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Pab1-based synthetic proteins and yeast robustness

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When exploited as cell factory, Saccharomyces cerevisiae is exposed to different kinds of stress that impair the titer, yield and productivity of the fermentative processes. Therefore, the development of robust strains represents a pivotal challenge for the implementation of cost-effective bioprocesses.

We have previously identified the poly(A) binding protein Pabl as a promising target to improve stress tolerance. Pabl is a component of stress granules and a master regulator of mRNA metabolism. It is composed of four RNA Recognition Motifs (RRM), a flexible linker rich of proline (for this reason named P domain) and a carboxy-terminal domain (C domain); this modularity is responsible of the binding to mRNA poly(A) tails and of the simultaneous interaction with diverse proteins involved in mRNA biogenesis and decay.

Recently, the modularity of Pab1 has been exploited to create a library for the expression of synthetic variants in which the domains are randomly mixed, repeated or even deleted. Thirty-nine variants have been selected by screening for their ability to improve acetic acid tolerance in S. cerevisiae. Here, we show the preliminary studies on these synthetic proteins carried out to find a correlation between their functions/localization and yeast robustness.

