

SUPPLEMENTARY FIGURE LEGENDS

Suppl. Figure 1. PDE activity of purified EAL domains: bis-*p*NPP hydrolysis.

Suppl. Figure 2. Sequence conservation in the EAL domain.

The sequence logo is based on an alignment of 3766 distinct sequences of EAL domains from sequenced bacterial genomes generated using the WebLogo program

(<http://weblogo.berkeley.edu>, Crooks C.E. et al., 2004 Genome Res. 14: 1188-1190).

The residue numbers of TBD1265 (Q3SJE6_THIDA) are shown below the logo. The height of each letter represents the degree of conservation of the corresponding amino acid residue in that position, whereas the total height of each column reflects statistical importance of the given position. The residues are colored as follows: acidic (D and E), red; positively charged (K, R, H), blue; small (G, S, C), green; polar uncharged (N, Q, T), purple; hydrophobic (A, F, L, M, I, P, V, W, Y), dark yellow.

