

CLUSTAL X (1.83) multiple alignment of SET-domain sequences from the SET 3/4 family. Species abbreviations: *Saccharomyces cerevisiae* (Sc), *S. bayanus* (Sb), *Schwanniomyces castelli* (Sca), *Candida glabrata* (Cg), *Ashbya gossypii* (Ag), *Candida albicans* (Ca), *Kluyveromyces lactis* (Kl), *Kluyveromyces waltii* (Kw), *Yarrowia lioplytica* (Yl) and *Debaryomyces hansenii* (Dh).

```

NP_012430 Sc          EVRKSSNERDFGVFAADSCVKGELIQEYLGKIDFQKNYQTDPNNDYRLMGTTKPKVLFHHPWPLYIDSRETGGLTRYIRRSCPEPNVEL
AACAO1000375.1(6257-6931) Sb  DIKSSNGKDLGVFISNSCVKGQLIQN-IAKLTFKKITRQHASNNYRLMGTTQPKVLFHHPWPLFIDSREVGGLTRYIRRSCPEPNV-L
XP_446555 Cg          KPLASKDIQDFGVFTSIPCSKKDYIQEYSGMISFSKQYVNNNAENKYDILGTPTRNLFHHPWPLYINTSGTKGAHEHLRCSCNPVEL
AACF01000014.1(32239-32583) Sca -----CLKGDLIDEFLGVVDFQKNYIMDPINQYRLWGTTRKRVIFHSQWPLLIDAREKSGRFRSLRRSCNPVEL
NP_012954 Sc          YSRTPYGF TKLG VYLKKDCIKGDFIQEILGELDFYKNYLTDPRNHYRIWGTAKRRVIFHSHWPIYIDARLSGNSTRYLRRSCQPNVEL
AACG02000197.1(8320-7895) Sb  YSRTPYGF TKLG VYLKRDCMKGDFVQEF LGELDFRKNYLTDSRNHYRIWGTTPKRRVIFHHPWPIYIDARSSGNLTRYLRRSCQPNVEL
XP_448906 Cg          YARTFPAHTKLG VFTKEYC NNGDLIEEFTGQVDFLKYTLDDTKNHYRIWGTAKNRVIFHHPWPIYIDARSKGNLTRFLRGCKPNVEL
XP_455210 Kl          HSRLEFPGYPKLAVY LKQGCDEGDYIDEFLGEIDFQRKYLEDPNNYRVWGTAKPKVIFHHPWPIYIDARLSGNLTRYLRRSCNPVEL
NP_985624 Ag          HSRVFHGF PKLGVYSQQPCA KDTLIAEFLGEVDFQRKYLEDPNNYRL LGIPNPKVLFHHPWPIYIDARLCGNLTRYLRRSCYPVEL
AADM01000081.1(81822-82199) Kw HSRSFTGLSKMGLFVKQACPVGT YIEEVLGEVDFSKYYADPRNNYRIFGTTPKPKVLFHHPWPIYIDCRLSGNITRFMRRCYPVEL
AACF01000109.1(21368-21757) Sca YSRTFPGFPKLGTFLPEGCNESALIQEFLGELNFKEDYLLDPRNMYRIWGTVKS KVV FHPNWPLCIDARSCGNLARYIRCCNPVGL
XP_504932 Yl          PKSKFCGFSKHGLVANQPIQKDRFIEYVGHVSHKDQYKADPINQYRIHPVPKSSVLFHPTLPLVIDGRLVGNDA RFMRRCNPNCRV
EAK95983 Ca          -ALFISSNGGSGGSLTIPENTPIIEYLGEIDL FKNYCRDSINQYRMWGS PKPKVLKTTILDIVLDSRFVGNESRFIRKACSANCRI
NC_006044 Dh          -----KDLKYEKEIIVPQETPIIEYLGEIDLFDNYVNDQVNQYSAFGTTPKPKVLKVDLLEIVSDSRFVGNESRFIRKACTSNCKI

NP_012430 Sc          VTVRPLDEKPRGDND-CRVKFVLR AIRDIRKGEEISVEWQWDLRNP
AACAO1000375.1(6257-6931) Sb  ITVRPLNEKQRGESD-CRVTFVLMATRD IKVGEEISLKWQWDLRNP
XP_446555 Cg          VTVRIMDNKPR-----IKFVIRAIRDIAEGEELQIAWQWDINHP
AACF01000014.1(32239-32583) Sca VTVKLGQDQDKHWGD-STVKFMIRAKRTIQAGEELHINWQWDLRHP
NP_012954 Sc          VTIKLQD TDNRNDKSSSRIKFVLRALRDIS EDEELYIKWQWDSKHP
AACG02000197.1(8320-7895) Sb  VTIRLQDLDHENVNSVSKIKFVLRALRDIS EDEELYIKWQWDLKQP
XP_448906 Cg          VTVCLPSAGEEK-----DIKFILRATRDIDEGEELLIDWKWDLRHP
XP_455210 Kl          VTIKLTNSNNQD-----EIKFVLRALRFIDKGEELHIKWDWDLRHP
NP_985624 Ag          VTIKMPADDRQASDVNKS VKFVLKALRDLERGEELHIKWDWDLRHP
AADM01000081.1(81822-82199) Kw VSMRMNDE-----SNVKFVLRALRDIDDD EELQIGWQWDL SHP
AACF01000109.1(21368-21757) Sca STVKIKETN-----EIKFVLRALRDINPGEELHLSWHWDKKHP
XP_504932 Yl          ATVVVNNTD-----IIFVVFATEPIKPGTELT LAW EWDTHHP
EAK95983 Ca          ETVYVPEQNKFR---FLVFTSKPITL KSENQDEELRLPWEWDVDHP
NC_006044 Dh          KPIYIPETNTFR---LLVVTSKPIILSSNTNEEELRLDWEWDRLHP

```