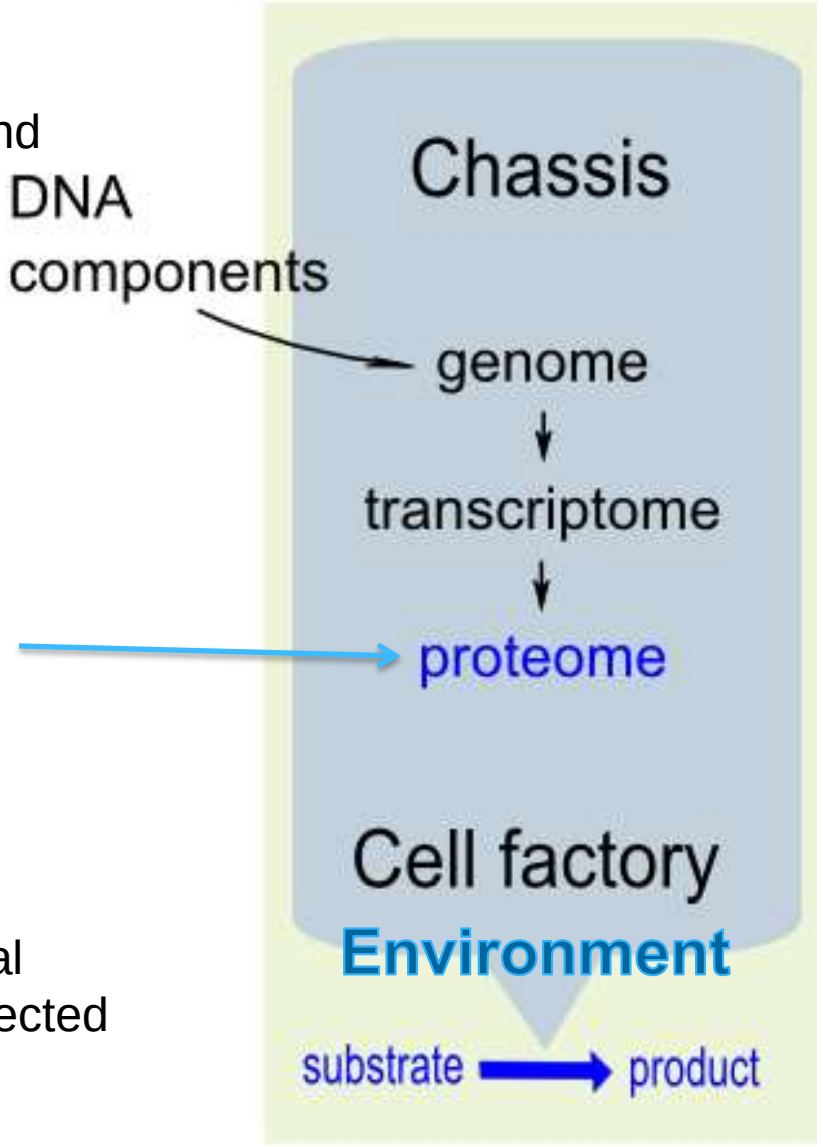
A gap between components and the endogenous systems

Understanding of interactions!



Native targets are used as general indicators (i.e. independent from the specific product formation pathway) for tracking different kind of perturbations and flux changes of the chassis.

NOVEL TOOLS
for quantification of
key proteins of chassis
AND components
in changing conditions.



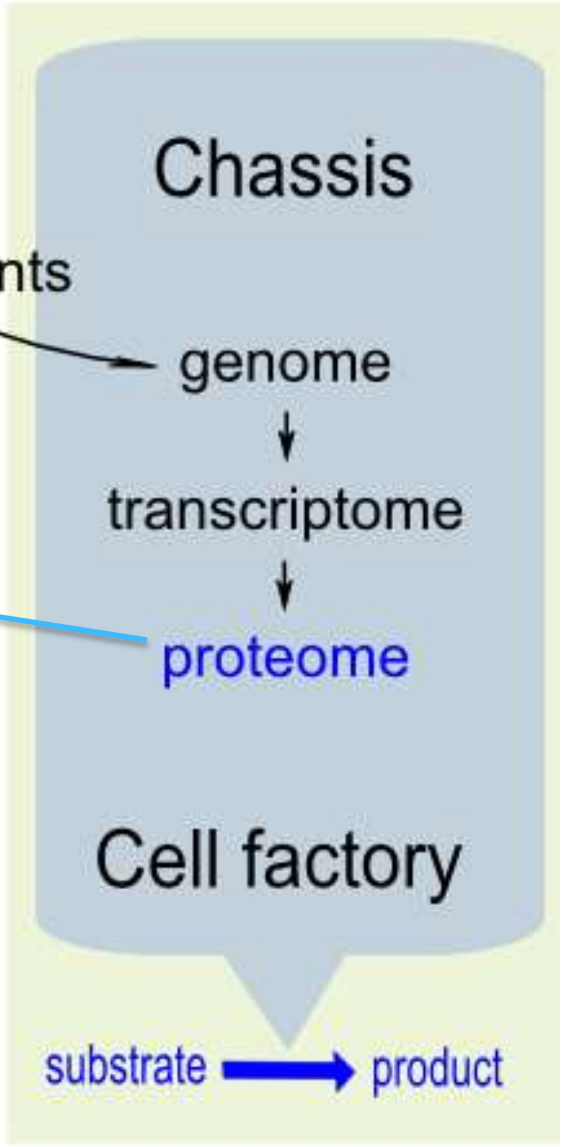
Non-native targets encodes essential activities for the product and are selected from a well-characterized DNA components library.

$$x_i = \sum a_j r_j \qquad (i = 1, 2, \ldots, m; \quad j = 1, 2, \ldots, n)$$

MODEL:

$$C_i^J = \frac{dJ}{dE_i}\left(\frac{E_i}{J}\right)$$

quantification of
<u>key proteins of chassis</u>
AND <u>components</u>



By integrating quantitative informations to the model, factors affecting the product formation can be identified and the yields can be improved by removing bottlenecks (eg. <u>rate limiting steps</u>).

Eg. by changing the expression levels of components or knocking out native genes to force the flux from the substrate towards the product.

Chassis?

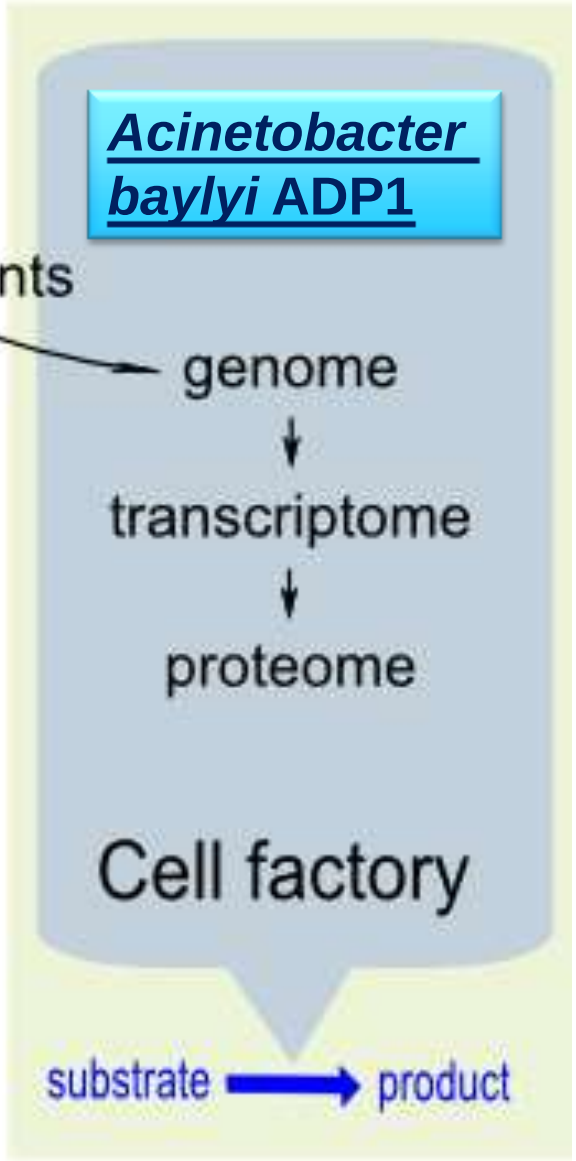
1) **Easily genome-engineerable** (allows high-throughput engineering)

- Natural transformation & homologous recombination

2) **No IPR-issues** (allows open source policy)

With traditional strains, excessive IPR stacking can be problematic

3) **Similarity to *Escherichia coli***



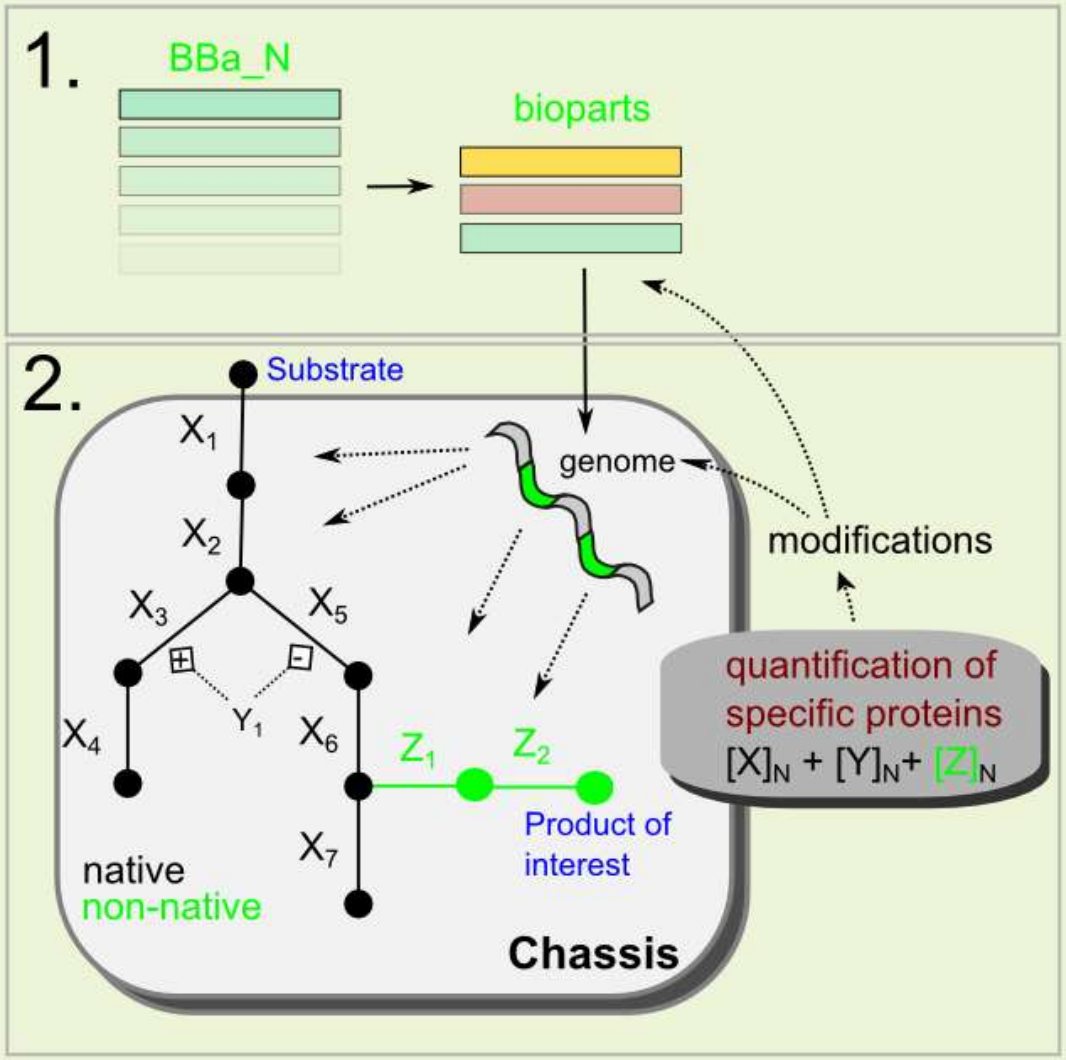
proChassis toolset

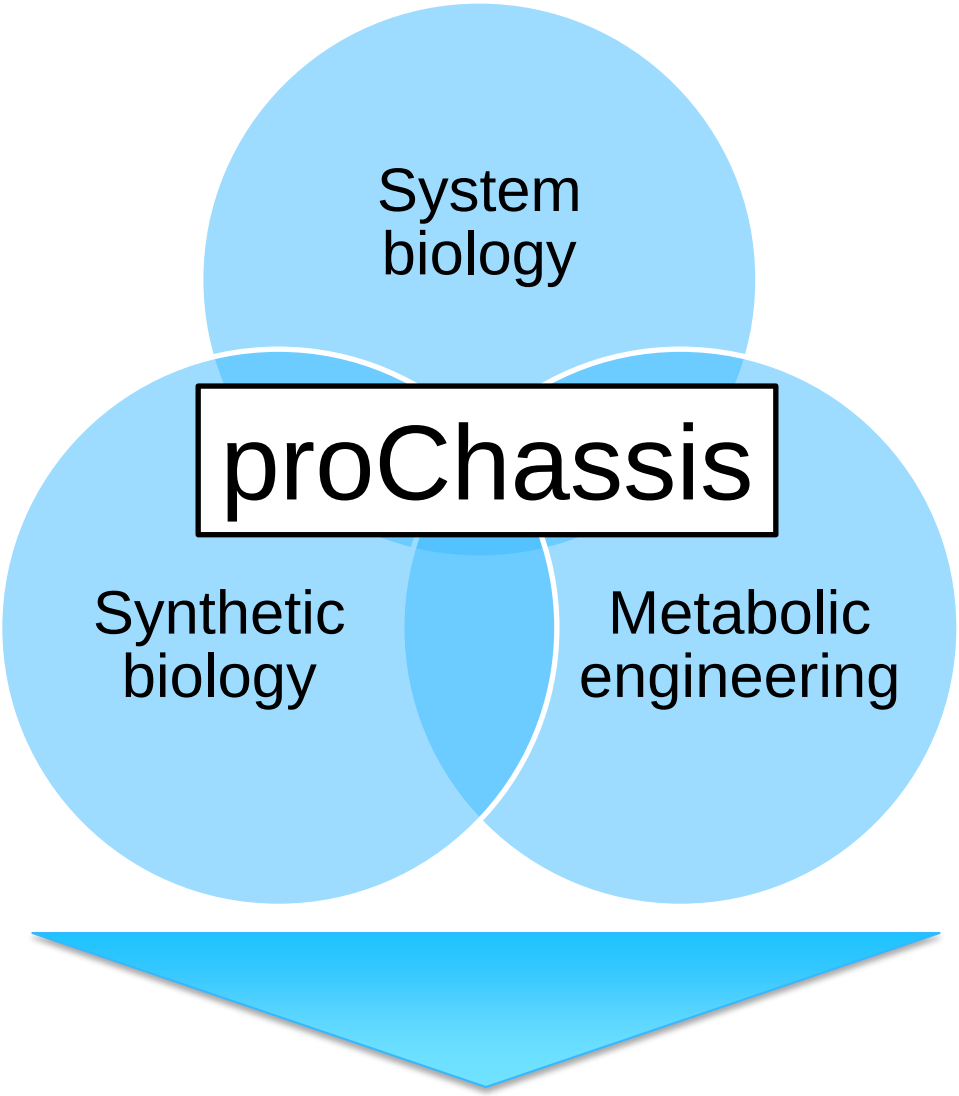
easily genome-engineerable chassis

quantitative monitoring of the expression of integrated bioparts and the key components of the host

computational approaches for system design and analysis

substrate → product





Sustainable biofuel production