

Colhig2	1	MYTSTLIL--SLVAAAAA	ACTGG--KNKTAE--AAAPGAKA--CCALQFDGRIPKAF	TAAD
Colch12	1	MFTSTLFL--SLVAAAAA	ACNGK--PNDT---DSSSGVKC--CCALQFDGRIPKAF	TAAD
Colfio2	1	MFASTIFL--SLVAAAAA	ACDGTTPKNNTG---AVSPGAKA--CCALQFDGRIPKTFKAAD	
Colsim2	1	MFASTIFL--SLVAAAAA	ACDGTTPKNNTG---AVSPGAKA--CCALQFDGRIPKTFKAAD	
Colinc2	1	MFTSTLFL--SLVAAAAA	ACDGST-KNNTA---GATPGAKA--CCSLQFDGRIPKAF	TAAD
Coltof2	1	MFTSTLFL--SLVAAAAA	ACDGST-KNNTA---GATPGAKA--CCSLQFDGRIPKAF	TAAD
Colgra2	1	MYTSTLIF--SLLAAA-----	-----GAKAQCTLQFDGRIPKAS	TVAD
Colorb2	1	MFASTIIL--SLVAAVAAD	CGSKS-GNNSYSSGPALPGAQA--CTLQFDGRIPKAF	TAAD
Lompro2	1	MALSR-----ALLSILL	SAA-----PLVSAQECTLQFDGRVPDGF	AAAD
Sceapi2	1	MSPRS-----ALLSLILL	SAL-----PLVSAQECTLQFDGRIPDGF	AAAD
Rosnec2	1	MAGFYPL--ALLVGI	IPTL-----VVSQCCDLQFDGRVP	SDFVAAT
Conlig2	1	MASPYLLSVSSIL	TLLALTS-----AQKCP	LQFDGRIPSTFTPTS
Grocla2	1	MLARH-----SLVLLAS	ATT-----AVLAKTCALQFDGRVP	STENLTT
Ophpic2	1	MISQYL-----SLLAL	PVLAA-----AQKCSLQFDGRIPSNL	TLAA
Spobra2	1	MMYPLSI---AFLAL	PLLAS-----AQKCTLQFDGRVP	STFTAAS
Spoins2	1	MRSSASL---ALLAL	PLLAS-----AQKCATLQFDGRIP	SSFAAT
Phamin2	1	MASLIRNY-FSLLP	ILLELS-----VVLAQSCDLQFDGRVP	SAGSAVAD
Podans2	1	MHKHGI---PLL	FASLVTS-----VSAQSCRLHFDGRVP	PSFGVAG
Diaamp2	1	MFSQRLLT-QTTLV	SLASLA-----ASC	SATLQFDGRVPAGTQLSA
Diahel2	1	MFSQRLLT-QTSLF	SLASLA-----ASC	STLQFDGRVPAGTQLSA
Psevex2	1	MASHRSFI-PSFLS	LVTLVV-----AQOCTLQFDGRVP	SDFVAAT
Thiter2	1	MVHLQYY--SVAVS	LLPS-----WVAAQNCTLQFDGRVP	SDLVAAD
Gaetri2	1	MRYSFTST-LSLALS	SPIS-----GVWAAQCRKLQFDGRIP	NNFQVAQ
Magory2	1	MRSFTVAS--AIFG	GLLATS-----PVYGOQCKLQFDGRVP	PANFOPAN
Maggr2	1	MRSFTVAS--AILG	GLSATS-----PVYGOQCKLQFDGRIP	ENFELTG
Cerpla2	1	MQSL-----SLLALI	APVA-----AQVCQLAFDGRVP	AKDFALEG
Thipun2	1	MYSR-----SLTAA	AALAAA-----PAVAQVCPLAFDGRVP	DNFTLDT
Colglo2	1	MSLSFIST-LSLL	LSAAGAAN-----AAKCP	LQFDGRVP
Colnym2	1	MHFSSSSL-GALV	AVAAGAAD-----AAKCP	LQFDGRIP
Stacha2	1	MAPSLFRL-LPVL	AGVTAVA-----CQSCPLQFDGRIP	RNFTVAD
Stach12	1	MAPSLFRI-LPVL	AGVTAVA-----CQSCSLQFDGRIP	RNFTVAD
Clapur2	1	MRTYFAI---NFV	AVATAAASG-----LGREAATTTKCP	LMFVDFGRVP

Colhig2	54	FDG-KTSP	FNTANVFGKGLKFS	DLIK-LPGGQ---SL--FDV--NSTQ	PFEVTI-----
Colch12	52	FDG-KSSP	FNTANVFGKGLKFS	DLIK-LPGGQ---SL--FDV--NSTQ	PFEVTI-----
Colfio2	55	FDS-TSSP	FNTANVFGKGLKFSE	IVQ-LPGGN---SL--FDV--NSTQ	PFEVTI-----
Colsim2	55	FDS-TSSP	FNTANVFGKGLKFSE	IVQ-LPGGN---SL--FDV--NSTQ	PFEVTI-----
Colinc2	54	FDG-SSSP	FNTANVFGKGLKFS	DLVQ-LPGGQ---SL--FDV--NSTQ	PFEVTI-----
Coltof2	54	FDG-TSSP	FNTANVFGKGLKFS	DLVQ-LPGGQ---SL--FDV--NSTQ	PFEVTI-----
Colgra2	38	FDA-KTSP	FNPSNVFGQGLKFS	QLIQ-LPGGQ---SL--FDA--NATQ	PFEVTI-----
Colorb2	57	FDG-KTSP	FNADNVLGKGLKFSE	DLIK-LPEET---SL--FDG--NS	SKPFEVTI-----
Lompro2	41	FDG-ANDI	FSPDNVFGQGLSFG	QLIQ-LPNAGL---SL--FDD--GT	IPFEVTI-----
Sceapi2	40	FDQ-ANNI	FSPDNVFGQGLAFS	QLIQ-LPAIGA---SL--FDD--ATV	PFEVTI-----
Rosnec2	40	FNT-GNGV	EDNNVVGQGLSLGS	VVQ-LQDSLS---SL--FDV--GTN	PFEVTI-----
Conlig2	41	FDA-ANAF	FQSNNVLGQGLKFS	QLIQ-LPSITP---SL--FDT--ATV	PVGVTI-----
Grocla2	39	FDT-ANGV	FNPNNVFGKNLTLS	QLLR-LPAQKG---SL--FDE--NTV	PFEVTI-----
Ophpic2	37	FDS-NNNI	YNPSNVFGKGLKFSE	LLIQ-LPAVAG---SL--FDT--KT	VPFEVTI-----
Spobra2	38	FDT-NNNL	FNPSNVFGQGLKFS	QLIQ-LPAVTG---SL--FDV--NTV	PAEVTI-----
Spoins2	38	FDT-NNNV	FSPSNVFGQNLKLS	QLVE-LPAQTG---SL--FDV--DTV	PFEVTI-----
Phamin2	43	FDA-TNNL	FSTDNVFGQGLKFS	QLIE-LPAVTP---SLPKFDV--NTI	PFEVTI-----
Podans2	39	FDT-PNNF	FSETNVLGAGLSFS	QLIQ-LPAISA---SL--FDT--ETI	PFEVTI-----
Diaamp2	40	FDS-ENGL	FNPDNVFGKNLTF	SQLIQ-LPDVAP---SL--FDV--GTV	PFEVTI-----
Diahel2	40	FDS-DNGL	FNPDNVFGKNVSE	QLIQ-LPDVDP---SL--FDV--GTV	PFEVTI-----
Psevex2	40	FDTAANT	MFNPDFTFGANLS	ISDVVE-MPCVTS---SL--FDAKN	NATKAVEVTI-----
Thiter2	41	FDS-PNKFF	SEKFVLGQGLKFDQ	ALRVLPVAGG---SL--FDI--DVDA	QPVVLI-----
Gaetri2	43	FDA-ANNI	FNPKNVLGKDLAFS	KILQ-LPKTSG---SL--FDN--NGT	QPLEVTI-----
Magory2	42	FDT-ANNI	FNPSNVLGKGLKFSD	VIO-LPTLAQQ---SL--FDV--AGK	TKAVEVTI-----
Maggr2	42	FDS-SNNL	FSSSNVLGKGLKFSE	LLIQ-FPANGNQTKIL--FD	TAGTKPFEVTIKYFTPP
Cerpla2	35	FDA-DTSP	FNPSNVFGKGLKSE	ILIK-FPEGNG---GL--FDV--DTK	PFEVTI-----
Thipun2	38	FDS-NNGV	FNPSFVLGANLT	WSEELQ-LPGGS---SL--FSD--NTQ	PFEVTI-----
Colglo2	42	FDT-SASP	FNNGFVFGKGLKAS	DVVT-IPTGLN---SL--FDA--NF	SKPFEVNI-----
Colnym2	41	FDT-SASP	FNNGFVFGKGLKAS	DVVT-IPTGLS---SL--LDG--PANK	PFOVNI-----
Stacha2	40	FDT-QNGI	YNPDFVKGRDLAFS	DIIE-LETDA---TL--FDT--NSV	PFTVQI-----
Stach12	40	FDT-QNGI	YNPDFVKGRDLAFS	DIIE-LETDT---TL--FDT--NSV	PFTVQI-----
Clapur2	47	FDV-KNNV	FNPSFVVGANQTF	SSVLR-FDNRGTSH--SL--FDR	VGVTKPFEVTI-----

Colhig2	99	---	DDKSIFAPSADNVQIGFRR	AEMLP	LSNDGK	DASTQG	IKTLHFS	LQKDD	KRPLNLS	SHE
Colchl2	97	---	NDKSIFAPSETNVQVGFRRA	ELLP	LSNDGQ	DASTDG	IKTLHFS	LKKDP	QRPLNLS	SHE
Colfio2	100	---	NDKSIFAPSETNVQVGFRRA	ELLP	LSNDGK	DASTQG	IKTLHFS	LQKDA	QRPLNLS	SHE
Colsim2	100	---	NDKSIFAPSETNVQVGFRRA	ELLP	LSNDGK	DASTQG	IKTLHFS	LQKDA	QRPLNLS	SHE
Colinc2	99	---	NDKSIFAPSETNVQVGFRRA	ELLP	LSNDGK	DASTQG	IKTLHFS	LQKDA	QRPLNLS	SHE
Coltof2	99	---	NDKSIFAPSATNVQVGFRRA	ELLP	LSNDGK	DASTQG	IKTLHFS	LQKDA	QRPLNLS	SHE
Colgra2	83	---	NDKSIFAPSANNVQIGFRR	AELP	ASNDGT	DPSTDG	IKTLHFS	LMKDA	QRSLNLS	SHE
Colorb2	102	---	NDKSIFAPSETNVQVGFRRA	ELLP	LSNDGK	DDSTVG	IKTLHFS	LKKDD	QRPLNLS	SHE
Lompro2	86	---	SDDSIFAPSADNVQIGFRR	AELLP	ASNDGT	DPSTTG	IKTLHFS	LMKDN	ARFNL	SHE
Sceapi2	85	---	SDDSIFAPSADNVQIGFRR	AELLP	ASNDGT	DPSTTG	IKTLHFS	LMKDN	ARAFNL	SHE
Rosnec2	85	---	SDDSIFAPSADNVQIGFRR	AELLP	ASNDGT	DASTTG	IKTLHFS	LMKDT	NRPLNL	THE
Conlig2	86	---	SDKSIFAPSADNVQIGFRR	AELLP	ASNSGT	DASTAG	IKTLHFS	VMKD	ARPLNLS	SHE
Groc1a2	84	---	SDESIFAPSASNVQIGFRR	AELP	ASNSGT	DPSTTG	IKTLHFS	LMKDS	ERPLNLS	SHE
Ophpic2	82	---	SDASIFAPSADNVQIGFRR	AELLP	ASNSGT	DASTLG	IKTLHFS	LMOD	PQRPLNL	THE
Spobra2	83	---	SDKSIFAPSADNVQIGFRR	AELLP	ASNSGT	DPSTQG	IKTLHFS	VMQDA	QRPLNL	THE
Spoins2	83	---	SDQSIFAPSADNVQIGFRR	AELLP	ASNSGT	DPSTQG	IKTLHFS	VMQDA	QRPLNLS	SHE
Phamin2	90	---	SDQSIFAPSADNVQIGFRR	AELLP	ASNSGT	DPSTTG	IKTLHFS	VMKDA	DRPLNLS	SHE
Podans2	84	---	SDASIF-----	NGQ	TGFRRA	ELLP	ASNSGT	DDSTTG	IKTLHFS	LQKDA
Diaamp2	85	---	SDESIFAPSADNVQLGFRRA	ELLP	ASNSGT	DASTLG	IKSLHFS	LMKDA	ARPLNLS	SHE
Diahel2	85	---	NDDSIFAPSADNVQLGFRRA	ELLP	ASNSGT	DPSTQG	IKSLHFS	LMKDA	ARPLNLS	SHE
Psevex2	88	---	DDKSIFTPSADNVQLGFRRA	ELMITS	NSDGT	DDSTLG	IKTLHFS	LMKDA	ARPLNLS	SHE
Thiter2	89	---	SDNSIF-----	NGQ	VGFRRA	ELLP	ASNSGT	DPSTQG	IKTLHFS	VMKDA
Gaetri2	89	---	DDKSIFVFNADTVQNGFR	RV	ELLA	ASNSGT	DDSTKG	IKTLHFS	IAKDC	ORALNL
Magory2	90	---	NDKSIFVFNADTVQNGFR	RT	ELL	IASNSGT	DDSTKG	IKTLHFS	IAKDLK	QPLNL
Maggr2	98	GIP	SDKSIFVFNPDTVQNGFR	RT	ELL	IASNSGT	DDSTKG	IKTLHFS	IAKDA	QRPLNL
Cerpla2	80	---	NDTSIFAPSETNVQNGFRRA	ELLP	ASNSGT	DPSTTG	IKTLHFS	LKKDA	QRPLNLS	SHE
Thipun2	82	---	NDKSIFAPSPDNVQVGFRRA	ELLP	ASNSGT	DNSTLG	IKTLHFS	LKKDI	TRPLNLS	SHE
Colglo2	88	---	DDRSIFAPTETNVQIGFRR	AELP	MSNGT	DPSTAG	IKTVHFS	MMKDP	KRPLNL	THE
Colnym2	87	---	DDRSIFAPTETNVQIGFRR	AELP	MSNGT	DPSTSG	IKTVHFS	MMKDP	KRPLNL	THE
Stacha2	84	---	DDSSIFAPSADNVQIGFRR	VELLP	ASNSGT	DDSTLG	IKTLHFS	VMKDV	TRPLNLS	SHE
Stach12	84	---	DDSSIFAPSADNVQIGFRR	VELLP	ASNSGT	DDSTLG	IKTLHFS	VMKDI	TRPLNLS	SHE
Clapur2	96	---	NDRSIFAPSVSNVQVGFR	RT	ELL	IASNSG	KDISTG	IKTLHFS	IAKDP	ARPLNLD

Colhig2	156	YQLA	FLESAD	FSTNQ	IVLKT	GTIL	-GQ-N--	TE	DPDTL	QLFGN	VATSP	-PPEL	FKTK	KFTF
Colchl2	154	YQLV	FLESAD	FSTNQ	IVLKT	GTIL	-GQ-N--	TA	DPDTL	QLFGN	VNSSP	-VPEL	FKTK	KFTE
Colfio2	157	YQLV	FLESAD	FSTNQ	IVLKT	GTIL	-GQ-N--	TA	DPDTL	QLFGN	VNSSP	-VPEL	FKTK	KFTA
Colsim2	157	YQLV	FLESAD	FSTNQ	IVLKT	GTIL	-GQ-N--	TA	DPDTL	QLFGN	VNSSP	-VPEL	FKTK	KFTA
Colinc2	156	YQLV	FLESAD	FSTNQ	IVLKT	GTIL	-GQ-N--	TE	DPDTL	QLFGN	VASSP	-TPEL	FKTK	KFTF
Coltof2	156	YQLV	FLESAD	FSTNQ	IVLKT	GTIL	-GQ-N--	TA	DPDTL	QLFGN	VASSP	-TPEL	FKTK	KFTF
Colgra2	140	YQLV	FLESAD	FSTNQ	IVLKT	GSIL	-CQ-N--	TA	DPDTL	QLFGN	VNSNP	-VPEL	FQTK	KFTF
Colorb2	159	YQLV	FLESAD	FSTNQ	IVLKT	GSIL	-GE-N--	TA	DPDTL	QLFGN	VASSP	-VPQL	FSTK	KFTF
Lompro2	143	YQLV	FLESND	FSTNQ	IVLKT	GTIL	-GV-N--	TA	DPDTL	QLFGN	VNQG---	NILF	STPF	FTA
Sceapi2	142	YQLV	FLESAD	FSTNQ	IVLKT	GTIL	-GG-N--	TA	DPDTL	QLFGN	VNQG---	QILF	STPF	FTA
Rosnec2	142	YQLV	FLESND	FSTNQ	IVLKT	GSIL	-GA-N--	TA	DPDTL	QLFGN	VNANP	-VQTL	FSVP	PFTE
Conlig2	143	YQLV	FLESND	FSTNQ	IVLKT	GTIL	-GA-G--	AG	DPDTL	QLFGN	VNESP	-PKV	LFST	PFQA
Groc1a2	141	YQLV	FLESSD	FSTNQ	IVLKT	GTIL	-GQ-E--	TA	NPDTL	QLFGN	VNVNP	-PQV	LFST	PFLLP
Ophpic2	139	YQLV	FLESAD	FSTNQ	IVLKT	GTIL	-GSTD--	GV	DPNTL	QLFGN	VNANP	-PQV	LFST	PFFTP
Spobra2	140	YQLV	FLESND	FSTNQ	IVLKA	GTIL	-CQAG--	NV	DPNTL	QLFGN	VNSNP	-PQV	LFST	PFFTP
Spoins2	140	YQLV	FLESND	FSTNQ	IVLKT	GTIL	-CGAA--	GV	DPNTL	QLFGN	VNANP	-PQV	LFST	PFFTP
Phamin2	147	YQLV	FLESND	FSTNQ	IVLKT	GTIL	-GQ-A--	TA	DPDTL	QLFGN	VNDG--	-ANV	LFST	PFVVD
Podans2	136	YQLV	FLESND	FSTNQ	IVLKT	GTIL	-GGDT--	AV	DPDTL	QLFGN	VNQTP	-SKL	LFST	VPFLD
Diaamp2	142	YQLV	FVLESSD	FSTNQ	IVLKT	GTIL	-DTATQ	GGV	DPDSL	ILFGN	VKQS---	QILF	NTAF	TFTE
Diahel2	142	YQLV	FVLESSD	FSTNQ	IVLKT	GTIL	-DTATQ	KG	VDPSL	ILFGN	VKQS---	EQ	LFST	PFTE
Psevex2	145	YQLF	FLESAD	FSTNQ	IVLKT	GSIL	-GA-D--	TP	NPDTL	QLFGN	VNSSP	-LQ	TLFST	NFTE
Thiter2	141	YQLV	FLESND	FSTNQ	IVLKT	GTIL	-GQ-N--	TA	DPDTL	QLFGN	VNQG---	QILF	STPF	VVD
Gaetri2	146	YQLV	FLEDNS	FSTNQ	IVLKT	GTIA	-GQ-N--	GN	PDTL	QLFGN	VKESP	-PKV	LFST	PFFAA
Magory2	147	YQLV	FLEDNKF	FSTNQ	IVLKT	GTID	-GQ-A--	NT	PDTL	QLFGN	VASSP	-PKL	LFST	PFPGA
Maggr2	158	YQLV	FLEDNKF	FSTNQ	IVLKT	GTIA	-CQ-T--	SN	TNTL	QLFGN	VNASP	-PKL	LFST	PFFAA
Cerpla2	137	YQLV	FLEDNST	FSTNQ	IVLKT	GTILT	-GQ-N--	AS	DPDTL	QLFGN	VNQKE	-PGM	IFSAP	FTF
Thipun2	139	YQLV	FLEDNST	FSTNQ	FALK	GTIL	-GQ-N--	TN	PDTL	QLFGN	VNDAK	-PGL	IFSAP	FTTA
Colglo2	145	YQM	VFLESS	IFSSNQ	YALK	YGDIL	-GI-H--	PA	DPDV	LHLFGN	SNTKP	FPQ	ELFRT	KFTD
Colnym2	144	YQM	VFLESS	IFSSNQ	FALK	YGDIL	-GI-H--	PA	DPDV	LHLFGN	SNTNP	-SPE	LFKTK	FTE
Stacha2	141	YQLV	FLESAD	YSNSQ	FDIK	GTIL	-GR-D--	TP	DPDT	IQVYGN	INAG--	-AALL	YSTP	PFTE
Stach12	141	YQLV	FLESAD	YSNSQ	FDIK	GTIL	-GR-D--	TP	DPDT	IQVYGN	INAG--	-AALL	YSTP	PFTE
Clapur2	153	YQLS	FLEDSS	FSTNQ	FVLKT	GNIT	-GV-N--	TL	DPDSL	TLFGN	TNKF--	-GDV	LFST	PFFTA

Colhig2	211	GVFHNFAIKLDEFTANTTEVFYSQGTSALKSQGAAPNIAGQGQYHFGILKKPVNGGADI
Colchl2	209	GVFHNFAIKLDFTKNTTEVFYSQGN SALKSQGAPVSNLAGKGQYHFGMLKKPVNGGSDI
Colfio2	212	GVFHNFAIKLDFTKNTTEVFYSQGN SALKSTGAAVTNNLAGQGQYHFGMLKKPVNGGSDI
Colsim2	212	GVFHNFAIKLDFTKNTTEVFYSQGN SALKSTGAAVANNLAGQGQYHFGMLKKPVNGGSDI
Colinc2	211	GVFHNFAIKLDEFTANTTEVFYSQGN SALKSQGA VANNLAGQGQYHFGMLKKPVNGGADI
Coltof2	211	GVFHNFAIKLDEFTANTTEVFYSQGN SALKSQGAPVANNLAGQGQYHFGILKKPVNGGDDI
Colgra2	195	GVFHNFAIKLDEFTANTTQVFYSQGN SALKSQGAPVANNLAGKGQFHFGVLKKPVNGGADI
Colorb2	214	GVFHNFAIKLDFTKNTTEVFYSTDN SALKSQGA VANNLAGQGQYHFGVLKKPVNAGSDM
Lompro2	196	GVFHNFGITLDEFDALTTQVFYSTGDDPLEQQTDAANDVSGQGQFHFGVLKKPTDSAGDI
Sceapi2	195	GVFHNFGVVLDEFDALTTQVLYSTGDDPLEAQTDADNDVSGEGQFHFGVLKKPTDSAGDI
Rosnec2	197	DVFHNFAVTLDFDALTTQVFYSQGVDA LVAQTEALANDVSGQGQFHFGVLKKGLNGGDDI
Conlig2	198	GVFHNFGVMLDFDKLTSQVFHSTGTTALKAVTQALANDVSGQGQFHFGVLKKGI-GGNNI
Grocla2	196	DVFHNFAVTLDFENNLTTQVFHSTGNSSLKAVTQALSNDISGQGEFHFGMLKKPIDGGSDI
Ophpic2	195	GVFNFAVTLDFENNLTSQVFHSTGKSP LKPVTQALSNDVSGQGQFHFGMLKKPIDGGNDI
Spobra2	196	GVFHNFAVTLDFENKLTSQVFHSTGTTALKSVTQALANDVSGQGQFHFGVLKKPVNPGADI
Spoins2	196	GVFQNFVTLDFDKLTSQVFHSTGTSPLKAQTQALSNDVSGQGQFHFGVLKKGLDGGDDI
Phamin2	201	GAFHNFGVTLDFENNLTTQVFHSACTDALEAVTQPLANDVSGQGQFHFGVLKKGLNGGDDI
Podans2	192	GVFHNFAVTLDEDTLTTQVFHSAGGDPLEVVNQVSNNDVSGQGQFHFGLLKKPTDAVGDI
Diaamp2	198	GVFHNFGITLDFDANTTQVFYSTGNDPLAQVTEPLPNDISGQGQYHFGVLKKGVNGGDDI
Diahel2	198	GVFHNFGITLDFENANTTQVFYSTGNEPLAQVTDALPNDISGQGQYHFGVLKKGVNGGSDI
Psevex2	200	GVFHNFAVTLDFEDKNTTQVFYSQDSSALEAQTEPLANDVSGQGQYHFGVLKKGIGGDVDI
Thiter2	194	GVFHNFAIKLDFDQSTTQVFHSAGEDPLKAVTGVLNDISGQGQFHFGVLKKPVGGQGI
Gaetri2	201	NGFHNFGITLDFENKNTVQVLESTGAQPLKAVTQPLANDESGGGQYHFGMLKKGLGGGADI
Magory2	202	DGFHNFAVTLDFTKNTTQVFHSTGNSPLKAVSKAEPNDVSGGGQFHFGCLKKGVGVKVDV
Maggri2	213	EGFHNFAIKLDEDKNTTQVFHSTGSEALKAVSKEESNDVSGGGQFHFGILKKGVGNAKDI
Cerpla2	193	GTfHNFGIKLDEFTANTTQVFYSTGNCELTQQTTEPLNNDVSGQGQFHFGILKKPTGETTDV
Thipun2	194	GKFHNFAIKLDFENANTTQVFYSTGNCSLSQQTTEALANDVSGQGQFHFGILKKPTGNFTDI
Colglo2	201	GVFHNFAVTLDFTKNMTQVLYSQGSAP LVAQGKPVENDISGQGQFHFGVLKKSINGTGDT
Colnym2	199	GVFHNFAVTLDFGKNLTQVLYSQGNAP LVAQGQPVENDISGQGQFHFGVLKKSINGTGDL
Stacha2	195	GVIHNFAIRLDYETGTTQVLYSQDCAQLQSVTDIANDISGQGQYHIGLKKPTGSDGDI
Stachl2	195	GVIHNFAIRLDYETGTTQVLYSQDCAQLQSVTDIANDISGQGQYHIGLKKPTGSDGDI
Clapur2	207	GTfHNFAIRLDFTRNTEVRYSTGLHALKSVTGPRANDISGQGQYHFGILKKGLNGNGD-

Colhig2	271	TKSGDQPADIDEGIIYAGIFQEDSANGCISLSP
Colchl2	269	TKSGDQPSGINEGIIYGGIFQEDSSSGCISLSP
Colfio2	272	TKSGDQPTGINEGIIYGGIFQEDSSAGCISLSP
Colsim2	272	TKSGDQPTGINEGIIYGGIFQEDSSAGCISLSP
Colinc2	271	TKSGDQPSGINEGIIYAGIFQEDSANGCISLSP
Coltof2	271	TKSGDQPSGINEGIIYAGIFQEDSSSTGCISLSP
Colgra2	255	SKSGEQPANINEGIIYGGIFEDSSSTGCISLSP
Colorb2	274	TKSGDQPANIDEGIIYGGIFQEDSSSGCISLSP
Lompro2	256	TKDGFQEQAGIDEGIIYAGIFQEDSSDGCISLSL
Sceapi2	255	TKDGFQEQAGIDEGIIYAGIFQEDSSDGCISLSL
Rosnec2	257	VKNGEQEPGIDEGIIYGGIFEDSSDGCITLSV
Conlig2	257	VKDGVQEQAGIDEGIIYGGIFEDSSAGCVSLSP
Grocla2	256	VHNGTQESDIDEGIIYGGIFEDSSSTGCVSLSP
Ophpic2	255	VHNGTQEDGIDEGIIYGGIFEDSSSTGCISLCA
Spobra2	256	VHSGTQEPGINEGIIYGGIFEDSSSTGCISLSP
Spoins2	256	VHDGIQEPGINEGIIYGGIFEDSSSTGCVSLSP
Phamin2	261	VKNGEQEQAGINEGIIYGGIFEDSSSTGCISLSP
Podans2	252	TRNGFQEDGIDEGIIYGGIFQEDSSAGCVSLRP
Diaamp2	258	TKDGGQPPAGIDEGIIYGGIFQEDSAASSITLSLSP (40)
Diahel2	258	TRDAQQPSGISEGIIYGGIFLEDSSASTITLSLSP (34)
Psevex2	260	TRLAQFPAGIDEGIIYGGIFQEDSADGCISLSA
Thiter2	254	TKNGFQEQAGINEGIIYGGIFEDSSAVGCIILAG (3)
Gaetri2	261	VRNGVQPPAGINEGIIYGGIFMEDSSSTGCVSLAP (16)
Magory2	262	VREGIQEPNINEGIIYGGIFEDSSANGCISLSA (56)
Maggri2	273	IRDGIQEPANINEGIIYSGIFMEDSSADGCVSLST (22)
Cerpla2	253	TKSGFQPADIDEGIIYSGIFSEDSADGCVSLSP (4)
Thipun2	254	TKSGFQESGINEGIIYSGIFMEDSADDCITLSLR (4)
Colglo2	261	TKTGFHESGINEGIIYGGIFEDSSADGCVSLSP
Colnym2	259	TKSGFHESGINEGIIYSGIFEDSSIDGCVTLSL
Stacha2	255	TRRGFQSSGINEAVIYGGIFLEDSSADGCISLGP (15)

Stachl2 255 TREGFQSSGINEAVLYGGIFLEDSADGCLSLGP(15
 Clapur2 266 SKKGTQETGINEGLIYGGIFMEDSSENCRCNY-

Sordariomycetes

Hypocreomycetidae - Glomerellales (Colletotrichum but not Verticillium)

Colchl2 = OLN97937.1 hypothetical protein CCHL11_02648 [Colletotrichum chlorophyti]
 Colfio2 = EXF80808.1 hypothetical protein CFIO01_01179 [Colletotrichum fiorinae 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 Torrubia 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]
 Stachl2 = 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)
 Maggri2 = XP_030976736.1 hypothetical protein PgNI_11158 [Pyricularia grisea]

Sordariomycetidae - Ophiostomataceae

Grocla2 = XP_014171689.1 hypothetical protein CMQ_2256 [Grosmanella 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 [Podospira anserina S mat+] corrected for upstream methionine start and unrecognised intron
 Thermostelomyces thermophilus - no orthologue found
 Thiter2 = SPQ19874.1 44879d5e-d898-4d54-8381-2fd604ce673d [Thermostielavioides 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
Hypoxyton 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.