

BAD43124.1 | [Arabidopsis thaliana] (identical to AHP5)
 AAV59314.1 | [Oryza sativa (japonica cultivar-group)] (identical to XP_475732)
 NP_916056.1 | [Oryza sativa (japonica cultivar-group)] (identical to BAD87913)
 NP_746476.1 | [Pseudomonas putida KT2440]
 AAN69940.1 |
 ZP_00600877.1 | [Rubrobacter xylanophilus DSM 9941]
 EAN36092.1 | [Rubrobacter xylanophilu
 ZP_01055360.1 | [Roseobacter sp. MED193]
 EAQ46303.1 | [Rose
 ZP_00601697.1 | [Rubrobacter xylanophilus DSM 9941]
 gb|EAN35240.1 | [Rubrobacter xylanophilu
 ABA73286.1 | [Pseudomonas fluorescens PfO-1]
 YP_347275.1 |
 AAA50632.2 | [Caenorhabditis elegans]
 NP_498471.1 | [Caenorh
 |S44641 Caenorhabditis elegans
 BAA17056.1 | [Synecocystis sp. PCC 6803]
 NP_440376.1 |
 AAM65769.1 | [Arabidopsis thaliana] (identical to AHP5)
 NP_850649.1 | [Arabidopsis thaliana] (identical to AHP2)

AHP2(A13g29350): global tree
 File name: AHP2.mltree0.svg
 101 aa residues 78 OTU included.

Assemble Job Id: EWrsOM
 Tree job id: OjQiWk
 BP values out of 100
 Analyzed by ku-bo@nibb.ac.jp
 Date: Thu Jun 08 18:59:32 JST 2006

Comments
 result of bl2seq(blastN) of NP_916056 and BAD87913
 Score = 808 bits (420), Expect = 0.0
 Identities = 420/420 (100%), Gaps = 0/420 (0%)
 Score = 252 bits (131), Expect = 2e-63
 Identities = 131/131 (100%), Gaps = 0/131 (0%)

were removed from this tree.

