



Phylogenetic tree of the Clp1/Grc3 protein family.

The tree is based on an alignment of selected Clp1 and Grc3 protein family members. Distances were calculated with PROTDIST and the tree was generated with NEIGHBOR of the PHYLIP package (Felsenstein, J. 1993. PHYLIP (Phylogeny Inference Package) version 3.5c. Distributed by the author. Department of Genetics, University of Washington, Seattle), using default parameters. TreeView was used for the graphical representation (Page, 1996). The length of the branch is the number of nucleotide changes that are expected in that particular branch in the tree. Support for the three major branches is provided by bootstrap probabilities (1000 replicates). Organism abbreviations and protein accessions are the following: Bacteria/Archaea group: *Archaeoglobus fulgidus* (Af, NP_070873.1), *Candidatus Korarchaeum cryptofilum* (Ck, YP_001737707.1), *Geobacter uraniireducens* (Gu, YP_001232219.1), *Pyrobaculum aerophilum* (Pb, NP_558890.1, NP_559872.1), *Pyrococcus furiosus* (Pf, NP_577841.1), *Rhodothermus marinus* (Rm, YP_003291740.1); Clp1/Grc3 group: *Aspergillus nidulans* (An, CBF90066.1/ XP_662203.1), *Caenorhabditis elegans* (Ce, NP_001040858.1/NP_502588.1), *Coccidioides immitis* (Ci, XP_001239523.1/ XP_001248112.1), *Cryptosporidium parvum* (Cp, XP_626224.1/ XP_627494.1), *Dictyostelium discoideum* (Dd, XP_638095.1/ XP_642025.1), *Drosophila melanogaster* (Dm, NP_610876.1/ NP_611084.2), *Homo sapiens* (Hs, NP_006822.1/ Q5SY16.1), *Laccaria bicolor* (Lb, XP_001874797.1/ XP_001878778.1), *Ostreococcus lucimarinus* (Ol, XP_001416530.1/XP_001415935.1), *Saccharomyces cerevisiae* (Sc, NP_014893.1/NP_013065.1), *Schizosaccharomyces pombe* (Sp, NP_593741.1/NP_588473.1), *Sorghum bicolor* (Sb, XP_002451771.1/ XP_002457221.1), *Trichoplax adhaerens* (Ta, XP_002110634.1/ XP_002111887.1), *Ustilago maydis* (Um, XP_759217.1/ XP_761015.1).