

## Short Abstract Template

### **Development of an Integrated Database of Completely Sequenced Plastids and Cyanobacteria Genomes**

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Plastids descended from a cyanobacterium that adopted an intracellular, endosymbiotic lifestyle within early eukaryotes. Comparisons of their genomes provide new challenges to various biological questions. We have been developing a gene order database of plastid genomes, and now cyanobacterial genomes have been included. A normalizing gene-labeling system across the genomes were developed so that broad comparisons are made available without having to go back to sequence analysis. Many incorrect coordinates of tRNA-encoding regions found in the major databases were corrected. We distinctively labeled tRNA genes using the anticodon sequence. The integrated database will allow researchers to compile target data for comparative analysis of plastid/cyanobacteria genes and genomes.