

Colhig2

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1 MYTSTLIL--SLVAAAAA ACTGG--KNKTAE--AAAPGAKA--CCALQFDGRIPKAFIAAD
Colch12 1 MFTSTLFL--SLVAAAAA ACNKG--PNDT----DSSSGVKC--CCALQFDGRIPKAFIAAD
Colfio2 1 MFASTIFL--SLVAAAAA ACDGTTPKNNTG--AVSPGAKA--CCALQFDGRIPKTFKAAD
Colsim2 1 MFASTIFL--SLVAAAAA ACDGTTPKNNTG--AVSPGAKA--CCALQFDGRIPKTFKAAD
Colinc2 1 MFTSTLFL--SLVAAAAA ACDGST--KNNTA---GATPGAKA--CCSLQFDGRIPKAFIAAD
Coltof2 1 MFTSTLFL--SLVAAAAA ACDGST--KNNTA---GATPGAKA--CCSLQFDGRIPKAFIAAD
Colgra2 1 MYTSTLIF--SLLAAA-----GAKAQCCTLQFDGRIPKASIVAD
Colorb2 1 MFASTIIL--SLVAAVAADCGSKS--GNNSYSSGPALPGAQA--CCTLQFDGRIPKAFIAAD
Lompro2 1 MALSRS----ALLSILLSAA-----PLVSAQECTLQFDGRIPDGFAAAD
Sceapi2 1 MSPRS----ALLSILLSAL-----PLVSAQECTLQFDGRIPDGFAAAD
Rosnec2 1 MAGFYPL--ALLVGI IPTL-----VVSQQCDLQFDGRIPSDFVAAT
Conlig2 1 MASPILLSVSSILTLALTS-----AQKCP LQFDGRIPSTFTPTS
Grocla2 1 MLARH----SLVLLASATT-----AVLAKTCALQFDGRIPSTFNLT
Ophpic2 1 MISQYL---SLLALPVLAA-----AQKCSLQFDGRIPSNLTLAA
Spobra2 1 MMYPLSI---AFLALPLLAS-----AQKCTLQFDGRIPSTFTAAS
Spoins2 1 MRSSASL---ALLALPLLAS-----AQKCALQFDGRIPSSFSAA
Phamin2 1 MASLIRNY--FSLLPILLELS-----VVLAQSCDLQFDGRIPSAGSAVAD
Podans2 1 MHKHGI---PLLFA SLVTS-----VSAQSCRLHFQDGRIPPSFGVAG
Diaamp2 1 MFSQRLLT--QTTLVSLASLA-----ASC SATLQFDGRIPAGTQLSA
Diahel2 1 MFSQRLLT--QTSLFSLASLA-----ASCSTLQFDGRIPAGTQLSA
Psevex2 1 MASHRSFI--PSFLSLVTLVV-----AQCC TLQFDGRIPSDFVAAT
Thiter2 1 MVHLQYY--SVAVSL LPS-----WVAAQNC TLQFDGRIPSDLVAAD
Gaetri2 1 MRYSFTST--LSLALS SPIS-----GVWAQCRK LQFDGRIPNNEQVAQ
Magory2 1 MRSFTVAS--AIFGGL LATS-----PVYGOQCK LQFDGRIPANEQPAN
Maggr12 1 MRSFTVAS--AILGGL SATS-----PVYGOQCK LQFDGRIPNEFELTG
Cerpla2 1 MQSL-----SLLALI APVA-----AQVCQLAFDGRIPAKDFALEG
Thipun2 1 MYSR-----SLTAAALAAA-----PAVAQVCPLAFDGRIPDNFILD
Colglo2 1 MSLSFIST--LSLLLSAAGAN-----AAKCP LQFDGRIPNFTPTD
Colnym2 1 MHFSSSSL--GALVAVAAGAAD-----AAKCP LQFDGRIPNFTPAT
Stacha2 1 MAPSLFRL--LPVLAGVTAVA-----CQSCPLQFDGRIPRNFIVAD
Stach12 1 MAPSLFRI--LPVLAGVTAVA-----CQSCSLQFDGRIPRNFIVAD
Clapur2 1 MRTYFAI---NFVAVATAAASG-----LGREAATTTKCP LQFDGRIPNEFLEQ

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Colhig2

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54 FDG-KTSPFNTANVFGKGLKFSDLIK--LPGGQ---SL--FDV--NSTQPFEVTI-----
Colch12 52 FDG-KSSPENTANVFGKGLKFSDLIK--LPGGQ---SL--FDV--NSTQPFEVTI-----
Colfio2 55 FDS-TSSPENTANVFGKGLKFSEIVQ--LPGGN---SL--FDV--NSTQPFEVTI-----
Colsim2 55 FDS-TSSPENTANVFGKGLKFSEIVQ--LPGGN---SL--FDV--NSTQPFEVTI-----
Colinc2 54 FDG-SSSPFNTANVFGKGLKFSDLVQ--LPGGQ---SL--FDV--NSTQPFEVTI-----
Coltof2 54 FDG-TSSPENTANVFGKGLKFSDLVQ--LPGGQ---SL--FDV--NSTQPFEVTI-----
Colgra2 38 FDA-KTSPFNPSNVFGQGLKFSQLIQ--LPGGQ---SL--FDA-NATQPFEVTI-----
Colorb2 57 FDG-KTSPFNADNVLGKGLKFSELIK--LPEET---SL--FDG-NSKQPFEVTI-----
Lompro2 41 FDA-ANDIFSPDNVFGQGLSFGQLIQ--LPPNAGL---SL--FDD--GTIPFEVTI-----
Sceapi2 40 FDQ-ANNIFSPDNVFGQGLAFSQLIQ--LPAIGA---SL--FDD--ATVPFEVTI-----
Rosnec2 40 FNT--GNGVFDENNVVQGLSLGSVVQ--IQDSLS---SL--FDV--GTNPFEVTI-----
Conlig2 41 FDA-ANAFESQSNVLGQGLKFSQLIQ--LPSITP---SL--FDT--ATVPVGVTI-----
Grocla2 39 FDT-ANGVFNPNVFGKNTLSQLLR--LPAQKG---SL--FDE--NTVPFEVTI-----
Ophpic2 37 FDS-NNNIYNPSNVFGKGLKFSELIQ--LPAVAG---SL--FDT--KTVPFEVTI-----
Spobra2 38 FDT-NNNLFNPSNVFGQGLKFSQLIQ--LPAVTG---SL--FDV--NTVPAEVTI-----
Spoins2 38 FDT-NNNVFSPSNVFGQNLKLSQLVE--LPAQTG---SL--FDV--DTVPFEVTI-----
Phamin2 43 FDA-TNNLFSTDNVFGQGLKFSQLIE--LPAVTP---SLPKFDV--NTIPFEVTI-----
Podans2 39 FDT-PNNFFSETNVLGAGLSFSQLIQ--LPAISA---SL--FDT--ETIPFEVTI-----
Diaamp2 40 FDS-ENGLFNPDNVFGKNTLFSQLIQ--LPDVAP---SL--FDV--GTVPEVTI-----
Diahel2 40 FDS-DNGLFNPDNVFGKNTLFSQLIQ--LPDVDP---SL--FDV--GTVPEVTI-----
Psevex2 40 FDTAANTMFNPDFTFGANLSISDVVE--VPCVTS---SL--FDAKNATKAEVTI-----
Thiter2 41 FDS-PNKFFSEKFLVGGQGLKFDQALRVLPVAGG---SL--FDV--DVDAQPEVTI-----
Gaetri2 43 FDA-ANNIFNPKNVLGKDLAFSKTIQ--LPKTSG---SL--FDN--NGTQPEVTI-----
Magory2 42 FDT-ANNIFNPSNVLGKGLKFSDLVQ--LPTLAQQ---SL--FDV--AGKTKAEVTI-----
Maggr12 42 FDS-SNNLFSNNVLGKGLKFSELIQ--FPANGNQTKIL--FDTAGKTKPFEVTIKYFTTP
Cerpla2 35 FDA-DTSPFNPSNVFGKGLKFSSELIK--FPEGNG---GL--FDV--DTKPFVTI-----
Thipun2 38 FDS--NNGVFNPSFVLGANLTFSEELIQ--LPGGS---SL--FSD--NTQPEVTI-----
Colglo2 42 FDT-SASPFNNGFVFGKGLKASDVVT--LPTGLN---SL--FDA--NFKQPFEVNI-----
Colnym2 41 FDT-SASPFNNGFVFGKGLKASDVVT--LPTGLS---SL--LDG--PANKPFOVNI-----
Stacha2 40 FDT-QNGIYNPDEFVKGRDLAFSDIE--LETDA---TL--FDT--NSVPFTVQI-----
Stach12 40 FDT-QNGIYNPDEFVKGRDLAFSDIE--LETDT---TL--FDT--NSVPFTVQI-----
Clapur2 47 FDV-KNNVFNPSFVVGANQTFSSVLR--FDNRGTSH--SL--FDRVGVTKPFEVTI-----

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Colhig2 99 ---DDKSIFAPSDNVQIGFRRRAEMLPASNDGKDASTQGIKTLHFSLQKDDKRPPLNLSHE
Colch12 97 ---NDKSIFAPSETNVQVGFRRRAELLPASNDGQDASTDGIKTLHFSLKQDPORPLNLSHE
Colfio2 100 ---NDKSIFAPSETNVQVGFRRRAEMLPASNDGKDASTQGIKTLHFSLQKDAQORPLNLSHE
Colsim2 100 ---NDKSIFAPSETNVQVGFRRRAEMLPASNDGKDASTQGIKTLHFSLQKDAQORPLNLSHE
Colinc2 99 ---NDKSIFAPSETNVQVGFRRRAEMLPASNDGKDASTQGIKTLHFSLQKDAQORPLNLSHE
Coltof2 99 ---NDKSIFAPSATNVQVGFRRRAEMLPASNDGKDASTQGIKTLHFSLQKDAQORPLNLSHE
Colgra2 83 ---NDKSIFAPSANNVQIGFRRRAEMLPASNDGTDPTDGNKTLHFSLMKDAQORSNLSHE
Colorb2 102 ---NDKSIFAPSETNVQVGFRRRAELLPASNDGKDDSTVGIKTLHFSLKDDQORPLNLSHE
Lompro2 86 ---SDDSIFAPSDNVQIGFRRRAELLPASNDGTDPTDGNKTLHFSLMKDNARPFNLSHE
Sceapi2 85 ---SDDSIFAPSDNIGTGFRRRAELLPASNDGTDPTDGNKTLHFSLMKDNARAFNLSHE
Rosnec2 85 ---SDDSIFAPSDNVQIGFRRRAELLPASNDGTDASTDGNKTLHFSLMKDTNRPLNLTHE
Conlig2 86 ---SDKSIFAPSDNVQIGFRRRAELLPASNSGTDASTAGVKTLLHFSVMKDAARPLNLSHE
Grocla2 84 ---SDESIFAPSASNVQIGFRRRAELLPASNSGTDPTDGNKTLHFSLMKDSEARPLNLSHE
Ophpic2 82 ---SDASIFAPSDNVQIGFRRRAELLPASNSGTDASTLGNKTLHFSLMODPQRPLNLTHE
Spobra2 83 ---SDKSIFAPSDNVQIGFRRRAELLPASNSGTDPTDGNKTLHFSLMODAQRPLNLTHE
Spoins2 83 ---SDQSIFAPSDNIGTGFRRRAELLPASNSGTDPTDGNKTLHFSLMODAQRPLNLSHE
Phamin2 90 ---SDQSIFAPSDNVQIGFRRRAELLPASNSGTDPTDGNKTLHFSLMKDADRPLNLSHE
Podans2 84 ---SDASIF-----NGQIGFRRRAELLPASNSGTDSTLGNKTLHFSLGKDAQORPLNLSHE
Diaamp2 85 ---SDESIFAPSDNVQLGFRRRAELLPASNNGTDASTLGNKSLHFSLMKDAARPLNLSHE
Diahel2 85 ---NDDSIFAPSDNVQLGFRRRAELLPASNSGTDPTDGNKSLHFSLMKDAARPLNLSHE
Psevex2 88 ---DDKSIFTPSDNVQLGFRRRAELMITSNDGTDSTLGNKTLHFSLMKDAARPLNLSHE
Thiter2 89 ---SDNSIF-----NGQVGFRRRAELLPASNDGTDPTDGNKTLHFSLVKKDAERPLNLSHE
Gaetri2 89 ---DDKSIFVFNADTVQNGFRRVELLAASNSGTDSTKGNKTLHFSLAKDCORALNLTHE
Magory2 90 ---NDKSIFVFNADTVQNGFRRTELLIASNNGTDSTKGNKTLHFSLAKDLKQRPLNLTHE
Maggr12 98 GIPSDKSIFVFNADTVQNGFRRTELLIASNNGTDSTKGNKTLHFSLAKDAQRPLNLTHE
Cerpla2 80 ---NDTSIFAPSETNVQNGFRRRAELLPASNSGTDPTDGNKTLHFSLKDAQRPLNLSHE
Thipun2 82 ---NDKSIFAPSPDNVQVGFRRRAELLPASNSGTDNSTLGNKTLHFSLKDDITRPLNLSHE
Colglo2 88 ---DDRSIFAPTEETNVQIGFRRRAELPMNSNNGTDPTDSTAGIKTVHFSVMKDPKQRPLNLTHE
Colnym2 87 ---DDRSIFAPTEETNVQIGFRRRAELPMNSNNGTDPTDSTAGIKTVHFSVMKDPKQRPLNLTHE
Stacha2 84 ---DDSSIFAPSDNVQIGFRRVELLPASNSGTDSTLGNKTLHFSLVAKDVTRPLNLSHE
Stach12 84 ---DDSSIFAPSDNVQIGFRRVELLPASNSGTDSTLGNKTLHFSLVAKDITRPLNLSHE
Clapur2 96 ---NDRSIFAPSVSNVQVGFRRTELLIASNSGKDIISTDGNKTLHFSLAKDPAARPLNLDHE

Colhig2 156 YQLAFLESADFSTNQVVLKTGTIL-GQ-N--TEDPDTLQLFGNVATSP-PEPELFKTKFTF
Colch12 154 YQLVFLESADFSTNQVVLKTGTIL-GQ-N--TADPDTLQLFGNVNSSP-VPEPELFKTKFTE
Colfio2 157 YQLVFLESADFSTNQVVLKTGTIL-GQ-N--TADPDTLQLFGNVNSSP-VPEPELFKTKFTA
Colsim2 157 YQLVFLESADFSTNQVVLKTGTIL-GQ-N--TADPDTLQLFGNVNSSP-VPEPELFKTKFTA
Colinc2 156 YQLVFLESADFSTNQVVLKTGTIL-GQ-N--TEDPDTLQLFGNVASSP-TPEPELFKTKFTF
Coltof2 156 YQLVFLESADFSTNQVVLKTGTIL-GQ-N--TADPDTLQLFGNVASSP-TPEPELFKTKFTF
Colgra2 140 YQLVFLESADFSTNQVVLKTGSIL-GQ-N--TADPDTLQLFGNVNSNP-VPEPELFQTKFTF
Colorb2 159 YQLVFLESADFSTNQVVLKTGSIL-GE-N--TADPDTLQLFGNVASSP-VPEPELFKTKFTF
Lompro2 143 YQLVFLESADFSTNQVVLKTGTIL-GV-N--TADPDTLQLFGNVNQG---NQLFSTPFFTA
Sceapi2 142 YQLVFLESADFSTNQVVLKTGTIL-GG-N--TADPDTLQLFGNVNQG---QILFSTPFFTA
Rosnec2 142 YQLVFLESADFSTNQVVLKTGSIL-GA-N--TADPDTLQLFGNVNANP-VQTLFSTVPFTE
Conlig2 143 YQLVFLESADFSTNQVVLKTGTIL-GA-G--ADPDTLQLFGNVNESP-PKVLFSTPFQA
Grocla2 141 YQLVFLESADFSTNQVVLKTGTIL-GQ-E--TADPDTLQLFGNVNANP-PQVLFSTPFPLP
Ophpic2 139 YQLVFLESADFSTNQVVLKTGTIL-GSTD--GVDNPTLQLFGNVNANP-PQVLFSTPFPTP
Spobra2 140 YQLVFLESADFSTNQVVLKAGTIL-GQAG--NVDNPTLQLFGNVNANP-PQVLFSTPFPTP
Spoins2 140 YQLVFLESADFSTNQVVLKTGTIL-CGAA--GVDNPTLQLFGNVNANP-PQVLFSTPFPTP
Phamin2 147 YQLVFLESADFSTNQVVLKTGTIL-GQ-A--TADPDTLQLFGNVNDG--ANVLFSTPFVD
Podans2 136 YQLVFLESADFSTNQVVLKTGTIL-GGDT--AVDPDTLQLFGNVNQTP-SKLLFSTVPFLD
Diaamp2 142 YQLVFLESADFSTNQVVLKTGTIL-DTATQGGVDPDSLILFGNVKQS---QILFNTAFTE
Diahel2 142 YQLVFLESADFSTNQVVLKTGTIL-DTATQKGVDPDSLILFGNVKQS---EQLFSTPFTE
Psevex2 145 YQLVFLESADFSTNQVVLKTGSIL-GA-D--TPNPDTLQLFGNVNSSP-LQTLFSTNFTE
Thiter2 141 YQLVFLESADFSTNQVVLKTGTIL-GQ-N--TADPDTLQLFGNVNQG---QILFSTPFVD
Gaetri2 146 YQLVFLESADFSTNQVVLKTGTIL-GQ-N--GNPDTLQLFGNVKESP-PKVLFSTPFPA
Magory2 147 YQLVFLESADFSTNQVVLKTGTIL-GQ-A--NTNPDTLQLFGNVASSP-PKLLFSTPFPA
Maggr12 158 YQLVFLESADFSTNQVVLKTGTIL-GQ-T--SNNTNLTNFGNVNASP-PKLLFSTPFPA
Cerpla2 137 YQLVFLESADFSTNQVVLKTGTIL-GD-G--ASDPDTLQLFGNVNQKE-PGMIFSAFPTP
Thipun2 139 YQLVFLESADFSTNQVVLKTGTIL-GQ-N--TTPNPDTLQLFGNVNDAK-PGLIFSAFPTA
Colglo2 145 YQMVFLESADFSTNQVVLKTGTIL-GI-H--PADPDVLLVFGNSNTKPFQPELFRTKFTD
Colnym2 144 YQMVFLESADFSTNQVVLKTGTIL-GI-H--PADPDVLLVFGNSNTNTP-SPEPELFKTKFTE
Stacha2 141 YQLVFLESADFSTNQVVLKTGTIL-GR-D--TPDPDTLQVYGNINAG--AALLYSTPFTE
Stach12 141 YQLVFLESADFSTNQVVLKTGTIL-GR-D--TPDPDTLQVYGNINAG--AALLYSTPFTE
Clapur2 153 YQLVFLESADFSTNQVVLKTGTIL-GV-N--TLDPDSLILFGNVNKF--GDVLFSTPFFTA

Colhig2 211 GVFNHFAIKLDFETANTTEVFYSQGTSALKSQGAAV PNI TAGOGQYHFGILKKPVNGGADI
Colch12 209 GVFNHFAIKLDFETKNTTEVFYSQGN SALKSQGAPV SNN TAGKGOYHFGMLKKPVNGGSDI
Colfio2 212 GVFNHFAIKLDFETKNTTEVFYSQGN SALKSTGAAV TNN TAGOGQYHFGMLKKPVNGGSDI
Colsim2 212 GVFNHFAIKLDFETKNTTEVFYSQGN SALKSTGAAV ANN TAGOGQYHFGMLKKPVNGGSDI
Colinc2 211 GVFNHFAIKLDFETANTTEVFYSQGN SALKSQGAAV ANN TAGOGQYHFGMLKKPVNGGADI
Coltof2 211 GVFNHFAIKLDFETANTTEVFYSQGN SALKSQGAPV ANN TAGOGQYHFGILKKPVNGGDDI
Colgra2 195 GVFNHFAIKLDFETANTTQVFYSQGN SALKSQGAPV ANN TAGKQGFHFGVLKKPVNGGADI
Colorb2 214 GVFNHFAIKLDFETKNTTEVFYSTDN SALKSQGAAV ANN TAGOGQYHFGVLKKPVNAGSDM
Lompro2 196 GVFNHFGITLDFDALTTQVFYSTGDDPLEQQTDA ANDV SGQGQFHFGVLKKPTDSAGDI
Sceapi2 195 GVFNHFGVVLDFDALTTQVLYSTGDDPLEAQTDAL DNDV SGEQGFHFGVLKKPTDSAGDI
Rosnec2 197 DVFNHFAVTLDFDALTTQVFYSQGV DALVAQTEAL ANDV SGQGQFHFGVLKKGLNGGDDI
Conlig2 198 GVFNHFGVMLDFDKLTSQVFEHSTGTTALKAVTQAL ANDV SGQGQFHFGVLKKGI -GGNNI
Grocla2 196 DVFNHFAVTLDFENNLTTQVFEHSTGNS SALKAVTQAL SNDV SGQGEFHFGMLKKPIDGGSDI
Ophpic2 195 GVFNHFAVTLDFENNLTSQVFEHSTGK SPLKPVTOAL SNDV SGQGQFHFGMLKKPIDGGNDI
Spobra2 196 GVFNHFAVTLDFENKLT SQVFEHSTGTTALKSVTQAL ANDV SGQGQFHFGVLKKPVNPGADI
Spoins2 196 GVFNHFAVTLDFDKLTSQVFEHSTGTS PLKAQTOAL SNDV SGQGQFHFGVLKKGLDGGDDI
Phamin2 201 GAFHNFGVTLDFENNLTTQVFEH SACTDALEAVTQP ANDV SGQGQFHFGVLKKGLNGGDDI
Podans2 192 GVFNHFAVTLDFEDTLTTQVFEH SAGGDPLEVVNQV SNDV SGQGQFHFGVLKKPTDAVGD I
Diaamp2 198 GVFNHFGITLDFDANTTQVFYSTGN DPLAQVTEPEPNDV SGQGQYHFGVLKKGVNGGDDI
Diahel2 198 GVFNHFGITLDFENANTTQVFYSTGN EPLAQVTDALPNDV SGQGQYHFGVLKKGVNGGSDI
Psevex2 200 GVFNHFAVTLDFEDKNTTQVFYSQD S SALLEAQTEPEL ANDV SGQGQYHFGVLKKGIGGDVDI
Thiter2 194 GVFNHFAIKLDFEQSTTQVFEH SAGEDPLKAVTGVLENDV SGQGQFHFGVLKKPVGGQDI
Gaetri2 201 NGFNHFGITLDFENKNTVQVLEH STGAQPLKAVTQPEL ANDV SGGGQYHFGMLKKGLGGGADI
Magory2 202 DGFHNFAVTLDFETKNTTQVFEH SKGSEALKA VSKAEPNDV SGGGQFHFGCLKKGVGKVKDV
Magri2 213 EGFHNFAIKLDFEDKNTTQVFEH SKGSEALKA VSKAEPNDV SGGGQFHFGILKKGVGNAKDI
Cerpla2 193 GTFNHFGIKLDFETANTTQVFYSTGN CELTQQT EPEPNDV SGQGQFHFGILKKPTGETTDV
Thipun2 194 GKFNHFAIKLDFENANTTQVFYSTGN CSLSQQT EAL ANDV SGQGQFHFGILKKPTGNFTDI
Colglo2 201 GVFNHFAVTLDFETKNTTQVYYSQGS AP LVAQKPVENDV SGQGQFHFGVLKKSINGTGDT
Colnym2 199 GVFNHFAVTLDFGKNLTQVYYSQGN AP LVAQGPVENDV SGQGQFHFGVLKKSINGTGDL
Stacha2 195 GVITHNFALRLDYE TGTTOIFYSQDQAQLQSVTDI ANDV SGQGQYHFGILKKPTGSDGDI
Stach12 195 GVITHNFALRLDYE TGTTOIFYSQDQAQLQSVTDI ANDV SGQGQYHFGILKKPTGSDGDI
Clapur2 207 GTFHNFAVTLDFETRNTEVRYSTGL HALKSVTGPRANDV SGQGQYHFGILKKGLNGNGD-

Colhig2 271 TKSGDQPADIDEGLIYAGIFQEDSANGCISLSP
Colch12 269 TKSGDQPSGINEGLIYGGIFQEDSSSGCISLSP
Colfio2 272 TKSGDQPTGINEGLIYGGIFQEDSSAGCISLSP
Colsim2 272 TKSGDQPTGINEGLIYGGIFQEDSSAGCISLSP
Colinc2 271 TKSGDQPSGINEGLIYAGIFQEDSANGCISLSP
Coltof2 271 TKSGDQPSGINEGLIYAGIFQEDSSTGCISLSP
Colgra2 255 SKSGEQPANINEGLIYGGIFEDSSTGCISLSP
Colorb2 274 TKSGDQPANIDEGLIYGGIFQEDSSSGCISLSP
Lompro2 256 TKDGFQEQAGIDEGLIYAGIFQEDSSDGCISLSL
Sceapi2 255 TKDGFQEQAGIDEGLIYAGIFQEDSSDGCISLSL
Rosnec2 257 VKNGEQEQAGIDEGLIIFGGIFEDSSDGCILSV
Conlig2 257 VKDGVQEQAGIDEGLIIFGGIFEDSSAGCVSLSP
Grocla2 256 VHNQTQESDIDEGLIYGGIFEDSSTGCVSLSP
Ophpic2 255 VHNQTQEDGIDEGLIYGGIFEDSSTGCISLCA
Spobra2 256 VHSQTQEQAGINEGLIIFGGIFEDSSTGCISLSP
Spoins2 256 VHDGIQEQAGINEGLIIFGGIFEDSSTGCVSLSP
Phamin2 261 VKNGEQEQAGINEGLIIFGGIFEDSSTGCISLSP
Podans2 252 TRNGEQEQAGIDEGLIIFGGIFQEDSSAGCVSLRP
Diaamp2 258 TKDGGQEQAGIDEGLIYGGIFQEDSAASSIILSP (40)
Diahel2 258 TRDAQQPSGISEGLIYGGIFLEDSSASTIILSP (34)
Psevex2 260 TRLAQEQAGIDEGLIYGGIFQEDSADGCISLSA
Thiter2 254 TKNGEQEQAGINEGLIIFGGIFEDSAVGCILAG (3)
Gaetri2 261 VRNGVQEQAGINEGLIYGGIFMEDSSTGCVSLAP (16)
Magory2 262 VREGIQEQPNINEGLIYGGIFEDSANGCISLSA (56)
Magri2 273 IRDGIQEQANINEGLIYSGIFMEDSADGCVSLST (22)
Cerpla2 253 TKSGEQEQPADIDEGLIYSGIFSEDSADGCVSLSP (4)
Thipun2 254 TKSGEQEQSGINEGLIYSGIFMEDSADDCVSLSR (4)
Colglo2 261 TKTGFHESGINEGLIIFGGIFEDSADGCVSLSP
Colnym2 259 TKSGFHESGINEGLIIFGSI FEDSIDGCVTLSL
Stacha2 255 TRREGFQSSGINEAVLYGGIFLED SADGCISLGP (15)

Stach12 255 TRREGFQSSGINEAVLYGGIFLEDSADGCLSLGP(15
Clapur2 266 SKKGTQETGINEGLIYGGIFMEDSSENCRCNY-

Sordariomycetes

Hypocreomycetidae - Glomerellales (Colletotrichum but not Verticillium)

Colch12 = OLN97937.1 hypothetical protein CCHL11_02648 [Colletotrichum chlorophyti]
Colfio2 = EXF80808.1 hypothetical protein CFIO01_01179 [Colletotrichum fioriniae PJ7]
Colglo2 = KAF3811743.1 hypothetical protein GCG54_00014494 [Colletotrichum gloeosporioides]
Colgra2 = XP_008098621.1 hypothetical protein GLRG_09745 [Colletotrichum graminicola M1.001]
Colhig2 = TID06827.1 hypothetical protein CH35J_000821 [Colletotrichum higginsianum], which is equivalent to CH063_00647 described by Anasontzis et al. (2019) except the signal peptide sequence is correct
Colinc2 = KZL82458.1 hypothetical protein CI238_03137, partial [Colletotrichum incanum]
Colnym2 = KXH25668.1 hypothetical protein CNYM01_07213 [Colletotrichum nymphaeae SA-01]
Colorb2 = TDZ16663.1 hypothetical protein Cob_v010277 [Colletotrichum orbiculare MAFF 240422]
Colsim2 = KXH47399.1 hypothetical protein CSIM01_05336 [Colletotrichum simmondsii]
Coltof2 = KZL71646.1 hypothetical protein CT0861_07364 [Colletotrichum tofieldiae]

Hypocreomycetidae - Hypocreales - Clavicipitaceae (in Claviceps purpurea and other Claviceps species but not Metarhizium, Moelleriella libera, Pochonia chlamydosporia or Torrubietta hemipterigena)

Clapur2 = KAG6202730.1 hypothetical protein E4U50_006098 [Claviceps purpurea]

Hypocreomycetidae - Hypocreales - Cordycipitaceae - no orthologues found

Hypocreomycetidae - Hypocreales - Hypocreaceae - no orthologues found

Hypocreomycetidae - Hypocreales - Nectriaceae - no orthologues found

Hypocreomycetidae - Hypocreales - Ophiocordycipitaceae - no orthologues found

Hypocreomycetidae - Hypocreales - Stachybotryaceae

Stacha2 = KFA47799.1 hypothetical protein S40293_09048 [Stachybotrys chartarum IBT 40293]
Stach12 = KFA69030.1 hypothetical protein S40285_08453 [Stachybotrys chlorohalonata IBT 40285]

Hypocreomycetidae - Microascales

Cerpla2 = KKF95434.1 hypothetical protein CFO_g2225 [Ceratocystis platani]
Thipun2 = KKA28951.1 hypothetical protein TD95_005422 [Thielaviopsis punctulata]
Lompro2 = PKS05998.1 hypothetical protein jhhlp_007831 [Lomentospora prolificans]
Sceapi2 = XP_016645553.1 hypothetical protein SAPIO_CDS1553 [Scedosporium apiospermum]

Sordariomycetidae - Coniochaetales

Conlig2 = OIW32631.1 hypothetical protein CONLIGDRAFT_699488 [Coniochaeta ligniaria NRRL 30616]

Sordariomycetidae - Togniniales

Phamin2 = XP_007911498.1 hypothetical protein UCRPA7_713 [Phaeoacremonium minimum UCRPA7]

Sordariomycetidae - Diaporthales

Coniella lustricola - no orthologue found
Diaamp2 = KKY30855.1 hypothetical protein UCDDA912_g09201 [Diaporthe ampelina]
Diahel2 = POS74227.1 hypothetical protein DHEL01_v207386 [Diaporthe helianthi]

Sordariomycetidae - Magnaporthales

Gaetri2 = XP_009219288.1 hypothetical protein GGTG_03245 [Gaeumannomyces tritici R3-111a-1]
Magory2 = QBZ65172.1 hypothetical protein PoMZ_06877 [Pyricularia oryzae] (syn. Magnaporthe oryzae)
Maggr2 = XP_030976736.1 hypothetical protein PgNI_11158 [Pyricularia grisea]

Sordariomycetidae - Ophiostomataceae

Grocla2 = XP_014171689.1 hypothetical protein CMQ_2256 [Grosmania clavigera kw1407]
Ophpic2 = EPE10934.1 hypothetical protein F503_06029 [Ophiostoma piceae UAMH 11346]
Spobra2 = XP_040620669.1 uncharacterized protein SPBR_02939 [Sporothrix brasiliensis 5110]
Spoins2 = OAA67092.1 hypothetical protein SPI_01668 [Sporothrix insectorum RCEF 264]
Sposch2 = XP_016591024.1 hypothetical protein SPSK_07672 [Sporothrix schenckii 1099-18]

Sordariomycetidae - Sordariales - Sordariales incertae sedis

Madurella mycetomatis - no orthologue found

Sordariomycetidae - Sordariales - Chaetomiaceae

Chaetomium thermophilum var. thermophilum - no orthologue found
Podans2 = XP_001908978.1 uncharacterized protein PODANS_3_2140 [Podospora anserina S mat+] corrected for upstream methionine start and unrecognised intron
Thermothelomyces thermophilus - no orthologue found
Thiter2 = SPQ19874.1 44879d5e-d898-4d54-8381-2fd604ce673d [Thermothielavioides terrestris](syn. Thielavia terrestris)with corrected N-terminal sequence in place of erroneous starting methionine

Sordariomycetidae - Sordariales - Sordariaceae - no orthologues found

Xylariomycetidae - Xylariales

Eutypa lata - no orthologue found

Daldinia sp. - no orthologue found
Hypoxyylon sp. - no orthologue found
Microdochium bolleyi - no orthologue found
Pestalotiopsis fici - no orthologue found
Psevex2 = XP_040720469.1 uncharacterized protein BCR38DRAFT_334322 [Pseudomassariella vexata]
Rosnec2 = GAP88082.1 hypothetical protein SAMD00023353_3201390 [Rosellinia necatrix]

Supplementary Figure S7. ChGluc131A alignment. Multiple protein-sequence alignment of ChGluc131A orthologues in the Fol-EC4 clade of Sordariomycete GH131 (glycosyl-hydrolase 131) sequences. All sequences shown were the highest blastP matches to ChGluc131A (= Colhig2 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 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. The number of C-terminal residues removed manually for the purposes of alignment are shown in brackets at the end of the alignment.