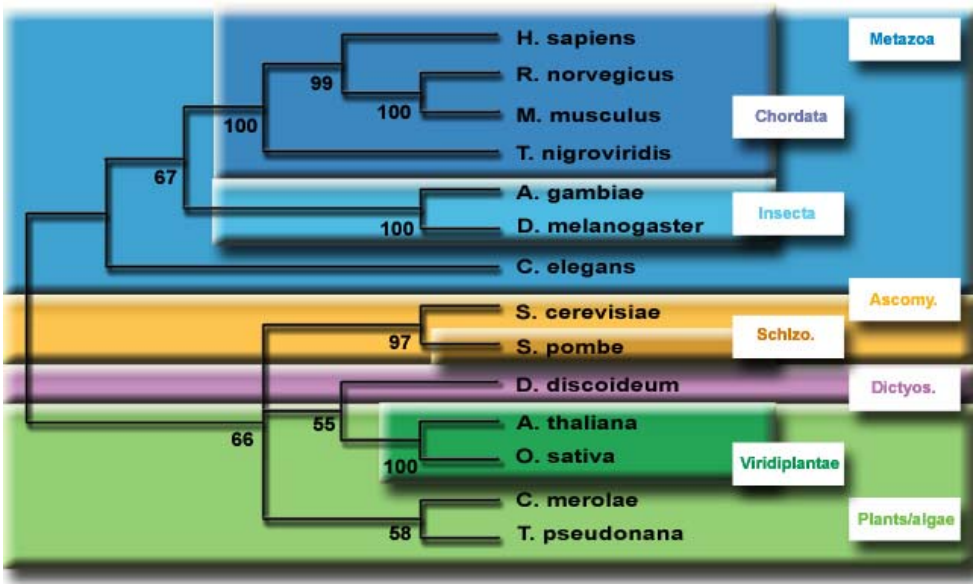
Supplementary Figure 1



Supplementary Figure 1. Peroxisomal phylogenetic Supertree. The set of 25 proteins used to generate is depicted in Figure 1. Numbers correspond to bootstrap values over 50%, reached after 500 replications. The tree is divided into two main branches: (1) metazoan and (2) Fungi, Protozoa and Plants/algae. Ascomy: Ascomycota, Dictyos: Dictyostellida and Schizo: Schizosaccharomycetes.

Supplementary Table I

Protein	Domain	Function	Compartiment	% region of similarity in Bacteria/Archaea
Pex1	AAA	Protein import	Cytosol and docking sites with the peroxisomal membrane	29%
Pex6	AAA	Protein import	Cytosol and docking sites with the peroxisomal membrane	32%
Pex5	TPR	Target signal receptor	Cytosol and docking sites with the peroxisomal membrane	18%
Pex5R	TPR	Target signal receptor?	Cytosol and docking sites with the peroxisomal membrane	18%
Pex7	WD repeats	Target signal receptor	Cytosol and docking sites with the peroxisomal membrane	43%
Pex14	PXXP	Docking of receptors	Peroxisomal membrane	16%

Supplementary Table I: List of the 6 peroxins showing restricted motifs of homology in Bacteria/Archea genomes. Only 6 Pex out of the established 35 peroxins exhibit bacterial homology after 5 iterations by PSI-BLAST analysis (E value cutoff of 10^{-3}). Among them, the 2 receptors that recognize both PTSs (Peroxisomal Target Signals), and the 2 Pexs that enharbour the AAA domain (ATPases associated with various cellular activities). The % region of similarity corresponds to the length of the region of homology between the closest Bacterial/Archeal homolog of the given peroxisomal protein and the latter, calculated in % to the total length of the given protein.