



Identification and validation of small proteins in *Pseudomonas putida* KT--2440

Yang, Xiaochen; Ingemann Jensen, Sheila; Wulff, Tune; Harrison, Scott James; Long, Katherine S.

Published in:

Book of Abstracts. DTU's Sustain Conference 2015

Publication date:

2015

Document Version

Publisher's PDF, also known as Version of record

[Link back to DTU Orbit](#)

Citation (APA):

Yang, X., Ingemann Jensen, S., Wulff, T., Harrison, S. J., & Long, K. S. (2015). Identification and validation of small proteins in *Pseudomonas putida* KT--2440. In *Book of Abstracts. DTU's Sustain Conference 2015* [B-9] Technical University of Denmark.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Identification and validation of small proteins in *Pseudomonas putida* KT-2440

Xiaochen Yang, Sheila Ingemann Jensen, Tune Wulff, Scott James Harrison, Katherine S. Long*

DTU Biosustain

kalon@bio.dtu.dk

Small proteins (s-proteins) that contain 50 or fewer amino acids have been overlooked due to difficulties in their annotation and identification. Recent research indicates that s-proteins widely exist in bacteria and are involved in various biological processes. Our research focuses on identification and validation of s-proteins in the production organism *Pseudomonas putida*. By using proteomics, bioinformatics tools and the *Pseudomonas* genome database (PGD), we have identified 283 putative small open reading frames (sORFs) in the *P. putida* KT2440 genome. The transcription, conservation and genome contexts of sORFs were analyzed and 32 conserved sORFs with evidence of transcription selected for validation. The sORFs are validated by expressing them with a C-terminal SPA-tag (Sequential peptide affinity tag) followed by Western blotting⁽²⁾. The expression of 3 sORFs has been confirmed and testing of 20 additional sORF candidates is currently in progress. This will be followed by functional characterization of selected sORFs.