

C.muc. JCM9939 Ste3 1 MPDVAFITFISGLGLVLLVLLPPLQWRARNIGTLNVLGWFSCFTFIYFINSILWWDTYEV-FAHVWCDIS-----VKLIVGLNSGLA 80
C.der. JCM11170 Ste3 1 MPDVAFITFISGLGLVLLVLLPPLQWRARNIGTLNVLGWFSCFTFIYFINSILWWDTYEV-FAHVWCDIS-----VKLIVGLNSGLA 80
C.cya. JCM31833 Ste3 1 MNHLFFTYSYSGIGLVLLVLLPPLQWRARNITAILNMTWIFASAFVFNLSILWRQRTEV-FAHVWCDIS-----AKITITVYIGLA 80
V.fra. JCM1530 Ste3 1 MHDVAFVFFAGLALVLLVLLPPLQWRARNITAILNLSLWVWNTLVSFINTLLWWDTYEV-FGHVWCDIS-----KVISIGFETGLA 80
T.fae. 002_949 Ste3 1 MNDLAFTLIFAGISLLVLLVLLPPLSLHWRVGMCTVFLLLNCFVTCVHFVFNMSILWVGSTEV-FAKVVWCDIC-----VKLIVSFPVGLT 80
T.cor. 011_338 Ste3 1 MNDLAFTLIFAGISLLVLLVLLPPLSLHWRVGMCTVFLLLNCFVTCVHFVFNMSILWVGSSDK-TAKVWCDISSTYSSATRAYFSGVKILSSFAVGLT 92
T.ovo. 001_800 Ste3 1 MNDPAFILFAGISVFLVLLPPLWQWRAGTGTVLLLLWCFVTCVHFVFNMSILWVNSKRI-FAMVWCDICV-----KVLVSFPETGLA 80
T.ovo. 014_240 Ste3 1 MNDPAFTFFAGISLLVLLVLLPPLWQWRVGNCTVLLLVWCFVTCVHFVFNMSILWVNSKEI-FAKVVWCDICESRGC-----GKLVLSFPTGLA 85
V.hum. CBS8242_02_253 Ste3 1 MHDTPHTLFSGLGLVLLVLLPPLTQWRARNITIFNLNLSLWFLVDFVAFINSIMWWDNYRA-YGLVWGDIS-----AKLITASVCLIA 80
A.dom. 002_745 Ste3 1 MFDPAFFSFGIGLIVLLVLLPPLQWKAINTSTLNLNLSLWFLVDFVAFINSIMWWDNYRA-FAPVWCDISTLCQVRELTPG-VKISFALPTALA 91
C.neo. Ste3 mat alpha CNAG_06808 1 MHDLSLVIFSGIGLIVLLVLLPPLHWRARNAGTLLLIAMFLIANFIFVDFGIVWVNSYDLPSSPIWCDIAS-----KLFIVGVPVGIS 81
C.gat. Ste3 mat alpha CGB_I1090W 1 MHDLSLVIFSGIGLIVLLVLLPPLHWRARNAGTLLLIAMFLIANFIFVDFGIVWVNSYDLPSSPIWCDIAS-----KLFIVGVPVGIS 81
T.tep. JCM11965 Ste3 1 -----MLFCGISLIVLLVLLPFPQWKAINTSTILNLIWFLANLIVLVNAWVYDITG-NYAPVWCDIS-----IKIMTGFICILT 74
C.neo. Ste3 mat a AAN75624.1 1 MLHPDYPFWNLTALVLLVLLPAPWHWRARNIATVSLVIVLWTFANLCCGINTIIMAGNYAD-KSPVWCDIS-----SRVPLLVGYAIP 80
C.gat. Ste3 mat a AEG78597.1 1 MLHPDYPFWNLTALVLLVLLPAPWHWRARNIATVSLVIVLWTFANLCCGINTIIMAGNYAD-KSPVWCDIS-----SRVPLLVGYAIP 80
C.ole. Ste3 Triol1|339518 1 MRHPDYPFWSCLSLVLLVLLPAPWHWRARNIATVSLVIVLWTFANLCCGINTIIMAGNYAD-KSPVWCDIS-----SRVPLLVGYAIP 80
C.muc. JCM9939 Ste3 1 MRHPDYPFWSFVSLVLLVLLPAPWHWRARNIATVSLVIVLWTFANLCCGINTIIMAGNYAD-RAPVWCDIS-----GRCTVILFFAIP 80
C.arb. JCM14201 Ste3 1 MRHPDYPFWSFVSLVLLVLLPAPWHWRARNIATVSLVIVLWTFANLCCGINTIIMAGNYAD-RAPVWCDIS-----ARIASAVFFAIP 80
C.cur. Ste3.1 1 MRHPDYAFWSVSLVLLVLLPAPWHWRARNIATVSLVIVLWTFANLCCGINTIIMAGNYAD-TSPVWCDIS-----SRITILSDAVI 80
C.das. JCM11166 Ste3 1 MRHPDYAFWSVSLVLLVLLPAPWHWRARNIATVSLVIVLWTFANLCCGINTIIMAGNYAD-TSPVWCDIS-----ARVIAIIFFAIP 80
V.hum. JCM1457_001_295 Ste3 1 -MPADYPLWNIIGLAVLLVLLPSPWHWRAGNISTCLIAWLSVYHLTSFANTLIWAENVAD-SHPVWCDIS-----SRVTAVIQFAIP 79
V.hum. UJ1 Ste3 1 -MPADYPLWNIIGLAVLLVLLPSPWHWRAGNISTCLIAWLSVYHLTSFANTLIWAENVAD-SHPVWCDIS-----SRVTAVIQFAIP 79
T.asa. EJT49421.1 1 -----MLPISG-----ARVSTK-----HTPLADTAG-----KFLIADVPIYAPV 34
T.cor. 023_151 Ste3 1 MRHPDYPIWISFCILIVLLVLLPSPWHWRARNIATVSLVIVLWTFANLCCGINTIIMAGNYAD-TAPVWSEIS-----CRFTALVPIYAPV 80
T.ink. 003_120 Ste3 1 MRHPDYPAWSFICVLLVLLVLLPSPWHWRARNIATVSLVIVLWTFANLCCGINTIIMAGNYAD-TAPVWSEIS-----CRISAVVPTIIP 80
T.kor. JCM12878 Ste3 1 MLHPDYPFWTLVGAIVVLLVLLPVRWHWRARNIATVSLVIVLWTFANLCCGINTIIMAGNYAD-VAPVWCDIS-----SRILVLIYFAIP 80

C.muc. JCM9939 Ste3 81 AASLCINRRLAGITASA-RSVLVDKQKRRSVVVDLIIIGVGIIVAVMAASVVFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
C.der. JCM11170 Ste3 81 AASLCINRRLAGITASA-RSVLVDKQKRRSVVVDLIIIGVGIIVAVMAASVVFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
C.cya. JCM31833 Ste3 81 AASLCINRRLAGITASA-RSVLVDKQKRRSVVVDLIIIGVGIIVAVMAASVVFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
V.fra. JCM1530 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
T.fae. 002_949 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
T.cor. 011_338 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
T.ovo. 001_800 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
T.ovo. 014_240 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
V.hum. CBS8242_02_253 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
A.dom. 002_745 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
C.neo. Ste3 mat alpha CNAG_06808 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
C.gat. Ste3 mat alpha CGB_I1090W 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
T.tep. JCM11965 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
C.neo. Ste3 mat a AAN75624.1 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
C.gat. Ste3 mat a AEG78597.1 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
C.ole. Ste3 Triol1|339518 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
C.muc. JCM9939 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
C.arb. JCM14201 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
C.cur. Ste3.1 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
C.das. JCM11166 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
V.hum. JCM1457_001_295 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
V.hum. UJ1 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
T.asa. EJT49421.1 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
T.cor. 023_151 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
T.ink. 003_120 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172
T.kor. JCM12878 Ste3 81 ASLGVNRRRIARIASS-RSVTQQAQKRRREYIDLALGLGLPAMVMAISYIFQPHRFDMIGVGCPEVLWNSCIGMVLLIQLPPIALNLVSAAY 172

C.muc. JCM9939 Ste3 173 G-----AYAIHFFISRRVQVNAVLLKSSQSGIDLSHYFRLIGLATADILVGLPIALYFFCVNVQQLG----TWGSWS 239
C.der. JCM11170 Ste3 173 G-----AYAIHFFISRRVQVNAVLLKSSQSGIDLSHYFRLIGLATADILVGLPIALYFFCVNVQQLG----TWGSWS 239
C.cya. JCM31833 Ste3 173 G-----AYATRYFVLRBAQVKALRRS-QGSELSHYLKILIGLATSIDVGLPVSISYIYLAGAISR----PWGSWD 238
V.fra. JCM1530 Ste3 173 G-----IYARPFIFISHAQFRTVLRSSQSGISSHMFRLIGLATSADVDFGLPAEYIFLVVAQNAL----PWGSWK 239
T.fae. 002_949 Ste3 172 -----LISVYAYFFVVRRAQIKELKSSQSGIELAHCVRIILISTIDIILCLPMGLFTLVNSLQNRV----VWDSWD 240
184 GREC-----RWAQLTSVYRAYFFVRSQIKELKSSQSGIELAHCVRIILISTIDIILCLPMGLFTLVNSLQNRV----VWDSWA 261
T.cor. 011_338 Ste3 172 G-----LYARFVFLRCAQVTELLKTSQNGSELAHCVRIILAMIDIILCLPMVMSVNSIQNRV----VWDSWE 238
T.ovo. 001_800 Ste3 176 GRESF-----AHVCQLTVVYAVHFFVRRRAQVKELLKSSQSGIELAHCVRIILISTIDIILCLPMVMSVNSIQNRV----EWDSE 258
T.ovo. 014_240 Ste3 172 G-----CIAVRFVRSRRRLRSLSLHSSGIDVGLQRLRIGLATSADLCLGPFVSVYIYFEASQNLN----PWSWN 234
V.hum. CBS8242_02_253 Ste3 176 -----AYAWFFFTTRACVKAVLDHNSGIDLSHYFRLIMALASTDVAFGIPLSVYPLVTTIPVLR----PWSWS 241
A.dom. 002_745 Ste3 174 G-----AIALRFLYLRLLQHTVLRSSRSRSDSRHYLRIMALASVDIILGLPATLFTLIVNIRQR----SYPSWD 240
C.neo. Ste3 mat alpha CNAG_06808 174 G-----VVALRFLYLRLLQHTVLRSSRCSDRHYLRIMALASVDIILGLPATLFTLIVNIRQR----SYPSWD 240
C.gat. Ste3 mat alpha CGB_I1090W 174 G-----ALAIRFLYLRLLQHTVLRSSRSDSRHYLRIMALASVDIILGLPATLFTLIVNIRQR----SYPSWD 233
T.tep. JCM11965 Ste3 173 A-----ALAVRWFLLRRLQFRTILASSDAKLSIGRFRILIALAVTDSVVVIVYAAANALSDSSLPMPYRPNWA 243
C.neo. Ste3 mat a AAN75624.1 173 A-----ALAVRWFLLRRLQFRTILASSDAKLSIGRFRILIALAVTDSVVVIVYAAANALSDSSLPMPYRPNWA 243
C.gat. Ste3 mat a AEG78597.1 173 A-----ALAVRWFLLRRLQFRTILASSDAKLSIGRFRILIALAVTDSVVVIVYAAANALSDSSLPMPYRPNWA 243
C.ole. Ste3 Triol1|339518 174 A-----ALAMRWFVRRRAQFRLSILSGG--ITTGVYLRLLGLAITSILMLGTFVFNLLILFVHGADIQPTSDW 242
C.muc. JCM9939 Ste3 174 A-----GLAMRWFVRRRAQFRLSILSGG--ITTGVYLRLLGLAITSILMLGTFVFNLLILFVHGADIQPTSDW 242
C.arb. JCM14201 Ste3 174 A-----SLATRWFLLRRLQFRTILASSDAKLSIGRFRILIALAVTDSVVVIVYAAANALSDSSLPMPYRPNWA 242
C.cur. Ste3.1 173 A-----GIAMRYAFKHAEBVYKHLRGTGA--INSGRYMRLIAGLAVVDFCLFCLFCTLELLIGRFAVYHDLIMPYKSWK 241
C.das. JCM11166 Ste3 173 A-----ALAVRWFLLRRLQFRTILASSDAKLSIGRFRILIALAVTDSVVVIVYAAANALSDSSLPMPYRPNWA 241
V.hum. JCM1457_001_295 Ste3 172 A-----CVATRWFLLRRLQFRTILASSDAKLSIGRFRILIALAVTDSVVVIVYAAANALSDSSLPMPYRPNWA 240
V.hum. UJ1 Ste3 172 A-----CVATRWFLLRRLQFRTILASSDAKLSIGRFRILIALAVTDSVVVIVYAAANALSDSSLPMPYRPNWA 240
T.asa. EJT49421.1 127 AGEHPENHLSPPAYRFGSADRQGLAVYVFKRSQFRLSILSGG--ITTGRVFRILAAALMSDVSISLFTLNFVLRIVVYHTGTPYVSWA 217
T.cor. 023_151 Ste3 173 A-----GLAVYRFLKRSRFRSILSGG--ITTGRVFRILAAALMSDVSISLFTLNFVLRIVVYHTGTPYVSWA 217
T.ink. 003_120 Ste3 173 A-----GLAVYRFLKRSRFRSILSGG--ITTGRVFRILAAALMSDVSISLFTLNFVLRIVVYHTGTPYVSWA 241
T.kor. JCM12878 Ste3 173 A-----GMALRFLYLRLLQHTVLRSSRCSDRHYLRIMALASVDIILGLPATLFTLIVNIRQR----SYPSWD 242

Ste3 α group
Ste3 a group

A.dom. Apiotrichum domesticum
C.gat. Cryptococcus gattii
C.neo. Cryptococcus neoformans
C.arb. Cutaneotrichosporon arboriformis
C.cur. Cutaneotrichosporon curvatus
C.cya. Cutaneotrichosporon cyanovorans
C.das. Cutaneotrichosporon daszewskae
C.der. Cutaneotrichosporon dermatis
C.muc. Cutaneotrichosporon mucoides

C.ole. Cutaneotrichosporon oleaginosa
T.kor. Takashimella koratensis
T.tep. Takashimella tepidaria
T.asa. Trichosporon asahii
T.cor. Trichosporon coremiiforme
T.fae. Trichosporon faecale
T.ovo. Trichosporon ovoides
V.fra. Vanrija fragicola
V.hum. Vanrija humicola