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Agn1p   MKLVL----FLVLLFSALINL----------------TNADKMVVAHFIVGN-TYPYTVSNWEEDIQDA 48
Th MutA MLGVVRRLGLGALAAAALSSLGSAAPANVAIRSLEERASSADRLVFCHFMIGIVGDRGSSADYDDDMQRA 70
Pp MutA M-------KVSSAFAATLSAI-IAACSALPSDSMVSRRSTSDRLVFAHFMVGIVSDRTSASDYDADMQGA 62

Agn1p   IAVGIDGFALNMGSDAWQVERIEDAYDAAASVSSDFKLFISFDMSI-ISADADFIEGVVRRFADKPNQLY 117
Th MutA KAAGIDAFALNIGVDGYTDQQLGYAYDSADR--NGMKVFISFDFNWWSPGNAVGVGQKIAQYASRPAQLY 138
Pp MutA KAYGIDAFALNIGTDTFSDQQLGYAYESAAN--NDMKVFISFDFNWWSTSQATEIGQKIAQYGSLPGQLM 130

Agn1p   YDGKVFVSTFAGETDTFGYSDVSTGWDSAVKEPLASAGYPIYFVPSWTSLGQGALEESVADGFLSWNAWP 187
Th MutA VDNRPFASSFAGD-------------GLDVNALRSAAGSNVYFVPNFHPGQSSP-SN--IDGALNWMAWD 192
Pp MutA YDDKIFVSSFAGD-------------GVDVAALKSAAGGNVFFAPNFHPSYGTDLSD--VDGLLNWMGWP 185

Agn1p   TTDADMN----------DNDDIGYQNLANSLGKLYVAPVSPWFYTHL----SY-KNWAYKSDWLIIDRWNE 243
Th MutA NDGNNKAPKPGQTVTVADGDNAYKNWLG--GKPYLAPVSPWFFTHFGPEVSYSKNWVFPGGPLIYNRWQQ 260
Pp MutA SNGNNKAPTAGANVTVEEGDEEYITALD--GKPYIAPASPWFSTHFGPEVTYSKNWVFPSDLLFYQRWND 253

Agn1p   MLSVQPDMIEVLTWNDYGESHYIGNIQGA-LPAGSEGYVDGFDHTAWRYLMSPYISAYK---LGLSEPYI 309
Th MutA VLQQGFPMVEIVTWNDYGESHYVGPLKSKHFDDGNSKWVNDMPHDGFLDLSKPFIAAYKNRDTDISK-YV 329
Pp MutA LLNLGPQFIEVVTWNDYGESQYVGPLNSPHTDDGSSRWANDMPHDGWLDLAKPYIAAFHDGATSLSSSYI 323

Agn1p   NFESLFYWYRPTPK-----SATATADSLSYPSGGDY----------MEDEIFVLVYLLQSAEVTVTCGST 364
Th MutA QNEQLVYWYRRNLKALDCDATDTISNRPANNGSGNYFMGRPDGWQTMDDTVYVAALLKTAGSVTVTSGGT 399
Pp MutA TEDQLIYWYRPQPRLMDCDATDT-CMVAANNDTGNYFEGRPNGWESMEDAVFVVALLQSAGTVQVTSGPN 392

Agn1p   TQTFSGVPGVNQFTIPMETNASPSFTVARQGGTLASGTGPEIVDSL---SIYNFNAYIGVL--------- 422
Th MutA TQTFQANAGANLFQIPASI-GQQKFALTRNGQTVFSGTSLMDITNVCSCGIYNFNPYVGTIPAGFDDPLQ 468
Pp MutA TETFDAPAGASAFQVPMGF-GPQSFSLSRDGETVLSGTSLKDIIDGCLCGIYNFNAYVGSLPATFSDPLE 461
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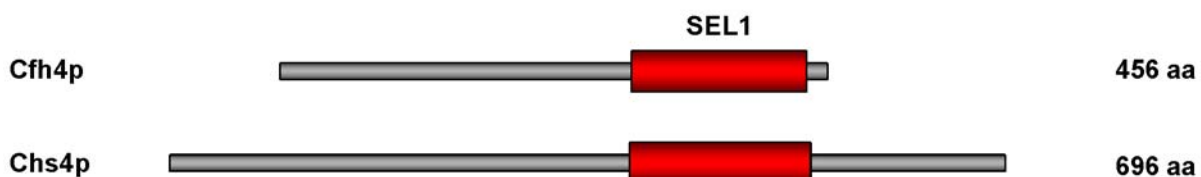
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Cfh4p [====== SEL1 ======] 456 aa

Chs4p [====== SEL1 ======] 696 aa

B

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Chs4p MASSPQVHPYKKHLMQSQHINFDNRGLQFQNSSLKVGQDFSDNKENRENRDNEDFSTADLPKRSANQPLI  70

Cfh4p SDVLP---------ETNNAHEE----VSSSSWSLSSSDSIMSYDSLSD---------------------  86
Chs4p NEHLRAASVPLLSNDIGNSQEEDFVPVPPPQLHLNNSNNT-SLSSLGSTPTNSPSPGALRQTNSSTSLTK 139

Cfh4p ----------DVSVLSFLDCPLTT--FETAPSIASFSNSAADVSSHSRSSSSWSAKLS------------ 132
Chs4p EQIKKRTRSVDLSHMYLLNGSSDTQLTATNESVADLSHQMISRYLGGKNNTSLVPRLKTIEMYRQNVKKS 209

Cfh4p -------RFTKHASKPSLSSNSSDSSFSKSGSESNALSSRGSFEL--EPHGIHRHVS-----RAKRLLSK 188
Chs4p KDPEVLFQYAQYMLQTALTIESSNALVQDSDKEGNVSQSDLKLQFLKEAQSYLKKLSIKGYSDAQYLLAD 279

Cfh4p FYS-----KFHHKKEDSSFDPLAPLVFAPNTSRVLRVTNEANASAISLEKATSL----SSQEQPGSEIKK 249
Chs4p GYSSGAFGKIENKEAFVLFQAAAKHGHIESAYRASHCLEEGLGTTRDSRKSVNFLKFAASRNHPSAMYK- 348

Cfh4p ELSLYDHEFDQILDLAIKAKKDGNLENAIEFLEYIMPEVASQQNFVPYELAELYKQ---RGTSQDLKSIL 316
Chs4p -LGLY--SFYGRMGLPTDV--NTKLNGVKWLSRAAARANELTAAAPYELAKIYHEGFLDVVIPDEKYAM  412

Cfh4p PLYMLAASLGHDRSSFLVGEAFFYGTYGARENKLRALQYYHLANDKGNADAMLALCKLYLRGLPGHIFPS 386
Chs4p ELYIQAASLGHVPSATLLAQIYETGNDTVGQDTSLSVHYYTQAALKGDSVAMLGLCAWYLLGAEPAFEKD 482

Cfh4p SRRAFEYAHRAAMLGHAPACYVLGKFYETGVGC----------------------VKDLAKSEAGF---- 430
Chs4p ENEAFQWALRAANAGLPKAQFTLGYFYEHGKGCDRNMEYAWKWYEKAAGNEDKRAINKLRSRDGGLASIG 552

Cfh4p ----------------------RAGLINDSPIT---------------DADALQI--------------- 448
Chs4p KKQHKKNKSISTLNLFSTVDSQTSNVGSNSRVSSKSETFFTGNPKRDREPQGLQINMNSNTNRNGIKTGS 622

Cfh4p --------------------------ASTLV----------------------------- 453
Chs4p DTSIRKSSSSAKGMSREVAEQSMAAKQEVSLSNMGSSNMIRKDFPAVKTESKKPTSLKNKKDKQGKKKKD 692

Cfh4p -LLQ 456
Chs4p CVIM 696
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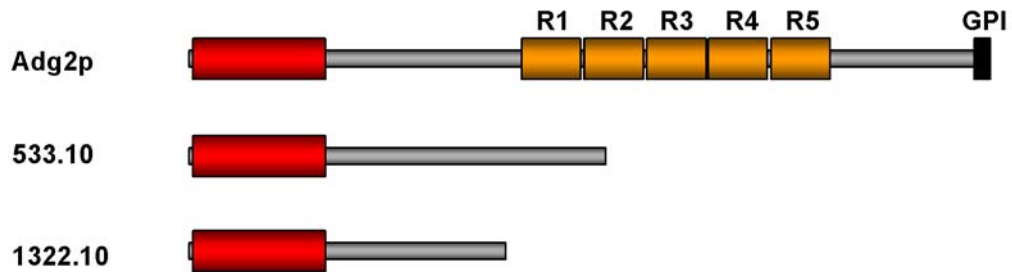
A

Adg2p — [red] — [grey] — R1 R2 R3 R4 R5 [orange] — [grey] — GPI

533.10 — [red] — [grey]

1322.10 — [red] — [grey]

B

```
Adg2p    MRRLT-ISGLLISLAKLCA-GMEINVPSSSDVWTSGHIEPLEWSVVSTDPLQANVWLINEVEYPPTSRYI  68
553.10   ML-FK-ISFLALIASAL---AMSINSPTNGDTWQTNGEEQITWNVVSTDEPSAALYLTNFAVYPTVTQYL  65
1322.10  MLARV-GTTLFFLANALAAYAVSVTSPTRDTTWSGQVNTVTWSSVSTDPEEMVIMLVNNAHYPNQNFNL  69
An       MRSSICFTVFAILFDSLAA-AISITEPTANSTFAAGSTITVKWTTVDTDPSYFSLYLVNFVSWPPSYIAL  69
Nc       MRV----LALAALAAPLVS-ALQFTDPVANATLHKGETFDLKWSTVDTDPTDFSVYLVNFVNWPPYYTPL  65
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Adg2p    M-TINTFDENATFPALDLS--PGYGYQISF-TSIRDDSVIYAQSGTFYIVGG-EGISSTTGSTFQSM     130
553.10   D-TVDTSTGSYTTNTTNWP--TGQGFQINM-AYPGRPEQIYAQSQQFNIV                     111
1322.10  G-TVQSSAGSLDTDISISSDLPTDGWQIYFNGATSQNQGSLAQSEQFDFEG                    119
An       ALDVPSADESHTVQIPCDTN-PEWGYQLS-AINGTNVYIIYAQGERFTVSNPLNGSHC-VDSVPSDTTC   135
Nc       AYNIEPSSGELSVTIPCDID-SSYGWQFN-AINGTNVYVIYAQTPKFYIS----GGPCSVDSPFPTGAP  128
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C

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R1  TGSTTTTGSAT-VSSSPFYSNSSVI-PTSVPSS--VSSFTSS---SSSYTTTLTASNTSV
R2  TYTGTGTGSATFTSSPPFYSNSSVI-PTSVPSS--VSSFTSS---NSSYTTTLTASNTSI
R3  TYTGTGTGSATFTSSPPFYSNSSVI-PTSVPSS--VSSFTSS---NSSYTTTLTASNTTV
R4  TFTGTGTGSATFTSSPPFYSNSSVI-PTSAPSS--VSSFTSS---NSSYTTTLTASNTTV
R5  TFTGTGTGSATATSSSPYYSNSSIIVPTTVSTSGSVSSFSSSPSPTSSFSGT-SALSSSS
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A

SUN

Adg3p

Sun4p

BgIAp

Ymr244wp
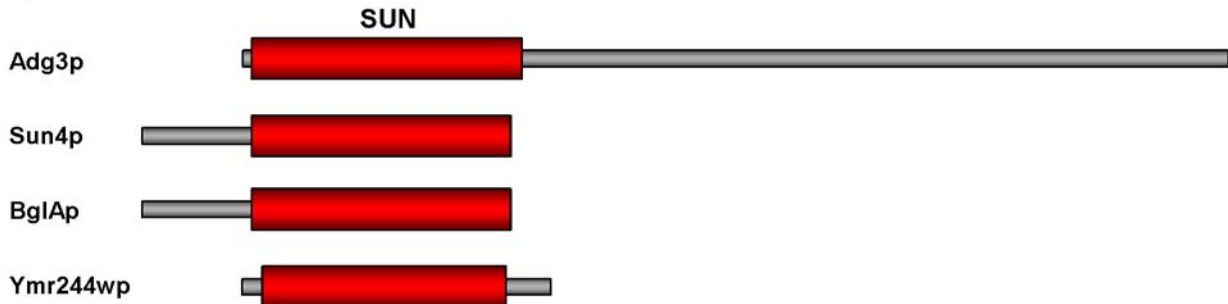
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D.han      GGNTCD-FPSNKGLVSVTSKSSNGGWA-----MSPDQQCTEGNYCPYACPPGKLMAQWDSSATSYSYPE   89
A.gos      G--TCA-FPHGKMVAVQTEGKNAGWA------MHSDQECKPGTWCPYACPAGOLMGQWNPQVTAYTYPG   91
Ymr244wp   GG-TCA-FPNYDGMVAVQKGGSNGGWA-----MSPDQECSYGSWCPYACKPGOLMGQWDPSATTYSYPK  109
BgIAp      GVISCSDFPVGQGVIPLNNLG-FGGWSGIYHSDTSTGGSCTEGSYCSYACQPGMSKTQWPSDQPA---NG  232
SUN4p      GTIPCGQFPSGQGVIPISWLD-EGGWSGVENTDTSTGGSCKEGSYCSYACQPGMSKTQWPSDQPS---DG  231

Adg3p      SMYGGLYCNSDGVAVKPFPSKDY-CYPGVGDLSVVDQT-GDGIAFCQTVLPGNEAMLIPTWVAPDSEQVL  199
A.nid      SMNGGLYCNEDGEIEKPFPDKPY-CRDGTGAVEAVNKC-GDVVSFCQTVLPGNEAMLIPTLVEEVS--TL  168
D.han      SQNGGLKCNQDGTVSKPFSNKDY-CVDGKGTVEVNNKA-SDNVAFCQTVLPGNEAMLIPTNVDGSGTQTL  157
A.gos      SMEGGLFCDESGNLQTPYPDKPY-CYDGKGTVIAENKA-GADVAFCQTVLPGNEEMLIPTLVGGGSSQTL  159
Ymr244wp   CQNGGLYCDSNGNLQKPNSDKDY-CYDGKGTVIAKNNANSGDVAFCQTVLPGNEAMLIPTLVGSGSKQTL  178
BgIAp      VSVGGLLCKG-GKLYKSSS-SDYLCEWGVDAARVVSEI-SDVVSICRTDYPGTENMVIPTAVEGGDEAIL  299
SUN4p      RSIGGLLCKD-GYLYRSNTDTDYLCEWGVDAAYVVSEL-SNDVAICRTDYPGTENMVIPTYVQAGDSLPL  299

Adg3p      AVPDIS-Y--WDE--TAAHYYVNPPGVSTTDGCVWGTSANPYGNWAPYVAGANMDENNITYVKLGANPIY  264
A.nid      AVPDLS-Y--WCE--TAAHFYINPPGKDPETACVWGTSSNPWGNWAAYVAGANTDGDGNTFVKIIGWNPIY  233
D.han      AVPGSD-Y--WDG--TAAHYYINPPGVSTDDGCVWGTKDKSQGNWAPYVAGANMDDSGKTYVKIGWNPKY  222
A.gos      AVPGTD-Y--WAG--TAAHYYVNPPGVSVKDACIWGTKENARGNWAPYVTGANQDAEGNTFVTVGWNPIY  224
Ymr244wp   AVPGTD-Y--WAS--SASHYYVNAPGVSVEDACQWGSSANPOGNWAPFVAGSNMDDNQNTFVKIGWNPVY  243
BgIAp      TVVNGETYYQWEGMTTSAQYYVNNAGVSYEDGCIWGDSNGDIGNWAPLNFGAGYDG-GISYLSLIPNP--  366
SUN4p      TVVDQDTYYTWQGLKTSAQYYVNNAGISVEDACVWGSSSSGVGNWAPLNFGAGSSD-GVAYLSLIPNP--  366

Adg3p      LDDSY-WSTVKPTYGLALECEGDT-CSGLPCYVDPRENGVQG--CPEGSPIGAGGACFCVVGFQQGTIAK  330
A.nid      LEDTTPFRSTRPDFGVEIECDGDG-CNGLPCKIDPAENDVNEVT--GSSSDGAGGANFCVVTVPKGEKAR  300
D.han      IDD---FSNKKPNFGIRVTCD-DGDCDGLDCEIDPSKTGYNGV--SGSSSGKQEGASYCIVTAKNKSKAQ  286
A.gos      LEPETPFRNVKPSYGLRIVCDNEEDCVGLPCGIDPSVNGVNEIQ--GSGSTGAGGANFCVVTAKKGAKAR  292
Ymr244wp   LESSCPFKNVKPSFGIRITCDDESQCEGLPCSIDPSSNGVNEVTSSGGGSSGAGGGNFCVVTARNGAKAN  313
BgIAp      -NNKNAL-----NFNVKIIAYDDKSNVNGECVYE-----------NGSYNGDGTDGCTVAVTSG-KAK  416
SUN4p      -NNGNAL-----NFNVKIVAADDSSTVNGECIYE-----------NGSFSG-GSDGCTVSVTAG-KAK  415

Adg3p      IVVVDYSEEMASSSSSA--------------------SAT                               350
A.nid      LVVFDSSSGS                                                            310
D.han      IEVFST                                                                292
A.gos      VEVFSTGG----NAKRSLEHTHN-RGNLSDIH-RTVTTIAMN                             328
Ymr244wp   IEVFDVGSGSSSSKGKRELNPLDVITTTVTETKYKTVTVTAKT                            355
BgIAp      YVLY                                                                  420
SUN4p      FVLYN                                                                 420
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SUPPLEMENTARY FIGURE LEGENDS

Fig. S1. Alignment of Agn1p with the catalytic domain of α-glucanases. Agn1p shows sequence similarity to the catalytic domain of α-glucanases (mutanases) from *Trichoderma harzianum* (Th MutA, AAF27911) and *Penicillium purporogenum* (Pp MutA, AF214481). The complete amino acid sequence of Agn1p was aligned with the catalytic domains of *T. harzianum* MutAp (from 1 to 468) and *P. purporogenum* MutAp (1 to 461) using the CLUSTAL program. Black boxes indicate sequence identities and dashes indicate gaps.

Fig. S2. Domain architecture and alignment of Cfh4p with the *S. cerevisiae* Csh4p. (A) Domain architecture of Cfh4p and Chs4p. Both proteins contain a SEL1 domain, a subfamily of the tetratricopeptide repeat (TPR) proteins. (B) Sequence alignment of Cfh4p and Chs4p. Cfh4p shows low sequence similarity (17.6% identity) to the *S. cerevisiae* Chs4p (CAA84882), which is more apparent in the SEL1 domain (double underlined). Global alignment of the two sequences was performed using the ALIGN program. Black boxes indicate sequence identities and dashes indicate gaps.

Fig. S3. Domain architecture and similarities of Adg2p. BLAST searches revealed the presence of a region at the N-terminal end of Adg2p (amino acids 1 to 130, red box) that shows sequence similarity to two *S. pombe* proteins of unknown function (SPCC553.10p and SPCC1322.10p) and to proteins from *Aspergillus nidulans* (XP_407395) and *Neurospora crassa* (XP_324909). (A) Domain architecture of Adg2p, SPCC553.10p (CAA19262) and SPCC1322.10p (CAA22863). The red box indicates the N-terminal region common to the three proteins. The orange boxes indicate the position of the five repeats present in Adg2p (R1 to R5), and the black box at the C terminus represents the putative GPI attachment site. (B) Alignment of the N-terminal region of Adg2p, SPCC553.10p (553.10), SPCC1322.10p (1322.10), *A. nidulans* (An) and *N. crassa* (Nc) proteins. The sequences were aligned using the CUSTAL program, with black boxes indicating sequence identities and dashes indicating gaps. (C) Alignment of the

five repeats of Adg2p. The sequence of the five repeats present in Adg2p were aligned using the CUSTAL program, with black boxes indicating sequence identities and dashes indicating gaps.

Fig. S4. Domain architecture and similarities of Adg3p. (A) Domain architecture of Adg3p and similar proteins. Adg3p contains a domain at the N-terminus (amino acids 69-350, red box) that belongs to the SUN family of proteins, followed by a large region (amino acids 350-1131) which is Ser/Thr-rich (51% of the amino acids). The SUN domain is also present in other fungal proteins, such as *S. cerevisiae* Sun4p or Ymr244wp, or the putative β-glucosidase BglAp of *Candida wickerhamii*. (B) Alignment of the SUN domain of Adg3p and related proteins. The protein sequence of Adg3p was aligned using the CLUSTAL program with related proteins from *A. nidulans* (XM_404863; A.nid), *Debaryomyces hansenii* (XM_462085; D.han), *Ashbya gossypii* (NM_209901; A.gos), *S. cerevisiae* (Ymr244p and Sun4p) and *C. wickerhamii* (BglAp). Black boxes indicate sequence identities and dashes indicate gaps.