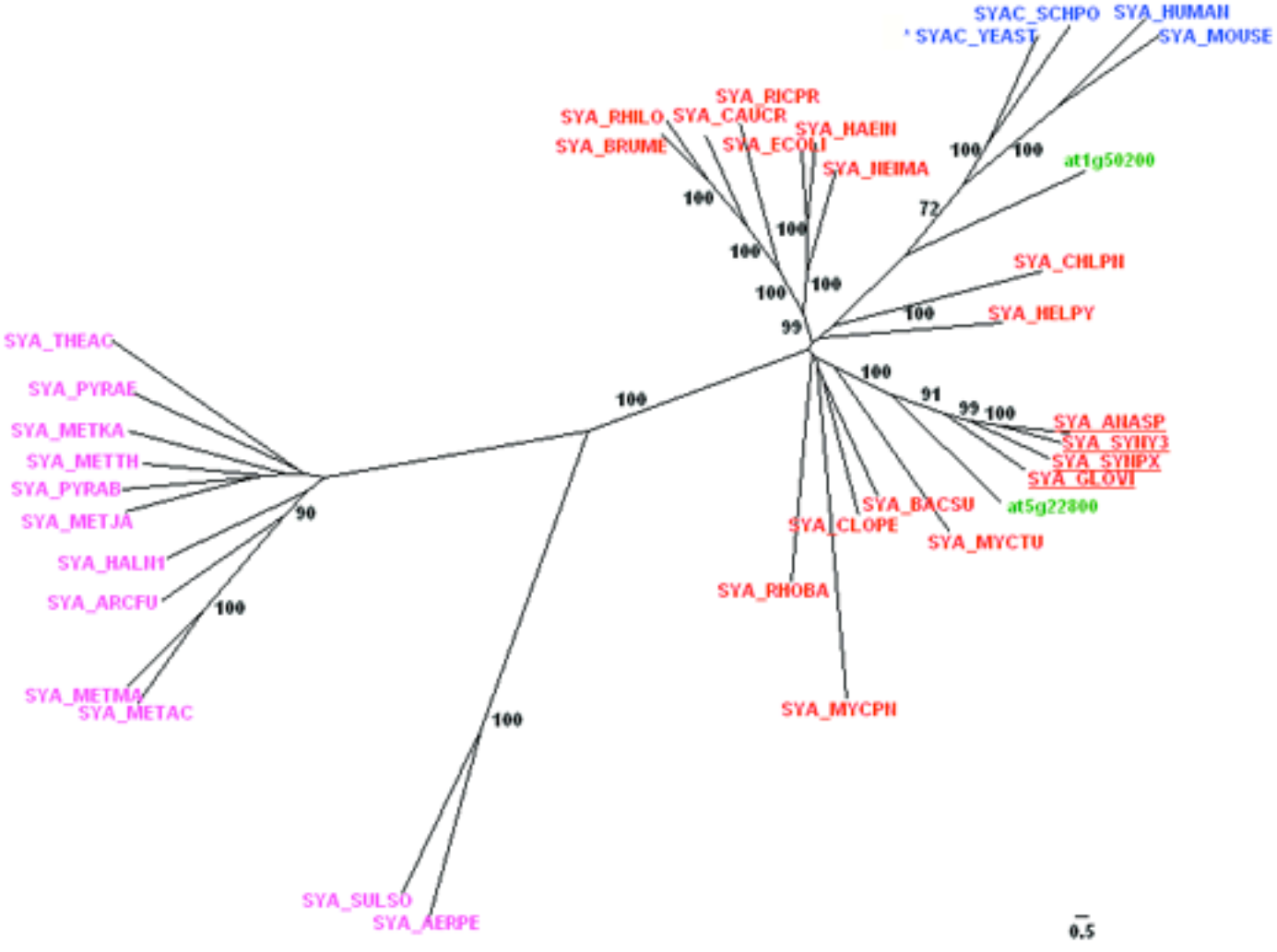
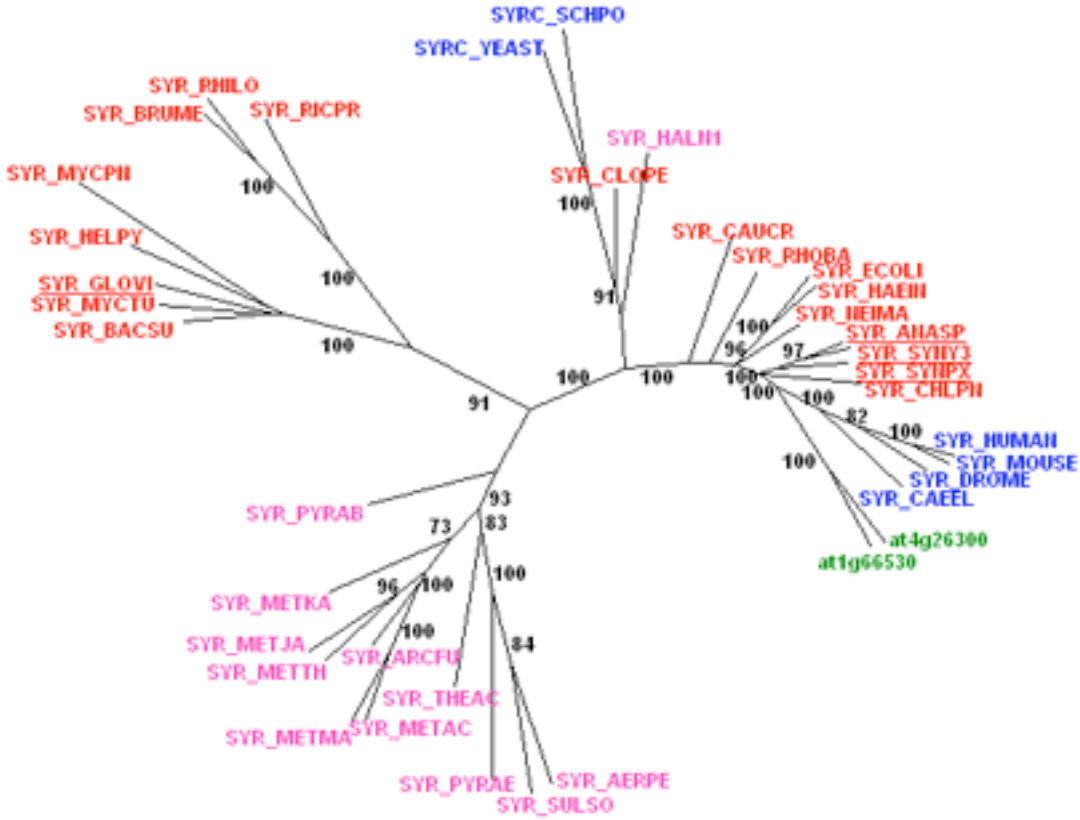
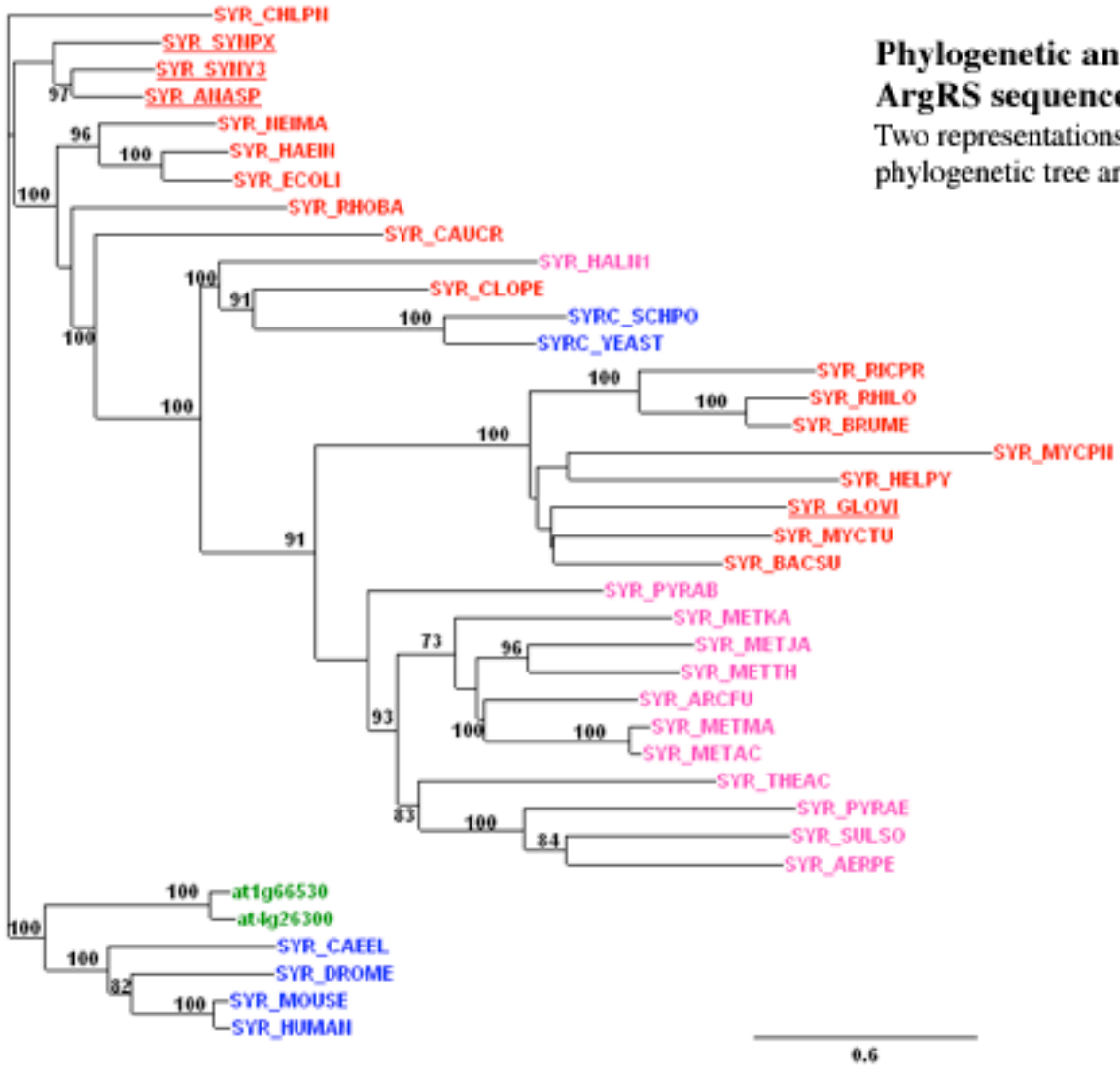
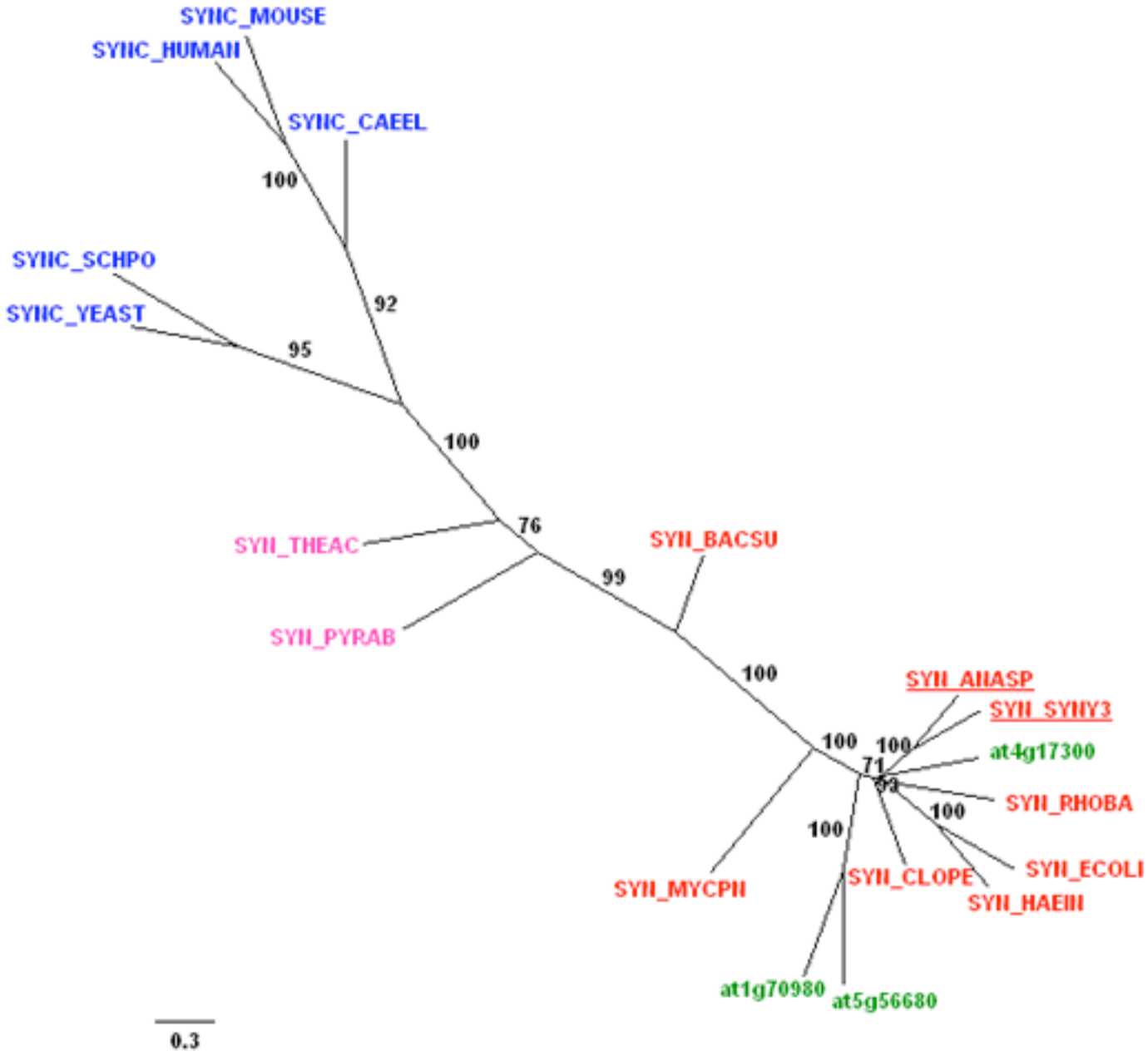

SYAC_SCHPO
SYA_HUMAN
SYAC_YEAST
SYA_MOUSE
SYA_RICPR
SYA_RHILO
SYA_CAUCR
SYA_HAEIN
SYA_BRUME
SYA_ECOLI
SYA_NEIMA
at1g50200
SYA_CHLPN
SYA_HELPY
SYA_THEAC
SYA_PYRAE
SYA_METKA
SYA_METTH
SYA_PYRAB
SYA_METJA
SYA_HALN1
SYA_ARCFU
SYA_METMA
SYA_METAC
SYA_ANASP
SYA_SYNY3
SYA_SYNPX
SYA_GLOVI
SYA_BACSU
at5g22800
SYA_CLOPE
SYA_MYCTU
SYA_RHOBA
SYA_MYCPN
SYA_SULSO
SYA_AERPE
100
100
72
100
100
100
100
100
100
99
100
100
91
99
100
100
90
100
100
0.5



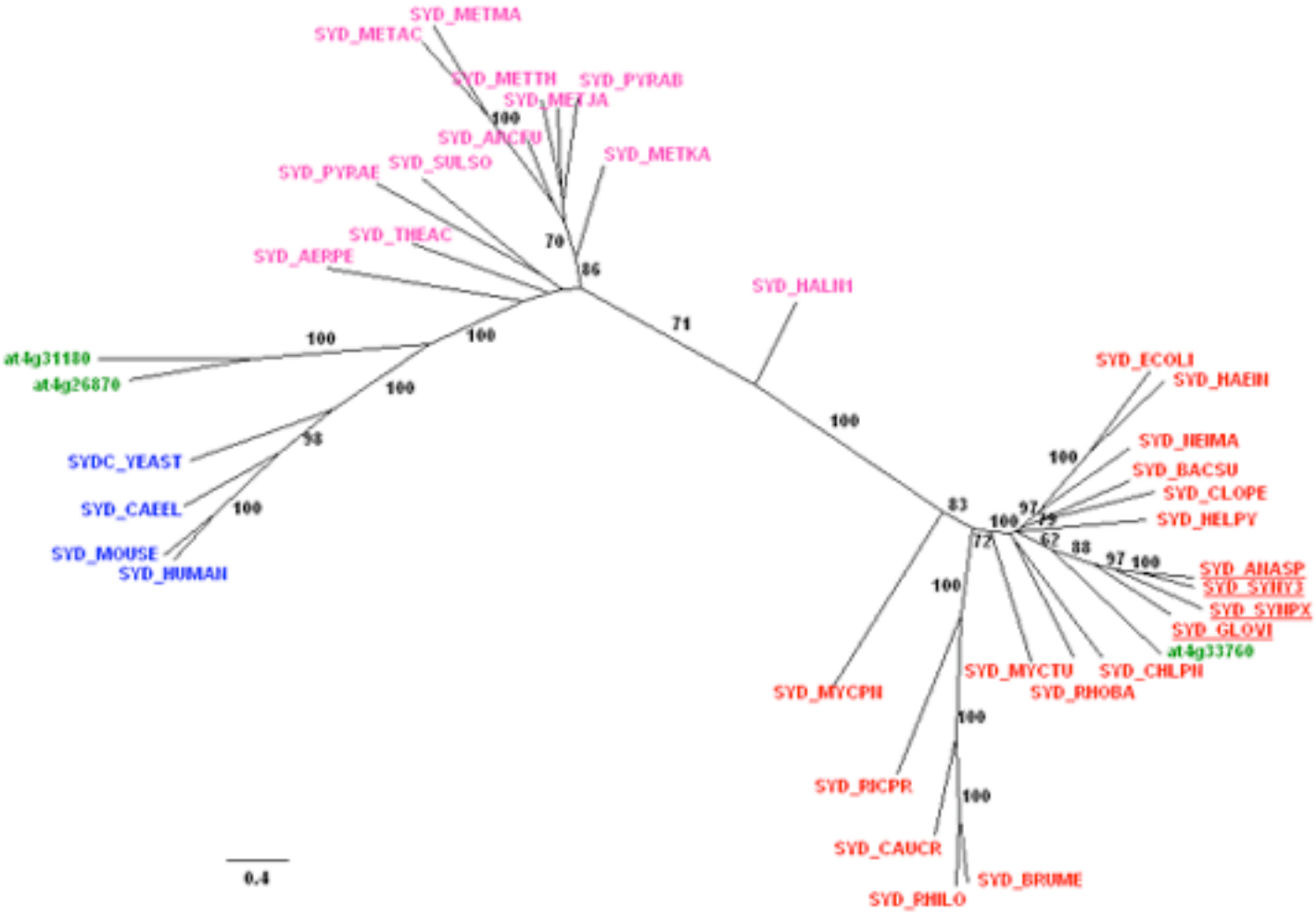


Phylogenetic analysis of ArgRS sequences

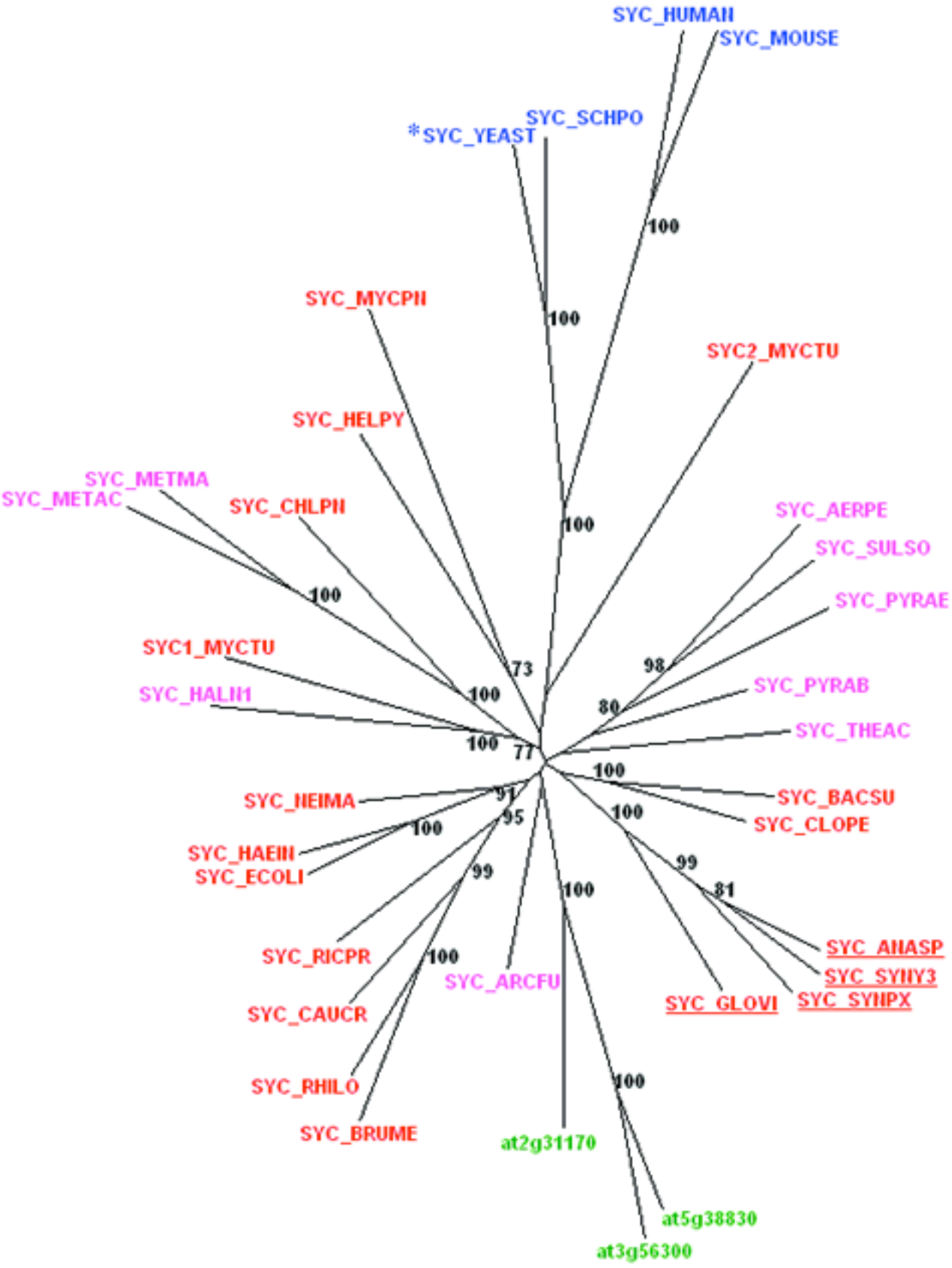
Two representations of the phylogenetic tree are given



Phylogenetic analysis of AsnRS sequences

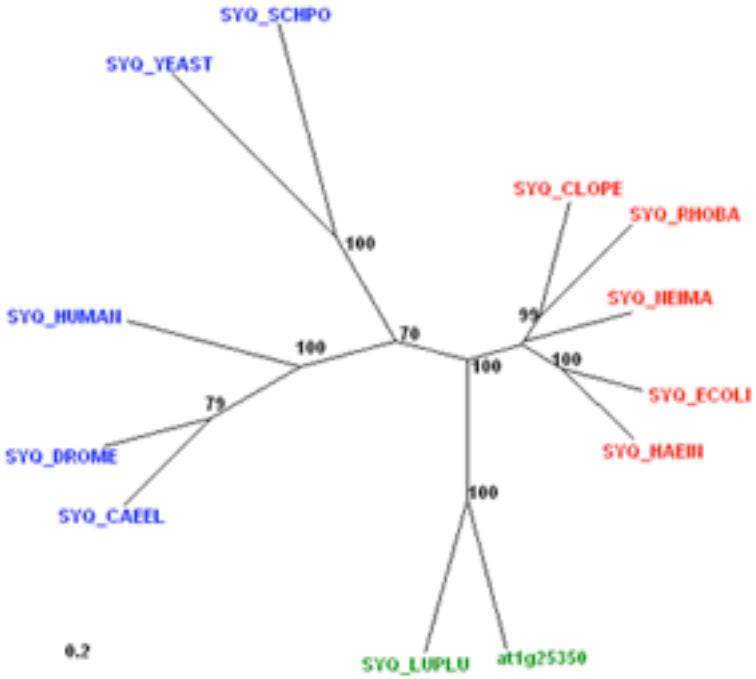


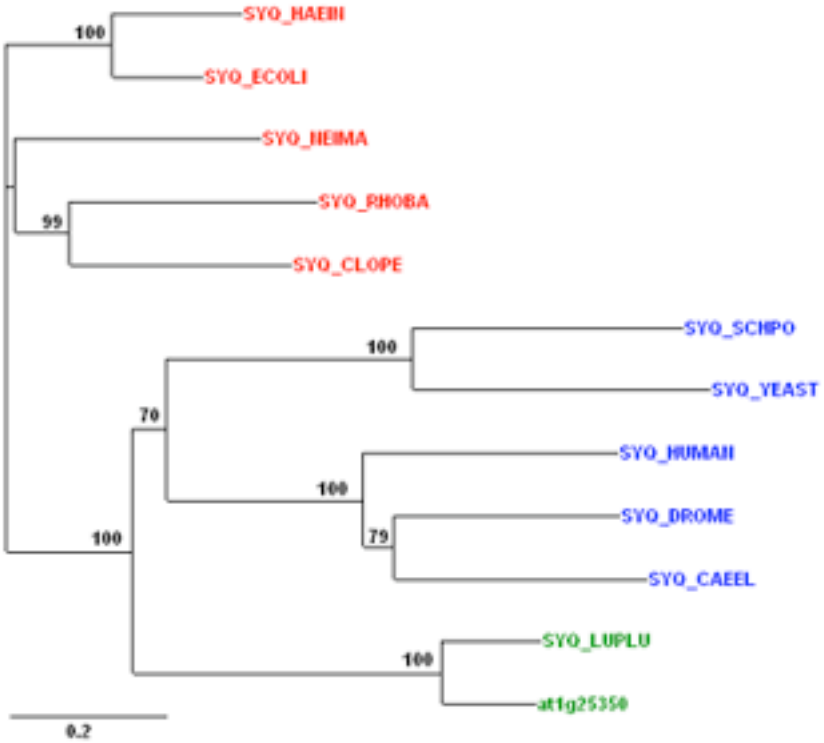
Phylogenetic analysis of AspRS sequences



Phylogenetic analysis of CysRS sequences

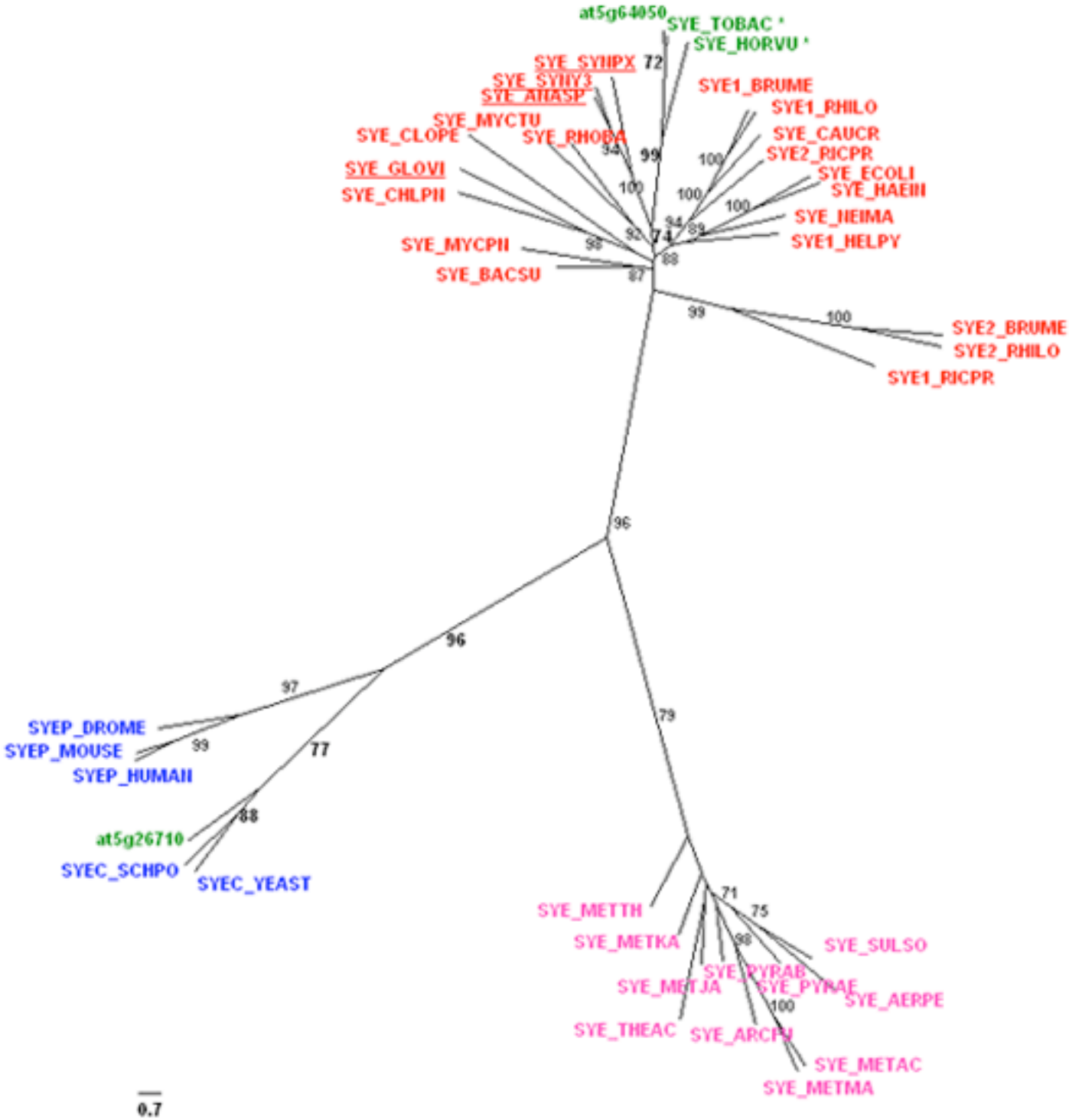
* predicted to be also mitochondrial (http://mips.gsf.de)





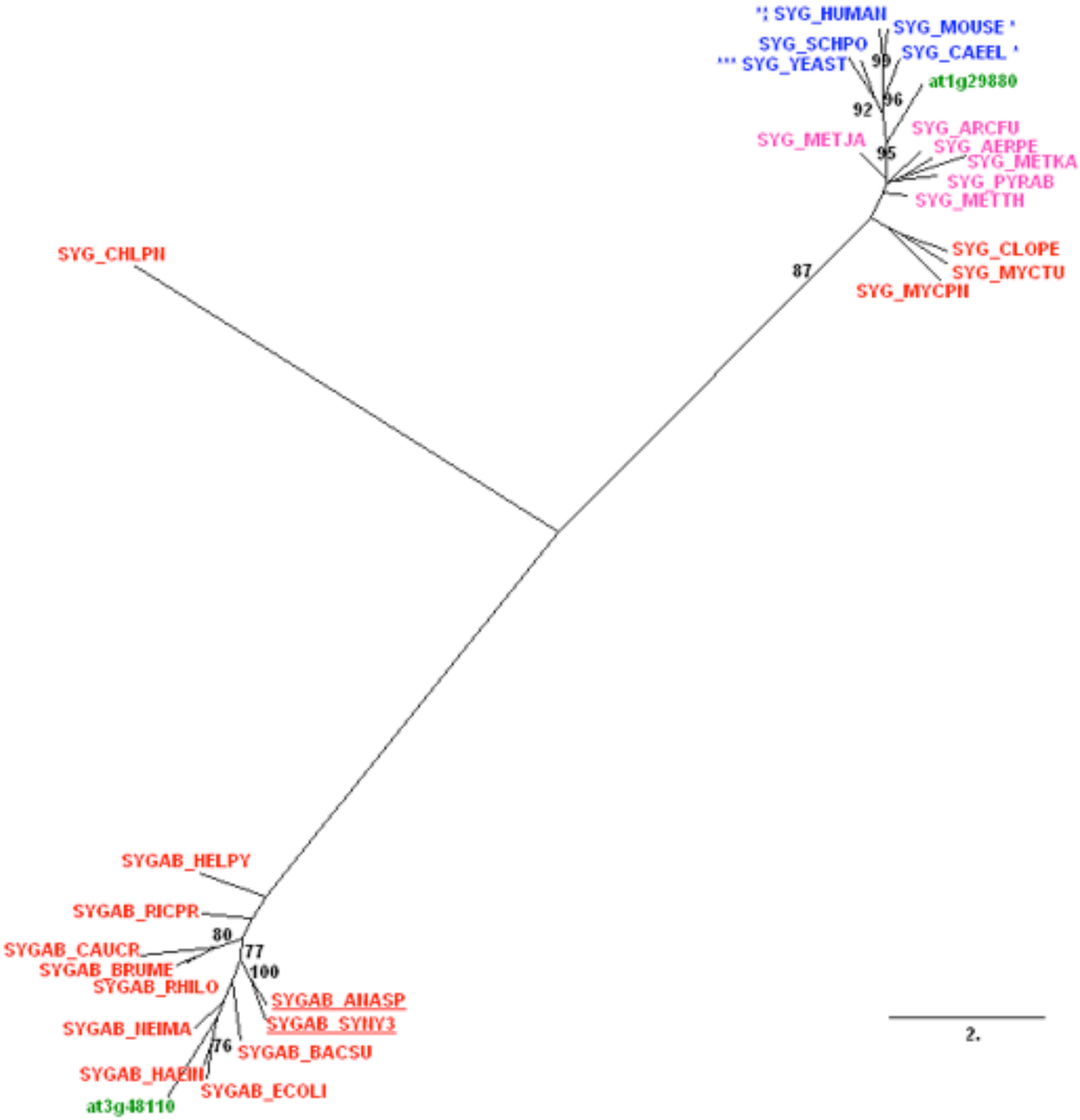
Phylogenetic analysis of GlnRS sequences

Two representations of the phylogenetic tree are given



Phylogenetic analysis of GluRS sequences

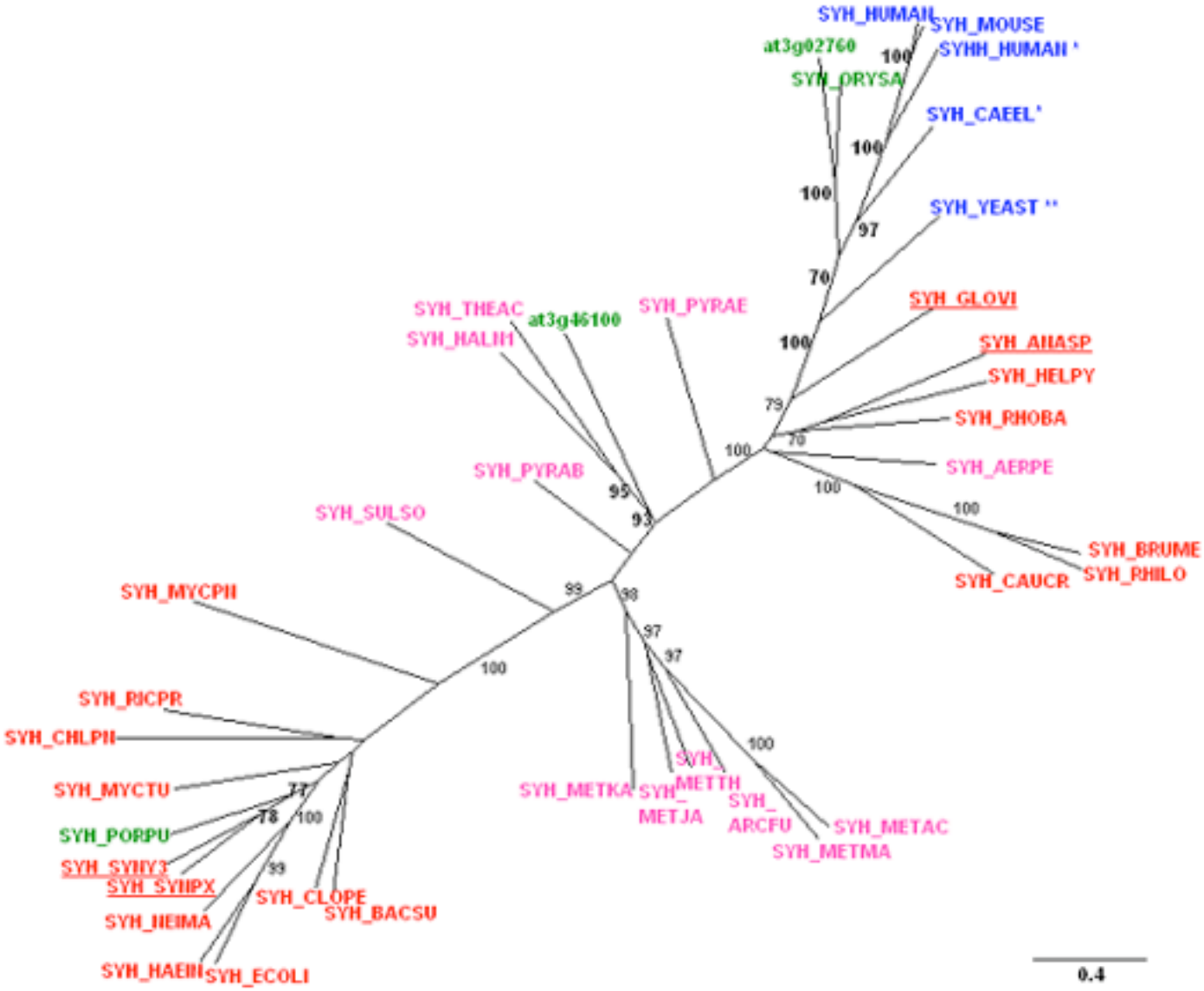
* possibly mitochondrial and/or plastid
(http://genoplante-info.infobiogen.fr/predotar/predotar.html)



Phylogenetic analysis of GlyRS sequences

In the case of eubacterial enzymes, the alpha and beta subunits were fused to make the alignments and phylogenetic analysis.

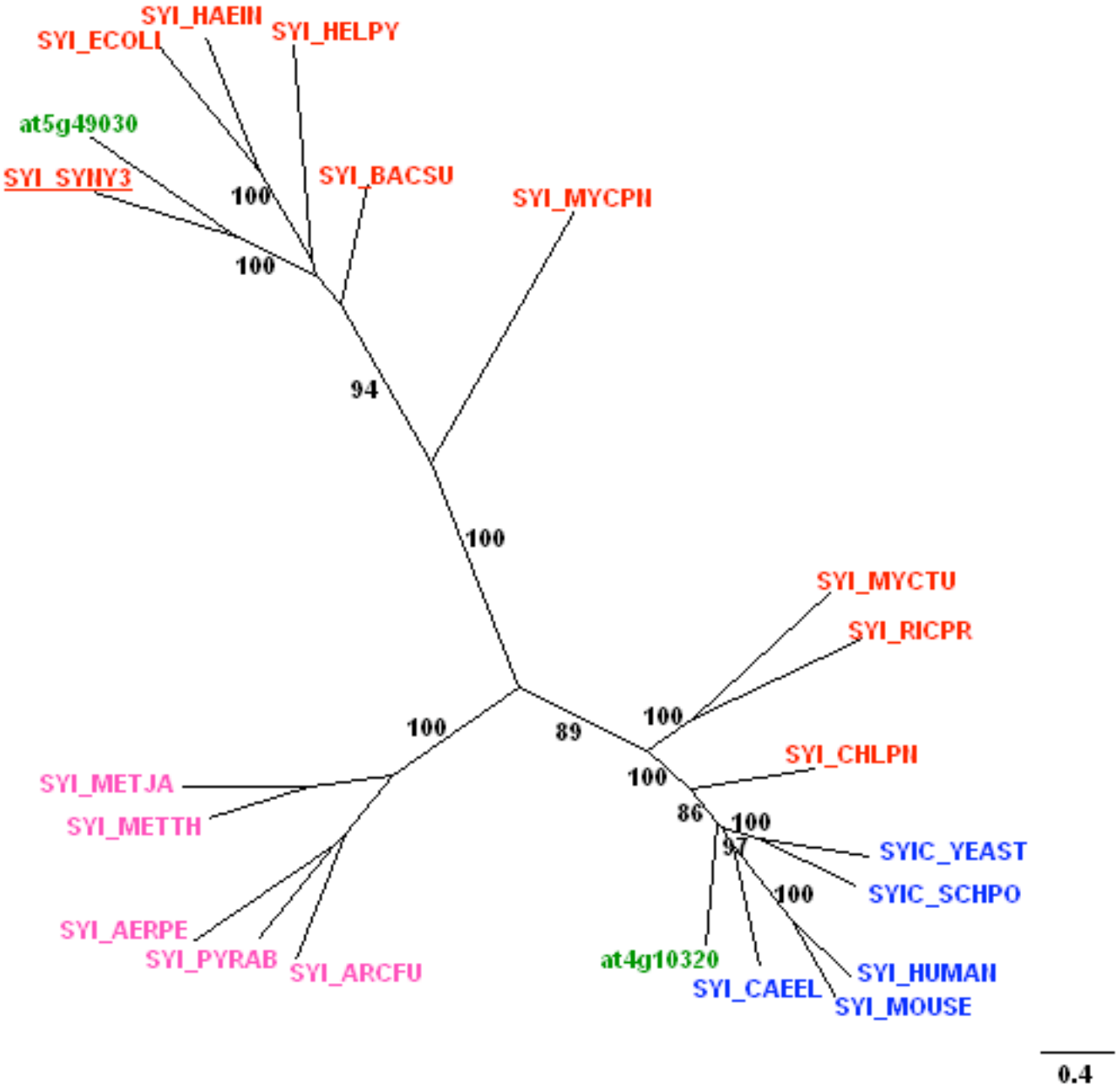
* possibly mitochondrial (Predotar, TargetP)
** the cytosolic and mitochondrial enzymes are encoded by the same gene (Shiba et al. J. Biol. Chem (1994) 269: 30049-30055)
*** predicted to be also mitochondrial (http://mips.gsf.de)



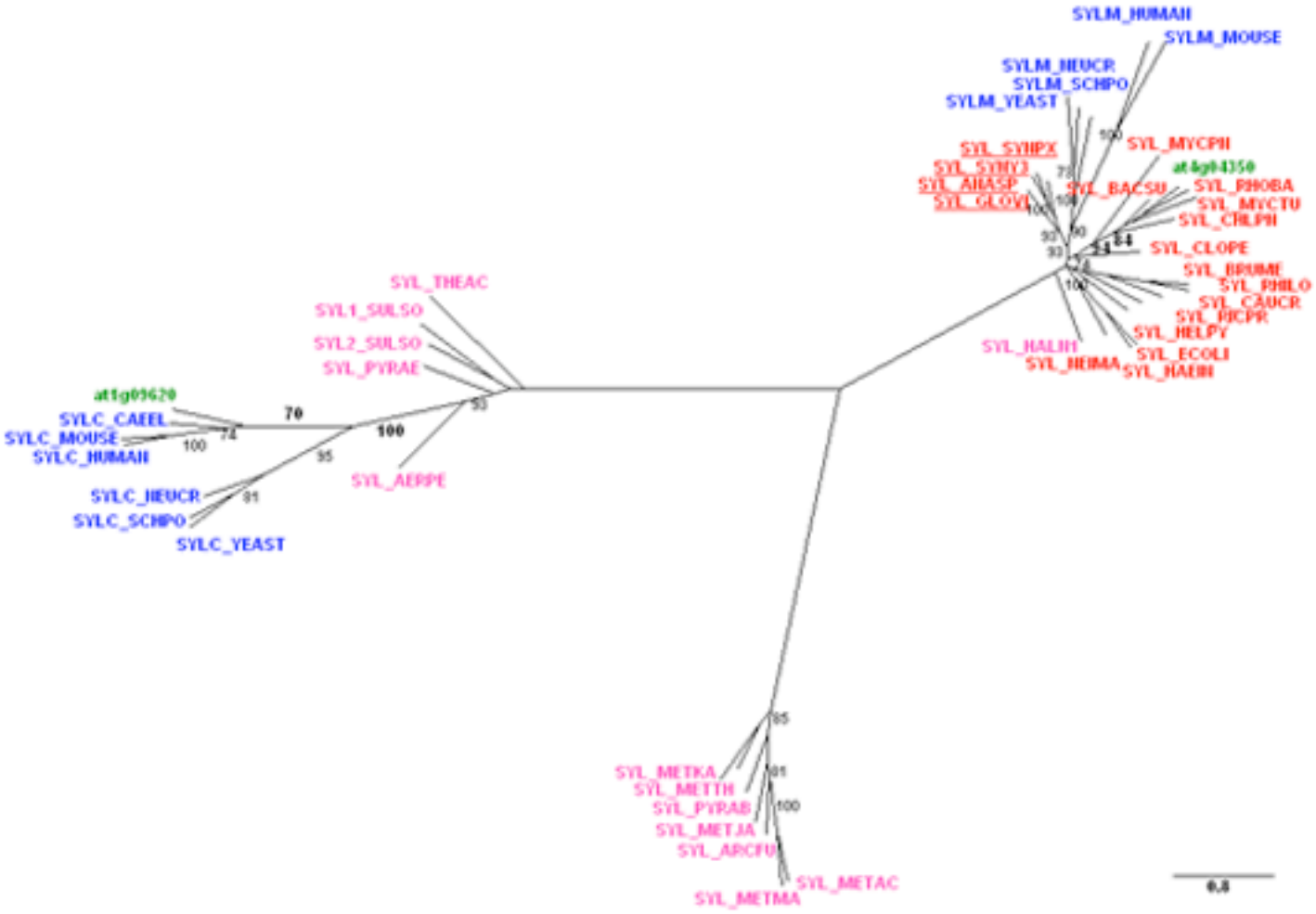
Phylogenetic analysis of HisRS sequences

* possibly mitochondrial (Predotar, TargetP)

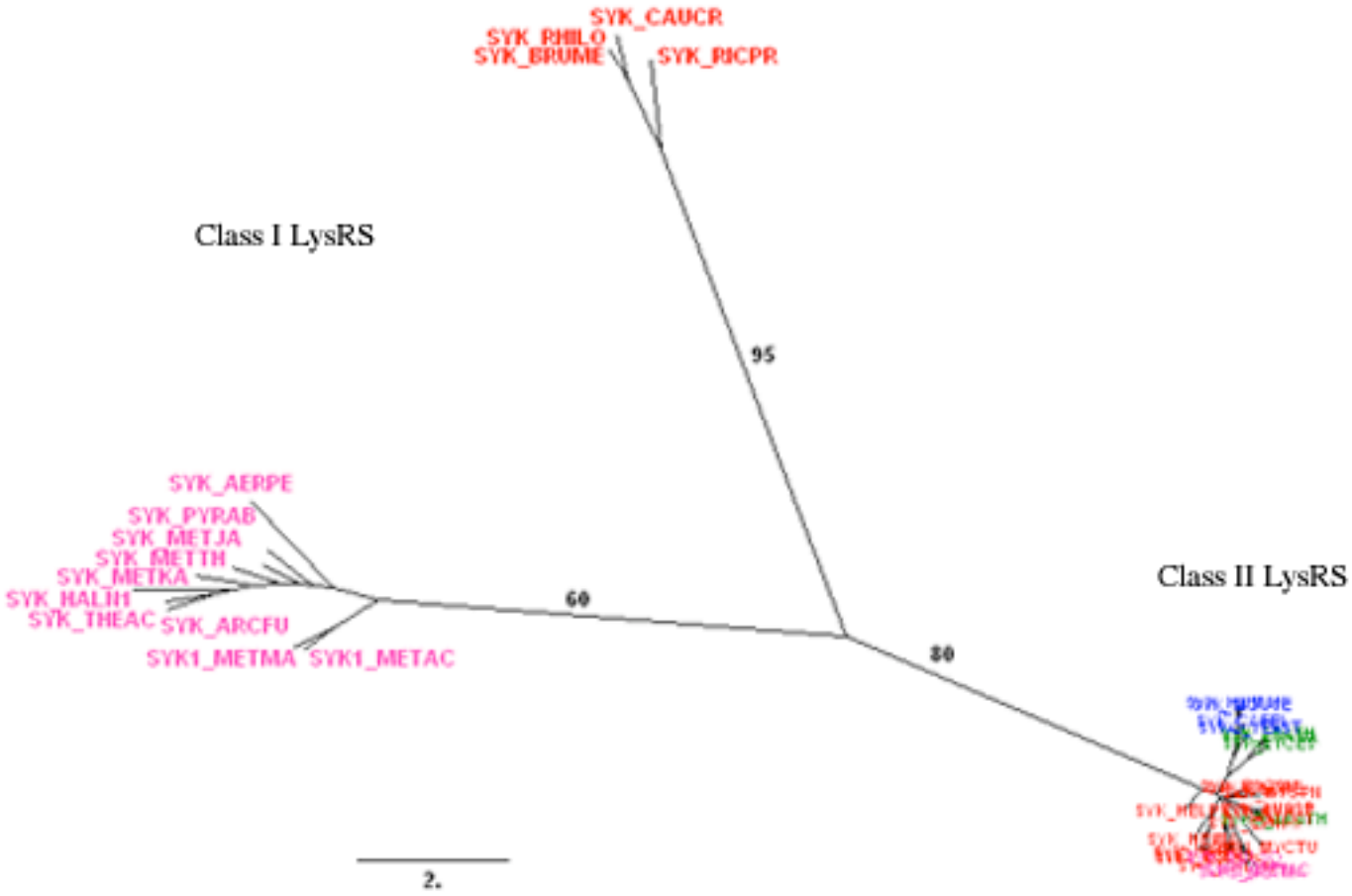
** the cytosolic and mitochondrial enzymes are encoded by the same gene (Natsoulis et al. Cell (1986) 46: 235-243)



Phylogenetic analysis of IleRS sequences

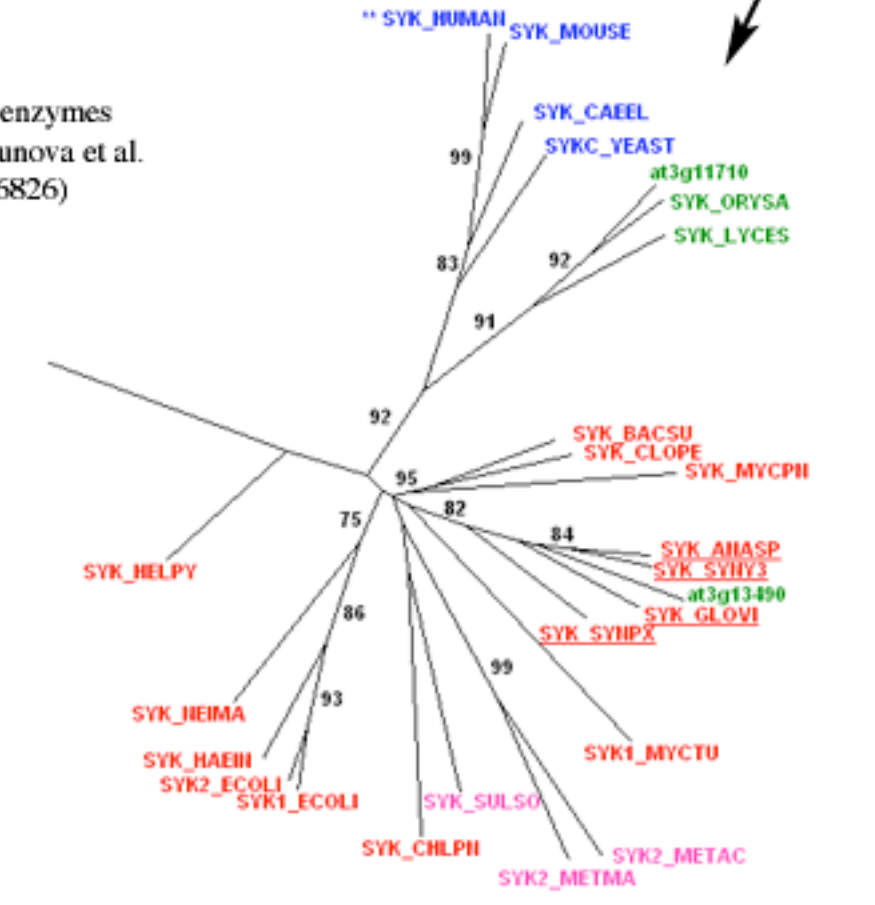


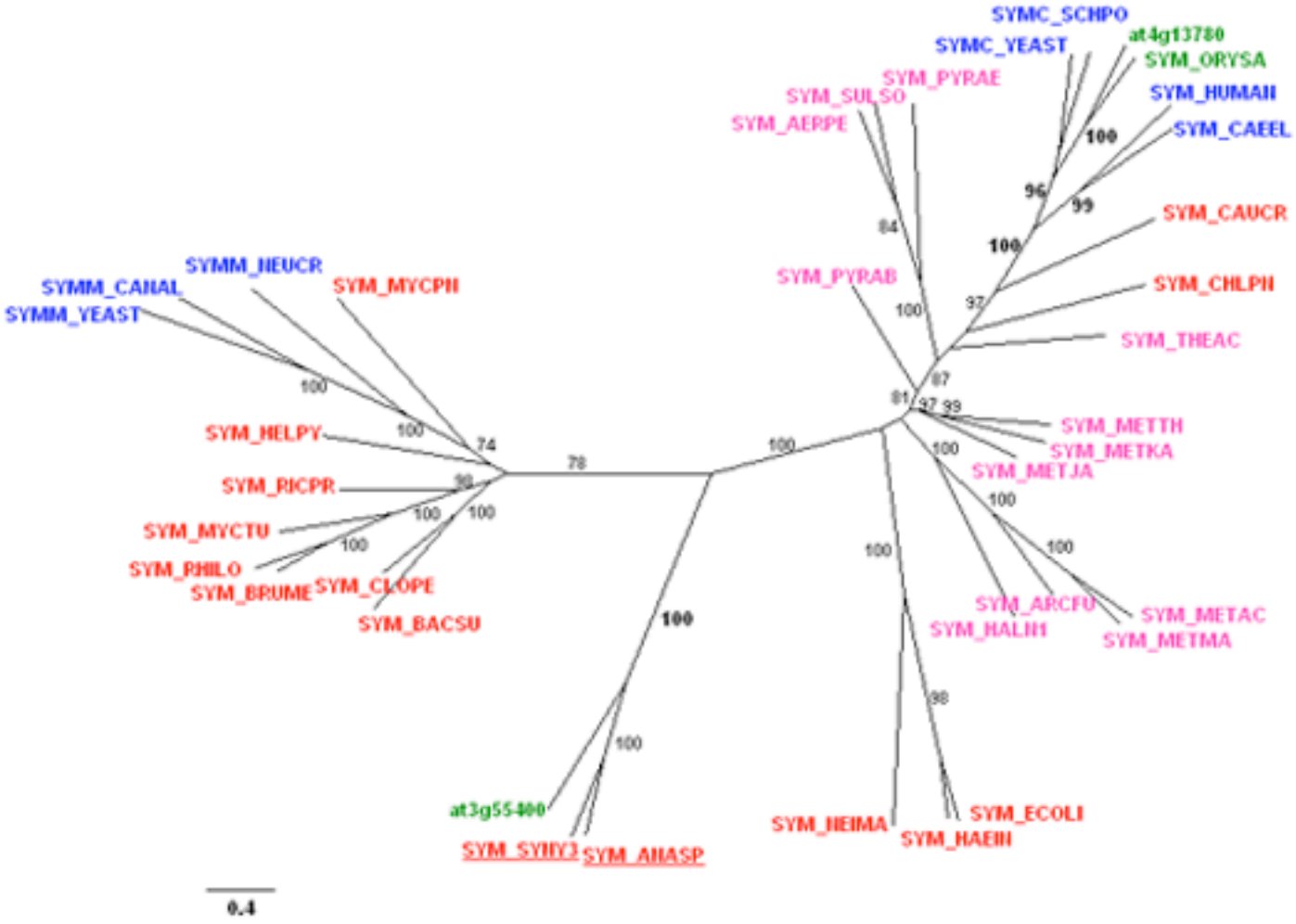
Phylogenetic analysis of LeuRS sequences



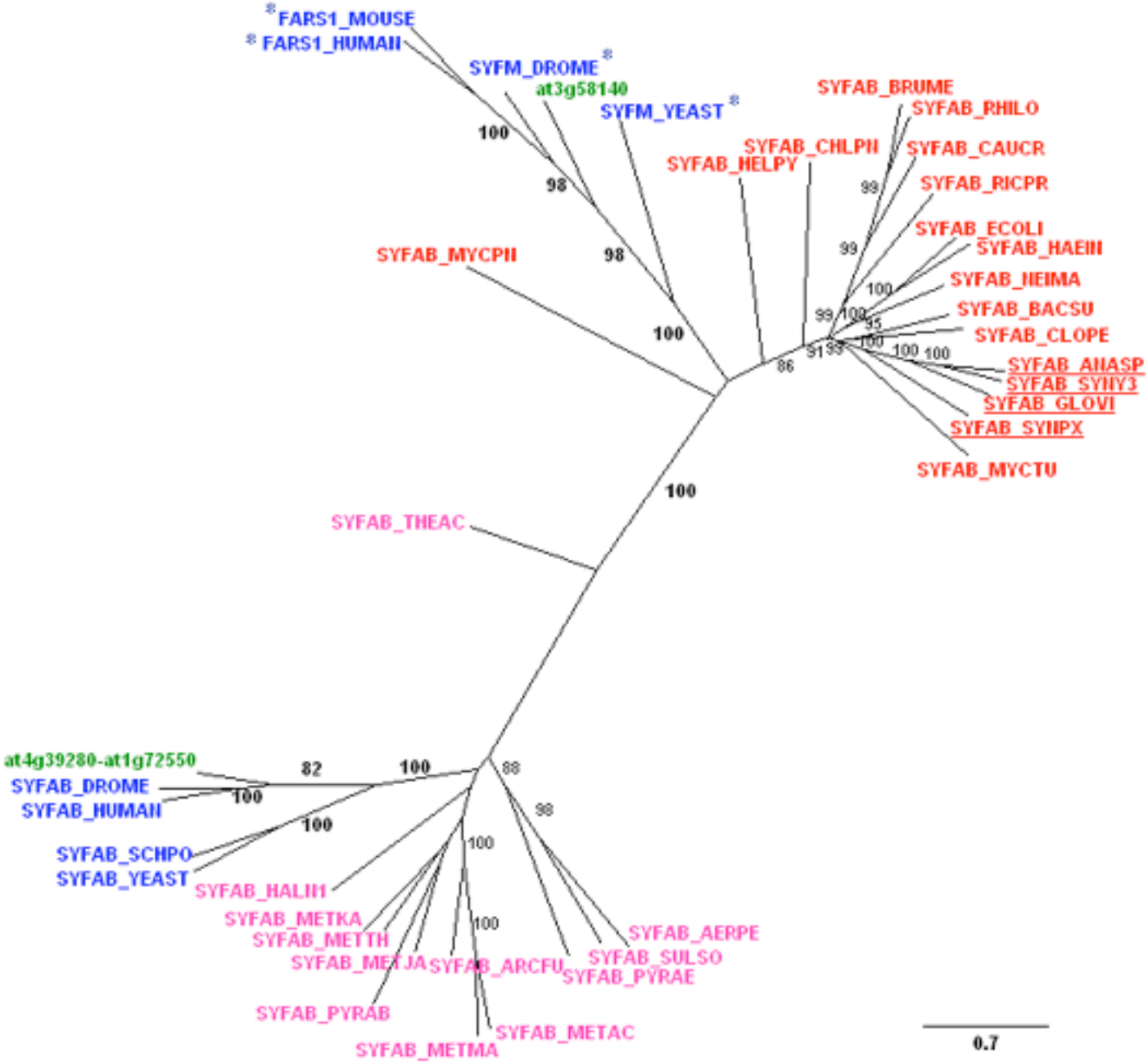
Phylogenetic analysis of LysRS sequences

** The cytosolic and mitochondrial enzymes are encoded by the same gene (Tolkunova et al. J. Biol. Chem. (2000) 275: 16820-16826)





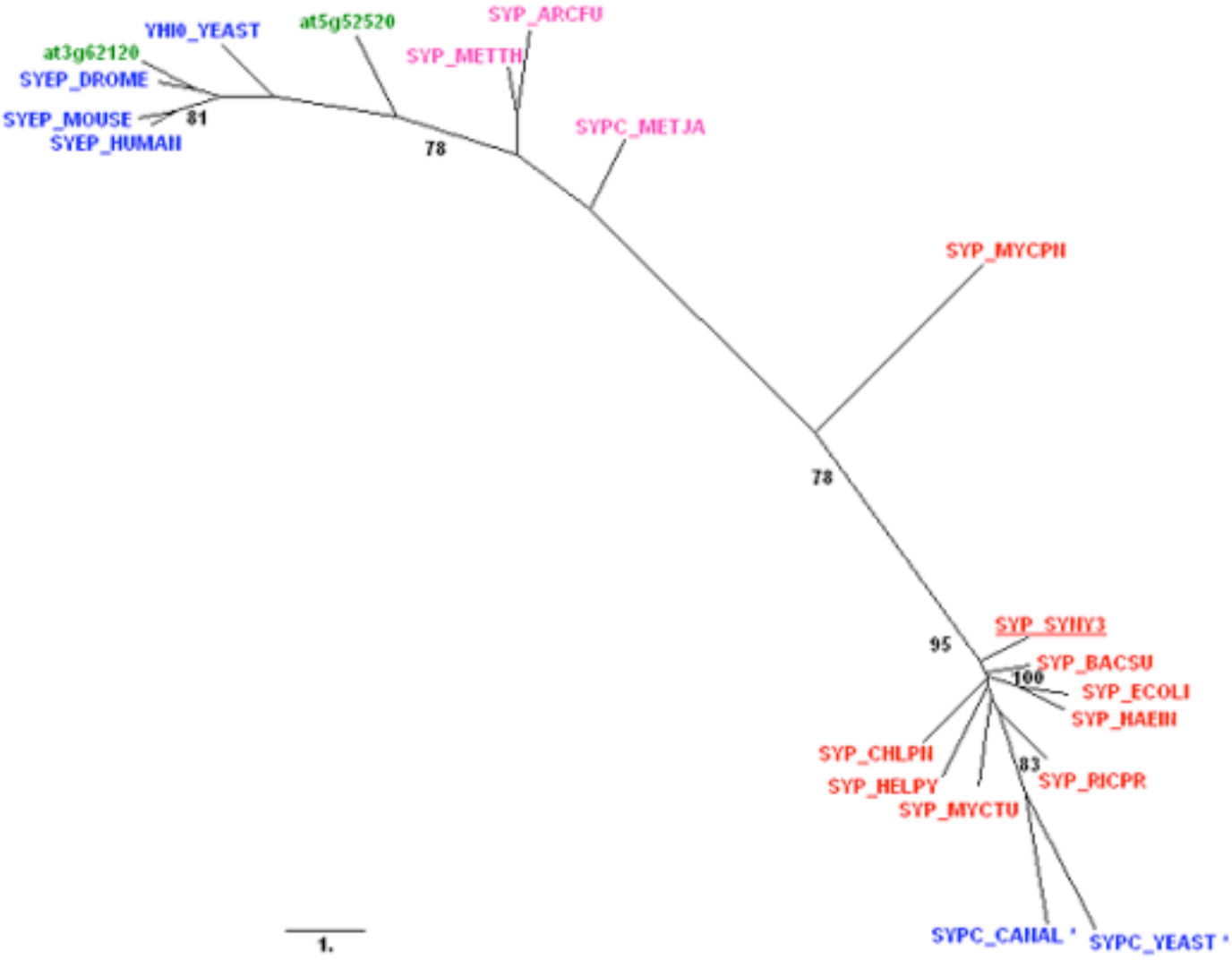
Phylogenetic analysis of MetRS sequences



Phylogenetic analysis of PheRS sequences

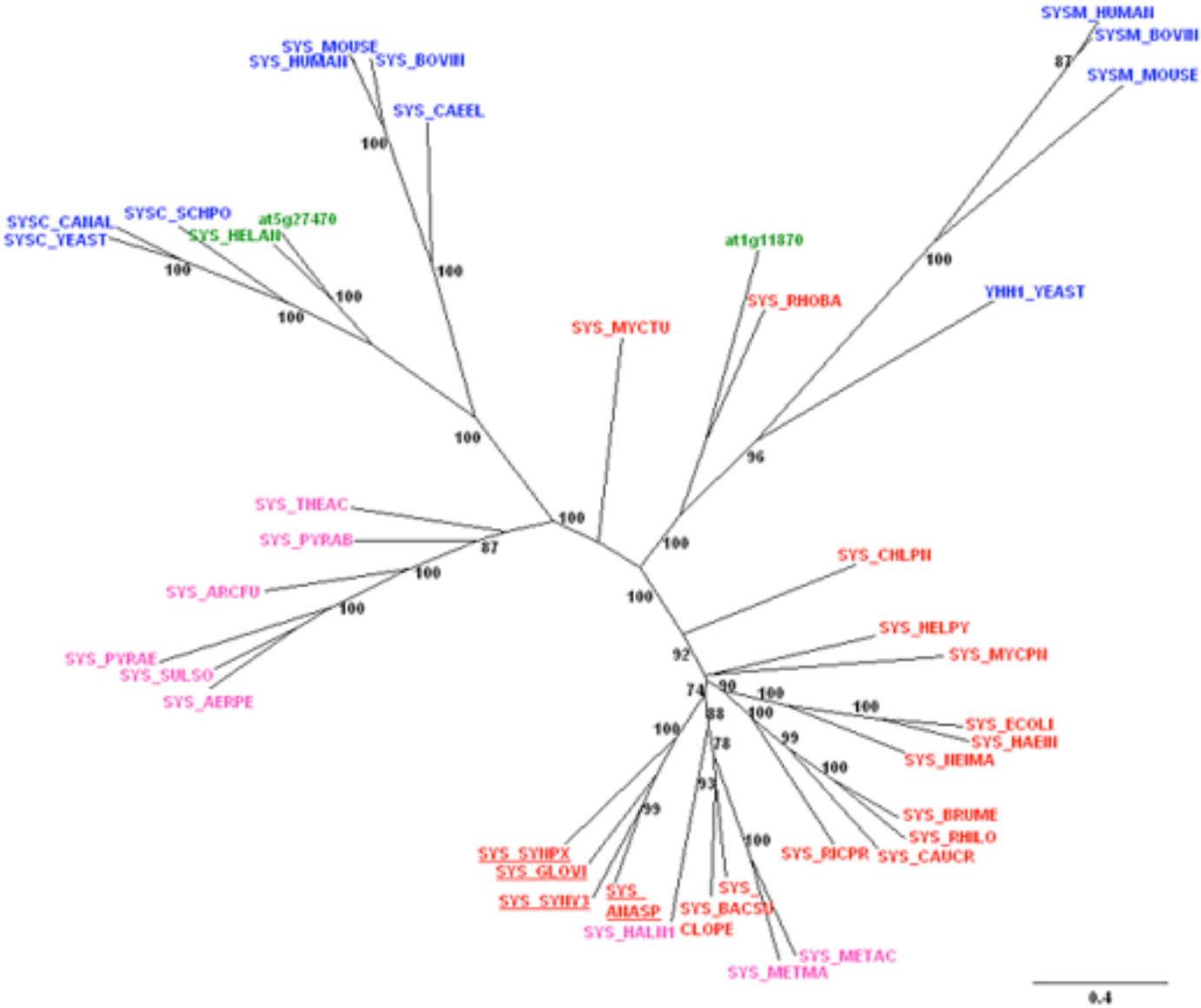
The alpha and beta chains were fused to make the alignments

* predicted to be mitochondrial (http://mips.gsf.de or http://www.expasy.org)

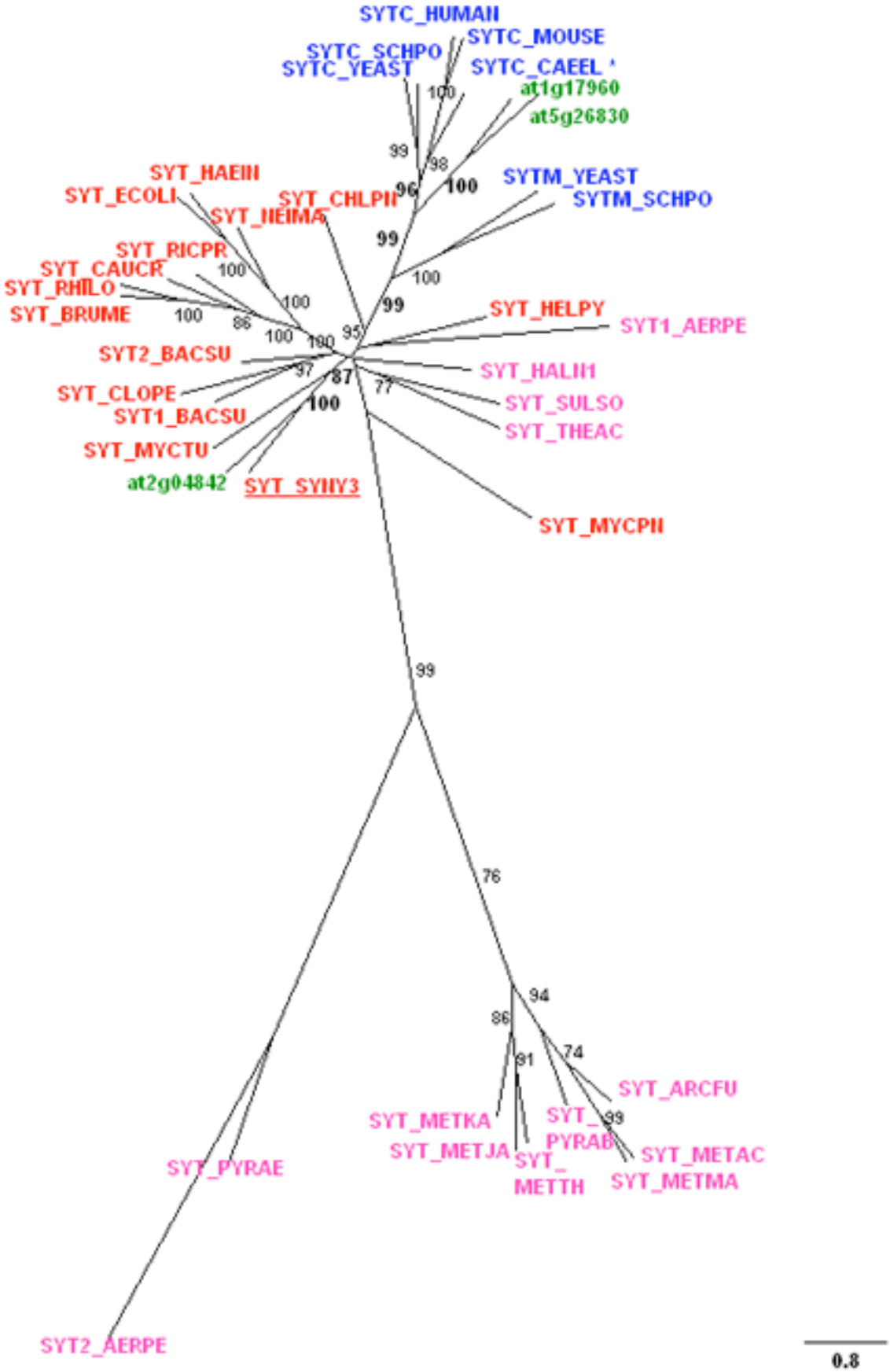


Phylogenetic analysis of ProRS sequences

* possibly mitochondrial (Predotar and/or TargetP)
For SYEP_HUMAN, SYEP_DROME and SYEP_MOUSE, the part of sequence corresponding to the GluRS was removed (about 800 first aminoacids) prior to alignments and phylogenetic analysis.

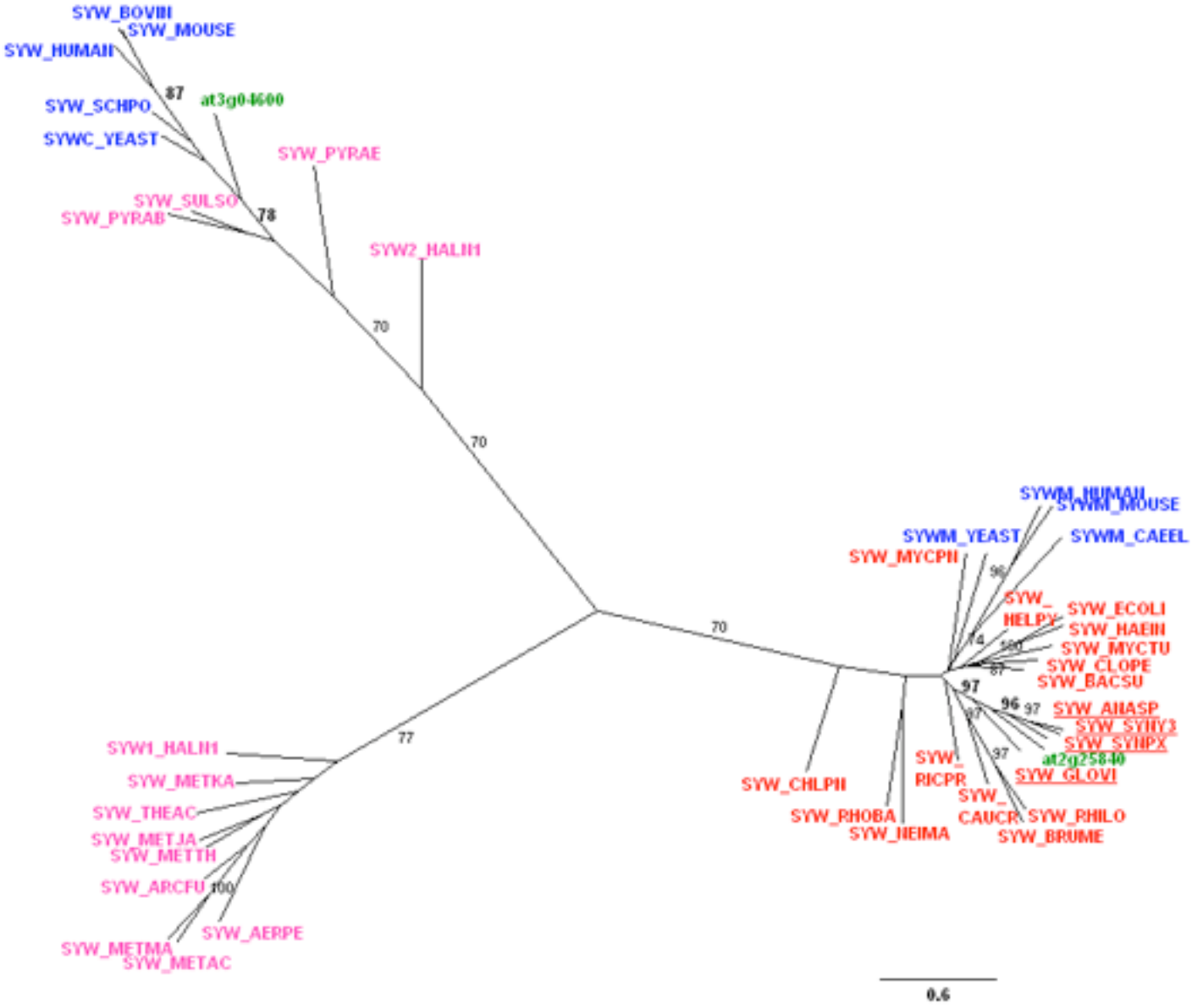


Phylogenetic analysis of SerRS sequences

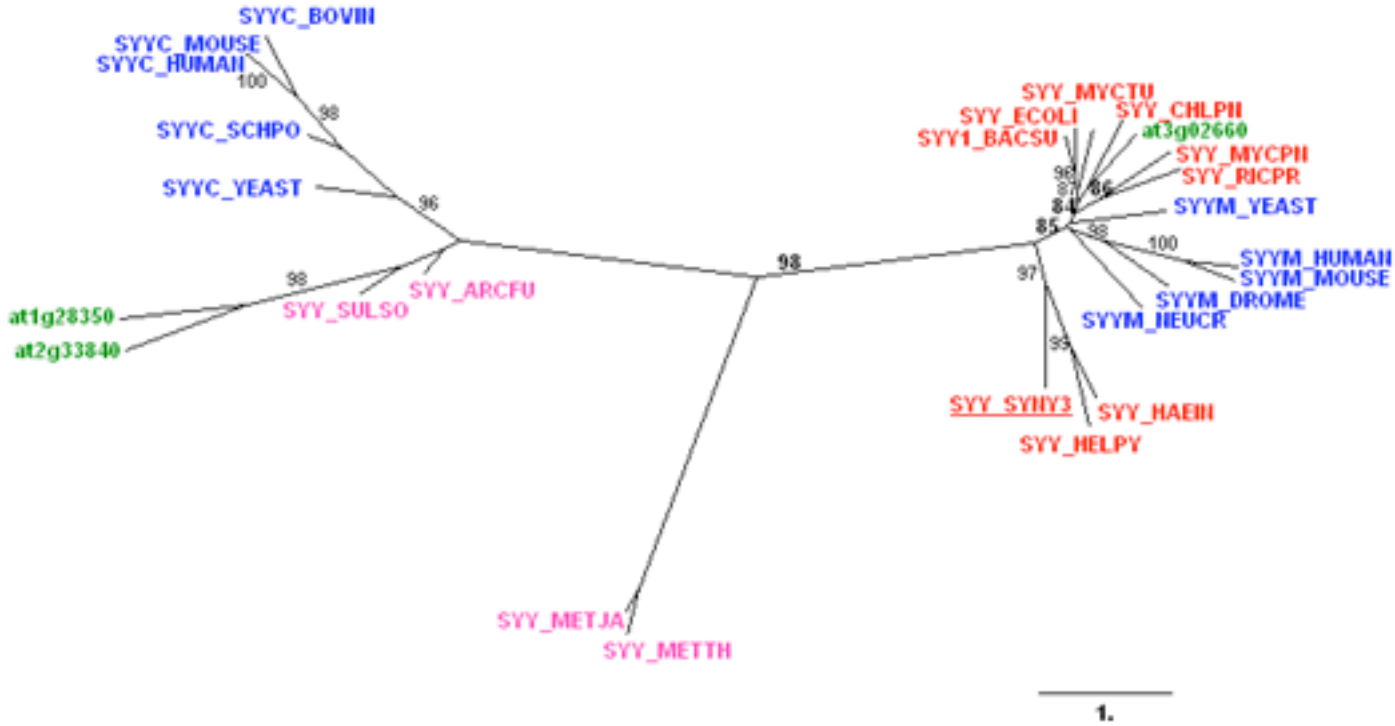


Phylogenetic analysis of ThrRS sequences

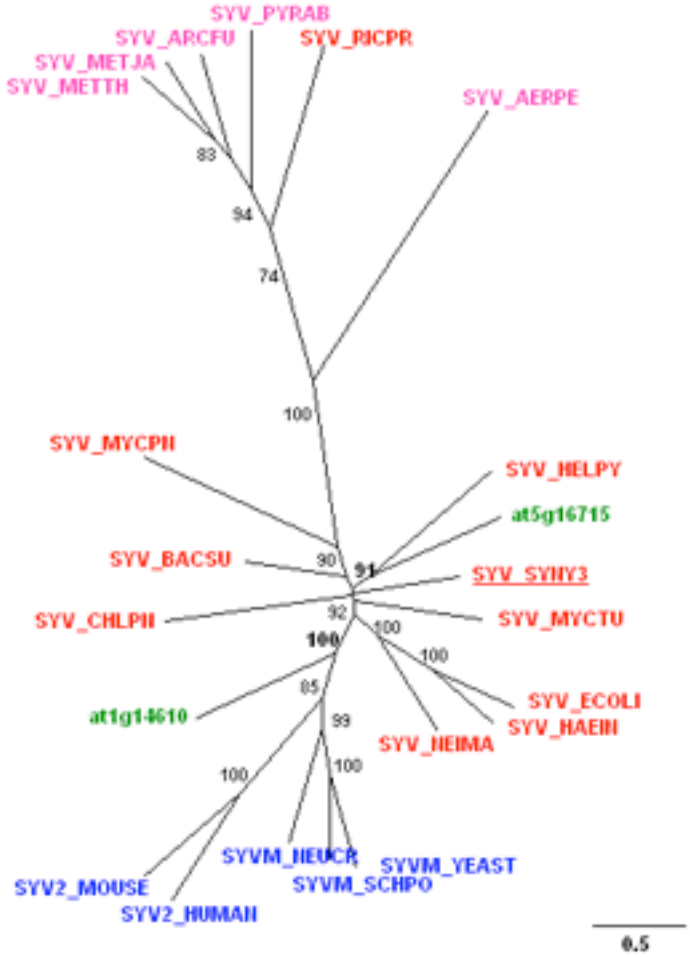
* possibly mitochondrial (Predotar and/or TargetP)

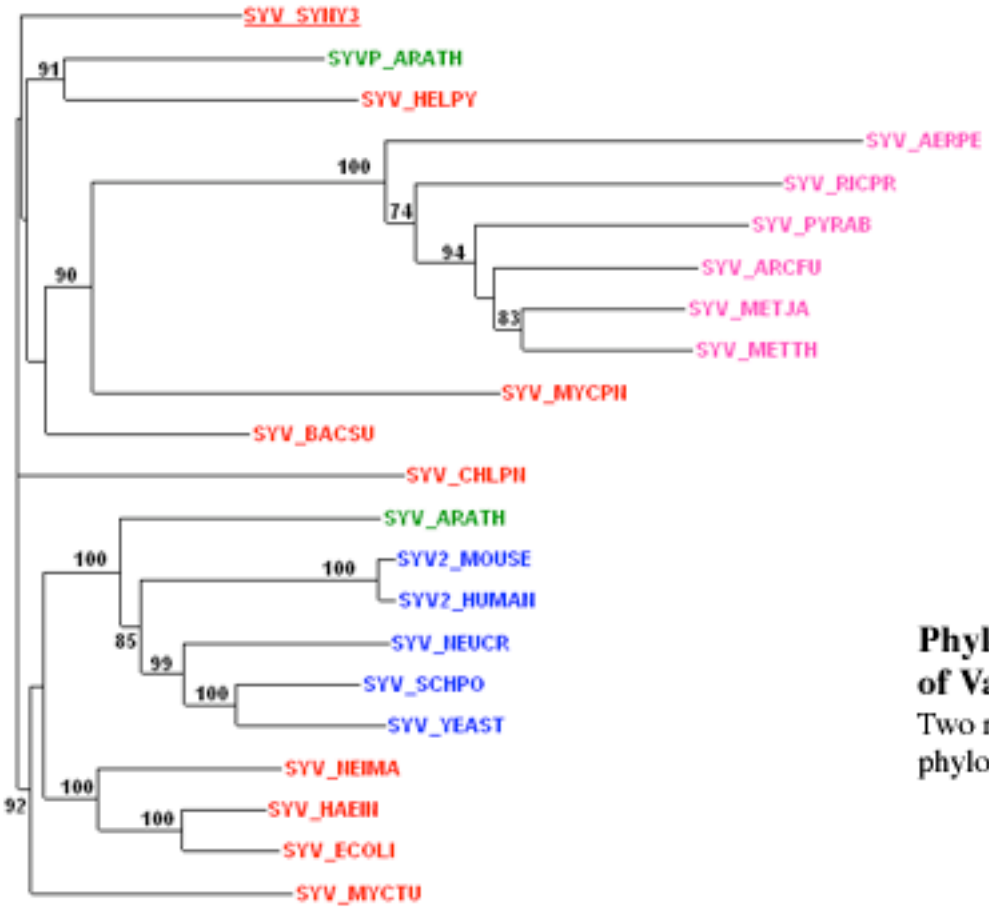


Phylogenetic analysis of TrpRS sequences



Phylogenetic analysis of TyrRS sequences





Phylogenetic analysis of ValRS sequences

Two representations of the phylogenetic tree are given