

Supplementary figure 1: Sequence alignment of TDs from different sources:

Escherichia coli K12 (ecTD), *Nicotiana attenuata* (naTD), *Arabidopsis thaliana* (atTD), *Pseudoalteromonas tunicata* D2 (ptTD), *Saccharomyces cerevisiae* (scTD), *Lactococcus lactis* (llTD), *Streptococcus thermophilus* (stTD), *Bacillus subtilis* (bsTD), *Corynebacterium diphtheriae* (cdTD). Sequences were aligned using the CLUSTALW program¹ with default parameters. Secondary structure elements of *ecTD* (PDB file 1TDJ) are indicated by arrows (β -strands), spirals (α - and η -helices) and T's (turns). Figure was prepared using ESPript² using the default representation style; completely conserved residues are shown highlighted in white on red background and conserved residues shown in red, Conserved residues or stretches of residues are outlined in blue. The two ACT-like regulatory subdomains in *ecTD* extend from secondary elements β 11 to β 14 and from β 15 to β 18, respectively, and are marked with blue bars under the alignment. The green triangles below the sequences indicate the positions mutated in this study. The red triangle indicates the position of the conserved lysine, which forms the internal aldimine with PLP.

¹. CLUSTAL W: Julie D. Thompson, Desmond G. Higgins and Toby J. Gibson, modified; any errors are due to the modifications.

². Gouet, P., Courcelle, E., Stuart, D. & Metoz, F. ESPript: analysis of multiple sequence alignments in PostScript. *Bioinformatics* **15**, 305-308 (1999).