Table 5. Type II MADS domain sequences

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             ◄──────────────────────────────── MADS Domain ──────────────────────

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 5         15         25         35         45         55
SEP1         MGRGRVELKR IENKINRQVT FAKRRNGLLK KAYELSVLCD AEVALIIFSN RGKLYEFCSS
SEP2         MGRGRVELKR IENKINRQVT FAKRRNGLLK KAYELSVLCD AEVSLIVFSN RGKLYEFCST
SEP3         MGRGRVELKR IENKINRQVT FAKRRNGLLK KAYELSVLCD AEVALIIFSN RGKLYEFCSS
AGL3         MGRGKVELKR IENKINRQVT FAKRRNGLLK KAYELSVLCD AEIALLIFSN RGKLYEFCSS
AGL13        MGRGKVEVKR IENKITRQVT FSKRKSGLLK KAYELSVLCD AEVSLIIFST GGKLYEFSNV
AGL6         MGRGRVEMKR IENKINRQVT FSKRRNGLLK KAYELSVLCD AEVALIIFSS RGKLYEFGSV
CAL          MGRGRVELKR IENKINRQVT FSKRRTGLLK KAQEISVLCD AEVSLIVFSH KGKLFEYSSE
AP1          MGRGRVQLKR IENKINRQVT FSKRRAGLLK KAHEISVLCD AEVALVVFSH KGKLFEYSTD
FUL          MGRGRVQLKR IENKINRQVT FSKRRSGLLK KAHEISVLCD AEVALIVFSS KGKLFEYSTD
AGL79        MGRGRVQLRR IENKIRRQVT FSKRRTGLVK KAQEISVLCD AEVALIVFSP KGKLFEYSAG
FLF          MGRKKLEIKR IENKSSRQVT FSKRRNGLIE KARQLSVLCD ASVALLVVSA SGKLYSFSSG
SHP1         LGRGKIEIKR IENTTNRQVT FCKRRNGLLK KAYELSVLCD AEVALVIFST RGRLYEYANN
SHP2         IGRGKIEIKR IENTTNRQVT FCKRRNGLLK KAYELSVLCD AEVALVIFST RGRLYEYANN
AG           SGRGKIEIKR IENTTNRQVT FCKRRNGLLK KAYELSVLCD AEVALIVFSS RGRLYEYSNN
AGL11        MGRGKIEIKR IENSTNRQVT FCKRRNGLLK KAYELSVLCD AEVALIVFST RGRLYEYANN
AGL12        MARGKIQLKR IENPVHRQVT FCKRRTGLLK KAKELSVLCD AEIGVVIFSP QGKLFELATK
AGL70        MGRRKVEIKR IENKSSRQVT FSKRRKGLIE KARQLSILCE SSIAVVAVSG SGKLYDSASG
MAF2I        MGRKKVEIKR IENKSSRQVT FSKRRNGLIE KARQLSILCE SSIAVLVVSG SGKLYKSASG
MAF1         MGRRKIEIKR IENKSSRQVT FSKRRNGLID KARQLSILCE SSVAVVVVSA SGKLYDSSSG
MAF5I        MGRRRVEIKR IENKSSRQVT FCKRRNGLME KARQLSILCG SSVALFIVSS TGKLYNSSSG
MAF4I        MGRRKVEIKR IENKSSRQVT FCKRRNGLME KARQLSILCE SSVALIIISA TGRLYSFSSG
AGL17        MGRGKIVIQK IDDSTSRQVT FSKRRKGLIK KAKELAILCD AEVCLIIFSN TDKLYDFASS
AGL21        MGRGKIVIQR IDDSTSRQVT FSKRRKGLIK KAKELAILCD AEVGLIIFSS TGKLYDFASS
ANR1         MGRGKIVIRR IDNSTSRQVT FSKRRSGLLK KAKELSILCD AEVGVIIFSS TGKLYDYASN
AGL16        MGRGKIAIKR INNSTSRQVT FSKRRNGLLK KAKELAILCD AEVGVIIFSS TGRLYDFSSS
AGL15        MGRGKIEIKR IENANSRQVT FSKRRSGLLK KARELSVLCD AEVAVIVFSK SGKLFEYSST
AGL18        MGRGRIEIKK IENINSRQVT FSKRRNGLIK KAKELSILCD AEVALIIFSS TGKIYDFSSV
SVP          MAREKIQIRK IDNATARQVT FSKRRRGLFK KAEELSVLCD ADVALIIFSS TGKLFEFCSS
AGL24        MAREKIRIKK IDNITARQVT FSKRRRGIFK KADELSVLCD ADVALIIFSA TGKLFEFSSS
AGL19        MVRGKTEMKR IENATSRQVT FSKRRNGLLK KAFELSVLCD AEVALVIFSP RSKLYEFSSS
AGL14        MVRGKTEMKR IENATSRQVT FSKRRNGLLK KAFELSVLCD AEVALIIFSP RGKLYEFSSS
SOC1         MVRGKTQMKR IENATSRQVT FSKRRNGLLK KAFELSVLCD AEVSLIIFSP KGKLYEFASS
AGL72        MVRGKIEIKK IENVTSRQVT FSKRRSGLFK KAHELSVLCD AQVAAMIFSQ KGRLYEFASS
AGL71        MVRGKIEIKK IENVTSRQVT FSKRRSGLFK KAHELSVLCD AQVAAIVFSQ SGRLHEYSSS
AGL42        MVRGKIEMKK IENATSRQVT FSKRRNGLLK KAYELSVLCD AQLSLIIFSQ RGRLYEFSSS
PI           MGRGKIEIKR IENANNRVVT FSKRRNGLVK KAKEITVLCD AKVALIIFAS NGKMIDYCCP
AP3          MARGKIQIKR IENQTNRQVT YSKRRNGLFK KAHELTVLCD ARVSIIMFSS SNKLHEYISP
TT16         MGRGKIEIKK IENQTARQVT FSKRRTGLIK KTRELSILCD AHIGLIVFSA TGKLSEFCSE
AGL63        MRKGKRVIKK IEEKIKRQVT FAKRKKSLIK KAYELSVLCD VHLGLIIFSH SNRLYDFCSN
AGL104       MGRVKLEIKR IENTTNRQVT FSKRRNGLIK KAYELSILCD IDIALIMFSP SDRLSLFSGK
AGL66        MGRVKLEIKR IENTTNRQVT FSKRRNGLIK KAYELSILCD IDIALLMFSP SDRLSLFSGK
AGL67        MGRVKLELKR IEKSTNRQIT FSKRKKGLIK KAYELSTLCD IDLALLMFSP SDRLCLFSGQ
AGL94        MGRVKLKIKK LQNMNGRQCT YTKRRHGIMK KAKELSILCD IDVVLLMFSP MGKASICIGK
AGL30        MGRVKLKIKK LENTNGRQST FAKRKNGILK KANELSILCD IDIVLLMFSP TGKAAICCGT
AGL65        MGRVKLKIKR LESTSNRQVT YTKRKNGILK KAKELSILCD IDIVLLMFSP TGRATAFHGE
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             ►◄──────────────────────── I Region ─────────────────────────────

             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  65         75         85         95        105        115
SEP1         SN-------- ---------M LKTLDRYQK- --CSYGSIEV NNKPAKEL-- ----------
SEP2         SN-------- ---------M LKTLERYQK- --CSYGSIEV NNKPAKEL-- ----------
SEP3         SS-------- ---------M LRTLERYQK- --CNYGAPEP NV-PSREALA VE--------
AGL3         PS-------- -G-------M ARTVDKYRK- --HSYATMDP NQ-SAKDL-- ----------
AGL13        G--------- ---------V GRTIERYYR- --CKDNLLD- ND-TLEDT-- ----------
AGL6         G--------- ---------I ESTIERYNR- --C-YNCSLS NNKPEETT-- ----------
CAL          SC-------- ---------M EKVLERYER- --YSYAERQL IA-PDSHVNA Q---------
AP1          SC-------- ---------M EKILERYER- --YSYAERQL IA-PESDVN- ----------
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FUL          SC-------- ---------M ERILERYDR- --YLYSDKQL VGR--DVSQS ----------
AGL79        SS-------- ---------M ERILDRYER- --SAYAG-QD IPTPNLDSQ- ----------
FLF          DN-------- ---------L VKILDRYGK- --QHADDLKA L--------- ----------
SHP1         S--------- ---------V RGTIERYKK- --ACSDAVN- PPSVTEANT- ----------
SHP2         S--------- ---------V RGTIERYKK- --ACSDAVN- PPTITEANT- ----------
AG           S--------- ---------V KGTIERYKK- --AISDNSN- TGSVAEINA- ----------
AGL11        N--------- ---------I RSTIERYKK- --ACSDSTN- TSTVQEINA- ----------
AGL12        GT-------- ---------M EGMIDKYMK- ---CTGGGRG SSSATFTAQE QLQPPNL---
AGL70        DN-------- ---------M SKIIDRYEI- --HHADELKA L--------- ----------
MAF2I        DN-------- ---------M SKIIDRYEI- --HHADELEA L--------- ----------
MAF1         DD-------- ---------I SKIIDRYEI- --QHADELRA L--------- ----------
MAF5I        DS-------- ---------M AKIISRFKI- --QQADDPET L--------- ----------
MAF4I        DS-------- ---------M AKILSRYEL- --EQADDLKT L--------- ----------
AGL17        S--------- ---------V KSTIERFNT- --AKMEEQEL MNPASEV--- ----------
AGL21        S--------- ---------M KSVIDRYNK- --SKIEQQQL LNPASEV--- ----------
ANR1         SS-------- ---------M KTIIERYNR- --VKEEQHQL LNHASEI--- ----------
AGL16        S--------- ---------M KSVIERYSD- --AKGETSSE NDPASEI--- ----------
AGL15        G--------- ---------M KQTLSRYGN- --HQSSSASK A--------- ----------
AGL18        C--------- ---------M EQILSRYGY- --TTASTEHK QQREHQLLIC ASHGNEA---
SVP          S--------- ---------M KEVLERHNL- --QSKNLEKL DQPSLELQ-- ----------
AGL24        R--------- ---------M RDILGRYSL- --HASNINKL MDPPSTHL-- ----------
AGL19        S--------- ---------I AATIERYQR- --RIKEIGNN HKRNDNS--- ----------
AGL14        SS-------- ---------I PKTVERYQK- --RIQDLGSN HKRNDNS--- ----------
SOC1         N--------- ---------M QDTIDRYLR- --HTKDRVST KPVSEENM-- ----------
AGL72        D--------- ---------I RNTIKRYAE- --YKREYFVA ETHPIEQYV- ----------
AGL71        Q--------- ---------M EKIIDRYGK- --FSNAFYVA ERPQVERYL- ----------
AGL42        D--------- ---------M QKTIERYRK- --YTKDHETS NHDSQIHL-- ----------
PI           SM-------- -D-------L GAMLDQYQK- --LS-G-KKL WDAKH----- ----------
AP3          NT-------- -T-------T KEIVDLYQT- --IS-D-VDV WATQY----- ----------
TT16         QN-------- -R-------M PQLIDRYLH- --TN-G-LRL -PDHHDDQ-- ----------
AGL63        ST-------- -S-------M ENLIMRYQK- --EKEGQTTA EHSFHSDQCS ----------
AGL104       TR-------- ---------I EDVFSRFINL PKQERESALY FPDQNRRPDI QNK-------
AGL66        TRFFVTFSLD TSIFLIKNER SKLTFQGFNR FSKDIP-LIL FPDQSRRPYI SRAKRYVIRL
AGL67        TR-------- ---------I EDVLARYINL PDQERENAIV FPDQSKRQGI QNK-------
AGL94        HS-------- ---------I GEVIAKFAQL SPQERAKRKL ENLEALRKTF MKANHD----
AGL30        RR-------- -CFSFESSEL EENFPKVGSR CKYTRIYSLK DLS------- ----------
AGL65        HR-------- -YNYQNHSYA LKKTFKKLDH DVNIHDFLGA RNQTIE---- ----------
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             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                125        135        145        155        165        175
SEP1         ------ENSY REYLKLKGRY EN-LQRQQRN LLGEDLGPLN SKELEQLERQ LDGSLKQVRS
SEP2         ------ENSY REYLKLKGRY EN-LQRQQRN LLGEDLGPLN SKELEQLERQ LDGSLKQVRC
SEP3         ------LSSQ QEYLKLKERY DA-LQRTQRN LLGEDLGPLS TKELESLERQ LDSSLKQIRA
AGL3         ------QDKY QDYLKLKSRV EI-LQHSQRH LLGEELSEMD VNELEHLERQ VDASLRQIRS
AGL13        ------QGLR QEVTKLKCKY ES-LLRTHRN LVGEDLEGMS IKELQTLERQ LEGALSATRK
AGL6         ------QSWC QEVTKLKSKY ES-LVRTNRN LLGEDLGEMG VKELQALERQ LEAALTATRQ
CAL          ------TNWS MEYSRLKAKI EL-LERNQRH YLGEELEPMS LKDLQNLEQQ LETALKHIRS
AP1          ------TNWS MEYNRLKAKI EL-LERNQRH YLGEDLQAMS PKELQNLEQQ LDTALKHIRT
FUL          ------ENWV LEHAKLKARV EV-LEKNKRN FMGEDLDSLS LKELQSLEHQ LDAAIKSIRS
AGL79        ------GECS TECSKLLRMI DV-LQRSLRH LRGEEVDGLS IRDLQGVEMQ LDTALKKTRS
FLF          -------DHQ SKALNYGSHY EL-LELVDSK LVGSNVKNVS IDALVQLEEH LETALSVTRA
SHP1         ------QYYQ QEASKLRRQI RD-IQNSNRH IVGESLGSLN FKELKNLEGR LEKGISRVRS
SHP2         ------QYYQ QEASKLRRQI RD-IQNLNRH ILGESLGSLN FKELKNLESR LEKGISRVRS
AG           ------QYYQ QESAKLRQQI IS-IQNSNRQ LMGETIGSMS PKELRNLEGR LERSITRIRS
AGL11        ------AYYQ QESAKLRQQI QT-IQNSNRN LMGDSLSSLS VKELKQVENR LEKAISRIRS
AGL12        -------DPK DEINVLKQEI EM-LQKGISY MFGGGDGAMN LEELLLLEKH LEYWISQIRS
AGL70        -------DLA EKIRNYLPHK EL-LEIVQSK LEESNVDNVS VDSLISMEEQ LETALSVIRA
MAF2I        -------DLA EKTRNYLPLK EL-LEIVQSK LEESNVDNAS VDTLISLEEQ LETALSVTRA
MAF1         -------DLE EKIQNYLPHK EL-LETVQSK LEEPNVDNVS VDSLISLEEQ LETALSVSRA
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MAF5I        -------DLE DKTQDYLSHK EL-LEIVQRK IEEAKGDNVS IESLISMEEQ LKSALSVIRA
MAF4I        -------DLE EKTLNYLSHK EL-LETIQCK IEEAKSDNVS IDCLKSLEEQ LKTALSVTRA
AGL17        ------KFWQ REAETLRQEL HS-LQENYRQ LTGVELNGLS VKELQNIESQ LEMSLRGIRM
AGL21        ------KFWQ REAAVLRQEL HA-LQENHRQ MMGEQLNGLS VNELNSLENQ IEISLRGIRM
ANR1         ------KFWQ REVASLQQQL QY-LQECHRK LVGEELSGMN ANDLQNLEDQ LVTSLKGVRL
AGL16        ------QEMY IVTLEKYAYS EE-L-VLDRQ MMGEELSGLS VEALQNLENQ LELSLRGVRM
AGL15        ------EEDC AEVDILKDQL SK-LQEKHLQ LQGKGLNPLT FKELQSLEQQ LYHALITVRE
AGL18        ------VLRN DDSMK--GEL ER-LQLAIER LKGKELEGMS FPDLISLENQ LNESLHSVKD
SVP          ------LVEN SDHARMSKEI AD-KSHRLRQ MRGEELQGLD IEELQQLEKA LETGLTRVIE
AGL24        ------RLEN CNLSRLSKEV ED-KTKQLRK LRGEDLDGLN LEELQRLEKL LESGLSRVSE
AGL19        ------QQAR DETSGLTKKI EQ-LEISKRK LLGEGIDACS IEELQQLENQ LDRSLSRIRA
AGL14        ------QQSK DETYGLARKI EH-LEISTRK MMGEGLDASS IEELQQLENQ LDRSLMKIRA
SOC1         ------QHLK YEAANMMKKI EQ-LEASKRK LLGEGIGTCS IEELQQIEQQ LEKSVKCIRA
AGL72        ------QGLK KEMVTMVKKI EV-LEVHNRK MMGQSLDSCS VKELSEIATQ IEKSLHMVRL
AGL71        ------QELK MEIDRMVKKI DL-LEVHHRK LLGQGLDSCS VTELQEIDTQ IEKSLRIVRS
AGL42        ------QQLK QEASHMITKI EL-LEFHKRK LLGQGIASCS LEELQEIDSQ LQRSLG----
PI           ------ENLS NEIDRIKKEN DS-LQLELRH LKGEDIQSLN LKNLMAVEHA IEHGLDKVRD
AP3          ------ERMQ ETKRKLLETN RN-LRTQIKQ RLGECLDELD IQELRRLEDE MENTFKLVRE
TT16         ------EQLH HEMELLRRET CN-LELRLRP FHGHDLASIP PNELDGLERQ LEHSVLKVRE
AGL63        ------DCVK -TKESMMREI EN-LKLNLQL YDGHGLNLLT YDELLSFELH LESSLQHARA
AGL104       ------ECLL RILQQLKTEN DIALQVTNPA AINSDVEELE HE-VCRLQQQ LQ--MA----
AGL66        SILCMCHYLL RTLQQLKAEN DIALQLLYNY VICNNSEELE HE-VYKLQQQ LL--MA----
AGL67        ------EYLL RTLEKLKIED DMALQINIDF GMEMEQQLEN FS-WVRTDEN MN--VPI---
AGL94        ------IDIS KFLDRISTPT VE-VCTTTMM LINDSEVSSN SFRDTGIFRC LAKKSDSY--
AGL30        ------TQAR ILQARISEIH GR-LSYWTEP DKINNVEHLG QLEIS-IRQS LDQ-LRAH--
AGL65        ------VWID HL-RFMNFLG YFLLSCWTNI DRIENTEHLD LLEES-LRKS IER-IQIH--
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                                                  C terminal region
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                185        195        205        215        225        235
SEP1         IKTQYMLDQL SDLQNKEQML LETNRALAMK LD-------- ------D--- -MI----GVR
SEP2         IKTQYMLDQL SDLQGKEHIL LDANRALSMK LE-------- ------D--- -MI----GVR
SEP3         LRTQFMLDQL NDLQSKERML TETNKTLRLR LA-------- ------D--G YQM----P-L
AGL3         TKARSMLDQL SDLKTKEEML LETNRDLRRK LE-------- ------D--S DAAL---T--
AGL13        QKTQVMMEQM EELRRKEREL GDINNKLKLE TE-------- ------D--H DFK-------
AGL6         RKTQVMMEEM EDLRKKERQL GDINKQLKIK FE-------- ------TEGH AFK----T--
CAL          RKNQLMNESL NHLQRKEKEI QEENSMLTKQ IK-------- ------E--- --R----E-N
AP1          RKNQLMYESI NELQKKEKAI QEQNSMLSKQ IK-------- ------E--- --R----E-K
FUL          RKNQAMFESI SALQKKDKAL QDHNNSLLKK IK-------- ------E--R EKK----T--
AGL79        RKNQLMVESI AQLQKKEKEL KELKKQLTKK VK-------- ------A--G ER-----E--
FLF          KKTELMLKLV ENLKEKEKML KEENQVLASQ ME-------- ---------- -------N--
SHP1         KKNELLVAEI EYMQKREMEL QHNNMYLRAK IA-------- --------EG ARL----NPD
SHP2         KKHEMLVAEI EYMQKREIEL QNDNMYLRSK IT-------- --------ER TGL----Q--
AG           KKNELLFSEI DYMQKREVDL HNDNQILRAK IA-------- --------EN ERN----N--
AGL11        KKHELLLVEI ENAQKREIEL DNENIYLRTK VA-------- --------EV ER--------
AGL12        AKMDVMLQEI QSLRNKEGVL KNTNKYLLDK IE-------- --------NN ----------
AGL70        KKTELMMEDM KSLQEREKLL IEENQILASQ VG-------- ---------- -------K--
MAF2I        RKTELMMGEV KSLQKTENLL REENQTLASQ VG-------- ---------- -------K--
MAF1         RKAELMMEYI ESLKEKEKLL REENQVLASQ MG-------- ---------- -------K--
MAF5I        RKTELLMELV KNLQDKEKLL KEKNKVLASE VG-------- ---------- -KL----K--
MAF4I        RKTELMMELV KTHQEKEKLL REENQSLTNQ LI-------- --------KM GKM----K--
AGL17        KREQILTNEI KELTRKRNLV HHENLELSRK VQ-------- --------RI ----------
AGL21        RKEQLLTQEI QELSQKRNLI HQENLDLSRK VQ-------- --------RI ----------
ANR1         KKDQLMTNEI RELNRKGQII QKENHELQNI VD-------- --------IM RKE----N--
AGL16        KKDQMLIEEI QVLNREGNLV HQENLDLHKK VN-------- --------LM ----------
AGL15        RKERLLTNQL EESRLKEQRA ELENETLRRQ VQ-------- --------EL RSFL-P----
AGL18        QKTQILLNQI ERSRIQEKKA LEENQILRKQ V--------- ---------- -EML-G----
SVP          TKSDKIMSEI SELQKKGMQL MDENKRLRQQ VC-------- --------VL ----------
AGL24        KKGECVMSQI FSLEKRGSEL VDENKRLRDK LE-------- --------TL ----------
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AGL19         KKYQLLREEI EKLKAEERNL VKENKDLKEK WL-------- --------GM ----------
AGL14         KKYQLLREET EKLKEKERNL IAENKMLMEK CE-------- --------MQ ----------
SOC1          RKTQVFKEQI EQLKQKEKAL AAENEKLSEK WG-------- --------SH ----------
AGL72         RKAKLYEDEL QKLKAKEREL KDERVRLSLK KT-------- --------IY ----------
AGL71         RKAELYADQL KKLKEKEREL LNE--RKRLL EE-------- --------VN ----------
AGL42         -KAQLFKEQL EKLKAKEKQL LEENVKLHQK NV-------- --------IN ----------
PI            HQMEILISK- ---RRNEKMM AEEQRQLTFQ LQ-------- --------Q- --------Q-
AP3           RKFKSLGNQI ETTKKKNKSQ QDIQKNLIHE LE-------- --------L- --------R-
TT16          RKNELMQQQL ENLSRKRRML EEDNNNMYRW LH-------- --------EH RAAM-EFQQ-
AGL63         RKSEFMHQQQ QQ-QTDQKLK GKEKGQGSSW EQ-------- ---------L M---------
AGL104        ------EEEL RRYEPDP--I RFTTMEEYEV SE--KQLLDT LTHVVQRRDH LMSN-HLSSY
AGL66         ------EEEL MKYEPDP--I RFTTMEEYET CE--KQLMDT LTRVNQRREH ILSQDQLSSY
AGL67         ------EEED PNLQLHH--M YKDITCSASS AL-------- -------GNY SGLF-SKSSD
AGL94         ------WTDV DNIDSVD--V LQQLEHSLRQ SLAQIYGRKA SMPQRQQQQL MSSQ-CKNQT
AGL30         -------KMQ DGI-QIP--L EQQLQSMSWI LN-------- ---------- ----------
AGL65         -------KEH YRK-NQL--L PIECAFHSGI QLPMFGSYPG YFGT------ ----------
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              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 245        255        265        275        285        295
SEP1          SHHMGG--WE GGEQ------ -NVTYAHHQA Q-SQGL-YQP ---------- LECNPTLQMG
SEP2          HHHIGGG-WE GGDQQ----- -NIAYGHPQA H-SQGL-YQS ---------- LECDPTLQIG
SEP3          QLNPNQEEVD HYGRH----- -HHQQQH--  --SQAF-FQP ---------- LECEPILQIG
AGL3          -----QSFWG SSAAEQQQQH QQQQQGMSSY Q-SNPP-IQE A--------- GFFKP-LQ-G
AGL13         --GF-QDLLL NPVLTAG--- --CSTDFSL- Q-STHQNYIS D--------- CNLGYFYRLG
AGL6          ---F-QDLWA NSAASVAG-- DPNNSEFPVE P-SHPN--VL D--------- CNTEPFLQIG
CAL           ILKTKQTQCE ----QLNRSV DDVP-QPQPF Q--HPHLYMI A--------- HQTSPFLNMG
AP1           ILRAQQEQWD -QQNQGHNMP PPLPPQQHQI Q--HP--YML S--------- HQPSPFLNMG
FUL           --G--QQEGQ LVQCSNSS-- -SVL-LPQYC VTS------- ---------- SRDGFVERVG
AGL79         --DF-QTQNL SHDLASLATP PFESPHELRR TIS-P----- ---------- --PPPPLSSG
FLF           --N--HHVGA EAEMEMS--- ----PAGQIS DNLP------ ---------- -VTLPLLN--
SHP1          QQE--SSVIQ GTTVYES--- ----GVSSHD QSQH------ ---------- -YNRNYIPVN
SHP2          QQE--SSVIH QGTVYES--- ----GVTSSH QSGQ------ ---------- -YNRNYIAVN
AG            -PS--ISLMP GGSNYEQ--- ----LMPPPQ TQSQPF---- ---------- -DSRNYFQVA
AGL11         --Y--QQHHH QMVSGSE--- ----INAIEA LASRN----- ---------- YFAHSIMTAG
AGL12         --N--SILDA NFAVMET--- -----NYSYP LTMP------ ---------- --SEIFQF--
AGL70         --K--TFLVI EGDRGMS--- ----RENGSG NKVP------ ---------- -ETLSLLK--
MAF2I         --K--TFLVI EGDRGMS--- ----WENGSG NKVR------ ---------- -ETLPLLK--
MAF1          --N--TLLAT DDERGMF--- ----PGSSSG NKIP------ ---------- -ETLPLLN--
MAF5I         --K--ILETG DERAVMS--- ----PENSSG HSPP------ ---------- -ETLPLLK--
MAF4I         --K--SVEAE DARAMS---- ----PESSSD NKPP------ ---------- -ETLLLLK--
AGL17         --H--QENVE LYKKAYG--- ----TSNTNG LGHH------ --ELVDAVYE SHAQVRLQLS
AGL21         --H--QENVE LYKKAY---- ----MANTNG FTHR------ --EVAVADDE SHTQIRLQLS
ANR1          IKL--QKKVH GRTNAIEG-- ----NSSVDP ISNG------ --------TT TYAPPQLQLI
AGL16         --H--QQNME LHEKVSE--- ----VEGVKI ANKNSLLT-- --NGLDMRDT SNEHVHLQLS
AGL15         -SF--THYVP SYIKCFAID- ----PKNALI NHDSKCS--- -------LQN TDSDTTLQLG
AGL18         -RG--SGPKV LNERPQDSS- ----P----E ADPE------ -------SSS SEEDENDNEE
SVP           --P--SLLIT NPFLLST--- ----INVHTP KFNP------ ---------- QLSTTHMFDH
AGL24         --E--RAKLT TLKEALE--- ----TESVTT NVSS------ ---------- YDSGTPLEDD
AGL19         --G--TATIA SSQSTLS--- ----SSEVNI DDN------- ---------- MEVETGLFIG
AGL14         --G--RGIIG RISSSSS--- ----TSELDI DDNE------ ---------- MEVVTDLFIG
SOC1          --E--SEVWS NKNQEST--- ----GRGDEE SSPS------ ---------- SEVETQLFIG
AGL72         --T--HLCQV GERPMGM--- ----PSG--- SKEK------ ---------- EDVETDLFIG
AGL71         --M--HHSSK GNTEGGH--- ----R----- TKHS------ ---------- SEVETDLFIG
AGL42         --P--WRGSS TDQQQEK--- ----YKV--- IDLN------ ---------- LEVETDLFIG
PI            ---------- ------E--- MAIASNARGM MMRDHDGQ-- ---------- ------FGYR
AP3           ------AEDP HYGLVDNG-- -G----DYDS V-LGYQIE-- ---------- --GSRAYALR
TT16          ---------- ------A--- GIDTKPGEYQ QFIEQLQCY- ---------- --------KP
AGL63         --W--QAERQ MMTCQRQ--- ----KDPAPA NEGG------ ---------- ---VPFLRWG
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AGL104       EAS--TMQPN IGGPFVNDVV EGWLPENGTN QTHLFDASAH SNQLRELSSA MYEPLLQGSS
AGL66        EASALQQQQS MGGPFGNDVV GGWLTENGPN EAHLFDASAH SAMYET---- ----LLQGSS
AGL67        ILQ--KLETG SIPGTSADPN QQFSNLSFLN DQKLKQLAEW NLLG-SPADY YVSQILEASY
AGL94        EID--AMGGN SSMQEAHSMS WLPDNDHQQT ILPGDSSFLP HREMDGSIPV YSSCFFESTK
AGL30        --S--NTTNI VTEEHNS--- --IPQREVEC SAS------- ---------- SSEPRFIPH-
AGL65        --------GK SPEMTIPGQE TSF-LDELNT GQ--LKQDTS SQQQFTNNNN ITAYNPNLHN
```

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             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                305        315        325        335        345        355
SEP1         YDNPVCS-E- --QITATTQA Q--------- ----AQPGNG YIP-GWML-- ----------
SEP2         YSHPVCS-E- --QMAVTVQG Q--------- ----SQQGNG YIP-GWML-- ----------
SEP3         YQGQQDG-M- --GAGPSV-- ---------- --------NN YML-GWLPYD TNSI------
AGL3         NVALQMSSHY N-----HNPA N------ATN SATTSQNVNG FFP-GWMV-- ----------
AGL13        FNN------- --TMSKVKDL R--------- ---------- ---------- ----------
AGL6         FQQ------- --HYYVQGEG S-------SV SKSNVAGETN FVQ-GWVL-- ----------
CAL          GLYQ------ --GEDQTAMR R-------NN LDLTLEPIYN Y-L-GCYAA- ----------
AP1          GLYQ------ --EDDPMAMR --------ND LELTLEPVYN CNL-GCFAA- ----------
FUL          GENGG----- --ASSLTEPN S--------- ----LLPA-- -----WMLRP TTTNE-----
AGL79        DTS------- -----QRDGV G-------EV AAGTLIRRTN ATLPHWMPQL TGE-------
FLF          ---------- ---------- ---------- ---------- ---------- ----------
SHP1         LLEPN----- -----QQFSG Q-------DQ PP------LQ LV-------- ----------
SHP2         LLEPN----- -----QNSSN Q-------DQ PP------LQ LV-------- ----------
AG           ALQPNN---- --HHYSSAGR Q-------DQ TA------LQ LV-------- ----------
AGL11        SGS------- -----GNGGS YS------DP DK------KI LHLG------ ----------
AGL12        ---------- ---------- ---------- ---------- ---------- ----------
AGL70        ---------- ---------- ---------- ---------- ---------- ----------
MAF2I        ---------- ---------- ---------- ---------- ---------- ----------
MAF1         ---------- ---------- ---------- ---------- ---------- ----------
MAF5I        ---------- ---------- ---------- ---------- ---------- ----------
MAF4I        ---------- ---------- ---------- ---------- ---------- ----------
AGL17        QPE------- -----QSHYK T-------SS NS-------- ---------- ----------
AGL21        QPE------- -----HSDYD T-------PP RANE------ ---------- ----------
ANR1         QLQP------ -----APREK S--------- ------IRLG LQLS------ ----------
AGL16        QP-------- -----QHDHE T-------HS KAIQLNYFSF IA-------- ----------
AGL15        LPGEAHD-RR TNEGERESPS SDSVTTNTSS ETAERGDQSS LANSPPEAKR QRFSV-----
AGL18        HHSDTSL-QL G----LSSTG YCTKRKKPKI ELVC------ DNSGSQVASD ----------
SVP          TV-------- ------R--- ---------- ---------- ---------- ----------
AGL24        SD-------- ------TSLK L-------GL PSWE------ ---------- ----------
AGL19        PPE------- ------TRQS K-------KF PPQN------ ---------- ----------
AGL14        PPE------- ------TRHF K-------KF PPSN------ ---------- ----------
SOC1         LPC------- -----SSRK- ---------- ---------- ---------- ----------
AGL72        FLK------- ------NRP- ---------- ---------- ---------- ----------
AGL71        LPV------- ------TRL- ---------- ---------- ---------- ----------
AGL42        LP-------- ------NRNC ---------- ---------- ---------- ----------
PI           VQPI------ -------QPN --------LQ -----EKIMS LVID------ ----------
AP3          FHQN------ ---HHHYYPN ------HGLH APSASDIITF HLLE------ ----------
TT16         --GE------ -------YQQ --------FL -----EQQQQ QPNSVLQLAT LPSEIDPTYN
AGL63        TTHR------ -----RSSPP ---------- ---------- ---------- ----------
AGL104       SSSNQNN-MS ECHVTNHNGE MFPEWAQAYS SSALFASMQQ QHEGVGPSIE EMMPAQQSDI
AGL66        SSSNQNNIMG ESNVSNHNGD MFQEWAQAYN STTAHNPSTL FPPMQHQHGL VVDPNIEEIE
AGL67        KPQIGGK-NN GASSETLPYV AVFDDPLYFW VNNGLFIIHL FSKLCYYWSC FADCF-----
AGL94        PEDQICS-NP GQQFEQLEQQ GNGCLGLQQL GEEYSYPTPF GTTLGMEEDQ EKKIKSEMEL
AGL30        ---------- ---------- ---------- ---------- ---------- ----------
AGL65        DMNHHQTLPP PPLPLTLPHA QVYIPMNQRE YHMNGFFEAP PPDSSAYNDN TNQTRFGSSS
```

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             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                365        375        385        395        405        415
SEP1         ---------- ---------- ---------- ---------- ---------- ----------
SEP2         ---------- ---------- ---------- ---------- ---------- ----------
SEP3         ---------- ---------- ---------- ---------- ---------- ----------
AGL3         ---------- ---------- ---------- ---------- ---------- ----------
AGL13        ---------- ---------- ---------- ---------- ---------- ----------
AGL6         ---------- ---------- ---------- ---------- ---------- ----------
CAL          ---------- ---------- ---------- ---------- ---------- ----------
AP1          ---------- ---------- ---------- ---------- ---------- ----------
FUL          ---------- ---------- ---------- ---------- ---------- ----------
AGL79        ---------- ---------- ---------- ---------- ---------- ----------
FLF          ---------- ---------- ---------- ---------- ---------- ----------
SHP1         ---------- ---------- ---------- ---------- ---------- ----------
SHP2         ---------- ---------- ---------- ---------- ---------- ----------
AG           ---------- ---------- ---------- ---------- ---------- ----------
AGL11        ---------- ---------- ---------- ---------- ---------- ----------
AGL12        ---------- ---------- ---------- ---------- ---------- ----------
AGL70        ---------- ---------- ---------- ---------- ---------- ----------
MAF2I        ---------- ---------- ---------- ---------- ---------- ----------
MAF1         ---------- ---------- ---------- ---------- ---------- ----------
MAF5I        ---------- ---------- ---------- ---------- ---------- ----------
MAF4I        ---------- ---------- ---------- ---------- ---------- ----------
AGL17        ---------- ---------- ---------- ---------- ---------- ----------
AGL21        ---------- ---------- ---------- ---------- ---------- ----------
ANR1         ---------- ---------- ---------- ---------- ---------- ----------
AGL16        ---------- ---------- ---------- ---------- ---------- ----------
AGL15        ---------- ---------- ---------- ---------- ---------- ----------
AGL18        ---------- ---------- ---------- ---------- ---------- ----------
SVP          ---------- ---------- ---------- ---------- ---------- ----------
AGL24        ---------- ---------- ---------- ---------- ---------- ----------
AGL19        ---------- ---------- ---------- ---------- ---------- ----------
AGL14        ---------- ---------- ---------- ---------- ---------- ----------
SOC1         ---------- ---------- ---------- ---------- ---------- ----------
AGL72        ---------- ---------- ---------- ---------- ---------- ----------
AGL71        ---------- ---------- ---------- ---------- ---------- ----------
AGL42        ---------- ---------- ---------- ---------- ---------- ----------
PI           ---------- ---------- ---------- ---------- ---------- ----------
AP3          ---------- ---------- ---------- ---------- ---------- ----------
TT16         LQLAQPNLQN DPTAQND--- ---------- ---------- ---------- ----------
AGL63        ---------- ---------- ---------- ---------- ---------- ----------
AGL104       PG-VTAETQV DHEVSDYETK VPQLSSQ--- ---------- ---------- ----------
AGL66        IPVMKKDAQA DHEVSDYDIR MPQLSSQ--- ---------- ---------- ----------
AGL67        ---------- ---------- ---------- ---------- ---------- ----------
AGL94        NNLQQQQQQQ QQQQQQDPSM YDPMANNNGG CFQIPHDQSM FVNDHHHHHH HHHQNWVPDS
AGL30        ---------- ---------- ---------- ---------- ---------- ----------
AGL65        SSLPCSISMF DEYLFSQMQQ PN-------- ---------- ---------- ----------
```

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              ....|....| ....|....| ..
                 425       435
SEP1          ---------- ---------- -*
SEP2          ---------- ---------- -*
SEP3          ---------- ---------- -*
AGL3          ---------- ---------- -*
AGL13         ---------- ---------- -*
AGL6          ---------- ---------- -*
CAL           ---------- ---------- -*
AP1           ---------- ---------- -*
FUL           ---------- ---------- -*
AGL79         ---------- ---------- -*
FLF           ---------- ---------- -*
SHP1          ---------- ---------- -*
SHP2          ---------- ---------- -*
AG            ---------- ---------- -*
AGL11         ---------- ---------- -*
AGL12         ---------- ---------- -*
AGL70         ---------- ---------- -*
MAF2I         ---------- ---------- -*
MAF1          ---------- ---------- -*
MAF5I         ---------- ---------- -*
MAF4I         ---------- ---------- -*
AGL17         ---------- ---------- -*
AGL21         ---------- ---------- -*
ANR1          ---------- ---------- -*
AGL16         ---------- ---------- -*
AGL15         ---------- ---------- -*
AGL18         ---------- ---------- -*
SVP           ---------- ---------- -*
AGL24         ---------- ---------- -*
AGL19         ---------- ---------- -*
AGL14         ---------- ---------- -*
SOC1          ---------- ---------- -*
AGL72         ---------- ---------- -*
AGL71         ---------- ---------- -*
AGL42         ---------- ---------- -*
PI            ---------- ---------- -*
AP3           ---------- ---------- -*
TT16          ---------- ---------- -*
AGL63         ---------- ---------- -*
AGL104        ---------- ---------- -*
AGL66         ---------- ---------- -*
AGL67         ---------- ---------- -*
AGL94         MFGQTSYNQV CVFTPPLELS R*
AGL30         ---------- ---------- -*
AGL65         ---------- ---------- -*
```

The 5′ of agamous and related sequences has been excluded.