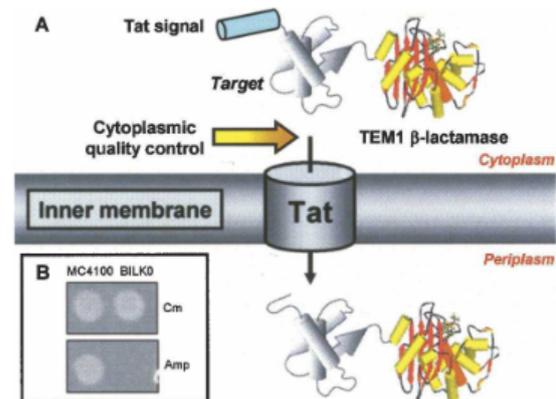


## Development of a high-throughput assay to identify possible foldable *de novo* proteins

**Background:** Different species have different proteins encoded in their genome. It has been thought that proteins evolve via gene duplication, but recently published work suggested, that there are proteins, called *de novo*, that don't show any similarity to other genes, meaning that they can't originate from duplication. The expression of the *de novo* proteins is still very difficult. Therefore, an assay which could help to test *de novo* protein folding in high-throughput would help to act as valuable starting point.

**Objectives:** In this project the different enzyme restriction sites (XhoI, HindIII, etc.) need to be implemented into the pSALect wildtype plasmid via PCR. In a next step this engineered plasmid will be self-ligated and cloned into *E. coli* (*E. coli*) cells. After sequencing to assure the correctness of the engineered plasmid, different kinds of *de novo* genes should be cloned into the pSALect vector using the new introduced restriction sites. In a follow up assay the possible folding of these *de novo* gene constructs should be controlled via ampicillin agar plates. The idea is that only cells, expressing the *de novo* protein ampicillin construct will grow.



**Figure 1:** Exploiting the Tat pathway's folding quality control feature for monitoring protein solubility.

### Requirements:

- Interest in evolution at the level of individual proteins
- Interest in lab work on DNA and protein level and basic knowledge of PCR, DNA-cloning, protein expression & purification

### Methods:

- Molecular biochemistry (DNA-cloning, PCR, restriction digest, ligase, etc.) & expression and purification of proteins
- Biochemical characterization of the proteins via SDS-gels

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### Selected Literature:

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4 Andreas Lange, Prajal H Patel, Brennen Heames, Adam M Damry, Thorsten Saenger, Colin J Jackson, Geoffrey D Findlay, Erich Bornberg-Bauer

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