Supplementary Information

Figure S1. Sequence Alignment of CheA Homologues from 61 Genera. The alignment, created with Jalview (*1*) using the ClustalW (*2*) alignment program, shows the full sequence for each CheA homologue. A BLAST (3) search was carried out using the sequence of *Salmonella typhimurim* CheA as a probe. The resulting sequences were ordered based on their degree of homology to the probe sequence, and the 61 most homologous sequences from different genera were chosen. The resulting species list extends from *S. typhimurim* to *Halobacterium salinarum*, thereby including examples of species from both the bacterial and archaeal superkingdoms. The color scheme follows that of alignments in ClustalW: Hydrophobic residues (A, C, I, L, M, F, W, V) are colored blue, basic residues (R, K) are colored red, polar residues (N, Q, S, T) are colored green, acidic residues are colored (D, E) magenta, glycines (G) are colored orange, histidines and tryptophans (H, Y) are colored cyan, and prolines (P) are colored yellow. A bar graph representing the alignment conservation score at each position is shown directly below the alignment. The value at each position is shown directly below the bar. The color of the bar, ranging from yellow to brown, also represents high to low conservation, respectively.

1. Clamp, M., Cuff, J., Searle, S. M., and Barton, G. J. (2004) The Jalview Java alignment editor. *Bioinformatics 20*, 426-7.
2. Thompson, J. D., Higgins, D. G., and Gibson, T. J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res 22*, 4673-80.
3. Zhang, Z., Schwartz, S., Wagner, L., and Miller, W. (2000), A greedy algorithm for aligning DNA sequences, *J Comput Biol 7*, 203-14.