

CKX7.(AT5G21482): global tree  
 File name: CKX7.njtree0.svg  
 204 aa residues 80 OTU included.  
 Results of 3 partial trees included. Smo\_CKX7\_9\_1, Smo\_CKX7720218613\_1  
 Assemble Job Id: vOpNqG  
 Tree job id: eg2e5A  
 BP values out of 100  
 Analyzed by ku-bo@nibb.ac.jp  
 Date: Thu Jun 01 13:46:50 JST 2006

AAS48511.1| [Fagopyrum esculentum]  
 AAK51494.1| [Triticum aestivum]  
 AAK51495.1| [Hordeum vulgare]  
 ZP 01195674.1| [Mycobacterium flavescens PYR-GCK]  
 EAS08013.1|  
 NP 849470.1| [Arabidopsis thaliana] (identical to AT4g29740)  
 AAZ54098.1| [Thermobifida fusca YX]  
 AAM78001.1| [Streptomyces carzinostaticus subsp. neocarzinostaticus]  
 ABD09733.1| [Frankia sp. Ccl3]  
 YP 479462.1|  
 XP 366189.1| [Magnaporthe grisea 70-15]  
 XP 384908.1| [Gibberella zeae PH-1]  
 EAA75691.1| XP 749210.1| [Aspergillus fumigatus Af293]  
 EAL87172.1| EAQ87374.1| [Chaetomium globosum CBS 148.51]  
 AAV70958.2| [Triticum aestivum]XP 384074.1| [Gibberella zeae PH-1]  
 EAA73366.1|XP 660955.1| [Aspergillus nidulans FGSC A4]  
 EAA63319.1|  
 Smo CKX7719787642 1 (not aligned)  
 BAE59774.1| [Aspergillus oryzae]  
 CAF19277.1| [Corynebacterium glutamicum ATCC 13032]  
 BAB97965.  
 were removed from this tree.

comments  
 result of bl2seq(blastN) of Smo\_CKX7\_9\_1 and Smo\_CKX7\_3\_1  
 Score = 2728 bits (1419), Expect = 0.0  
 Identities = 1501/1537 (97%), Gaps = 3/1537 (0%)  
 Score = 956 bits (497), Expect = 0.0  
 Identities = 553/567 (97%), Gaps = 5/567 (0%)

result of bl2seq(blastN) of Smo\_CKX7\_3\_1 and Smo\_CKX7720218613  
 Score = 962 bits (500), Expect = 0.0  
 Identities = 530/541 (97%), Gaps = 2/541 (0%)  
 Score = 579 bits (301), Expect = 6e-162  
 Identities = 318/324 (98%), Gaps = 1/324 (0%)

result of bl2seq(blastN) of Smo\_CKX7\_9\_1 and Smo\_CKX7719787642  
 No significant similarity was found

result of bl2seq(blastN) of Smo\_CKX7\_9\_1 and Smo\_CKX7720218613  
 No significant similarity was found

result of bl2seq(blastN) of Smo\_CKX7720218613 and Smo\_CKX7719787642  
 No significant similarity was found

result of bl2seq(blastN) of Smo\_CKX7\_3\_1 and Smo\_CKX7719787642  
 No significant similarity was found

result of bl2seq(blastN) of XP\_464684 and XP\_464685  
 Score = 1211 bits (630), Expect = 0.0  
 Identities = 990/1170 (84%), Gaps = 0/1170 (0%)  
 Score = 592 bits (308), Expect = 9e-166  
 Identities = 322/329 (97%), Gaps = 0/329 (0%)

