

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; [Synechocystis sp. PCC 6803]  
NP 440376.1;  
AAM65769.1; [Arabidopsis thaliana] (identical to AHP5)  
NP 850649.1; [Arabidopsis thaliana] (identical to AHP2)

AHP2(At3g29350): global tree  
File name: AHP2.njtree0.svg  
101 aa residues 78 OTU included.  
  
Assemble Job Id: EWrsOM  
Tree job id: 0jQiwk  
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.



0.100