P. Model

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Dear Peter -

In earlier missives, I suggested looking at ts-auxotrophs to identify proteins that needed chaperonin for folding in an in vitro system. You might (but wouldn't!) object that this would be characterizing a mutant - not a "normal" enzyme.

Further delving revealed (to me) that E. Z. Ron (+ Bernie Davis) had already identified O-succinyl homoserine synthetase as a critically ts-enzyme: a met⁻ phenotype

The thermal inactivation is reversible - they already sensed that "conventional denaturation" might not be the way to describe it. It may well be a depolymerization - but let's see what else the literature says about this enzyme

If hyperexpressed GroE suppresses that met⁻ phenotype, there would be a good grounding for an in vitro expt. Obviously you could also select for met⁺ at 42°.

The Matthews-Neidhardt paper imparts a confusing perspective, however, that methionine biosynthesis imparts HSP formation. The homoserine synthase is still a reasonable target. (Perhaps its allomer IS an HSP!)

Also enclosed - report that "bacteremic" E. coli are often nic⁻ at 42°. (I am surprised they did not pick up met⁻ - except in 1 case; most of Ron + Davis' strains were ts met⁻.

Anyhow that's a predigested lead.

J