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At_Ste24p -----MAFPMETVVG---FMVVMYIFVYDLRQUTALQPT-LPKTIVGVVSGQKPKKRAVSDSDSYFHFVHFVPT-ILMDSAIFPFIL
Sc_Ste24p -----MFDLKTLDHPNPKWKLISG---FSAQGFSSVYTVROYQKLSK-LDPVVEDEDDTTPHKSRNYSRAKAFSLGQDYN-LAQKLVFKYDLF
Hs_Zmpste24 -----MGWASLDALWEMPAKRFIFGAVLLFSWTYVWTFLAQRORRYKPTTHVPPPEGGIMDSPTPKSRVLYQDDSTSFWSGLYS-ETRTGLILFQGI
Ce_Ste24p -----MDASCLEKALLAT-----NWALFLWQVYTFRQYKAHNAVKRPNVKKELIGEDYKKAARDYKIDNHIFGFFHSWFN-QLLLTAQILGQYY
Dm_CG9000 -----SSLDADTVLISLFLVVIEN-----ALGIVESLRQVYQTKLVPAKSKHMGEDTTHKARVYGDQEKRFQKAVVMDVALLCMEVIGLI
Dm_CG9001 -----MSAFWDDPLALEYFIAPVLVDN-----LGVVEMLRDQVAKKQVQVAVSYFLPQBLDQKPKIKHROWVNTLLSAVILGIMEVTFEY
Dm_CG9002 -----MAFYDTPKVDPIVLLVCLILVLDNR-----LWEMTLTRKQLVCLNAWVPPKRGILPPVIVHRSVSRHTELOHWKYLID-LIITLCELTGFI
Dm_CG7573 MNSFALYQDPLRGEVLKISGNQIGMSVVPKLSFSDPILLRHILCLVIVVHNSFHILCCRQLKLCRRSVPKOMEKILSQABQAQRKQDHASSLIDFNIAID-TLVSCLDMLCTL
consensus -----m-----lm-llf-liv-----yaweilyt-Rqtri-k-t-vp-el-vi-e-f-kar-y-lkds-f-if-vv-ilm-velifg--

DMPFKNSG---AVLPRGLDPENLHTPTACVMTWSQITDPPSISHTFVLSSEHGFN--KQIIMMFPDMKRTFLSVLLGPFVAAIIFVQKGGPFLAIFDQKPFLLISIVM
RKHIMAYSLNLNVLDPVFMVMSVTAQSCPIGLGLSGLIVLDPVSYVGHVLESEHGFN--KQIVQLWQDMKSGSLTAYAGGPIVYLFKFDKFPFLDLMVIMVPLVQIDA
PVPVRLSG---RFGYAGFGPEYETOSVFLLLALTSALTGLPWSLVNTPVLESEHGFN--QOTLGFPMKDAKRFVVAICILLPVSSLLLYIKIGQYFFVAVLFLVVSIVL
PFLVYATA-----SYPLHVAVFLSINSHIETIDLPWLVSTFLEDAHGFN--KQIGFYFVDKIKKMLVGFALTMPIVYVGEWIVVNGQYFFVAVLFLVVSIVL
AVVWQDSV---QVVDKQWDSKNEHIVSCVFLISNVLSTFKGLPKIYKIFVLESEHGFN--KQIARFEAWDQKGFVIVQVLMIPITAAIFVIVQSGDNKPFVWLVWFTGVISIVL
AMVYGVAG---KCAISKWMSEHACVSYVFLVLLQVYFVMSKVPAMVSSCCRSKIQGFP--RPPWMSRCHPFDVLDVIGAMITLVVVALVYMFIDGKAPFLGMDPQSLILTRIV
Dm_CG9002 -----KTLQKTSQKMTVTHVYVFLYVICRPPVLYYKCHLQVLYMGS--FPWYLYCCIAMSILLQVLRDPLAAAVFQVKKIYKFFVWVWVWATTYDLE
APVWLVGVG---MYHYADSTWNVMTVTFVYLVVVKRLSLPDKKLVLDPRYVNDPEKTPPLGLCALVYVVFVQVAVIPLTATFMAHMLSEWYFFLFPVWGLVGLSVIV
consensus pvlw-lsg-----l-f---ei-vslvfl-lvslws-ik-lpf-ly-tviveerhgf--kqti--fi-d-ik-lvvaqilllpvaaiifv--gg-yffiywlfm-vlslll

MTIYVFLIADLEKQFPLDDE-DREKTEKLSSEKFFLKRIVVQSGSRSSHSNAYFYCF-KNKRIVFDPTLQOC-----KNEDEI
MTIYVFLIADLEKQFPLDDE-DREKTEKLSSEKFFLKRIVVQSGSRSSHSNAYFYCF-KNKRIVFDPTLQOC-----KNEDEI
VTVIADVIAPLADKFPPLDDE-KKKEEYVMKSIDPFLKVVVSGSRSSHSNAYFYCF-KNKRIVFDPTLLEYSVLNKKIQEDSGMEPRNEEENGSEIKAKVKKKQCKNDEB
Ce_Ste24p MTIYVFLIADLEKQFPLDDE-DKTKTEQDAASUSYPLDELIVVSGSRSSHSNAYFYCF-KNKRIVFDPTLLEYSVLNKKIQEDSGMEPRNEEENGSEIKAKVKKKQCKNDEB
Dm_CG9000 LPIYVFIAPLADKFPPLDDE-ALRQSEEDLAASIKFPLRIVVSGSRSSHSNAYFYCF-KNKRIVFDPTLLEYSVLNKKIQEDSGMEPRNEEENGSEIKAKVKKKQCKNDEB
Dm_CG9001 LLLIFVMIYVFGVQSVLENS-NMRTQVYVTRQVGFPMNSQVRIIRVHDPTGSAIYFC-CCIKRIVFDPTLLEYSVLNKKIQEDSGMEPRNEEENGSEIKAKVKKKQCKNDEB
Dm_CG9002 VFFLHCCFICIGQVQVVMQVATVMEKVKCDVVGPKMKRIFKIK-TRTMQSNAYFYCF-CCIKRIVFDPTLLEYSVLNKKIQEDSGMEPRNEEENGSEIKAKVKKKQCKNDEB
Dm_CG7573 LAFVGLGVGCLGSGRKMNS-DMDNSLKAVALDDPFG-PLVWHTFHVQ-RFPAWVGC-CCLEHDIHNLKRWGFS-----SDDFDGQMGALNDEQL
consensus mtiyvfliapif-kfplpdg-dlr--le-la-sl-fpltkvfvvsgsrsshsnayfygf--f-kkrivfdptll-nkkg-----e-e---d-grgm-edev

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VAVVAHELGHWRNHTHTYSPHAVOILAFLQGGYTLVRNSTDFRSFGEDTQ-----PVLIG-LIIFQHTVIFLQHWVSGELNLSVRAFEQADAFAVKLGVAKDRPAPAL
Sc_Ste24p TAVLAHELGHWRNHTHTYSPHAVOILAFLQGGYTLVRNSTDFRSFGEDTQ-----PVLIG-LIIFQHTVIFLQHWVSGELNLSVRAFEQADAFAVKLGVAKDRPAPAL
Hs_Zmpste24 LAVVGHELGHWRNHTHTYSPHAVOILAFLQGGYTLVRNSTDFRSFGEDTQ-----PVLIG-LIIFQHTVIFLQHWVSGELNLSVRAFEQADAFAVKLGVAKDRPAPAL
Ce_Ste24p VAVVAHELGHWRNHTHTYSPHAVOILAFLQGGYTLVRNSTDFRSFGEDTQ-----PVLIG-LIIFQHTVIFLQHWVSGELNLSVRAFEQADAFAVKLGVAKDRPAPAL
Dm_CG9000 LAVVGHELGHWRNHTHTYSPHAVOILAFLQGGYTLVRNSTDFRSFGEDTQ-----PVLIG-LIIFQHTVIFLQHWVSGELNLSVRAFEQADAFAVKLGVAKDRPAPAL
Dm_CG9001 VAVVAHELGHWRNHTHTYSPHAVOILAFLQGGYTLVRNSTDFRSFGEDTQ-----PVLIG-LIIFQHTVIFLQHWVSGELNLSVRAFEQADAFAVKLGVAKDRPAPAL
Dm_CG9002 AVVVAHELGHWRNHTHTYSPHAVOILAFLQGGYTLVRNSTDFRSFGEDTQ-----PVLIG-LIIFQHTVIFLQHWVSGELNLSVRAFEQADAFAVKLGVAKDRPAPAL
Dm_CG7573 AVVVAHELGHWRNHTHTYSPHAVOILAFLQGGYTLVRNSTDFRSFGEDTQ-----PVLIG-LIIFQHTVIFLQHWVSGELNLSVRAFEQADAFAVKLGVAKDRPAPAL
consensus vavlahelghwrnhthtysp-havoi-la-fl-qggy-tl-vr-nst-d-fr-sfg-ed-tq-----pvlig-liifqhtviflqhwvsgelnlsvrafeqadafa-klgvakdrpapal

VKIQEENLSAMNTDPLYSAYHVSHPPLVERLRNLDGEDKKTID----
Sc_Ste24p IDIQIKNLGMMNVDPLYSAYHVSHPPLVERLRNLDGEDKKTID----
Hs_Zmpste24 IKIKNDNLGMMNVDPLYSAYHVSHPPLVERLRNLDGEDKKTID----
Ce_Ste24p TKIKVDNLGMMNVDPLYSAYHVSHPPLVERLRNLDGEDKKTID----
Dm_CG9000 IKLNVNLDGMMNVDPLYSAYHVSHPPLVERLRNLDGEDKKTID----
Dm_CG9001 LKLVADNLGMMNVDPLYSAYHVSHPPLVERLRNLDGEDKKTID----
Dm_CG9002 VKIYADHMSFPVYDCCARWHTHTPTDORLAYOQKLDVYAMNAGTY
Dm_CG7573 LKIFSDYELGFPVDCCLMHLRLEVDQEDNDRQENMINGVSTA-
consensus vkiq-eenlsamntd-plys-ay-hvs-hpp-ler-lrn-l-d-ged-kkt-id----


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**Figure S1** Clustal W alignment of sequences for the type I prenyl protease and the *Drosophila* paralogs. All sequences were obtained through the relevant genome project websites. The canonical Zinc ion binding site (HEXXH) that comprises the active site of the enzyme is indicated with asterisks (\*). At: *Arabidopsis thaliana*; Sc: *Saccharomyces cerevisiae*; Ce: *C. elegans*; Hs: *Homo sapiens*; Dm: *Drosophila melanogaster*.