CLUSTAL X (1.81) MULTIPLE SEQUENCE ALIGNMENT

File: alignments-for-ancestor-plant
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                                                                                                  * *:** .*:*::.*   :   :******* :: *:.
gb|AAFD01000225.1_Tp ------------------------------------------------------------RTLKGHFGKVYAMHWNS-DSQTLVSASQDGKLIIWNAF    37
     tr_B0ETG9_ENTDI LSLTYMAEDLQAKIIQTRKEIDQIKEETRANREAKEDTTMKKFTSE---IPGISRSDHVKFKRGLRGHISKIYAMHWAS-DSTHLVSASQDGLMLTWDGQ    96
sp_P93398_GBB2_TOBAC ----MSVKELKERHMAATQTVNDLREKLKQKRLQLLDTDVSGYARSQGKTPVIFGPTDLVCCRILQGHTGKVYSLDWTP-EKNRIVSASQDGRLIVWNAL    95
sp_P93397_GBB1_TOBAC ----MSVTELKERHMAATQTVNDLREKLKQKRLQLLDTDVSGYARSQGKTPVTFGPTDLVCCRILQGHTGKVYSLDWTP-EKNRIVSASQDGRLIVWNAL    95
sp_Q40507_GBB3_TOBAC ----MSVTELKERHMAATQTVSDLREKLKQKRLQLLDTDVSGYARSQGKTPVTFGPTDLVCCRILQGHTGKVYSLDWTP-EKNRIVSASQDGRLIVWNAL    95
 sp_P93339_GBB_NICPL ----MSVTELKERHMAATQTVNDLREKLKQKRLQLLDTDVSGYARSQGKTPVTFGPTDLVCCRILQGHTGKVYSLDWTP-EKNRIVSASQDGRLIVWNAL    95
 sp_P93563_GBB_SOLTU ----MSVAELKERHMAATQTVNDLREKLKQKRLQLLDTDVSGYAKRQGKSPVTFGPTDLVCCRILQGHTGKVYSLDWTP-EKNRIVSASQDGRLIVWNAL    95
     tr_Q945H7_SOLTU ----MSVAELKERHMAATQTVNDLREKLKQKRLQLLDTDVSGYAKTQGKTPVTFGPTDLVCCRILQGHTGKVYSLDWTP-EKNRIVSASQDGRLIVWNAL    95
       tr_Q9SW94_PEA ----MSVAELKERHIAATETVNNLRERLKQRRLSLLDTDIAGYARSQGRAPVTFGPTDILCCRTLQGHTGKVYSLDWTS-EKNRIVSASQDGRLIVWNAL    95
  medicago|TC120865 ----MSVTELKERHIAATETVNNLRERLKQRRLSLLDTDIAGYAKSQGRTPVTFGPTDILCCRTLQGHTGKVYSLDWTS-EKNRIVSASQDGRLIVWNAL    95
 sp_P49177_GBB_ARATH ----MSVSELKERHAVATETVNNLRDQLRQRRLQLLDTDVARYSAAQGRTRVSFGATDLVCCRTLQGHTGKVYSLDWTP-ERNRIVSASQDGRLIVWNAL    95
 sp_Q40687_GBB_ORYSJ ---MASVAELKEKHAAATASVNSLRERLRQRRQMLLDTDVERYSRTQGRTPVSFNPTDLVCCRTLQGHSGKVYSLDWTP-EKNWIVSASQDGRLIVWNAL    96
 sp_P49178_GBB_MAIZE ---MASVAELKEKHAAATASVNSLRERLRQRRETLLDTDVARYSKSQGRVPVSFNPTDLVCCRTLQGHSGKVYSLDWTP-EKNWIVSASQDGRLIVWNAL    96
     tr_Q8LNY6_WHEAT ---MASVAELKEKHAAATASVNSLRERLRQRRQTLLDTDVEKYSKAQGRTAVSFNPTDLVCCRTLQGHSGKVYSLDWTP-EKNWIVSASQDGRLIVWNAL    96
     tr_O64944_AVEFA ---MASVAELKERHAAATASVNSLRERLRQRRQTLLDTDVEKYSKAQGRTAVSFNQTDLVCCRTLQGHSGKVYSLDWTP-EKNWIVSASQDGRLIVWNAL    96
     tr_Q8GU43_PHYPA ---MSVADSVRERYEVSKAEVQSLREQLHEKRASLLDTDGGPFIPAD--FVVVISFVFMVCVRTLQGHTGKIYSLDWAYRETSRIVSASQDGRLIVWNAI    95
               ruler 1.......10........20........30........40........50........60........70........80........90.......100

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gb|AAFD01000225.1_Tp TTNKVQAIPLRSSWVMTCAFEQSKGNLIACGGLDNVCSIYNTQQAS---TSNARASKELVAHDGYLSCCRFV--DEGHVVTSSGDSTCIYWDVNSGEVLK   132
     tr_B0ETG9_ENTDI TTNKIHCIRIRSSWVMTCAYAPS-MKFVACGGLDNIVSIYSIAPKSSSSEPLNNTTAELAGHVGYISCMRYV--DENRILTSSGDSTCCLWDVEQSAKIM   193
sp_P93398_GBB2_TOBAC TSQKTHAIKLPCAWVMTCAFSPS-GQSVACGGLDSVCSIFNLNSPIDK-DGNHPVSRMLSGHKGYVSSCQYVPDEDTHVITSSGDQTCVLWDITTGLRTS   193
sp_P93397_GBB1_TOBAC TSQKTHAIKLPCAWVMTCAFSPS-GQSVACGGLDSVCSIFNLNSPIDK-DGNHPVSRMLSGHKGYVSSCQYVPDEDTHLITSSGDQTCVLWDITTGLRTS   193
sp_Q40507_GBB3_TOBAC TSQKTHAIKLPCAWVMTCAFSPS-GQSVACGGLDSVCSIYNLNSPIDK-DGNHPVSRMLSGHKGYVSSCQYVPDEDTHLITSSGDQTCVLWDITTGLRTS   193
 sp_P93339_GBB_NICPL TSQKTHAIKLPCAWVMTCAFSPS-GHSVACGGLDSVCSIFNLNSPIDK-DGNHPVSRMLSGHKGYVSSCQYVPDEDTHLITSSGDQTCVLWDITTGLRTS   193
 sp_P93563_GBB_SOLTU TSQKTHAIKLPCAWVMTCAFSPS-GQSVACGGLDSACSIFNLNSPIDK-DGIHPVSRMLSGHKGYVSSCQYVPDEDTHLITSSGDQTCVLWDITTGLRTS   193
     tr_Q945H7_SOLTU TSQKTHAIKLPCAWVMTCAFSPS-GQSVACGGLDSACSIFNLNSPIDK-DGIHPVSRMLSGHKGYVSSCQYVPDEDTHLITSSGDQTCVLWDITTGLRTS   193
       tr_Q9SW94_PEA TSQKTHAIKLPCAWVMTCAFSPT-GQSVACGGLDSVCSIFNLNSPTDR-DGNLNVSRMLSGHKGYVSSCQYVPGEDTHLITGSGDQTCVLWDITTGLRTS   193
  medicago|TC120865 TSQKTHAIKLPCAWVMTCAFSPT-GQSVACGGLDSVCSIFNLNSPTDR-DGNLNVSRMLSGHKGYVSSCQYVPGEDTHLITGSGDQTCVLWDITTGLRTS   193
 sp_P49177_GBB_ARATH TSQKTHAIKLPCAWVMTCAFSPN-GQSVACGGLDSVCSIFSLSSTADK-DGTVPVSRMLTGHRGYVSCCQYVPNEDAHLITSSGDQTCILWDVTTGLKTS   193
 sp_Q40687_GBB_ORYSJ TSQKTHAIKLHCPWVMTCAFAPN-GQSVACGGLDSACSIFNLNSQADR-DGNIPVSRILTGHKGYVSSCQYVPDQETRLITSSGDQTCVLWDVTTGQRIS   194
 sp_P49178_GBB_MAIZE TSQKTHAIKLHCPWVMACAFAPN-GQSVACGGLDSACSIFNLNSQADR-DGNMPVSRILTGHKGYVSSCQYVPDQETRLITSSGDQTCVLWDVTTGQRIS   194
     tr_Q8LNY6_WHEAT TSQKTHAIKLHCPWVMECAFAPN-GQSVACGGLDSACSIFNLSSQADR-DGNMPVSRVLTGHKGYASSCQYVPDQETRLITGSGDQTCVLWDVTTGQRIS   194
     tr_O64944_AVEFA TSQKTHAIKLHCPWVITCAFAPN-GQSVACGGLNSACSIFNLNSQVDR-NGNMPVSKLLTGPKGYVLSCQYVPDQETRMITGSGDPTCVLWDVTTGQRIS   194
     tr_Q8GU43_PHYPA SSQKTYSLKLACAWVKAAISPG-GNTVACGGLDNVCSIFNLSSVPDK-EGNLPVSGTLAGHTGYLSSCKYMPTQEKHIVTSSGDHTCRFWDVETQCCIA   193
               ruler .......110.......120.......130.......140.......150.......160.......170.......180.......190.......200

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gb|AAFD01000225.1_Tp TF-----SDHKSDVMSVAISPENNNIFVSGSVDTTAKVWDIRNGK-CVQTHIGHEADINSVAFFPDGHAFGTGSDDASCRLFDMRSYGEVNKFKS-----   221
     tr_B0ETG9_ENTDI DF-----KDHQADVMCVSVSPD-QNTFVSGACDSMAKLWDIRMEN-CVATFTGHDADINAIAFHPSGNAFITGSDDFSCKLFDIRADRELMNYSS-----   281
sp_P93398_GBB2_TOBAC VFGGEFQSGHTADVQSVSISSSNPRLFVSGSCDSTARLWDTRVASRAQRTFYGHEGDVNTVKFFPDGNRFGTGSDDGTCRLFDIRTGHQLQVYYQPH--G   291
sp_P93397_GBB1_TOBAC VFGGEFQSGHTADVQSVSISSSNPRLFVSGSCDTTARLWDTRVASRAQRTFYGHEGDVNTVKFFPDGNRFGTGSEDGTCRLFDIRTEHQLQVYYQPH--G   291
sp_Q40507_GBB3_TOBAC VFGGEFQSGHTADVQSVSISSSNPRLFVSGSCDTTARLWDNRVASRAQRTFYGHEGDVNTVKFFPDGNRFGTGSEDGTCRLFDIRTGHQLQVYYQPH--G   291
 sp_P93339_GBB_NICPL VFGGEFQFGHTADVQSVSISSSNPRLFVSGSCDTTARLWDTRVASRAQRTFYCHEGDVNTVKFFPDGNRFGTGSEDGTCRLFDIRTGHQLQVYYQPH--G   291
 sp_P93563_GBB_SOLTU VFGGEFQSGHTADVLSVSISSSNPKLFVSGSCDTTARLWDTRVASRAQRTFHGHESDVNTVKFFPDGNRFGTGSDDGSCRLFDIRTGHQLQVYNQPH--G   291
     tr_Q945H7_SOLTU VFGGEFQSGHTADVSSVSISSSNPKLFVSGSCDTTARLWDTRVASRAQRTFHGHESDVTTVKFFPDGNRFGTGSDDGSCRLFDIRTGHQLQVYNQPH--G   291
       tr_Q9SW94_PEA VFGGEFQSGHTADVLSISINGSNSKLFVSGSCDATARLWDTRVASRAVRTFHGHEGDVNSVKFFPDGNRFGTGSEDGTCRLFDIRTGHQLQVYNQQH--Q   291
  medicago|TC120865 VFGGEFQSGHTADVLSISINGSNSKMFVSGSCDATARLWDTRVASRAVRTFHGHEGDVNSVKFFPDGNRFGTGSEDGTCRLFDIRTGHQLQVYNQQHS-G   292
 sp_P49177_GBB_ARATH VFGGEFQSGHTADVLSVSISGSNPNWFISGSCDSTARLWDTRAASRAVRTFHGHEGDVNTVKFFPDGYRFGTGSDDGTCRLYDIRTGHQLQVYQPHG---   290
 sp_Q40687_GBB_ORYSJ IFGGEFPSGHTADVLSLSINSSNSNMFVSGSCDATVRLWDIRIASRAVRTYHGHEGDINSVKFFPDGQRFGTGSDDGTCRLFDVRTGHQLQVYSREPDRN   294
 sp_P49178_GBB_MAIZE IFGGEFPSGHTADVQSVSINSSNTNMFVSGSCDTTVRLWDIRIASRAVRTYHGHEDDVNSVKFFPDGHRFGTGSDDGTCRLFDMRTGHQLQVYSREPDRN   294
     tr_Q8LNY6_WHEAT IFGSEFPSGHTADVLSLSINSLNANMFISGSCDTTVRLWDLRITSRAVRTYHGHEGDINSVKFFPDGQRFGTGSDDGTCRLFDMRTGHQLQVYNREPDRN   294
     tr_O64944_AVEFA IFGGEFPSGHTADVLSLSINSLNTNMFVSGSCDTTVRLWDLRIASRAVRTYHGHEGDINSVKFFPDGHRFGTGSDDGTCRLFDMRIRHQLQVYSREPDRN   294
     tr_Q8GU43_PHYPA VFGGDILTGHTGDVMSVSVSSSSPHVFISGSCDKSAKLWDVRTPARAQRTFYGHEGDVNTVNFLSEGRHFGTGSDDGSCRLFDIGTGHELQQYWDKQALA   293
               ruler .......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

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gb|AAFD01000225.1_Tp DKITCGITSVAFSRSGRLMFGGYD-DFNTYVWDTLSDADQCAFALPT--PHENRVSCLGVNKNGDALCTGSWDTNLKIWA--------   298
     tr_B0ETG9_ENTDI ESMQHGVTSVAISSTGRYLFCGYD-DLGCLWWDVLKGDYITKLTG-----HENRVSCLGVSPDGYALCTGSWDSTLRIWAN-------   356
sp_P93398_GBB2_TOBAC DGDIPHVTSMAFSISGRLLFVGYS-NGDCYVWDTLLAKVVLNLGAVQN-SHEGRISCLGLSADGSALCTGSWDTNLKIWAFGGHRSVI   377
sp_P93397_GBB1_TOBAC DGDIPHVTSMAFSISGRLLFVGYS-NGDCYVWDTLLAKVVLNLGGVQN-SHEGRISCLGLSADGSALCTGSWDTNLKIWAFGGHRSVI   377
sp_Q40507_GBB3_TOBAC DGDIPHVTSMAFSISGRLLFVGYS-NGDCYVWDTLLAKVVLNLGGVQN-SHEGRISCLGLSADGSALCTGSWDTNLKIWAFGGTEV--   375
 sp_P93339_GBB_NICPL DGDIPHVTSMAFSISGRLLFVRYS-NGDCYVWDTLLAKVVLNLGAVQN-SHEGXISCLGLSADGXXLCTGSWDTNLKIWAFGGHRSVI   377
 sp_P93563_GBB_SOLTU DGDIPHVTSMAFSISGRLLFVGYS-NGDCYVWDTLLAKVVLNLGSVQN-SHEGRISCLGLSADGSALCTGSWDTNLKIWAFGGHRSVV   377
     tr_Q945H7_SOLTU DGDIPHVTSIAFSISGRLLFVGYS-NGDCYVWDTLLAKVVLNLGSVQN-SHEGRISCLGLSADGSALCTGSWDTNLKIWAFGGHRSVI   377
       tr_Q9SW94_PEA DNEMAHVTSIAFSISGRLLIAGYT-NGDCYVWDTLLAKVVLNLGSLQN-SHEGRITCLGMSADGSALCTGSWDTNLKIWAFGGHRKVI   377
  medicago|TC120865 DNEMAHVTSIAFSISGRLLIAGYT-NGDCYVWDTLLAKVVLNLGSLQN-SHEGRITCLGLSADGSALCTGSWDTNLKIWAFGGHRKVI   378
 sp_P49177_GBB_ARATH DGENGPVTSIAFSVSGRLLFAGYASNNTCYVWDTLLGEVVLDLGLQQD-SHRNRISCLGLSADGSALCTGSWDSNLKIWAFGGHRRVI   377
 sp_Q40687_GBB_ORYSJ DNELPTVTSIAFSISGRLLFAGYS-NGDCYVWDTLLAEVVLNLGNLQN-SHEGRISCLGLSSDGSALCTGSWDKNLKIWAFSGHRKIV   380
 sp_P49178_GBB_MAIZE SNELPTVTSIAFSISGRLLFAGYS-NGDCYVWDTLLAEVVLNLGNLQN-SHDGRISCLGMSSDGSALCTGSWDKNLKIWAFSGHRKIV   380
     tr_Q8LNY6_WHEAT DNELPIVTSVAFSISGRLLFAGYS-NGDCYVWDTLLAEMVLNLGTLQN-SHEGRISCLGLSSDGSALCTGSWDKNLKIWAFSGHRKIV   380
     tr_O64944_AVEFA DNELPSVTSIAFSISGRLLFAGYS-NGDCYAWDTLLAEVVLNLGTLQN-SHEGRISCLGLSSDGSALCTGSWDKNLKIWAFSGHRKIV   380
     tr_Q8GU43_PHYPA RGPVN-VTSVAFSRSGRLLFAGYS-NGNCYVWDTLLAKVVANLGGGRDDGHTNRVSCLGLAADGDALCTGSYDATLKVWSCAGKKS--   377
               ruler .......310.......320.......330.......340.......350.......360.......370.......380........
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