Eukaryogenesis, a major transition in evolution of life, originated from the symbiogenic fusion of an archaea with a metabolically versatile bacterium. By general consensus, the latter organism belonged to a proteobacteria, subsequently evolving into the mitochondrial organelle of our cells. The consensus is based upon genetic and metabolic similarities between mitochondria and aerobic α proteobacteria but fails to explain the origin of several enzymes found in the mitochondria-derived organelles of anaerobic eukaryotes such as *Trichomonas* and *Entamoeba*. These enzymes are thought to derive from bacterial lineages other than a proteobacteria, e.g., *Clostridium* - an obligate anaerobe. [FeFe]-hydrogenase constitutes the characteristic enzyme of this anaerobic metabolism and is present in different types also in *Entamoeba* and other anaerobic eukaryotes. Here we show that a proteobacteria derived from metagenomic studies possess both the cytosolic and organelar type of [FeFe]-hydrogenase, as well as all the proteins required for hydrogenase maturation. These organisms are related to cultivated members of the Rhodospirillales order previously suggested to be close relatives of mitochondrial ancestors. For the first time, our evidence supports an α proteobacterial ancestry for both the anaerobic and the aerobic metabolism of eukaryotes. Reviewers: This article was reviewed by William Martin and Nick Lane, both suggested by the Authors.