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