- 99 CAK38995 Aspergillus niger
- XP 002152078 Penicillium marneffei
- 99 EAA62466 Aspergillus nidulans
- CAP83098 Penicillium chrysogenum
- XP 002374311 Aspergillus flavus
- 99 BAE58123 Aspergillus oryzae
- 99 EAA65188 Aspergillus nidulans
- EFX00699 Grosmannia clavigera
- 99 XP 002383590 Aspergillus flavus
- EGU84308 Fusarium oxysporum
- 99 XP 003049452 Nectria haematococca
- 99 EGU81639 Fusarium oxysporum
- 99 XP 774146 Cryptococcus neoformans
- 85 AAW44459 Cryptococcus neoformans
- XP 003047509 Nectria haematococca
- 99 XP 003007238 Verticillium albo-atrum
- 97 XP 003043719 Nectria haematococca
- 99 XP 001258340 Neosartorya fischeri
- 90 EGU84334 Fusarium oxysporum
- 99 XP 001212100 Aspergillus terreus
- EAA61403 Aspergillus nidulans
- 82 ***Xylaria polymorpha* GH78**
- 99 XP 002384747 Aspergillus flavus
- 99 BAE66403 Aspergillus oryzae
- 98 XP 365490 Magnaporthe oryzae
- XP 390862 Gibberella zeae
- 99 XP 003009324 Verticillium albo-atrum
- 99 XP 003041639 Nectria haematococca
- 93 EGU79091 Fusarium oxysporum
- 88 XP 388150 Gibberella zeae
- 99 XP 002839085 Tuber melanosporum
- XP 002617481 Clavispora lusitaniae
- 99 EFW97210 Pichia angusta
- XP 001258597 Neosartorya fischeri
- 99 EDP55326 Aspergillus fumigatus
- XP 002381436 Aspergillus flavus
- 90 XP 003039940 Nectria haematococca
- 99 EGU77919 Fusarium oxysporum
- 99 EGU76585 Fusarium oxysporum
- XP 003005195 Verticillium albo-atrum
- 99 XP 003048323 Nectria haematococca
- 81 EGU77788 Fusarium oxysporum
- 98 XP 389249 Gibberella zeae
- 99

Ascomycota

- YP 001362272 Kineococcus radiotolerans
- YP 004224831 Microbacterium testaceum
- 98 YP 831328 Arthrobacter sp.
- 99 YP 119613 Nocardia farcinica
- 99 Frankia spp.
- CAJ89979 Streptomyces ambofaciens
- YP 001359873 Kineococcus radiotolerans
- ZP 06416182 Frankia sp.
- YP 003493949 Streptomyces scabiei
- YP 003156189 Brachybacterium faecium
- 99 YP 004454486 Cellulomonas fimi
- ZP 03926090 Actinomyces urogenitalis
- YP 004399503 Lactobacillus buchneri
- 99 Bifidobacterium spp.
- 99 YP 002486514 Arthrobacter chlorophenolicus
- YP 004240987 Arthrobacter phenanthrenivorans
- 96 YP 004571383 Microlunatus phosphovorus
- YP 004575628 Microlunatus phosphovorus
- YP 001359874 Kineococcus radiotolerans
- YP 003156318 Brachybacterium faecium
- 87 99 YP 004372478 Coriobacterium glomerans
- ZP 03926094 Actinomyces urogenitalis
- YP 004224517 Microbacterium testaceum
- 98 YP 003511645 Stackebrandtia nassauensis
- 91 YP 004224876 Microbacterium testaceum
- YP 004223878 Microbacterium testaceum
- 99 YP 003324418 Thermobaculum terrenum
- 92 AAR96046 Thermomicrobia bacterium
- YP 001634000 Chloroflexus aurantiacus
- 99 YP 001504801 Frankia sp.
- 99 YP 003381436 Kribbella flavida
- YP 002883624 Beutenbergia cavernae
- YP 003099839 Actinosynnema mirum
- YP 003487952 Streptomyces scabiei
- 80 ADI05275 Streptomyces bingchenggensis
- YP 003494120 Streptomyces scabiei
- ZP 08528146 Agrobacterium sp.
- 99 Rhizobium spp.
- 99 YP 002546107 Agrobacterium radiobacter
- 99 YP 003378189 Kribbella flavida
- 99 ZP 08198428 Nocardioidaceae bacterium
- YP 003767933 Amycolatopsis mediterranei
- 99 YP 004085951 Asticcacaulis excentricus
- ZP 08265982 Asticcacaulis biprosthecum
- 99 YP 003592860 Caulobacter segnis
- NP 419794 Caulobacter crescentus
- 92 ZP 07029577 Acidobacterium sp.
- 99 YP 004219660 Acidobacterium sp.
- 99 YP 003343629 Streptosporangium roseum
- 99 YP 003767920 Amycolatopsis mediterranei
- YP 003392054 Conexibacter woesei
- YP 003342007 Streptosporangium roseum
- 94 YP 003767276 Amycolatopsis mediterranei
- 97 Streptomyces spp.
- 99 ZP 06242260 Victivallis vadensis
- 91 ZP 03725845 Opitutaceae bacterium
- 98 ZP 03726180 Opitutaceae bacterium
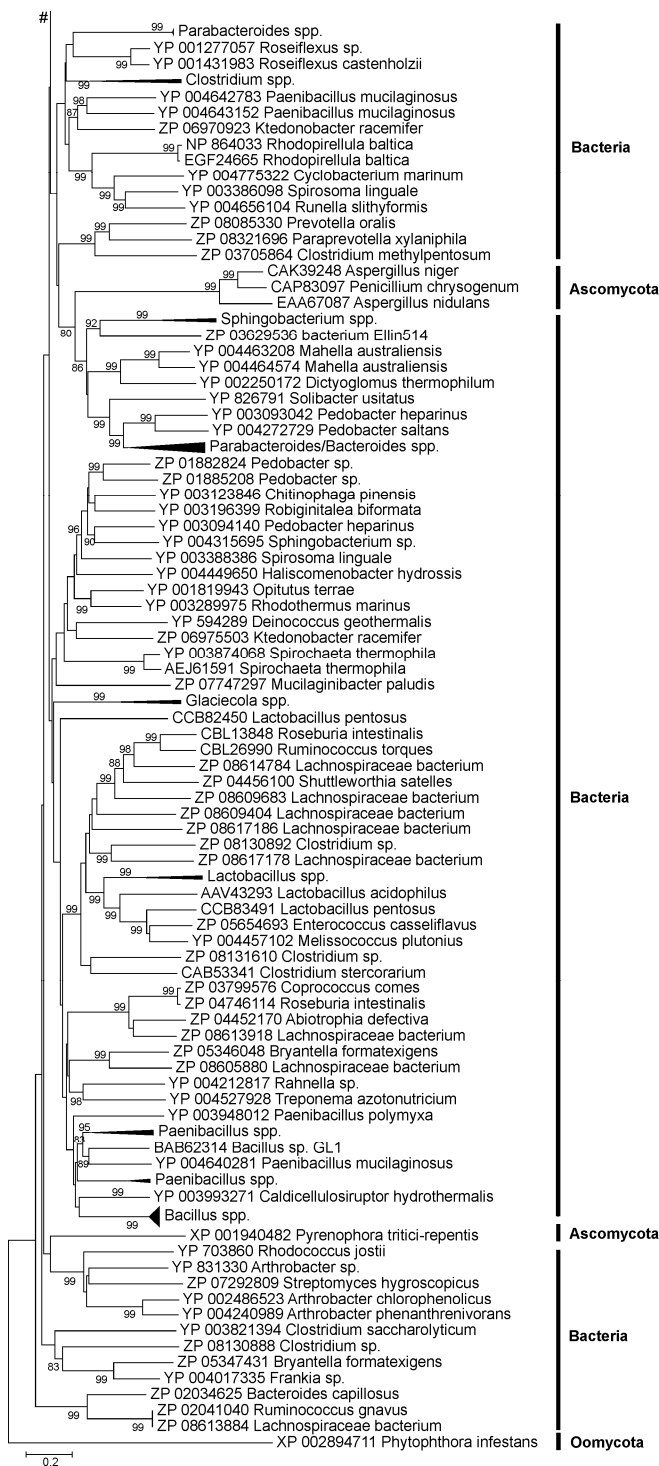- #

Bacteria

0.2

Figure S 3: Evolutionary relationship of eukaryotic and prokaryotic GH78 α-L-rhamnosidases of group I. The evolutionary history was inferred using the Neighbor-Joining method. The optimum tree with the sum of branch length = 67.95191309 is shown. The percentage of replicate trees, in which the associated taxa clustered together in the bootstrap test (1,000 replicates), is shown next to the branches. The evolutionary distances were computed using the Poisson correction method and are given in the units of the number of amino acid substitutions per site. The analysis included 248 amino acid sequences. All ambiguous positions were removed for each sequence pair. There are a total of 3,483 positions in the final dataset.