

MOL231: Benchmarking an Expression System in *Bacillus subtilis*

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Introduction

Bacillus subtilis is well-known for its important role in the industrial production of proteins and is thus an ideal organism to study mechanisms like protein expression (1). The aim of this experiment was to benchmark an expression system in our *B. subtilis* strain KO8, by utilizing six different enzymes, table 1. For this purpose, the plasmid pSP-FX_LipA, fig. 1, was used, as well as *B. subtilis* strain KO8 (2).

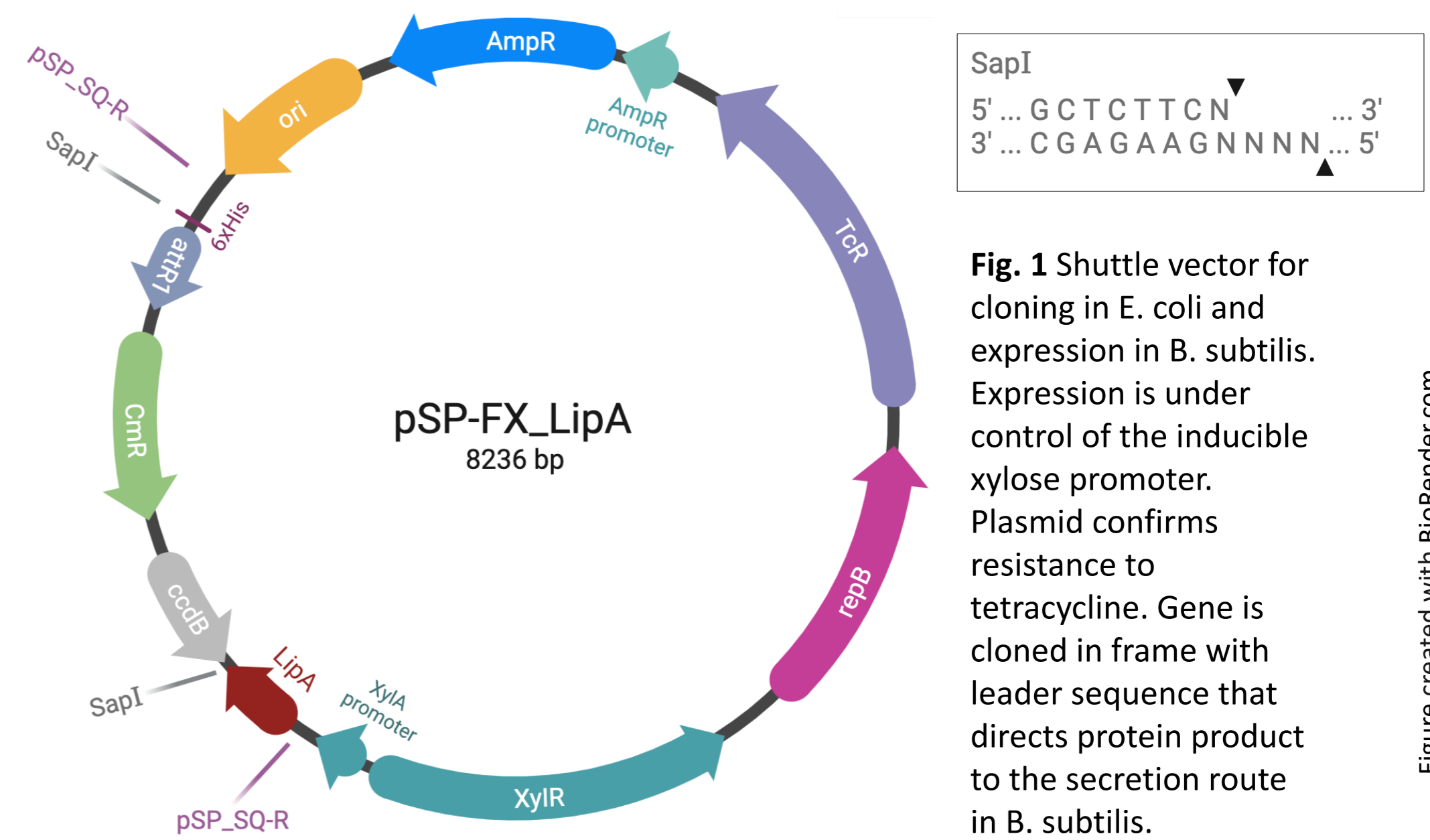
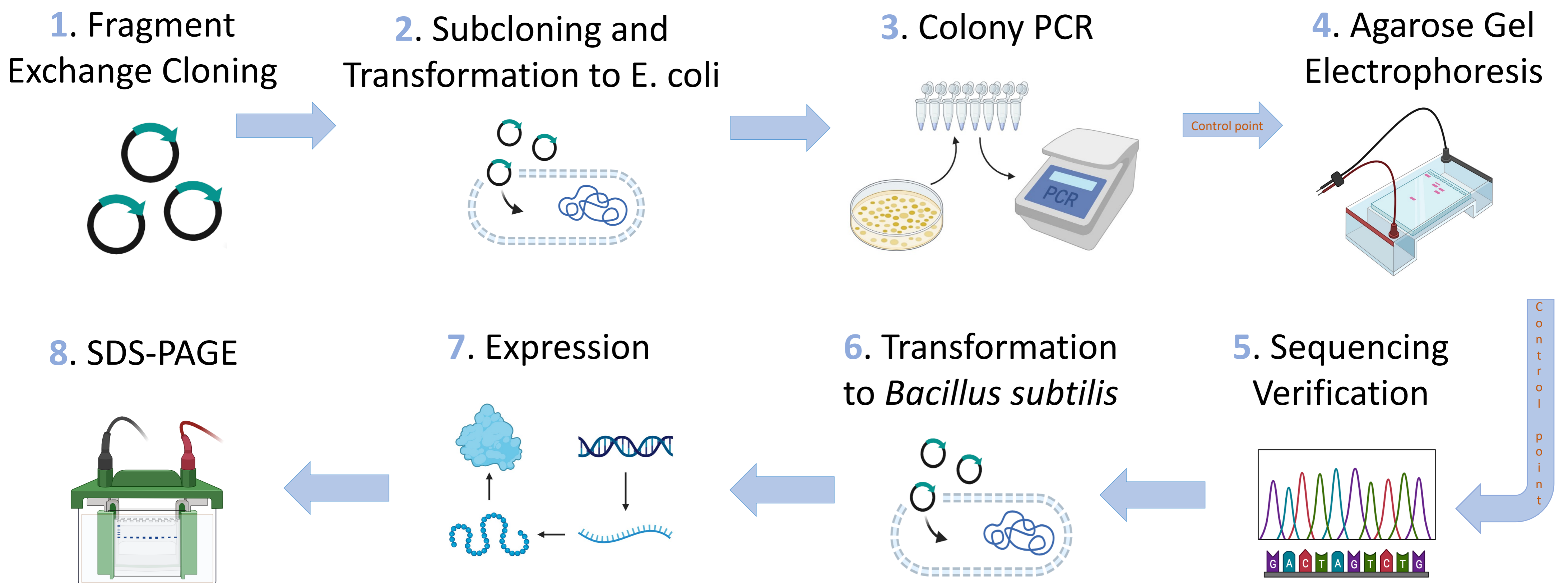


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Methods



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Table 1 The benchmarked enzymes in the study

| Target | Source | PCR-product (bp) | Pre-protein/mature (kDa) |
|--------|-------------------|------------------|--------------------------|
| T0307B | Tyrosinase | 2096 | 72.7 / 69.0 |
| T0308 | Alpha-amylase | 1583 | 54.4 / 50.7 |
| T0309 | Mannose isomerase | 1523 | 52.7 / 49.0 |
| T0310 | Catalase | 1733 | 60.1 / 56.4 |
| T0311 | Cutinase | 929 | 27.7 / 24.0 |
| T0312 | C1-peptidase | 1373 | 46.5 / 42.5 |

References:

- Cui W. *et al.* [2018] Exploitation of *Bacillus subtilis* as a robust workhorse for production of heterologous proteins and beyond. *World J Microbiol Biotechnol.*
- García-Moyano A. *et al* [2020] Fragment Exchange Plasmid Tools for CRISPR/Cas9-Mediated Gene Integration and Protease Production in *Bacillus subtilis*. *Appl Environ Microbiol.*

Results and Discussion

Successful analyzing of spent media using Sodium Dodecyl-Sulfate Polyacrylamide Gel Electrophoresis (SDS-PAGE). T0311 was confirmed to be expressed in the medium, as shown in fig. 2. The yield was measured to be 11.37%. The expression of the other samples could not be definitively confirmed. In future studies it should be considered to include analytical techniques such as Western blotting, RNA sequencing and codon optimization.

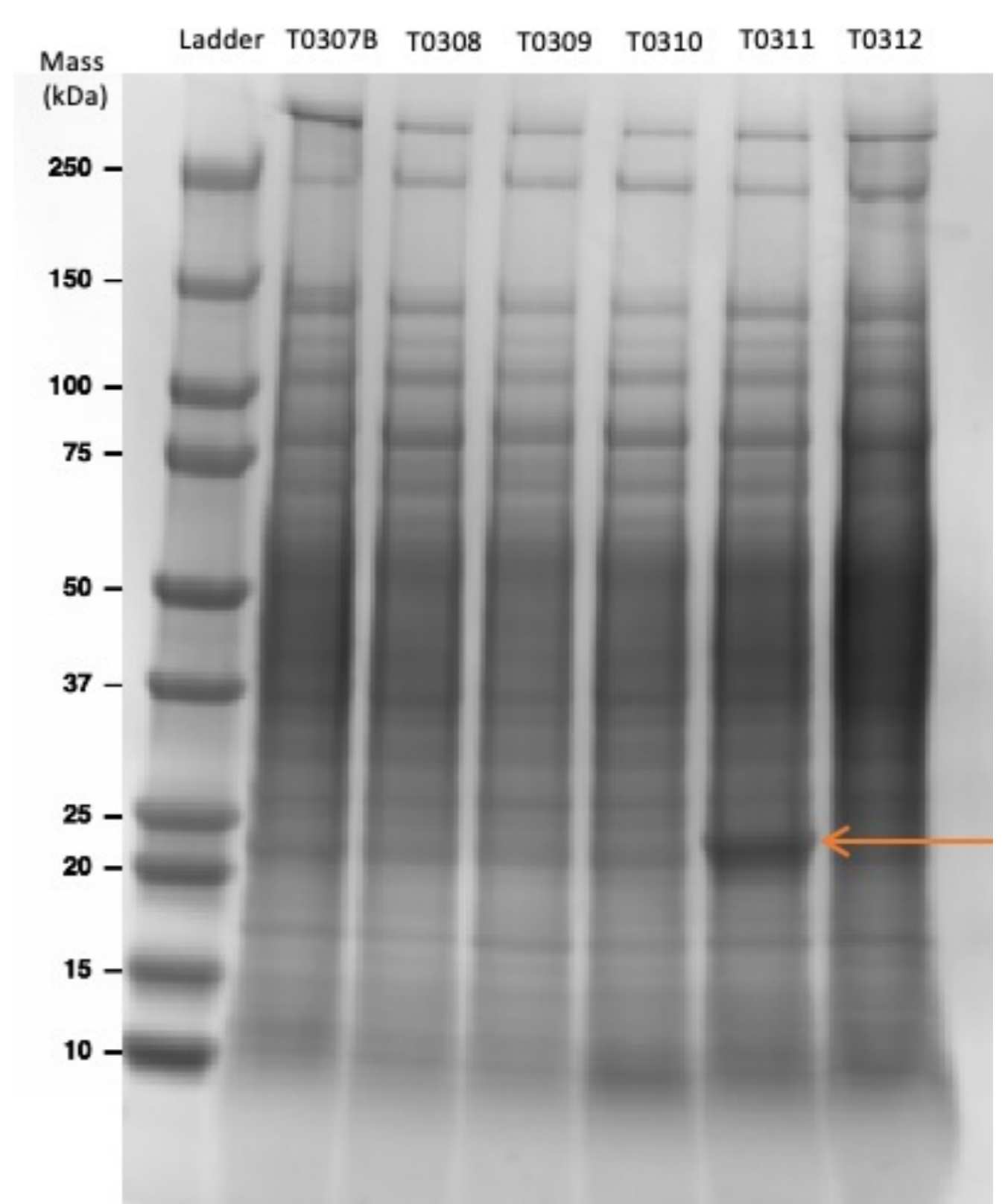


Fig. 2 SDS-PAGE of TCA concentrated spent media



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