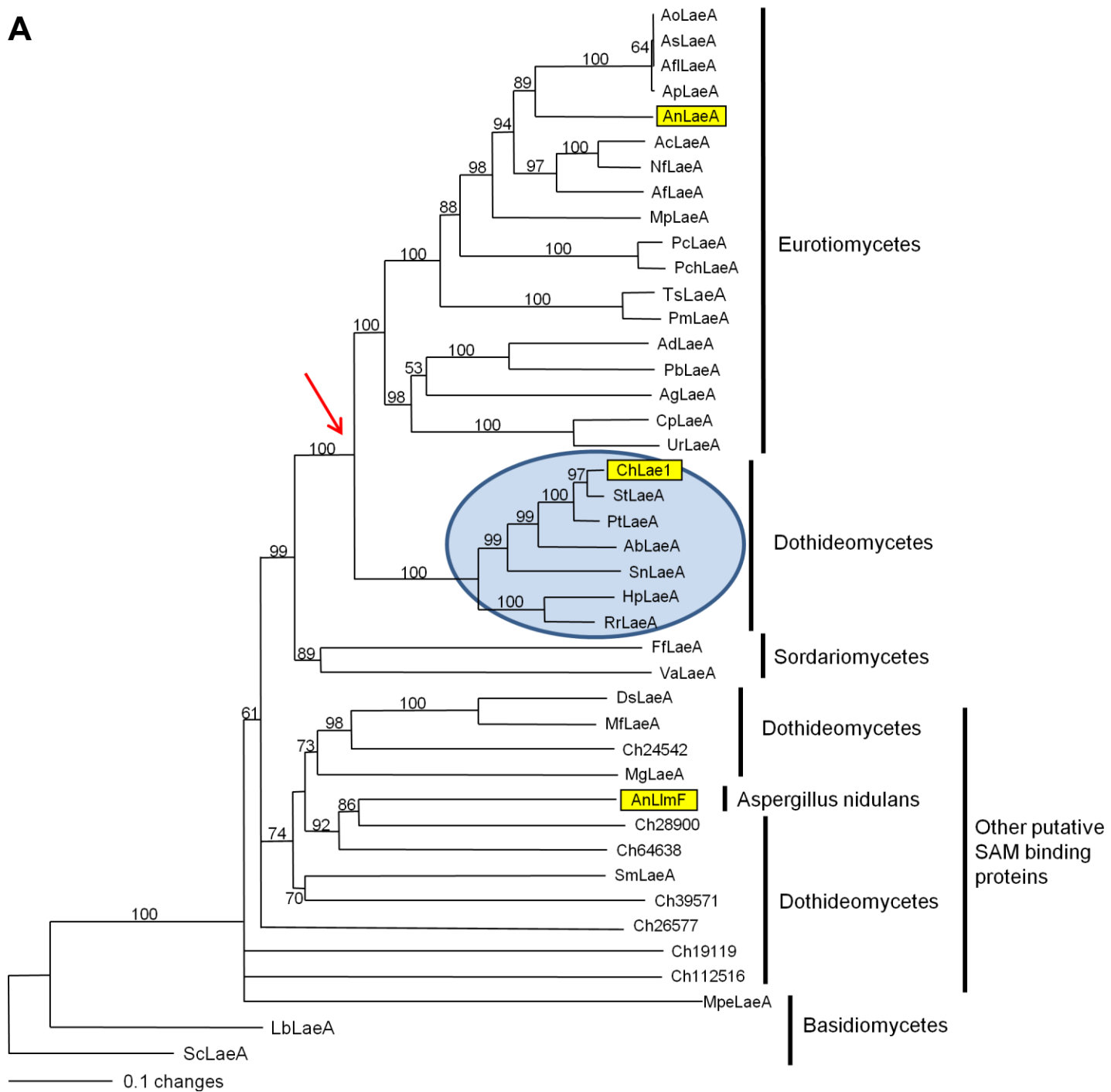


A

B

AfLaeA -----MLWTSIQSQTGVPLQR----ETRPLVVGTPMVPQVLIL 34
AnLaeA MFEMGPVGTRLPAMTSPAHNHYSYHSPTSDDRGRSRQNSDAMDIQSITEREPATRYAVAG 60
ChLae1 -----

AfLaeA PVASISLFPSSLLFSYSCSPFFRAAVKAENGRTYHGYRKG IYMLPCDEQE QDRLDIFHKL 94
AnLaeA GPAPWNRNGSPSPMYSNNSERNQFHEENGRTYHGFRRGMYFLPCDEQE QDRLDIFHKL 120
ChLae1 -----MENGRWYHGFRRGLYMYPCDEPEKDRMDIYHQF 33
**** ***:***:**** ***:***:***:****

AfLaeA FTVARVSDGLIYAPHPTN----GRFLD LGCCTGIWAIDVANKYPEAFVVGVDLAPIQPPN 150
AnLaeA FTVARVSESLIYAPHPTN----GRFLD LGCCTGIWAIEVANKYPDAFVAGVDLAPIQPPN 176
ChLae1 FAVARRGQ-LHQAPVPSEPHLQPRILD VGCCTGIWAIDMADKYLNAEVLGLDLVNIQPEK 92
*:*** .: * ** *:: ***:*****:***: ** * * ***: *** :

AfLaeA HPRNCDFYAPFD FESLWALGEDSWDLIHLMGSGSVASWP NLYRRIYSHLRPG-AWFEQV 209
AnLaeA HPKNCEFYAPFD FEAPWAMGEDSWDLIHLMGCGSVMGWP NLYRRIFAHLRPG-AWFEQV 235
ChLae1 IPPNLRFRVPRDYESPWTLGEDSWDLIHLMACGSVESWPELYQKIYTHLKP GTGWIEHI 152
* * * . * *:: ***:*****:*.*** ***:***:***:*** ***:*** .*:***:

AfLaeA EIDFEPRCDDRSLEG-LAIRQWYQLLKQATEETMRPVAHNSRETIRNLQEAGFTEIDHQM 268
AnLaeA EIDFEPRCDDRSLDG-TALRHWDCLKQATAETMRPIAHSSRDTIKDLQDAGFTEIDHQI 294
ChLae1 EIDMEPRCDDYTLPPDSMLRKWYGWLADATQRAYRPIAYEHR-TRQLLQAAGFIDIQETV 211
:** :* :*** * :** .: ***: . * * : ** *** :* . :

AfLaeA VGLPLNPWHEDEHERRVARWYNLAISESIETMSLAPFSRVFGWPIER- IKQIAADV KSEA 327
AnLaeA VGLPLNPWHQDEHERKVARWYNLAVSESIENLSLAPFSRVYRWPLER- IQQLAADV KSEA 353
ChLae1 IRVPYNTWPNDPHQKDIGRWYNLGLTEGLEALTFAPLTRVYHWDLNAHVRPIVEGVRREL 271
: : * * . * *:: .:*****:***:***:***: * : : : . . * : *

AfLaeA FNKEIHTYNI LHIYQARKPLAN 349
AnLaeA FNKEIHAYNI LHIYQARKPLR- 374
ChLae1 CNRKIHAYNNI HIWTARRPQQ- 292
::***:*** ***:***