Signal peptide

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Fol-EC14   1 MRTA-AF--I-TLLASVVSAT----PFGQR-----SQVLARASETCPVVFDGRVPANASL
Fuspro1    1 MRTA-AF--V-TLLASVVSAS----PFGQR-----SQVLARASETCPVVFDGRVPANASL
Fusman1    1 MRTA-AF--I-ALLASVVSAS----PFGQR-----SQVLARASETCPVVFDGRVPANASL
Fusfuj1    1 MRTA-AF--I-TLLASVVSAS----PFGQR-----SQVLARASETCPVVFDGRVPANASL
Fusnyg1    1 MRTA-AV--I-TLLASVVSAT----PFGQR-----SQVLARASETCPVIFDGRVPANASL
Fusver1    1 MRTA-SV--I-TLLASVVSAT----PFGQR-----SQVLPRASETCPVVFDGRVPANASL
Fuscul1    1 MRAA-AI--I-ALFASVAFAA----PADSR-------SCSKAKNTCPVVFDGRVPANASL
Fusgra1    1 MRAA-AI--I-ALFASVAFAA----PADSR-------SCSKAKNTCPVVFDGRVPANASL
Fuspse1    1 MRAA-AV--I-ALFASVAFAA----PADSR-------SCSKAKNTCPVVFDGRVPANASL
Fuslan1    1 MRAA-AI--I-TLLASVASAA----PADNR-------SCSKAKNTCPVVFDGRVPANASL
Fuspoa1    1 MRAA-AI--I-TLLASVASAA----PADDR-------SCSKAKNTCPVVFDGRVPANATL
Fusven1    1 MRAA-AI--I-TLLASVASAA----PADDR-------SCSKAKNACPVVFDGRVPANATL
Neodit1    1 MHRS-AV--F-ALLASAASAA----PF-HG-----FHAFTNKSSSCPVIFDGRVPANASL
Fussol1    1 MRAA-AF--F-ALVSSVVSAT----PLGHR-----FHTYSKASNSCAVVFDGRVPANASL
Colchl1    1 MPLQ-VI--I-LLTTVALAT----TKP---------CTPPPLTKCPVILDGRIPSFAIS
Colfio1    1 MRSSFLI-PL-LIAIPSSLAS----PSP---------CLTATIQCPLVFDGRVPVTATP
Colnym1    1 MRSPFLI-PI-LIAIPSALGS----PSP---------CTAAAIQCPLVFDGRVPATATP
Colsim1    1 MRSPFLI-PF-LIAIPSALAS----PSP---------CLTATIQCPLVFDGRAPATATP
Colglo1    1 MHP------L-TLLTLATPAL----SVTL--------TCRSL-IRCPLIFDGRVPSTAIP
Colgra1    1 MFSR-AA-LL-LLLTPATLAA----ATP---------NCHAAAVRCPIVFDGRVPAVATP
Colinc1    1 MFSH-TA--L-LLLAPAALAA----STL---------GCRAASLKCPIVFDGRVPATATP
Coltof1    1 MLPH-TA--L-LLLAPAAFTA----ATL---------NCRAASIKCPIVFDGRVPATATP
Colhig1    1 MIPP-AA--L-LLLALAILAA----SSPS--------NCGAASIRCPLIFDGRVPAAAVP
Colorb1    1 MRLF----LLSILFLSLTLAA-------------SLRCSAPSIQCPLIFDGRVPSTAIP
Veralf1    1 MLPS-VLTVL-SALVASSIAK----PVT---------KCRQAAVTCPIVFDGRVPQTATV
Verdah1    1 MLPS-VLTVL-SALVASSLAK----PVT---------KCRQAAVTCPIVFDGRVPQTAKV
Verlon1    1 MLPS-VLTVL-SALVASSFAK----PVT---------KCRQAAVTCPIVFDGRVPQTATV
Lompro1    1 MFRS-----L-FFLALAQAAF----ALP----------AAEPSCPVVFDGRVPADAEP
Sceapi1    1 MFRS-----L-LLLALTQGIF----ALP----------AAEPSCPIVFDGRVPKDASL
Chathe1    1 MHR--SI-LL-TLITTAIAVLARP-PSRHPHS--PSAAAAPGTIKCPIIFDGRIKTTTQL
Madmyc1    1 MHH--AI-LL-SLL-TAGTAVTAR-PSFSQEP--PINQHVATAIQCPIVFDGRVGATTEL
Thiter1    1 MHR--AT-LV-GLLAAAATTVTGA-PSCSG-----VHAAAPGTVKCPLVFDGRVKATAAL
Thethe1    1 MHST-TT-LL-SLLSAAAAANGASLPRDSV-------CGAAAEIQCPIVFDGRVSADAQP
Conlig1    1 MVHQ-TI-LL-ALLSALTVSAR---P-----------SKCAAEPKCPIVLDGRVKTTLVP
Daldsp1    1 MISS-AL-FTGFLLASSASAR----PT----------KRGTGEIKCPIILNGFVPADLTP
Hyposp1    1 MISS-AL-LTGLLLTSSASAH----PT----------KRGTGEIKCPVVLSGFVPVDKTP
Rosnec1    1 MVSS-TL-LLGGILAAATLSFALP-PSPPE-------RRGAGAIKCPVVLNGLVGVSLTP
Phamin1    1 MVSY-TL-VF-AALAAAVSCA----P-----------CASNATIKCPIVFDGRIAASAAL
Spobra1    1 MKAFSSL-LF-AGVAAAV------PTGQA----ADADTPAATVKCPIVFDGRVPSTLAL
Sposch1    1 MKAFSSL-LF-AGVAAAV------PTGQA----ADADAPAATVKCPIVFDGRVPSTLVL
Spoins1    1 MHALASL-LLTAGVAVAVPASSSS-SSAAASTP-TAAAAAAATVKCPIVFDGRVPPSLKL
Podans1    1 MHP--SL-LL-GLLAGTALAGTIRRPGRPR------PQAPTAETLCPIVFDGRPDSSLEP
Neucra1    1 MLT--PT-IL-TLLFTLATTALAV-PQPH----------AALIKCPVILDGRIKIHTQL
Neutet1    1 MLT--PT-IL-TLLFTLATTALAV-PHPH----------AALIKCPLIFDGRIKTRTQL
Sormac1    1 MHA--ST-IF-GFLAAAATAVLAV-PHPHK--------EKAAVKCPLIFDGRIKSRTLP
Pesfic1    1 MFS--QI-VMSSLLATLATAR----PSP----------RAAASCPVVLSGRVPASAQL
Psevex1    1 MFSV-AL-VF-GLTATAASAG----PL-----------LTPRIDITCPIVLEGRVASSTAL
Eutlat1    1 MVSS-TI-LV-SLFASLAVARR---PGRRQ---------GSGTITCPITLDGRVPVDTEL
Gaetri1    1 MTLA-RH-LANALLAVAVAVA-----------------GAAEVKCPIVFDGRVPASLAL
Magory1    1 MPLA-AL-IPALLLAAAAAAAAT-PLSPR------AADPAGPIRCPIVFDGRVPATLAA
Maggri1    1 MPLA-PL-FSVLLLAAAASAT----PLAVR------AADPTGTIQCPIVFDGRVPTTLVS
Conlus1    1 MLFT-SP-IL-ALSALVAIAT----ASPRICQTHASKTTNSSTIKCPIVLDGRVPANASL
Diaamp1    1 MFSA-SL-LL-ALGTTAVAAI----PYETR-------SPSSGVVQCPVILEGRIPASSVL
Diahel1    1 MFSV-SL-LL-GLGATIAAAI----PSGPR-------SLTSGSVKCPVVFEGRVPTSTTL
Micbo11    1 MALK-AF-FTTSLVALASLASALP-PVPGR------PGATATKISCPVVFSGQIPIAAKL
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Fol-EC14   48  TDFDTANGGGWNPYNPGFVKGNNISWSEILQLP---------------K-TKT--------K-SRF
Fuspro1    48  TDFDTANGGGWNPYNPGFVKGNNISWSEILQLP---------------K-TKT--------K-SRF
Fusman1    48  TDFDTANGGGWNPYNPGFVKGNNISWSEILQLP---------------K-TKT--------K-SRF
Fusfuj1    48  TDFDTANGGGWNPYNPGFVKGNNISWSEILQLP---------------K-TKT--------K-SRF
Fusnyg1    48  TDFDTANGGGWNPYNPGFVKGNNISWSEILKLP---------------K-TKT--------K-SRF
Fusver1    48  TDFDTANGGGWNPYNPGFVKGNNISWSEILKLP---------------K-TKT--------K-SRF
Fuscul1    46  ADFDKENGGGWNPYNPGFVKGNNISWSEIIKLP---------------Q-TTP----------SRF
Fusgra1    46  TDFDKENGGGWNPYNPGFVKGNNISWSEIIKLP---------------Q-TTP----------SRF
Fuspse1    46  TDFDKENGGGWNPYNPGFVKGNNISWSEIIKLP---------------Q-TTP----------SRF
Fuslan1    46  SDFDKENGGGWNPYNPGYVKGNNISWSEIVKLP---------------Q-TTP----------SRF
Fuspoa1    46  ADFDKENGGGWNPYNPGYVKGNNISWSEIIKLP---------------Q-TTP----------SRF
Fusven1    46  ADFDKENGGGWNPYNPGFVKGNNISWSEIVKLP---------------Q-TTP----------SRF
Neodit1    47  ADFDTARGGGWNPFNPGYVKGNNLSWSDILLLP---------------N-HVP--------A-SRF
Fussol1    48  TDFDTENGGGWNPFNPGYVKGNNISWSEILLLP---------------K-NTP--------R-SRF
Colchl1    44  IDFNTAQGGGWSPFNPDYVKGSSLAWSDILLLP---------------D-AVP--------P-SRF
Colfio1    45  RDFDTSLGGGWNPYNPDYVKGTNLSWSDIILLP---------------G-PAPVPTRPGSRS-SRF
Colnym1    45  QDFDTALGGGWNPYNPDYVKGASLSWSDIILLP---------------E-SAPVSTRPGSRS-SRF
Colsim1    45  QDFDTALGGGWNPYNPDYVKGTNLSWSDIILLP---------------E-SAPVSTRPGSRS-SRF
Colglo1    41  TDFDTPNGGGWNPFNPSYVKGNTLLWSDIVLLP------------------SGP--------T-SRF
Colgra1    45  QDFDTASGGGWNPYNPGYVKGEGLLWSDIILLPLPSPQEEEEE-AAP--------P-SRF
Colinc1    44  QDFDSASGGGWNPYNPGYVKGEGLLWSDIILLP---------------Q-VAP--------P-SRF
Coltof1    44  QDFDSASGGGWNPYNPGYVKGEGLLWSDIILLP---------------Q-VAP--------P-SRF
Colhig1    45  GDFDSASGGGWNPYNPDYVKGKGLLWSDIILLP---------------R-AGP--------P-SRF
Colorb1    43  TDFDSTT--WNPYNPSYVKGASLFWSEILLFP---------------PTP--------P-SRF
Veralf1    46  QDFDTAGGGGFNPFNPNFVKGNNLTWSEILLLP---------------T-ITP--------A-SRF
Verdah1    46  QDFDTAGGGGFNPFNPNFVKGNNLTWSEILLLP---------------T-ITP--------A-SRF
Verlon1    46  QDFDTAGGGGFNPFNPNFVKGNNLTWSEILLLP---------------T-ITP--------A-SRF
Lompro1    39  TDFDANNGGGWMPFNSGYVKGETLKWSEILQFP---------------E-VAE--------A-SRF
Sceapi1    39  TDFDANNGGGWMPFNPGYVKGETLKWSEILKLP---------------E-VAE--------A-SRF
Chathe1    54  TDFDSYST---SPFNPDYVKGQTLKWSDIIKFP---------------S--VS--------P-SRF
Madmyc1    53  TDFDSYGT---SIFNPDYVKGQNLKWSQIIKFP---------------E--VA--------N-SRF
Thiter1    51  TDFDSAST---SPFNPDYVKGNNLKWSQIIKFP---------------Q--TS--------N-ARF
Thethe1    51  TDFDSAST---SIFNPDYVKGNNLKWSDILQFP---------------D--AG--------T-THF
Conlig1    44  TDFDSYAT---SPFNPDYVKGNNLKWSDILQFP---------------T-DVG--------T-SRF
Daldsp1    45  TDFDSYAT---SPFNPDYIRGSE-KFSEILQFP---------------E--VE--------S-SRF
Hyposp1    45  TDFDSYAT---SPFNPDYIRGSE-KFSQILLFP---------------D--AG--------S-SRF
Rosnec1    51  ADFDSYAT---SPFNPDYVRGGE-KFSQTLRFP---------------A-VAA--------S-SRF
Phamin1    43  TDLDSSST---SPFNPDYVKGNSLKWSNIILFP---------------S--VP--------N-SRF
Spobra1    48  TDFDSYSKG--SPFNAEYVKGNDLKWSEILLLP---------------S--VP--------T-SRF
Sposch1    48  TDFDSYSKG--SPFNAEYVKGNDLKWSEILLLP---------------S--VP--------T-SRF
Spoins1    58  ADFDASGSG--SPFNPGYVKGNDLKWSDILLLP---------------S--VA--------APSRF
Podans1    51  LDFDDWNT---SPFNPDYVKGAGLPWSSILQFP---------------D-ISP--------P-ARF
Neucra1    45  TDFDSSAT---SLFNPDSVKGSSLKWSQIIQFP---------------EGDKG----------SRF
Neutet1    45  TDFDSSAT---SLFNPDNVKGSSLKWSQIIQFP---------------EGDKG----------SRF
Sormac1    47  TDFDSSST---SLFNPDNVKGSSLKWSQIVKFP---------------K-EKG----------SRF
Pesfic1    42  TDFDSSAT---SLFNPDYVRASAIPWSQILLFP---------------N--VT--------N-SRF
Psevex1    44  SDFDSYST---SIFNPDYVRGSQ-PWSQILVFS---------------N--TT--------N-SRF
Eutlat1    46  ADFDSYAT---SPFNPDYIRGDE-SHSETLLFP---------------D--VP--------N-SRF
Gaetri1    41  TDFDSPGRG--SPFGTGYVKGEGLLWSDILKFP---------------TAAAG--------P-PRF
Magory1    52  TDLDDAAR---SPFNTGYVKGEGLKWSDITEFP---------------A-GAG--------Q-PRF
Maggri1    49  TDLDDATR---SPFNTGYVKGEGLKWSDIIKFP---------------T-EVG--------Q-PRF
Conlus1    54  TSFDTAN----GLFNPDYVKGNNLSWSDILLFP---------------T-VAT--------N-SRF
Diaamp1    47  TDFDVEN----DLFNPGYTKGNNLSWSDILLFP---------------D--VA--------N-SRF
Diahel1    47  KEFDVEN----ELFNPDYVKGNNLTWSNVVRFP---------------D--VP--------N-SRF
Micbo11    52  TDFDAAAT---SLFNPNNVKGND-TWSQIIKFP-------AAAGAAP---GNAACGLARF
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Fol-EC14  89  DI------EAGTIPLEVTISDKSIFMKQLGFRRAGLQFNKDSNEGSPGSKGVKTLHFSIM
Fuspro1   89  DT------EAGTIPLEVTISDKSIFMKQLGFRRAGLQFNKDSNEGSPGSKGVKTLHFSIM
Fusman1   89  DT------EAGTIPLEVTISDKSIFMKQLGFRRAGLQFNKDSNEGSPGSKGVKTLHFSIM
Fusfuj1   89  DT------EAGTIPLEVTISDKSIFMKQLGFRRAGLQFNKDSNEGSPGSKGVKTLHFSIM
Fusnyg1   89  DT------EAGTIPLEVTISDKSIFMKQLGFRRAGLQFNKDSNEGSPGSKGVKTLHFSIQ
Fusver1   89  DT------EAGTIPLEVTISDKSIFMKQLGFRRAGLQFNKDSNEGSPGSKGVKTLHFSIQ
Fuscul1   86  DV------SGKTLPLEVTISDKSIFMKQLGFRRAGLQFSKDKNEGSPGSEGIKTLHFSIM
Fusgra1   86  DV------SGKTLPLEVTISDKSIFMKQLGFRRAGLQFSKDKNEGSPGSEGIKTLHFSIM
Fuspse1   86  DV------SGKTLPLEVTISDKSIFMKQLGFRRAGLQFSKDKNEGSPGSEGIKTLHFSIM
Fuslan1   86  DV------SGKTLPLEVTISDESIFMKQVGFRRAGLQFSKDKNEDSPGSEGIKTLHFSIM
Fuspoa1   86  DA------TGKTLPLEVTISDESIFMKQVGFRRAGLQFSKDKNEGSPGSEGIKTLHFSLI
Fusven1   86  DA------SGKTLPLEVTISDESIFMKQFGFRRAGLQFSKDKNEGSPGSEGIKTLHFSLM
Neodit1   88  DA------AAAVPVEVTIADESIFMKQNGFRRAGLQFNEDANEDSPASEGVVTLHFSLL
Fussol1   89  DA------VSRTVPLKVTISDESIFMQQHGFRRAGLQFAKDDNEKSPASEGVKTLHFSIL
Colchl1   85  DR------AQNQRPLEVTISDESIFMSQRGFRRAGLLFGADTNTGSPASTGVKTLHFSVR
Colfio1   94  DA-----AEKRRSLEVTISDASIFMNQQGLRRAGLLFSGDANEGSPAGEGVKTLHFSVR
Colnym1   94  DA-----AEKKRALEVTISDASIFMNRGFRRAGLLFAGDTNEGSPAGEGVKTLHFSVR
Colsim1   94  DA-----AEKKRALEVTLSDASIFMNQRGFRRAGLLFAGDTNEGSPAGEGVKTLHFSVR
Colglo1   81  DA-----AAGSRAVEVTISDESIFMSQRGFRRAGLQFAADANTGSPAGEGAKTLHFSVR
Colgra1   95  DA-----GGGTRPLEVTVSDRSIFMNQRGFRRAGLQFAADANVGSPAAAGVKTLHFSVR
Colinc1   85  DS-----REKKRPLEVTISDKSIFMSQRGFRRAGLQFAKDTNVGSPAGTGAKTLHFSVR
Coltof1   85  DA-----REEKRPLEVTISDKSIFMDQRGFRRAGLQFAMDANVGSPAGTGAKTLHFSVR
Colhig1   86  DA-----GEERRPLEVTISDASVFMDQRGFRRAGLLFAGDANVGGPAGAGVKTLHFSVR
Colorb1   81  DT------LPSTRAIEVTVSDDSIFMNQRGFRRAGLQFLADTNTGSPAAKGVVTLHFSVA
Veralf1   87  DA------AKNTRPVEVTISDESIFMTQLGFRRAELQFANDTGSGSPGSVGVKTLHFSVQ
Verdah1   87  DA------AKNTRPVEVTISDESIFMTQLGFRRAELQFANDTGSGSPGSVGVKTLHFSVQ
Verlon1   87  DA------AKNTRPVEVTISDASIFMTQLGFRRAELQFANDTGSGSPGSVGVKTLHFSVQ
Lompro1   80  DA------DAGTIPVEVTLSDKSIFMTQNGFRRAGLQFLKDTNEGSPATTGKKTIHFSLR
Sceapi1   80  DS------DSGTVPLEVTLSDKSIFMTQNGFRRAGLQFLKDSNEGSPASKGKKTIHFSLR
Chathe1   91  DD-----PDQHKPIEVTISDASIFMNQRGFRRAGLQFQGDSNTGSAGSKGVKTIHFSVR
Madmyc1   90  DN-------ETHKPFEVTISDASIFQSQRGFRRAGLQFQGDSNNGSPGSSGVKTIHFSVR
Thiter1   88  DN-------NSTKAEVTISDASIFQSQQGFRRAGLQFQGDTNNGSPGTTGVKTIHFSIK
Thethe1   88  DN-------ETHKPFEVTLSDESIFQSQQGFRRAGLQFNGDTNNGSPGSQGVKTIHFSVK
Conlig1   82  DN-------ASYKPFEVTISDASIFQQQNGFRRAGLQIQGDTNTGSPANTGVRTLHFSVR
Daldsp1   81  DN-------ESTRAVEVTINDKSIFQKQNGFRRAGLQIQGDTNENGPGTTGVRTLHFSVK
Hyposp1   81  DN-------ASTKSVEVTINDKSIFQTQNGFRRAGLQIQGDTNENGPGTTGVRTLHFSVK
Rosnec1   88  DN-------ASTKAVEVTINDRSIFQAQNGFRRAGLQIQGDTNEGGPGTVGIRTLHFSVK
Phamin1   80  DN-------ASHRPLEVTLSDKSVFQSQNGFRRAGLQFAGDSNNGSPGYTGIKTLHFSVK
Spobra1   86  DAAVNTSGAAFKALEVTLSDKSIFQKQNGFRRAGLQLNGDTNTGSPGFTGIKTLHFSVK
Sposch1   86  DAAVNTSGAAFKALEVTLSDKSIFQKQNGFRRAGLQLNGDTNTGSPGFTGIKTLHFSVK
Spoins1   97  DAAVNSSGAKPFQAVEVTLSDKSIFQKQQGFRRAGLQFNGDTNTGSPGYTGIKTLHFSVQ
Podans1   89  DD------PTYQKPFEVTINDSSIFNNQRGFRRAGLQFQGDTNRDSPGSSGIKTIHFSLK
Neucra1   83  DG-------CSHKPLEVTIADASVFKTQYGFRRAGLIFNGDKNIGSPASRGVKTLHFSVR
Neutet1   83  DS-------CSHKPLEVTIADASVFKTQYGFRRAGLIFNGDKNIGSPASRGVKTLHFSVR
Sormac1   84  DN-------CSHKPLEVTISDESVFKTQYGFRRAGLIFAADTNTGSPASKGVKTLHFSVR
Pesfic1   79  DG-------ADFKSVEVTISEKSIFQTQNGFRRAGLQLANDTNTQGPGTTGVRTLHWSVK
Psevex1   80  EN-------ASYKSIEVTISDQSIFQSQNGFRRAGLQINGDTNTGGPGSKGVKTLHWSVK
Eutlat1   82  DD-------EGFKSVEVTISDLSIFQEQNGFRRIGLQIQGDENEGGPGIVGVKTLHWSVK
Gaetri1   81  EN------ASLHKPITVTLSDRSIFQTQRGFRRAGLQFDGDSNTGGEGSAGVRTLHWSVK
Magory1   90  ED------AASHKPITVTLSDRSVFQTQRGFRRAGLQFRDDANAGGAGAVGVRTLHWSVK
Maggri1   87  EN------SSSHKPITVTLSDRSIFQTQRGFRRAGLQFKDDANTGGRGAVGVRTLHWSVK
Conlus1   91  DS----ADAAQYKPIEVNINNASVYQAQYGFRRAGLLFANDSNTGSLGYTGVKTLHWSVQ
Diaamp1   83  DN-------ASYKSVEVTISDESIFQKQYGFRRAGLLFANDINEGSLGYQGLKTLHWSVK
Diahel1   83  DN-------ASYKSVEVTISDQSIFQKQNGFRRAGLLFANDPNEGSFGYQGLRTLHWSVR
Micbo11   98  DD------PAKHKSFEVTINDRSIFKTQFGFRRAGLLFKNDTNAAGPGNTGVKTLHWSVK
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Fol-EC14 143 QDDKRPLNLSHEYLNVWHEKADFSGNQFQFQAGQLIGQ-N--GTAATWKLLDQDFKLLWE
Fuspro1  143 QDDKRPLNLSHEYLNVWHEKADFSGNQFQFQAGQLIGQ-N--GTAATWKLLDQDFKLLWE
Fusman1  143 QDDKRPLNLSHEYLNVWHEKADFSGNQFQFQAGQLIGQ-N--GTAATWKLLDQDFKLLWE
Fusfuj1  143 QDDKRPLNLSHEYLNVWHEKADFSGNQFQFQAGQLIGQ-N--GTAATWKLLDQDFKLLWE
Fusnyg1  143 QDDKRPLNLSHEYLNVWHEKADFSGNQFQFQAGQLIGQ-N--GTAATWKLLDQDFKLLWE
Fusver1  143 QDDKRPLNLSHEYLNVWHEKADFSGNQFQFQAGQLIGQ-N--GTAATWKLLDQDFKLLWE
Fuscul1  140 QDKSRPLNLSHEYINVWHEKADFSGNQFQFQSGTIIGQ-N--HTAATWKLFDEKMKLLWE
Fusgra1  140 QDKSRPLNLSHEYINVWHEKADFSGNQFQFQSGTIIGQ-N--HTAATWKLFDEKMKLLWE
Fuspse1  140 QDKSRPLNLSHEYINVWHEKADFSGNQFQFQSGTIIGQ-N--HTAATWKLFDEKMKLLWE
Fuslan1  140 QDKSRPLNLSHEYLNVWHEKADYSGNQFQFQAGTIIGQ-N--HAASTWKLFDEKMKLLWE
Fuspoa1  140 QDKNRPLNLSHEYLNVWHEKADYSGNQFQFQAGTIIGQ-N--HAAATWKLFDEKMKLLWE
Fusven1  140 QDKNRPLNLSHEYLNVWHEKADFSGNQFQFQAGTIIGQ-G--HAAATWKLFDEKMKLLWE
Neodit1  142 QDESRPLNLSHEYLNVWHEAADYSSNQFNFQTGAMIDQPT--LPKDTYKLLDRTNKEIWS
Fussol1  143 QDESRPLNLSHEYLNVWHEAGDYSSNQFNFEAGTIIGQ-D--LPKDTWKLLDRTNKQIWS
Colchl1  139 QDPSRPLNLTHEYLNVWHETAAYDANQFSFQAGTIFGQAG--FPKDTFKLLDRDNKLVWS
Colfio1  148 LNSERPLNLTHEYLNVWHETAAYDANQFNFQTGTIIGQPR--LPKDTFKLLDRDNKLIWS
Colnym1  148 LDLERPLNLTHEYLNVWHETAAYDANQFNFQTGTIIGQPE--LPKDTYKLLDRDNKLIWS
Colsim1  148 LDLERPLNLTHEYLNVWHETAAYDANQFNFQTGTIIGQPA--LPKDTFKLLDRDNKLLWL
Colglo1  135 QDAERPLNLTHEYLNVWHETAAYDANQFNFQTGTIIGQSG--LPEDTFKLLDRENRLVWS
Colgra1  149 QDAARPLNLTHEYLNVWHETAAYDANQFNFQTGTLIGREG-LLPKDTFKLLDRDNKLIWS
Colinc1  139 QDAAKPLNLTHEYLNVWHETAAYDANQFNFQTGTIIGQAG--LPKNTFKLLDRNNKLVWS
Coltof1  139 QDPARPLNLTHEYLNVWHETAAYDANQFNFQTGTIIGQAG--LPKNTFKLLDRDNKLVWS
Colhig1  141 QDAARPLNLTHEYLNVWHETAAYDANQFSFQTGTIIGQPG--LPRDTFKLLDRDNRLVWS
Colorb1  135 QDIERPLNLTHEYLNVWHETAAYDANQFNFQTGTIIGQEG--LPEKTWKLLDRNNQLMWS
Veralf1  141 TDAQRRFNESHEYLNVWHETAVFDANQFNFQTGTIIGQPE--LPANTWKLLDRNNALLWS
Verdah1  141 TDAQRRFNESHEYLNVWHETAAFDANQFNFQTGTIIGQPE--LPANTWKLLDRNNALIWS
Verlon1  141 TDAQRRFNGSHEYLNVWHETAAFDANQFNFQTGTIIGQPE--LPANTWKLLDRNNALIWS
Lompro1  134 TDPQRTLNLTHEYILVWHETAAYDANQFNFQTGTILGQTG--LPAETYKLLDRSNKQIWS
Sceapi1  134 TDPQRALNLTHEYILVWHETAAYDANQFNFQTGTILGQTG--LPRDTYKLLDRNNKQLWS
Chathe1  145 WDNARPLNLSHEYLNVWHETADYSANQFNFEGGAILGQTQ--LPADTWKVLDRNNRQIWA
Madmyc1  143 WDAQRALNLSHEYLNVWHEAADYSANQFNFQAGAILGQSS--LPRDTYKVLNRQNRQVWS
Thiter1  141 LDPQRPLNLSHEYLNVWHESADYSANQFNFEAGTIIGQSG--LPKNTWKVLNRQNQQIWS
Thethe1  141 IDPQRGLNLSHEYILVWHEAADYSANQFNFETGTIIGQEG--LPKDTYKVLNRNNQQIWS
Conlig1  135 QDPKRPLNLTHEYLNVWHEASDYSADQFMFEAGTIIDQTG--LPKNTFKVLNRQSKQIWS
Daldsp1  134 QDPERTLNLTHEYLNVWHESADYSANQFNFQSGTIIGKSG--SDKNNFKILNRQNTQVWS
Hyposp1  134 QDPERALNLTHEYLNVWHETSDYSANQFNFEAGTIIGKSG--SDKNSFKVLNRQNTQVWS
Rosnec1  141 QDPQRRLNLTHEYLNVWHETADYSANQFNFQAGTLIGRNS---NKNTFKVLNRQNTEVWS
Phamin1  133 QDPARALNLSHEYLNVWHEAADYSADQIMFETGTILGQTG--LPKNTFKFFDRNMKQIWS
Spobra1  146 QDAQRPLNLSHEYLNVWHEASDYSADQIMFQAGTLIDQAG--LPKNTFKVMSRQNKQIWS
Sposch1  146 QDAQRPLNLSHEYLNVWHEASDYSADQIMFQAGTLIDQAG--LPKNTFKVMSRQNKQIWS
Spoins1  157 QDAQRPLNLSHEYLNVWHESSDYSADQIMFQTGTLIDQAG--LPKNTWKVLSRTNKLIWS
Podans1  143 WDAQRPLNLSHEYLNVWHETADYSANQFNFQAGAILGQNS--LARDTWKVLNRQNRQVWS
Neucra1  136 QDEARGLNLTHEYLNVWHETSDWSANQFNFETGTIIGQEG-SLAKNTFKIMSRENKLIWS
Neutet1  136 QDEARGLNLTHEYLNVWHETSDWSANQFNFQTGTIIGQEG-SLAKNTFKIMSRENKLIWS
Sormac1  137 QDLKRPLNLTHEYLNIWHETSDWSANQFNFQTGTIIGQDTRKLPKNTFKIMSRENKLIWQ
Pesfic1  132 QDPTRTLNLTHEYLNVWHERADYNGNQFNFETGTIIDNSS--LDKNTFKITNRNSEVIWS
Psevex1  133 QDSSRPLNLTHEYLNVWHERADYNGNQFNFQTGTVIGQ-S--YAKDTFKILDRQNVLVWS
Eutlat1  135 QDPARTFNLIHETYGM--RRARYDGNQFNFETGTIIGRPG---NENTFKILDRQNTEVWS
Gaetri1  135 IDPGRALNLSHEYLNVWHETSDYSANQFNFEMGTILGQTS--LPRDTFKILNRQNRQIWS
Magory1  144 IDAARGLNLSHEYLNVWHETADYSANQFNFEMGSILGQPE--LPSDTFKILDRRNRQIWS
Maggri1  141 IDPARGLNLSHEYLNVWHETADYSANQFNFEMGSILGQPD--LPSDTFKILDRRNQQIWS
Conlus1  147 QDPQRALNLSHEYLNVWHESADYSADQIMFQAGSILAQPG--LARDTFKVFDRNSSLIWS
Diaamp1  136 QDSARALNLSHEYLNVWHESADYSGDQFMFQTGAMLDYPD--MPSDTFKFFDRNATLIWS
Diahel1  136 QDPALALNLSHEYLNVWHERADYSANQFSFQTGLMIDHPE--LSADSFKFFDRDGRLIWS
Micbo11  152 QDPARPLNLTHEYLNVWHEAGDFSSNHFHFTAGSLIGRPE--FPANTFKILNRKLDVIFS
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Fol-EC14  200  TPMLKK-VWQNFAITLNYEKNTIQAYYS-KGCKPLKVAT-QPIARNLTGQGQFQIGILKK
Fuspro1   200  TPMLKK-VWQNFAITLNYEKNTIQAYYS-KGCKPLKVAT-QPIARNLTGQGQFQIGILKK
Fusman1   200  TPMLKK-VWQNFAITLNYEKNTIQAYYS-KGCKPLKVAT-QPIARNLTGQGQFQIGILKK
Fusfuj1   200  TPMLKK-VWQNFAITLNYEKNTIQAYYS-KGCKPLNVAT-QPIARNLTGQGQFQIGILKK
Fusnyg1   200  TPMLKK-VWQNFAITLNYEKNTIQAYYS-KGCKPLKAAT-QPIARNLTGQGQFQIGILKK
Fusver1   200  TPMLKK-VWQNFAITLNYEKNTIQAYYS-KGCKPLKAAT-QPIARNLTGQGQFQIGILKK
Fuscul1   197  TPMLEG-KWQNFAITLNFDKNTIQAYYS-EGPKALKAAT-QPIARDLSGQGQYQIGMLKK
Fusgra1   197  TPMLEG-KWQNFAITLNFDKNTIQAYYS-EGSKALKAAT-QPIARDLSGQGQYQIGMLKK
Fuspse1   197  TPMLEG-KWQNFAITLNFDKNTIQAYYS-EGSKALKAAT-QPIARDLSGQGQYQIGMLKK
Fuslan1   197  TPMLKG-KWQNFAITLNFDKNTIQAYYS-EGSKPLKAAT-KPIARDLSGQGQYQIGMLKK
Fuspoa1   197  TPMLKG-KWQNFAITLNFDKNTIQAYYS-EGSKPLKAAT-KPIARDLSGQGQYQIGMLKK
Fusven1   197  TPMLKA-KWQNFAITLNFDKNTIQAYYS-EGSKPLKAAT-KPIARDLSGQGQYQIGMLKK
Neodit1   200  TPILPG-SWQNFAITLDFNNNTIQAWYS-EGNKPLLPAT-KPVANDNSGRGQYQIGILKK
Fussol1   200  TPILKD-VWQNFAITLDFDNNTIQAWYS-EGRKPLRAVT-EPISNDNSGRGQYQIGILKK
Colchl1   197  TPIVTDGSWQNFALTLDFSNNTMQVWYS-AGDAPLTKQG-SIISANLAGEGQYQIGILKK
Colfio1   206  TPMAMDGSWQNFALTLDFLYNTIQIWYS-AGDNPLARQG-GGVPVDLAGDGQYQIGILKK
Colnym1   206  TPIAKDGSWQNFALTLDFLNNTIQIWYS-AGNNPLARQG-GAVPVNLAGDGQYQIGILKK
Colsim1   206  TPMAKDGSWQNFALTLDFLNSTIQIWYS-AGNNPLARQG-GAVPVDLAGDGQYQIGILKK
Colglo1   193  TPMATDGSWQNFALTLDFDQNTIQVWYS-ANDEPLQKSG-DIISANLAGQGQYQIGMLKK
Colgra1   208  TPVATDGSWQNFALTLDFSKNTIQVWYS-TGGARLASQG-GAIPANLAGDGQYQIGILKK
Colinc1   197  TPIATDGSWQNFALTLDFSKNTIQVWYS-AGDAPLVKQG-GVISANLTGDGQYQIGILKK
Coltof1   197  TPMATDGSWQNFALTLDFSNNTIQAWYS-AGDAPLIKQG-GVVSANLAGDGQYQIGILKK
Colhig1   199  TPVATDGSWQNFALTLDFPNNTIQVWYS-AGNAPLARQG-GVIAANLLGDGQYQIGLLKK
Colorb1   193  TPLVDDGSWQNFALTLDFDQNTIQVWYS-GGGAPLTKQG-DGILADLAGGGQYQIGILKK
Veralf1   199  TPVLDG-VWQNFGLTLDFNANTIGVLYS-EGDKPLAPSGKGAFPANLAGEGQYHVGILKK
Verdah1   199  TPVVDG-VWQNFALTLDFNANTISVLYS-EGDKPLAPSGKGAFPANLAGEGQYHVGILKK
Verlon1   199  TPVLDG-VWQNFGLTLDFNANTIGVLYS-EGDKPLAPSGKGSFPANLAGEGQYHVGILKK
Lompro1   192  TPIKDD-TWQNFAITIDYTANTIQMWYS-EGDAELAKAT-DPINNNNAGEGQYQVGMLKK
Sceapi1   192  TPIKSD-TWQNFGITVDYTGNTIQVWYS-EGDEELAKAT-DPINNNNAGEGQYQVGMLKK
Chathe1   203  VKIERE-GWQNFAITVDYEKNTLQVYYS-KDDEPLTAVT-SAVYNNNAGEGQFQIGILKK
Madmyc1   201  TPILRD-DWQNFAITVDFNRNTLQVVYS-EGDEPLRSVT-SAVSNNNAGEGQYQIGLLKK
Thiter1   199  TPIVKD-DWQNFAITLDFNKNTLQVYYS-QGTDPLKSVT-SAVSNDNSGEGQYQIGILKK
Thethe1   199  TPILED-QWQNFAITLDFNQNTLQVYYS-EADEPLESVT-DVVSNNNAGEGQYQIGLLKK
Conlig1   193  TPIEST-AWQNFAITLDFNKNTLQVYYS-KGDDPLKSVT-SAVSNDNSGGGQYQIGILKK
Daldsp1   192  TPIDAT-AWQNFAITLDFVKNTLQVYYS-KDDEPLKAVT-EALQNDNSGGGQYQIGILKK
Hyposp1   192  TPIDAT-AWQNFAITLDFVKNTLQVYYS-KDDEPLKAVT-SALQNDNSGGGQYQIGILKK
Rosnec1   198  TPIDET-AWQNFAITLDFNKNTLQVYYS-RGDEPLRSVT-SALSNNNAGGGQYQIGILKK
Phamin1   191  TAVDGT-AWQNFAVTLNINSNTVQVYYS-KDDEPLKSVT-SAVSADLSGQGQFQIGILKK
Spobra1   204  TPISTT-DWQNFAFTLDFNKNTVQVYYS-KGTDPLASVL-KATADDLSGAGQFQIGILKK
Sposch1   204  TPISTT-DWQNFAFTLDFNKNTVQVYYS-KGTDPLASVL-KATADDLSGAGQFQIGILKK
Spoins1   215  TPLVAA-DWQNFALTLDFNKNTVQVYYS-QGSDPLKSVL-TATADDLTGAGEYQIGILKK
Podans1   201  TPILRN-EWQNFAISLDFVRNTLRVYYS-RGSEPLRSVT-NALTNNNAGEGQYQVGILRK
Neucra1   195  TPIEQK-EWQNFAITLDFNKNTLRLYYS-KGHEPLRSVT-QAVPNNNAGEGQYQIGILKK
Neutet1   195  MPIEQK-EWQNFAITLDFDKNTLRLYYS-KGHEPLRSVI-QAVPNNNAGEGQYQIGILKK
Sormac1   197  TPIEKK-EWQNFAITLDFNKNTLQVYYS-KGNEPLRSVT-KAVPNNNAGEGQYQFGILKK
Pesfic1   190  TPIDQS-AWQNFAVTLDYDNNTIQVYYS-LGTEPLTAVT-QAIANDNSGYGQFQIGILKK
Psevex1   190  TPIDAT-AWQNFAVTLDFDKNTLQVYYS-EGDAALAAVT-NVLTNDNSGEGQYQFGILKK
Eutlat1   190  TPIDES-EWQNFAVTLDFEQNTLQVYYS-VGDTPLEAVT-EALSNNNAGEGQYQIGILKK
Gaetri1   193  TKVDNT-AWNNFAIKIDYTKNTLQVYYS-KGDEPLKSVT-NAVQNDNSGKGQYQLGLLKK
Magory1   202  TPIDET-AWNNFAVTIDYVKNTLRVYYS-KNDEPLKAASCAPTPNDNSGEGQYQLGLLKK
Maggri1   199  TPIDET-AWNNFAVTIDYDKNTLRIYYS-KNDEPLKAASCTASPNDNSGEGQYQLGLLKK
Conlus1   205  VAMDLEGGWQNFAVTLDVTANTIQIYYS-TGTDPLQAVT-DVIPTDLSGDGQFQIGMIKK
Diaamp1   194  TPIDFS-EWQNFAITLDIDSNLVQIYYS-LGNAALEAVT-DFVPADLSGEGQFQLGILKK
Diahel1   194  TPIDFE-EWQNFAVMLNVDANLIQIYYS-LGDAALEAVT-DAEPLRLEGEGQYQLGILKK
Micbo11   210  TPINLRGEWQTFAVTLDYNANTIQVFTSPNANTPLKPAFPTPLPNDNSGFGQFQMGILKK
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Fol-EC14  257  PTG-TDDVANSGFQEANLNEGLIYGGIFLED-SADGCVSL
Fuspro1   257  PTG-TDDVANSGFQEANLNEGLIYGGIFLED-SADGCVSL
Fusman1   257  PTG-TDDVANSGFQEANLNEGLIYGGIFLED-SADGCVSL
Fusfuj1   257  PTG-TDDVANAGFQEANLNEGLIYGGIFLED-SADGCVSL
Fusnyg1   257  PTG-TDDVANSGFQEANLNEGLIYGGIFLED-SADGCVSL
Fusver1   257  PTG-TDDVANSGFQEANLNEGLIYGGIFLED-SADGCVSL
Fuscul1   254  PTG-TDDVANAGFQEANLNEGLIYGGIFLED-SKNNCVSL
Fusgra1   254  PTG-TDDVANAGFQEANLNEGLIYGGIFLED-SKNNCVSL
Fuspse1   254  PTG-TDDVANAGFQEANLNEGLIYGGIFLED-SKNNCVSL
Fuslan1   254  PTG-TDDVANAGFQEDNLNEGLIYGGIFLED-SKNDCVSL
Fuspoa1   254  PTG-TDDVANAGFQENNLNEGLVYGGIFLED-SKNDCVSL
Fusven1   254  PTG-TDDVANAGFQEDNLDEGLIYGGIFLED-SKNDCVSL
Neodit1   257  PTG-TADVVNSGFQESGLNEGLIYGGIFIED-STNYCVSK
Fussol1   257  PTG-TDDVVNSGFQESDLDEGLIYGGIFIED-SKDGCVSA
Colchl1   255  PTG-TSDVVNSGYQSSNLDEGQIYGGIFIED-SADGCVSI
Colfio1   264  PTG-TDDVVNSGYQSSNLNEGLIYGGIFIED-SADGCVSI
Colnym1   264  PTG-TDDVVNSGYQSSNLNEGLIYGGIFIED-SANGCVSI
Colsim1   264  PTG-TDDVVNSGYQSSNMNEGLIYGGIFIED-SANGCVSI
Colglo1   251  PTG-TDDVVNSGYQESDLDEGQIYGGIFIED-SADGCVSV
Colgra1   266  PTG-TSDVVNSGYQSSNLDEGQIYGGIFIED-GADGCVSL
Colinc1   255  PTG-TSDVVNSGYQSSNLNEGQIYGGIFIED-SADGCVST
Coltof1   255  PTG-TSDVVNAGYQSSNLNEGQIYGGIFIED-STNGCVST
Colhig1   257  PTG-TSDVVNEGYQSNNLDEGQIYGGIFIEE-SAGGCVST
Colorb1   251  PTG-TSDVVNSGYQASNLDEGQVYGGIFIED-STGGCVSI
Veralf1   257  PTG-TDDVVNSGFQESPLNEGLIYAGVFIED-SANGCVSK
Verdah1   257  PTG-TDDVVNSGFQESPLNEGLIYAGVFIED-SANGCVSK
Verlon1   257  PTG-TDDVVNSGFQESPLNEGLIYAGVFIED-SANGCVSK
Lompro1   249  PTG-TSDVVNSGYQESGLDEGLIYGGIFIED-SASDCVSK
Sceapi1   249  PTG-TSDVVNSGYQESGLDEGLIYGGIFIEDSSADTCVSK
Chathe1   260  PTG-TSDVVNSGYQSPNLDEGLLYGGLFVED-SAGGCVSL
Madmyc1   258  PTG-TSDVVNSGYQESNLNEGLIYGSLFVED-SADGCISL
Thiter1   256  PTG-TSDVVNSGYQESNLNEGLIYGSLFVED-SANGCISL
Thethe1   256  PTG-TDDVVNSGYQESGIDEGLIYGSLFVED-SANGCVSL
Conlig1   250  PTG-TSDVVNAGYQESKLNEGQIYGGLFIED-STNGCVSL
Daldsp1   249  PTG-TSDVVNSGYQETGINEGQIYGGIFLED-SANGCISL
Hyposp1   249  PTG-TSDVVNSGYQETGISEGQIYGGIFLED-SANGCVSL
Rosnec1   255  PTG-TSDVVNGGYQEKNLDEGQIYGGLFLED-GANGCISL
Phamin1   248  PTG-TSDVVNSGYQESGLNEGQIYGGLFIED-SSNGCISL
Spobra1   261  PTG-TSDVVNSGFQESGLKEGQIYGGIFIED-SANGCISL
Sposch1   261  PTG-TSDVVNSGFQESGLKEGQIYGGIFIED-SANGCISL
Spoins1   272  PTG-TSDVVNSGFQESGLKEGLIYGGIFIED-SANGCVSL
Podans1   258  PTG-TSDVVNSGYHQRNLNEGLIYGSVFVED-GEGGCVSL
Neucra1   252  PTG-TDDVVNSGYQESDIDEGQIYGGIFIED-SANGCVSL
Neutet1   252  PTG-TDDVVNSGYQESGIDEGQIYGGIFIED-SANGCVSL
Sormac1   254  PTG-TDDVVNKGYQESGIDEGQIYGGIFIED-SAGGCVSL
Pesfic1   247  PTG-TSDVVNSGYQESPISEGQIYGGIFLED-SANGCITL
Psevex1   247  PTG-TSDVVNSGYQEKGILEGQIYGGIFLED-SADGCISL
Eutlat1   247  PTG-TDDVVNSGYQETGIDEGQIYGSIFLED-SSDGCVSL
Gaetri1   250  PTG-TNDVVNSGYQSRNLNEGLIYGGIFLED-SAGGCISL
Magory1   260  PTG-TDDVVNSGYQASGIDEGLIYGGIFLED-SADGCVSL
Maggri1   257  PTG-TDDVVNSGYQASGIDEGLIYGGIFLED-SADGCVSL
Conlus1   263  PTG-TSDVVNAGYQEAPFEEGQIYGGLFVED-SAGGCISL
Diaamp1   251  PTG-TDDVVNSGFQESPLNEGQIYGGIFVED-STGGCVSL
Diahel1   251  PTG-SADVVNSGFQESPLNEGQIYGGIFVED-STAGCVSL
Micbo11   270  PTGETTDIVNKGFQSAGIDEGQIYGGVFLED-SAGGCVSL
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Sordariomycetes
Hypocreomycetidae - Glomerellales

Colchl1 = OLN97223.1 hypothetical protein CCHL11_02057 [Colletotrichum chlorophyti] after splicing out intron with putative non-canonical GCGCGT donor site, consistent with the findings of Rep et al. (2006)

Colfio1 = EXF74738.1 hypothetical protein CFIO01_05408 [Colletotrichum fioriniae PJ7]

Colglo1 = EQB57524.1 hypothetical protein CGLO_02337 [Colletotrichum gloeosporioides Cg-14]

Colgra1 = XP_008095341.1 hypothetical protein GLRG_06465 [Colletotrichum graminicola M1.001]

Colhig1 = XP_018153158.1 hypothetical protein CH63R_11343 [Colletotrichum higginsianum IMI 349063]

Colinc = KZL79130.1 hypothetical protein CI238_10245 [Colletotrichum incanum]

Colnym = KXH49624.1 hypothetical protein CNYM01_07617 [Colletotrichum nymphaeae SA-01]

Colorb = TDZ26553.1 hypothetical protein Cob_v001237 [Colletotrichum orbiculare MAFF 240422]

Colsim = KXH49371.1 hypothetical protein CSIM01_11916 [Colletotrichum simmondsii]

Coltof = KZL70738.1 hypothetical protein CT0861_13067 [Colletotrichum tofieldiae]

Veralf = XP_003005433.1 conserved hypothetical protein [Verticillium alfalfae VaMs.102]

Verdah = XP_009658131.1 uncharacterized protein VDAG_10367 [Verticillium dahliae VdLs.17]

Verlon = KAG7105666.1 hypothetical protein HYQ44_015124 [Verticillium longisporum]

Hypocreomycetidae - Hypocreales - Clavicipitaceae - none

Hypocreomycetidae - Hypocreales - Cordycipitaceae - none

Hypocreomycetidae - Hypocreales - Hypocreaceae - none

Hypocreomycetidae - Hypocreales - Nectriaceae

Fuspro = XP_031082440.1 related to endoglucanase c [Fusarium proliferatum ET1]

Fusfuj = KLO84549.1 endoglucanase c [Fusarium fujikuroi]

Fusman = XP_041680198.1 uncharacterized protein FMAN_08678 [Fusarium mangiferae

Fuscul = PTD05001.1 hypothetical protein FCULG_00002645 [Fusarium culmorum]

Fusgra = XP_011319797.1 hypothetical protein FGSG_08907 [Fusarium graminearum PH-1]

Fuslan = KPA46823.1 endoglucanase c [Fusarium langsethiae]

Fusnyg = PNP82107.1 hypothetical protein FNYG_04560 [Fusarium nygamai]

Fuspoa = KAG8671804.1 hypothetical protein FPOAC1_005062 [Fusarium poae]

Fuspse = KAF0636074.1 hypothetical protein FPSE5266_08205 [Fusarium pseudograminearum]

Fusven = XP_025584865.1 uncharacterized protein FVRRES_05581 [Fusarium venenatum]

Fusver = XP_018746004.1 hypothetical protein FVEG_02506 [Fusarium verticillioides 7600]

Neodit = KPM34483.1 hypothetical protein AK830_g12087 [Neonectria ditissima]

Fussol = XP_003052800.1 uncharacterized protein NECHADRAFT_67676 [Fusarium vanettenii 77-13-4] (syn. Fusarium solani)

Hypocreomycetidae - Hypocreales - Ophiocordycipitaceae - none

Hypocreomycetidae - Hypocreales - Stachybotryaceae - none

Hypocreomycetidae - Microascales

Ceratocystis platani - no orthologue

Thielaviopsis punctulate - no orthologue

Lompro = PKS06492.1 hypothetical protein jhhlp_007240 [Lomentospora prolificans]

Sceapi = XP_016644335.1 hypothetical protein SAPIO_CDS3558 [Scedosporium apiospermum]

Sordariomycetidae - Coniochaetales

Conlig = OIW34589.1 hypothetical protein CONLIGDRAFT_650979 [Coniochaeta ligniaria NRRL 30616]

Sordariomycetidae - Togniniales

Phamin = XP_007912622.1 hypothetical protein UCRPA7_1852 [Phaeoacremonium minimum UCRPA7]

Sordariomycetidae - Diaporthales

Conlus = PSR86977.1 hypothetical protein BD289DRAFT_433121 [Coniella lustricola]

Diaamp = KKY30718.1 hypothetical protein UCDDA912_g09348 [Diaporthe ampelina]

Diahel = POS74193.1 hypothetical protein DHEL01_v207411 [Diaporthe helianthi]

Sordariomycetidae - Magnaporthales

Gaetri = XP_009230278.1 hypothetical protein GGTG_14087 [Gaeumannomyces tritici R3-111a-1]

Magory = ELQ60567.1 hypothetical protein OOW_P131scaffold01278g3 [Pyricularia oryzae P131] (syn. Magnaporthe oryzae)

Maggri = XP_030977943.1 uncharacterized protein PgNI_09303 [Pyricularia grisea] (syn. Magnaporthe grisea)

Sordariomycetidae - Ophiostomataceae

Grosmannia clavigera - no orthologue

Ophiostoma piceae - no orthologue

Spobra = XP_040622012.1 uncharacterized protein SPBR_06066 [Sporothrix brasiliensis 5110]

Spoins = OAA67127.1 hypothetical protein SPI_01703 [Sporothrix insectorum RCEF 264]

Sposch = XP_016586072.1 hypothetical protein SPSK_04444 [Sporothrix schenckii 1099-18]

Sordariomycetidae - Sordariales - Sordariales incertae sedis

Madmyc = KXX74097.1 hypothetical protein MMYC01_208909 [Madurella mycetomatis]

Sordariomycetidae - Sordariales - Chaetomiaceae

Chathe = XP_006697564.1 hypothetical protein CTHT_0073070 [Chaetomium thermophilum var. thermophilum DSM 1495]

Podans = XP_001913072.1 uncharacterized protein PODANS_1_8450 [Podospora anserina S mat+] with intron prediction corrected

Thethe = XP_003659079.1 uncharacterized protein MYCTH_2295704 [Thermothelomyces thermophilus ATCC 42464]

Thiter = XP_003652516.1 uncharacterized protein THITE_2114094 [Thermothielavioides terrestris NRRL 8126] (syn. Thielavia terrestris)

Sordariomycetidae - Sordariales - Sordariaceae
Neucra = KHE89943.1 glycoside hydrolase family 131 protein [Neurospora crassa] after splicing out intron with non-canonical GCATGT donor site described by Rep et al. (2006) and removing spurious N-terminal sequence preceding correct start methionine
Neutet = EGZ77998.1 hypothetical protein NEUTE2DRAFT_80122 [Neurospora tetrasperma FGSC 2509] after splicing out intron with non-canonical GCATGT donor site described by Rep et al. (2006) and removing spurious N-terminal sequence preceding correct start methionine
Sormac = XP_024511214.1 uncharacterized protein SMAC_05957 [Sordaria macrospora k-hell]
Xylariomycetidae - Xylariales
Eutlat = EMR68142.1 hypothetical protein UCREL1_4850 [Eutypa lata UCREL1]
Daldsp = OTB14174.1 hypothetical protein K445DRAFT_140233 [Daldinia sp. EC12]
Hyposp = OTA63122.1 glycoside hydrolase family 131 protein [Hypoxylon sp. EC38]
Micbol = KXJ85933.1 hypothetical protein Micbo1qcDRAFT_220044 [Microdochium bolleyi]
Pesfic = XP_007828005.1 hypothetical protein PFICI_01233 [Pestalotiopsis fici W106-1]
Psevex = XP_040712670.1 uncharacterized protein BCR38DRAFT_398434 [Pseudomassariella vexata]
Rosnec = GAP92008.2 putative glycoside hydrolase family 131 protein [Rosellinia necatrix] corrected to remove spurious N-terminal sequence

Supplementary Figure S6. Fol-EC14 alignment. Multiple protein-sequence alignment of Fol-EC14 orthologues in the Fol-EC14 clade of Sordariomycete GH131 (glycosyl-hydrolase 131) sequences. All sequences shown were the highest blastP matches to Fol-EC14 obtained for each genome-sequenced species represented. Sequences were aligned using ClustalW at https://www.ebi.ac.uk/Tools/msa/mafft/. Amino-acid identities were highlighted in black and similarities in grey using BoxShade at https://embnet.vital-it.ch/software/BOX_form.html. Conserved cysteines have been highlighted manually in blue, residues conserved with the catalytic residues of PaGluc131A and CcGH131A in red and non-conserved residues in teal.