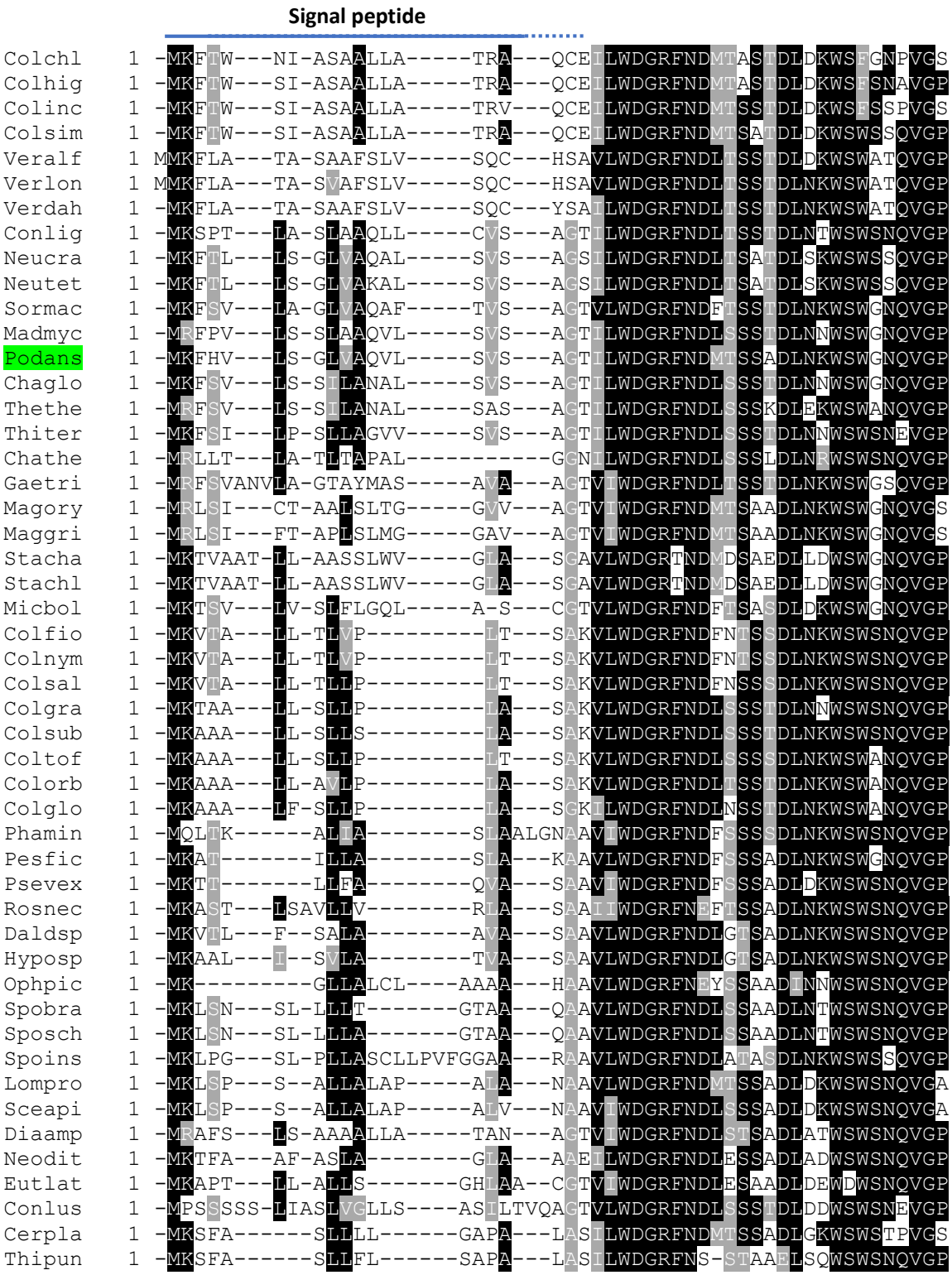
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Verlon 1 MMKFLA---TA-SVAFSLV-----SQC---HSAVLWDGRFNDLTSSTDLNKWSWATQVGP
Verdah 1 -MKFLA---TA-SAAFSLV-----SQC---YSAILWDGRFNDLTSSTDLNKWSWATQVGP
Conlig 1 -MKSPT---LA-SLAAQLL-----CVS---AGTILWDGRFNDLTSSTDLNTWSWSNQVGP
Neucra 1 -MKFTL---LS-GLVAQAL-----SVS---AGSILWDGRFNDLTSATDLSKWSWSSQVGP
Neutet 1 -MKFTL---LS-GLVAKAL-----SVS---AGSILWDGRFNDLTSATDLSKWSWSSQVGP
Sormac 1 -MKFSV---LA-GLVAQAF-----TVS---AGTVLWDGRFNDFTSSTDLNKWSWGNQVGP
Madmyc 1 -MRFPV---LS-SLAAQVL-----SVS---AGTILWDGRFNDLSSSTDLNNWSWGNQVGP
Podans 1 -MKFHV---LS-GLVAQVL-----SVS---AGTILWDGRFNDMTSSADLNKWSWGNQVGP
Chaglo 1 -MKFSV---LS-SILANAL-----SVS---AGTILWDGRFNDLSSSTDLNNWSWGNQVGP
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Chathe 1 -MRLLT---LA-TLTAPAL-----------GGNILWDGRFNDLSSSLDLNRWSWSNQVGP
Gaetri 1 -MRFSVANVLA-GTAYMAS-----AVA---AGTVIWDGRFNDLISSTDLNKWSWGSQVGP
Magory 1 -MRLSI---CT-AALSLTG-----GVV---AGTVIWDGRFNDMTSAADLNKWSWGNQVGS
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Micbol 1 -MKTSV---LV-SLFLGQL-----A-S---CGTVLWDGRFNDFTSASDLDKWSWGNQVGP
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Colsub 1 -MKAAA---LL-SLLS---------LA---SAKVLWDGRFNDLSSSTDLNKWSWSNQVGP
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Eutlat 1 -MKAPT---LL-ALLS-------GHLAA--CGTVIWDGRFNDLESAADLDEWDWSNQVGP
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Cerpla 1 -MKSFA------SLLLL------GAPA---LASILWDGRFNDMTSSADLGKWSWSTPVGS
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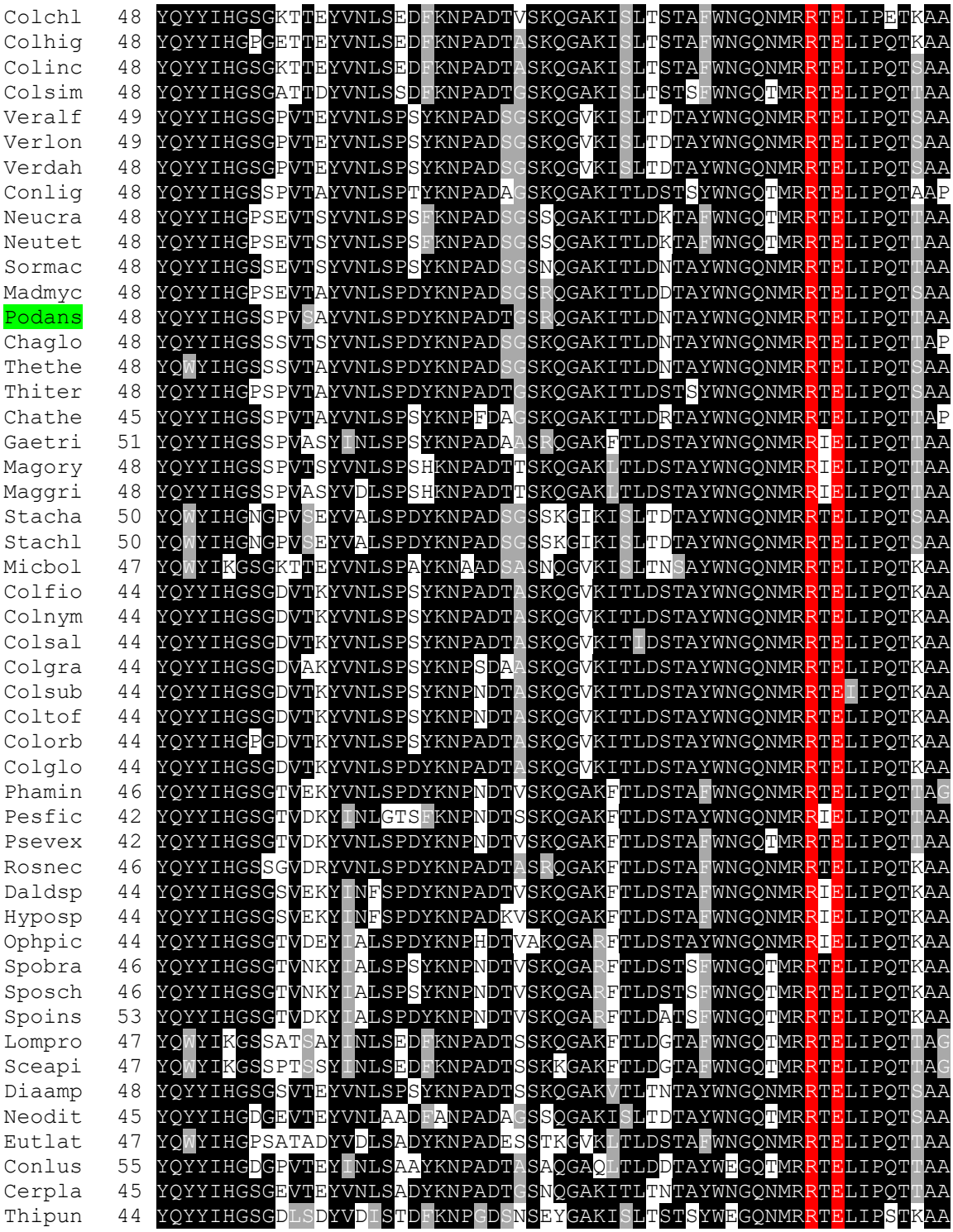
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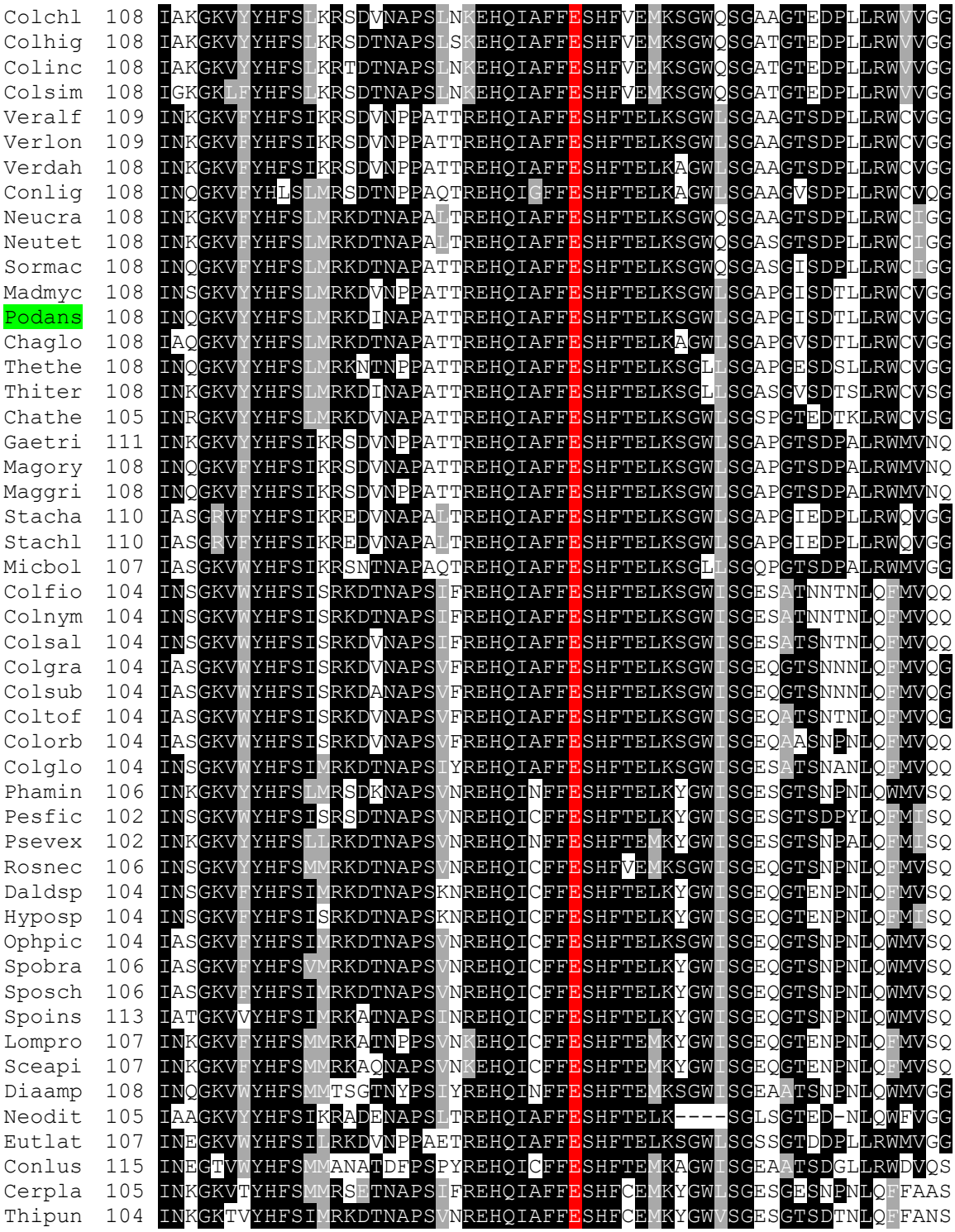
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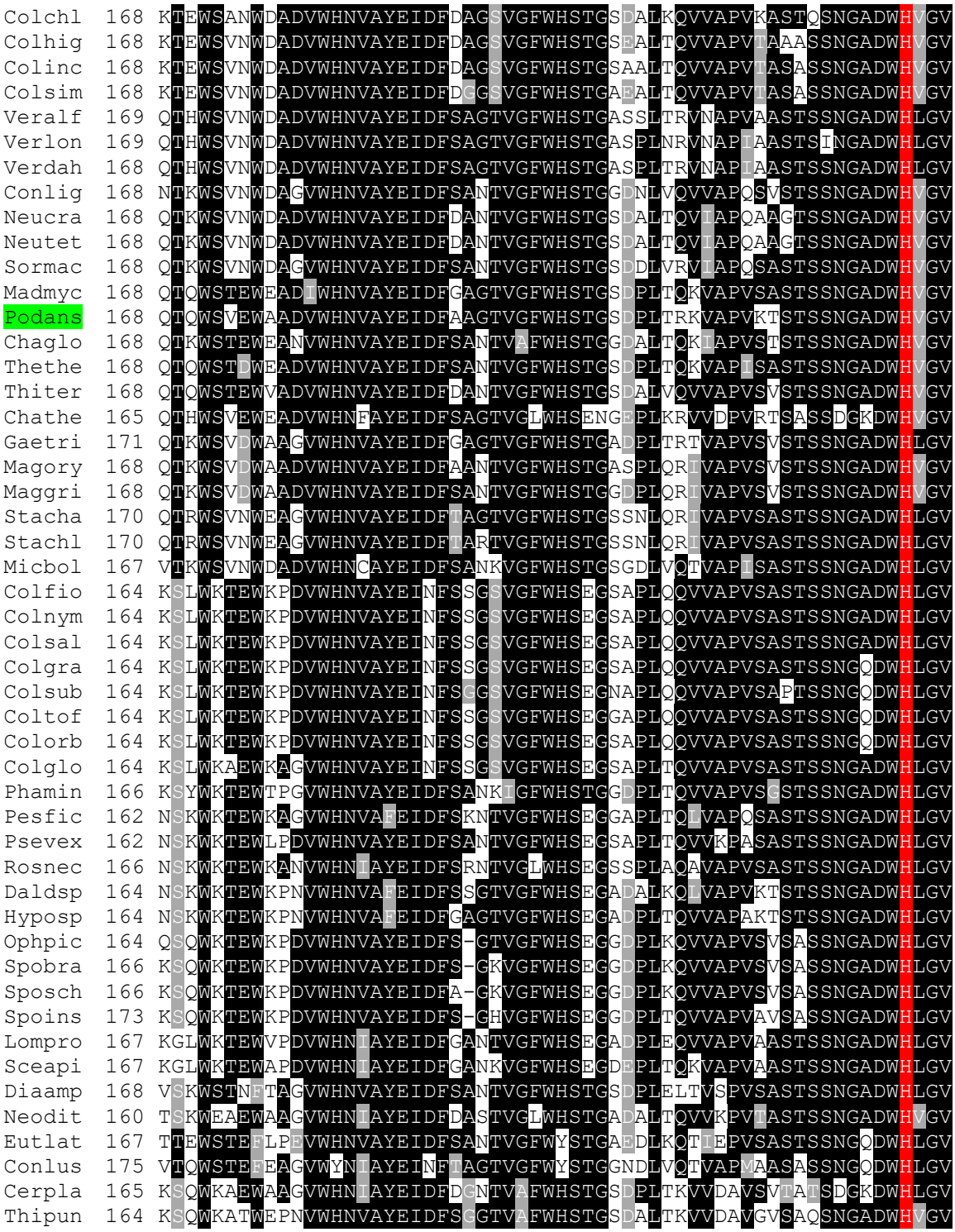
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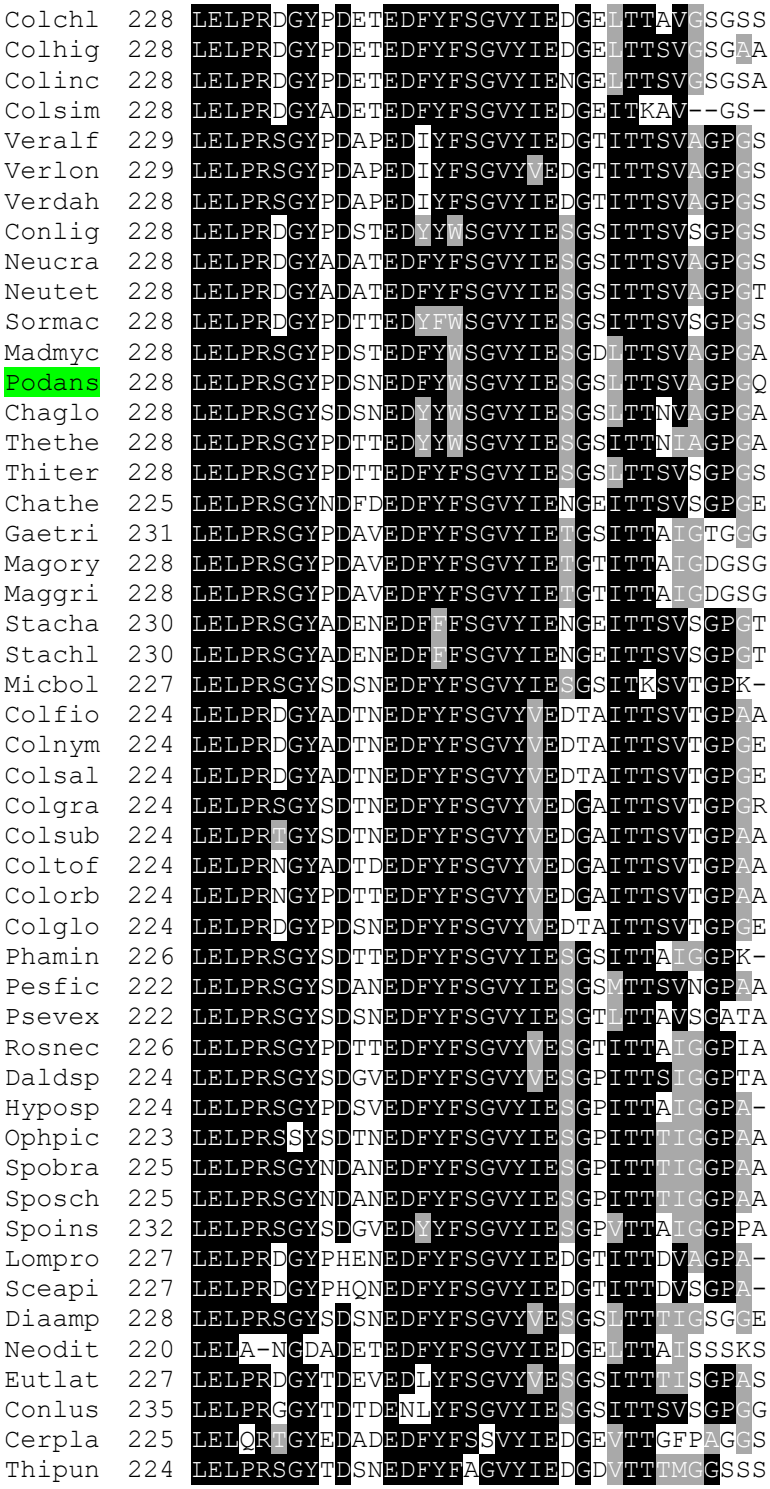
Cerpla 165 KSQWKAEWAAGVWHNIAYEIDFDGNTVAFWHSTGSDPLTKVVDAVSVTIATSDGKDWHLGV
Thipun 164 KSQWKATWEPNVWHNVAYEIDFSGGTVAFWHSTGSDALTKVVDAVGVSAQSNGADWHVGV



Sordariomycetes

Hypocreomycetidae - Glomerellales

Colchl = OLN87414.1 hypothetical protein CCHL11_09568 [Colletotrichum chlorophyti]
SAPAATASAKPACRRRRRRSNKAKRN
Colfio = EXF79761.1 hypothetical protein CFIO01_10221 [Colletotrichum fioriniae PJ7]
Colglo = EQB46944.1 hypothetical protein CGLO_13971 [Colletotrichum gloeosporioides Cg-14]
Colgra = XP_008089016.1 hypothetical protein GLRG_00140 [Colletotrichum graminicola M1.001]
Colhig = CCF34200.1 hypothetical protein CH063_06244 [Colletotrichum higginsianum]
Colinc = KZL80950.1 hypothetical protein CI238_10924 [Colletotrichum incanum]
Colnym = KXH48861.1 hypothetical protein CNYM01_04877 [Colletotrichum nymphaeae SA-01]
Colorb = TDZ18371.1 hypothetical protein Cob_v008530 [Colletotrichum orbiculare MAFF 240422]
Colsim = KXH30104.1 hypothetical protein CSIM01_00818 [Colletotrichum simmondsii]
Colsal = KXH61778.1 hypothetical protein CSAL01_07891 [Colletotrichum salicis]
Colsub = KDN72294.1 hypothetical protein CSUB01_06221 [Colletotrichum sublineola]

Coltof = KZL74381.1 carbohydrate-binding module family 1 protein [Colletotrichum tofieldiae] corrected to remove spurious N-terminal sequence
Veralf = XP_003008315.1 conserved hypothetical protein [Verticillium alfalfae VaMs.102]
Verdah = KAF3351428.1 Putative transcriptional regulatory protein [Verticillium dahliae VDG2]
Verlon = KAG7128176.1 hypothetical protein HYQ45_012077 [Verticillium longisporum]
Hypocreomycetidae - Hypocreales - Clavicipitaceae - no orthologues found
Hypocreomycetidae - Hypocreales - Cordycipitaceae - no orthologues found
Hypocreomycetidae - Hypocreales - Hypocreaceae - no orthologues found
Hypocreomycetidae - Hypocreales - Nectriaceae (but no orthologues found in Fusarium)
Neodit = KPM42463.1 hypothetical protein AK830_g4089 [Neonectria ditissima]
Hypocreomycetidae - Hypocreales - Ophiocordycipitaceae - no orthologues found
Hypocreomycetidae - Hypocreales - Stachybotrys
Stacha = KEY67053.1 hypothetical protein S7711_10884 [Stachybotrys chartarum IBT 7711]
Stachl - KFA65100.1 hypothetical protein S40285_03114 [Stachybotrys chlorohalonata IBT 40285]
Hypocreomycetidae - Microascales
Cerpla = KKF94894.1 hypothetical protein CFO_g2760 [Ceratocystis platani]
Thipun = KKA29646.1 hypothetical protein TD95_000695 [Thielaviopsis punctulata]
Lompro = PKS10019.1 hypothetical protein jhhlp_004644 [Lomentospora prolificans]
Sceapi = XP_016641373.1 hypothetical protein SAPIO_CDS7745 [Scedosporium apiospermum]
Sordariomycetidae - Coniochaetales
Conlig = OIW27922.1 carbohydrate-binding module family 1 protein [Coniochaeta ligniaria NRRL 30616]
Sordariomycetidae - Togniniales
Phamin = XP_007910843.1 putative carbohydrate-binding module family 1 protein [Phaeoacremonium minimum UCRPA7]
Sordariomycetidae - Diaporthales
Conlus = PSR77661.1 hypothetical protein BD289DRAFT_377636 [Coniella lustricola]
Diaamp = KKY33924.1 putative carbohydrate-binding module family 1 protein [Diaporthe ampelina]
Sordariomycetidae - Magnaporthales
Gaetri = XP_009223752.1 hypothetical protein GGTG_07663 [Gaeumannomyces tritici R3-111a-1]
Magory = >QBZ57551.1 hypothetical protein PoMZ_02480 [Pyricularia oryzae] (syn. Magnaporthe oryzae)
Maggri = XP_030981300.1 uncharacterized protein PgNI_07823 [Pyricularia grisea] (syn. Magnaporthe grisea)
Sordariomycetidae - Ophiostomataceae
Ophpic = EPE07306.1 carbohydrate-binding module family 1 protein [Ophiostoma piceae UAMH 11346]
Spobra = XP_040620187.1 uncharacterized protein SPBR_03181 [Sporothrix brasiliensis 5110]
Spoins = OAA53838.1 hypothetical protein SPI_09283 [Sporothrix insectorum RCEF 264]
Sposch = XP_016590501.1 hypothetical protein SPSK_07902 [Sporothrix schenckii 1099-18]
Sordariomycetidae - Sordariales - Sordariales incertae sedis
Madmyc = KXX78310.1 Feruloyl esterase B [Madurella mycetomatis]
Sordariomycetidae - Sordariales - Chaetomiaceae
Chaglo = XP_001228503.1 uncharacterized protein CHGG_10576 [Chaetomium globosum CBS 148.51]
Chathe = XP_006690661.1 hypothetical protein CTHT_0001080 [Chaetomium thermophilum var. thermophilum DSM 1495]
Podans = AFQ89876.1 beta-glucanase [Podospora anserina]
Thethe = XP_003667321.1 carbohydrate-binding module family 1 protein [Thermothelomyces thermophilus ATCC 42464]
Thiter = SPQ27187.1 1b90b30c-5168-4e91-890b-de3dbdb1dae1 [Thermothielavioides terrestris] (syn. Thielavia terrestris)
Sordariomycetidae - Sordariales - Sordariaceae
Neucra = XP_958348.1 hypothetical protein NCU09764 [Neurospora crassa OR74A]
Neutet = XP_009851721.1 hypothetical protein NEUTE1DRAFT_64374 [Neurospora tetrasperma FGSC 2508]
Sormac = XP_003344812.1 uncharacterized protein SMAC_09184 [Sordaria macrospora k-hell]
Xylariomycetidae - Xylariales
Eutlat = EMR71091.1 putative carbohydrate-binding module family 1 protein [Eutypa lata UCREL1]
Daldsp = OTB20440.1 hypothetical protein K445DRAFT_312903 [Daldinia sp. EC12]
Hyposp = OTA66562.1 glycoside hydrolase family 131 protein [Hypoxylon sp. EC38]
Micbol = KXJ89759.1 hypothetical protein Micbo1qcDRAFT_212247 [Microdochium bolleyi]
Pesfic = XP_007838550.1 hypothetical protein PFICI_11778 [Pestalotiopsis fici W106-1]
Psevex = XP_040719926.1 uncharacterized protein BCR38DRAFT_96685 [Pseudomassariella vexata]
Rosnec = GAP89226.2 putative carbohydrate-binding module family 1 protein [Rosellinia necatrix]

Supplementary Figure S5. PaGluc131A alignment. Multiple protein-sequence alignment of the N-terminal

glycosyl hydrolase domains of PaGluc131A orthologues in the PaGluc131A/CcGH131A clade of Sordariomycete GH131 (glycosyl-hydrolase 131) sequences. All sequences shown were the highest blastP matches to PaGluc131A (= Podans highlighted in green in the alignment) 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 back and similarities in grey using BoxShade at https://embnet.vital-it.ch/software/BOX_form.html. Residues conserved with the catalytic residues of PaGluc131A and CcGH131A have been highlighted manually in red. C-terminal extensions, including those containing CBM1 (carbohydrate binding module 1) domains, were removed manually for the purposes of alignment.