Prebiotic Chemical Kinetics Imprint on Positional Codon Usage

Ricardo Ferreira,*,a Kevin Lai^b and Roberto D. Lins^a

*^{a}Departamento de Química Fundamental, Universidade Federal de Pernambuco,
50740 Recife-PE, Brazil*

*^{b}Computational Biology and Bioinformatics, Pacific Northwest National Laboratory,
Richland, WA 99352, USA*

From the Refseq v22, all complete exon sequences of *Archaea* (28,206) and *Eukarya* (775,406) equal or longer than 75 codons were screened. A randomly chosen subset of the available Eubacterial genome (256,502 containing 75 equal or longer codon sequences) was used. This subset is comprised by all complete and non-redundant sequences of the following species: *Actinobacillus spp., Anabaena spp., Arthrobacter spp., Bacillus spp., Bacteroides spp., Bdellovibrio spp., Bifidobacterium spp., Borrelia spp., Brevibacillus spp., Burkholderia spp., Campylobacter spp., Chlamydia spp., Chlamydophila spp., Clostridium spp., Corynebacterium spp., Deinococcus spp., Desulfitobacterium spp., Desulfovibrio spp., Enterococcus spp., Erwinia spp., Flavobacterium spp., Fusobacterium spp., Geobacillus spp., Geobacter spp., Gordonia spp., Haemophilus spp., Helicobacter spp., Lactobacillus spp., Lactococcus spp., Legionella spp., Leptospira spp., Listeria spp., Mesoplasma spp., Micromonospora spp., Moraxella spp., Mycobacterium spp., Mycoplasma spp., Neisseria spp., Nitrosomonas spp., Nocardia spp., Paracoccus spp., Pasteurella spp., Porphyromonas spp., Prevotella spp., Pseudoalteromonas spp., Pseudomonas spp., Pyrobaculum spp., Rhizobium spp., Rhodobacter spp., Rhodococcus spp., Ruminococcus spp., Selenomonas spp., Shewanella spp., Sphingomonas spp., Spiroplasma spp., Staphylococcus spp., Streptococcus spp., Streptomyces spp., Thermoanaerobacter spp., Treponema spp., Vibrio spp., Weissella spp.*

*e-mail: rferreira100@yahoo.com