A.thaliana 1 MNHGGNTQAVAPMDPNSIENRYGVDGSQTQKYSYQYSTG-------------SESAPWTG  
H.sapiens 1 ------------MA-----A--NVGDQRSTDWSSQYSMVAGAGRENGMETPMHENPEWEK  
M.musculus 1 ------------MA-----A--NVGDQRAADWSSQYSMVTGNSRENGMETPMHENPEWEK  
D.melanogaster 1 -----------------------------------------------MSDAMSAPPPLIP  
C.elegans 1 ------------------------------------------------------------  
S.pombe 1 ------------------------------------------------------------  
S.cerevisiae 1 ------------------------------------------------------------  
  
  
A.thaliana 48 HSVENQAVENGNYSNSNYYHPQPTGPATGNVQEIPNTVSFTISSTSGTANVAQDYSGYTP  
H.sapiens 42 ARQALASISKSGAAGG-SAKSSSNGPVA---------SAQYVSQAEASALQ--QQQYYQW  
M.musculus 42 ARQALASISKAGATSS--SKASSSGPVA---------SAQYVSQAEASALQQQQQQYYQW  
D.melanogaster 14 QLQEMQ---------------------------------QQQQQSANPAQLAQQWSNYAW  
C.elegans 1 ------------------------------------------------------------  
S.pombe 1 ------------------------------------------------------------  
S.cerevisiae 1 ------------------------------------------------------------  
  
  
A.thaliana 108 YQTSSDPHNYSNTGYSNYYSGYQQQPSQSYPQPVGAYQNTGAPQPLSSFQNPGSYAGTPS  
H.sapiens 90 YQQYNY------------------------------------------------------  
M.musculus 91 YQQYNY------------------------------------------------------  
D.melanogaster 41 YANQNA------------------------------------------------------  
C.elegans 1 ------------------------------------------------------------  
S.pombe 1 ------------------------------------------------------------  
S.cerevisiae 1 ------------------------------------------------------------  
  
  
A.thaliana 168 YSGTYYNPADYQTAGGYQSTNYNNQTAGSYPSTNYSNQTPASNQGNYTDYTSNPYQNYTP  
H.sapiens 96 ------------------------------------------------------------  
M.musculus 97 ------------------------------------------------------------  
D.melanogaster 47 ------------------------------------------------------------  
C.elegans 1 ------------------------------------------------------------  
S.pombe 1 ------------------------------------------------------------  
S.cerevisiae 1 ------------------------------------------------------------  
  
  
A.thaliana 228 DAANTHSSTIATTPPVHYQQNYQQWTEY---YSQTE------VPC--APG---TEKLSTP  
H.sapiens 96 ----------------AYPYS--YYYPM--------------------------------  
M.musculus 97 ----------------AYPYS--YYYPM---SMYQSYGSPSQYGMASSYGSATAQQPSAP  
D.melanogaster 47 ----------------AYQQQYQQYYQY---YVRYQQQQQQQVTS---------------  
C.elegans 1 ----MGEEVMSIPVPMETGANSEAWKKANEALMKIQGGMSK--GLNASNGNNNT-----G  
S.pombe 1 ------------------------------------------------------------  
S.cerevisiae 1 ------------------------------------------------------------  
  
  
A.thaliana 274 TTSAYSQSFPVPGVTSE---MPASNSQP---APSYVQPWRPETDSSHPPS--------QQ  
H.sapiens 106 --------PPVPGMDES---MSYQAPPQ---QLPSAQPPQP----SNPPHGAHTLNSGPQ  
M.musculus 136 QHQGTLNQPPVPGMDES---MAYQASPQ---QLPAAQPPQP----SNSQHGTHSLSNGPQ  
D.melanogaster 73 ---TVSTSNAPPGFSNA---LA---APP---PLPSGPPPPPPPQIGQPPGQNKQQQQQQQ  
C.elegans 50 QNSWMNNSFSFPNPPSAYGQFGGGFHPSTWGSGPIVPPPPPQQSAV--------------  
S.pombe 1 ------------------------------------------------------------  
S.cerevisiae 1 ------------------------------------------------------------  
  
  
A.thaliana 320 PGAAVSTSNDTYWMHQAPSLQAHHPVPPQN-----NYQSPLETKPLYETPF-------QG  
H.sapiens 148 PGTAPA--T----------QHSQAGPATGQAYGPHTYTEP--------------------  
M.musculus 186 PGTAPS--T----------QHSQAGAPTGQAYGPHSYSEP--------------------  
D.melanogaster 121 QQQLQQQQQ----------QQQQQQQQQQKNFGGIRFNLNLNQKRLAGAPNPLQQQQQQQ  
C.elegans 96 ------------------------NATAQAAYNQASFNY---------APPP--------  
S.pombe 1 ------------------------------------------------------------  
S.cerevisiae 1 ------------------------------------------------------------

*atsac3a-3*/*gfw5-1*(Q375\*)

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A.thaliana 368 HQRATYP---------**Q**EMNSQS---SFHQAPLGY---RQPTQTAPLVDSQ---------  
H.sapiens 176 ------AKPKKGQQLWNRMKPAP-----G--TGGL---KFNIQKRPFAVTT---------  
M.musculus 214 ------AKPKKGQQLWTRMKPAP-----G--TGGL---KFNIQKRPFAVTS---------  
D.melanogaster 171 HQQQQHQQQQQVMQLYNNNNSNKKKRKRNNKNKNF---EQSTYSNPFANQTPATPQAPPP  
C.elegans 115 -----------PPQNWNNGYGRG----RGGGANNWNQQQRPQQFQPFALNRKNNSSAFP-  
S.pombe 1 ------------------------------------------------------------  
S.cerevisiae 1 ------------------------------------------------------------

A.thaliana 404 ---RVSKVQIPTNPRIASN---LP-SGFTKMD-----KD-STAASA-AQAPAYVSVSMPK  
H.sapiens 211 -----QSFGSNAEGQH---------SGFGPQPNPEK----VQNHSG--------------  
M.musculus 249 -----QSFSSNSEGQH---------SSFGPQPNSEN----TQNRSG--------------  
D.melanogaster 228 PIISASDVGVPINPDLSKPPPPLPLAIVAPTENPQHQKQQQQEHMAAQRAGEATSQTSNF  
C.elegans 159 ------HLTSTFVPQ---GGGPQPLMGVG-------------------------------  
S.pombe 1 ------------------------------------------------------------  
S.cerevisiae 1 ------------------------------------------------------------

A.thaliana 450 PKDHTT-AMSDPGTFPKSLRGFVERAFARCKDDKEKESCEVALRKIVKKAKEDNTLYTRD  
H.sapiens 239 SSARGN-LSGKPDDWPQDMKEYVERCFTACESEEDKDRTEKLLKEVLQARLQDGSAYTID  
M.musculus 277 PSGRGN-LSGKPDDWPQDMKEYVERCFTACESEEDKDRTEKLLKEVLQARLQDGSAYTID  
D.melanogaster 288 KRPNSF-QMASSDSWPNSLNQYVARCYSKCNTDLDKDQIDICLKGKIIAAANRNELWTRD  
C.elegans 179 -RGRGVPAPGPAKPPPPSAQRYMERAFEAANTVEDRQKTQEYLQKRLFPMLNAGNAHMVN  
S.pombe 1 -----M-KKEHHSPWPDSLKEFIGRCIQDAEENSQPE-LEDEVKLLISRQYEMGNIWNVD  
S.cerevisiae 1 ------------------------------------------------------------  
  
 *atsac3a-4*/*gfw5-2*(W509\*)

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A.thaliana 509 **W**DTEPLSTVTTTNVTNSESSSAQLSSLQNKSPTRRPKSRWEPLVEGKPFVKPASTFS---  
H.sapiens 298 WSREPLPGLTREPVAESPKK-----------------KRWEAASSLHPPRGAG-------  
M.musculus 336 WSREPLPGLTREPVAESPKK-----------------KRWEAPSSLHPSRGAG-------  
D.melanogaster 347 WDNEPMPTVYSERDGIDVVL-----------------SN------VPPPQQQRSNYFQKK  
C.elegans 238 WDNEPLPHEKNYELA----------------------PAWTPANKLPH---QANGFNRKK  
S.pombe 54 WSSMNLESLRKLTNAQNTII-----------------ED----------K----------  
S.cerevisiae 1 ------------------------------------------------MQNPYGHFTNNT  
  
 *atsac3a-5*/*gfw5-3*

(ss mutant: Stop after 13 aa from 582)

↓

A.thaliana 566 -----------------SAVKFGVWNHQNENNK**KS**SESFQKVD-AATGFKPT-------Y  
H.sapiens 334 -------SATRGGGAPSQRGTPGAGG----AGRARGNSFTKFG-NRNVFMKDNSSSSSTD  
M.musculus 372 -------SVTRGGGAQSQRGTPGAGG----AGRARGSSFTKFG-NRNVFMKDNSSSSSTD  
D.melanogaster 384 QEQERERERDREADKSPAKGSTGIVN----QFKQKGNQFNKAS-SSYGS---HHSSSSKY  
C.elegans 273 SPS------RRRSDEMSNSGAAGGGGQMKRARRDSDGASSDSD-NSDPL-----------  
S.pombe 77 ---------KR------KV-----------EKPVSGNQFSLLS-EED-------------  
S.cerevisiae 13 ---------TEDREASSQGGPFGQSL--N-RPLDYAGSFPSLTYNNNNFIAN--------

A.thaliana 601 SGQ------------NSAKKSFQRPVKR--------------------------------  
H.sapiens 382 SRSRSS--SRS------PTRHFRRSDSHSDSDS-SYSGNECHPVGRRNPPPKGRG----G  
M.musculus 420 SRSRSS--SRS------PTRHFRRSDSHSDSDS-SYSGNECHPVGRRNPPPKGRG----G  
D.melanogaster 436 SRSRSRSPSSSNSLKYSSKKRYSRSRSRSRSRSRSPRSRSCSRSSDASSPPARKIIRKSG  
C.elegans 315 -----------------EKMH---------------------------------------  
S.pombe 97 ------------------------------------------------------------  
S.cerevisiae 53 --QQPSLPLPE------PRLSWN-------------------NVNQVS------------  
  
  
A.thaliana 617 -------------------------QRFSGGAATAI-----DDEASSDS-DKDLTPYYSS  
H.sapiens 429 RGAH------------MDRGR----GRAQRGKRH-------DLAPTKRSRKK--------  
M.musculus 467 RGAH------------MDRGR----GRAQRGKRH-------DLAPTKRSRKK--------  
D.melanogaster 496 SNESLNFIPLT---ANLSRKQQK--MLMKKGKRA-------AAMASAQMKKKDTPHFYSN  
C.elegans 319 ------FSSMN---QKKTKAQ----KKAEKA----------ARKAAKKLQKQQTPQKVKN  
S.pombe 97 ------------------------------------------------------------  
S.cerevisiae 74 --NPLMVTPLPGLQKRMNKNIKKKLPRVSKKASALSNGVSGNVMSNSNI-VGHGAVGSAS

A.thaliana 646 AMALAGSAEE-KKRRDSRSKRFEKIQGHSRGNDLTKP--KNANVGNLHSRRATAL-----  
H.sapiens 458 MAALECEDPERELKKQKRAARFQH--GHSRRLRLEPLVL------------------Q--  
M.musculus 496 MAALECEDPERELKKQKRAARFQH--GHSRRLRLEPLVL------------------Q--  
D.melanogaster 544 QSSVGGAVDDDTARLQQRAARFSQ--QGSSSAKKSVVAIASSPFGLTTAKNKKKMVQQHQ  
C.elegans 356 AWKVAGG--DTEARREDRARRFAETLYNVSKPSVSV------------------------  
S.pombe 97 ----------EVDKKEKRRRRFEN--GSRSQNNAK-------------------------  
S.cerevisiae 131 GWKVEMGGSDELERRKRRAERFSQ--GPSATTNSNDN--LNEDFAN--------------

*atsac3a-6*/*gfw5-4*

　(ss mutant: Stop after 9 aa from 744)

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A.thaliana 698 -RLSKVFDESGSRAVEDIDWDALTVKGTCQEIEKRYLRLTSAPDPAT**VR**PEDVLEKALIM  
H.sapiens 496 ------M-SSLESSGADPDWQELQIVGTCPDITKHYLRLTCAPDPSTVRPVAVLKKSLCM  
M.musculus 534 ------M-SNLESSGADPDWQELQIVGTCPDITKHYLRLTCAPDPSTVRPVAVLKKSLCM  
D.melanogaster 602 QHQRSAF-YEDTEAASGIDLLDLHIVGTCRDLEKSFLRLTKAPSPSEVRPVEVLTHSLVN  
C.elegans 390 --------------PQHYFRRGQVIRGTCQNIEKSFFRLTAAPNPSEVRPLEVLRLSLQN  
S.pombe 120 ------------SEELKVNPENGAIIGRSTELEKRYLRLTSAPDPDTVRPLPVLKQTLEL  
S.cerevisiae 173 --------LNAISSKSHQYDKKIHVVGRCQTLEKSYLRLTSEPNPDLIRPPNILQKMYCL

*atsac3a-7*/*gfw5-5*

(ss mutant: Stop after 5 aa from 810)

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**SAC3\_superfamily**

A.thaliana 757 VQD---SQ-KNYLFKCDQLKSIRQDLTVQRIHNHLTAKVYETHARLALEAGDLPEY**NQ**CL  
H.sapiens 549 VKCHWKEK-QDYAFACEQMKSIRQDLTVQGIRTEFTVEVYETHARIALEKGDHEEFNQCQ  
M.musculus 587 VKSHWKEK-QDYAFACEQMKSIRQDLTVQGIRTEFTVEVYETHARIALEKGDHEEFNQCQ  
D.melanogaster 661 VKGKWRAN-QDYHYACDQLKSIRQDLTVQGIRDQFTVEVYETHARIAMEKGDHEEFNQCQ  
C.elegans 436 VRDKYRAR-AEYSYLTSQMRSIRQDLTVQVIRNEFTVEVYEINARISLENADREEFNKCQ  
S.pombe 168 LKKKWKEE-KNYAYICDQFKSLRQDLTVQRIQNEFSVLVYEIHARIALEKGDVGEYNQCQ  
S.cerevisiae 225 LMDKYQSKTATYTYLCDQFKSMRQDLRVQMIENSFTIKVYQTHARIALENGDLGEFNQCQ

A.thaliana 813 SQLKTLYAEG--VEGCSLEFAAYSLLYITLHSNNNRELLSS----MSRLSEEDKKDEAVR  
H.sapiens 608 TQLKSLYAEN--LPGNVGEFTAYRILYYIFTK-NSGDITTE----LAYLTRELKADPCVA  
M.musculus 646 TQLKSLYAEN--LAGNVGEFTAYRILYYIFTK-NSGDITTE----LAYLTREMKADPCVA  
D.melanogaster 720 TQLKMLYMEIGGKNANALEFTAYRILYYIFTK-NTLDITTV----MRSITADQRENPVIA  
C.elegans 495 SQLKLLYSEIEN-CANQAEFVAYRLLYYIAMD-NQIDINAL----LRELTPELKENDCVE  
S.pombe 227 TQLFHLYSFG--IPGNTKEFLAYRILYMLFTK-NRSEMNSL----LANLKEEDKTNAAVT  
S.cerevisiae 285 NRIMALFENPTIPKKSYSEFICYSVLYSMLTED-YPSISHLKLKLIDDGSSEILEDEHVK

A.thaliana 867 HALSVRAAVTSGNYVMFFRLYKTAPNMNSCLMDLYVEKMRYKAVNFMSRSCRPTIPV-SY  
H.sapiens 661 HALALRTAWALGNYHRFFRLYCHAPCMSGYLVDKFADRERKVALKAMIKTYVVPSSLLPL  
M.musculus 699 HALALRAAWALGNYHRFFRLYCHAPCMSGYLVDKFADRERKAALKAMIKTYVALHSAA--  
D.melanogaster 775 HALQFRSAWSLGNYCKLFSLYRTAPLMSGHMIEWFLERERKAALRVIIKSYRPNISV-DY  
C.elegans 549 FALNVRKAVTMNNYVKFFRLFKNAPRMCPYIMDLFVDRERKKALGIITKAFRPTITY-KL  
S.pombe 280 HALEVRSAMATGDYYKFFHLYLVAPNMGGYLMDLFIERERVQAMIMMCKAYRPSLTM-EF  
S.cerevisiae 344 MIFELSDMKLVGNYHYFMKNYLKLHKFEKCLINSFLNLEKLIFLTIICKSYNQVNL--DF

A.thaliana 926 IVQVLGFTGAASEGTDEKETDGMEDCLEWLKTHGANIIT------DSNG----DMLLD--  
H.sapiens 721 LFP--SF-------------RLVSSCIKLS-PCPLLP--------LPPV----FLLIFFS  
M.musculus 757 ------------------------FCAVAL-PRPLRI--------LVS-----LQLLCWS  
D.melanogaster 834 ITKILAF-------------DSSEKCKEWLDTFSLPYAA---------------------  
C.elegans 608 IAEFLSMKES--------------TLIDWLEEE-----------------------LKWT  
S.pombe 339 LANTLAF-------------EEMEDCVNFFRSCNAVYDS------KDPN----RILMK--  
S.cerevisiae 402 VKSEFNF-------------NSIEETTNFLNEQNLTEFILNKQITDSNGKSSNIKILN--

A.thaliana 974 TKATSTS-LFMPEPEDAVA---HGDRNLDVNDFFTRT  
H.sapiens 753 PFPPSLS-AFFPWFSTGKTVPLPPSSAM---------  
M.musculus 779 PLPVPCS------------------------------  
D.melanogaster 860 ---------------DGAQVDCKNAAAIAI-------  
C.elegans 631 DVEVGG--TFDP----------KIPRNI---------  
S.pombe 374 ---ESTD-RFEKCMKKHAVVDIKGQ--I---------  
S.cerevisiae 447 T--KGCRVQLIQNYMKSKKIDIKGQK-----------  
  
**Figure S5:** **Amino acid sequence alignments of Sac3a proteins in higher plant and metazoans species.**

Sac3a\_superfamily domain is indicated in blue line. Homologous protein search was done by NCBI protein BLAST using A.thaliana Sac3a protein as a query. The sequences were aligned by Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/). The alignment result was visualized by BOXSHADE (<http://www.ch.embnet.org/software/BOX_form.html>). NCBI ID numbers for the sequences shown; A.thaliana; NP\_181466; H.sapiens; Q96PV6; M.musculus; Q8CBY3; D.melanogaster; Q9VKP5; C.elegans; NP\_498274; S.pombe; Q1MTP1; S.cerevisiae; Q12049