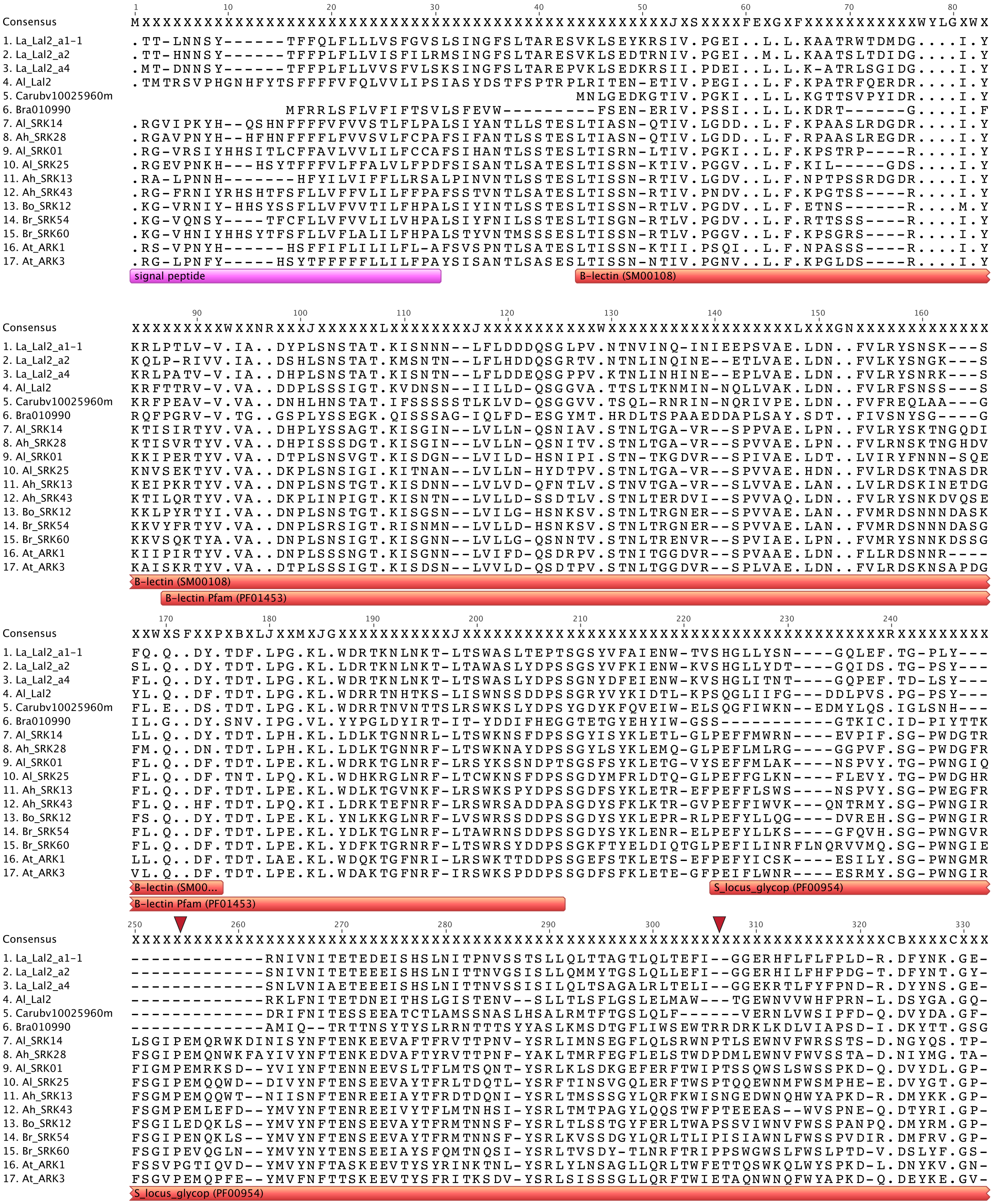
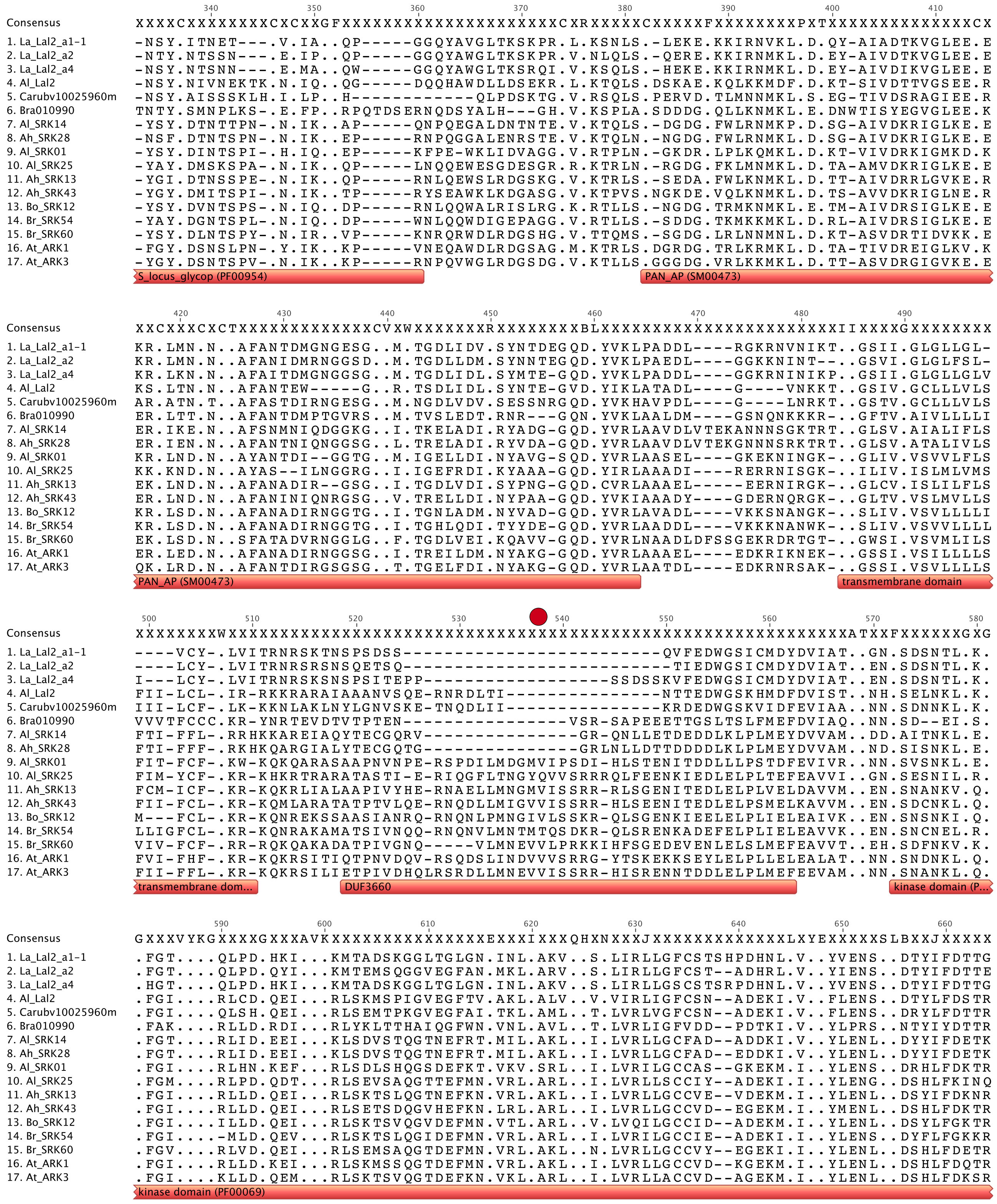


```
                      1        10        20        30        40        50        60        70        80
Consensus             MXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXJXSXXXXFEXGXFXXXXXXXXXXXWYLGXWX

1. La_Lal2_a1-1       .TT-LNNSY------TFFQLFLLLVSFGVSLSINGFSLTARESVKLSEYKRSIV.PGEI..L.L.KAATRWTDMDG....I.Y
2. La_Lal2_a2         .TT-HNNSY------TFFPLFLLVISFILRMSINGFSLTARESVKLSEDTRNIV.PGEI..M.L.KAATSLTDIDG....I.Y
3. La_Lal2_a4         .MT-DNNSY------TFFPLFLLVVSFVLSKSINGFSLTAREPVKLSEDKRSII.PDEI..L.L.K-ATRLSGIDG....I.Y
4. Al_Lal2            .TMTRSVPHGNHFYTSFFFFVFQLVVLIPSIASYDSTFSPTRPLRITEN-ETIV.PEGI..L.F.KPATRFQERDR....I.Y
5. Carubv10025960m                                               MNLGEDKGTIV.PGKI..L.L.KGTTSVPYIDR....I.Y
6. Bra010990                         MFRRLSFLVFIFTSVLSFEVW---------FSEN-ERIV.PSSI..L.L.KDRT------G....I.F
7. Al_SRK14           .RGVIPKYH--QSHNFFFFVFVVSTLFLPALSIYANTLLSTESLTIASN-QTIV.LGDD..L.F.KPAASLRDGDR....I.Y
8. Ah_SRK28           .RGAVPNYH--HFHNFFFFLFVVSVLFCPAFSIFANTLSSTESLTIASN-QTIV.LGDD..L.F.RPAASLREGDR....I.Y
9. Al_SRK01           .RG-VRSIYHHSITLCFFAVLVVLILFCCAFSIHANTLSSTESLTISRN-LTIV.PGKI..L.F.KPSTRP----R....I.Y
10. Al_SRK25          .RGEVPNKH---HSYTFFFVLFFALVLFPDFSISANTLSATESLTISSN-KTIV.PGGV..L.F.KIL-----GDS....I.Y
11. Ah_SRK13          .RA-LPNNH-------HFYILVIFFLLRSALPINVNTLSSTESLTISSN-RTIV.LGDV..L.F.NPTPSSRDGDR....I.Y
12. Ah_SRK43          .RG-FRNIYRHSHTFSFLLVFFVLILFFPAFSSTVNTLSATESLTISSN-RTIV.PNDV..L.F.KPGTSS----R....I.Y
13. Bo_SRK12          .KG-VRNIY-HHSYSSFLLVFVVTILFHPALSIYINTLSSTESLTISSN-RTLV.PGDV..L.F.ETNS------R....M.Y
14. Br_SRK54          .KG-VQNSY----TFCFLLVFVVLILVHPALSIYFNILSSTESLTISGN-RTLV.PGDV..L.F.RTTSSS----R....I.Y
15. Br_SRK60          .KG-VHNIYHHSYTFSFLLVFLALILFHPALSTYVNTMSSSESLTISSN-RTLV.PGGV..L.F.KPSGRS----R....I.Y
16. At_ARK1           .RS-VPNYH------HSFFIFLILILFL-AFSVSPNTLSATESLTISSN-KTII.PSQI..L.F.NPASSS----R....I.Y
17. At_ARK3           .RG-LPNFY-----HSYTFFFFFLLILFPAYSISANTLSASESLTISSN-NTIV.PGNV..L.F.KPGLDS----R....I.Y

                            90        100       110       120       130       140       150       160
Consensus             XXXXXXXXXWXXNRXXXJXXXXXXLXXXXXXXXJXXXXXXXXXXXWXXXXXXXXXXXXXXXXXXLXXXGNXXXXXXXXXXXXX

1. La_Lal2_a1-1       KRLPTLV-V.IA..DYPLSNSTAT.KISNNN--LFLDDDQSGLPV.NTNVINQ-INIEEPSVAE.LDN..FVLRYSNSK---S
2. La_Lal2_a2         KQLP-RIVV.IA..DSHLSNSTAT.KMSNTN--LFLHDDQSGRTV.NTNLINQINE--ETLVAE.LDN..FVLKYSNGK---S
3. La_Lal2_a4         KRLPATV-V.IA..DHPLSNSTAT.KISNTN--LFLDDEQSGPPV.KTNLINHINE--EPLVAE.LDN..FVLRYSNRK---S
4. Al_Lal2            KRFTTRV-V.VA..DDPLSSSIGT.KVDNSN--IILLD-QSGGVA.TTSLTKNMIN-NQLLVAK.LDN..FVLRFSNSS---S
5. Carubv10025960m    KRFPEAV-V.VA..DNHLHNSTAT.IFSSSSSTLKLVD-QSGGVV.TSQL-RNRIN-NQRIVPE.LDN..FVFREQLAA---G
6. Bra010990          RQFPGRV-V.TG..GSPLYSSEGK.QISSSAG-IQLFD-ESGYMT.HRDLTSPAAEDDAPLSAY.SDT..FIVSNYSG----G
7. Al_SRK14           KTISIRTYV.VA..DHPLYSSAGT.KISGIN--LVLLN-QSNIAV.STNLTGA-VR--SPPVAE.LPN..FVLRYSKTNGQDI
8. Ah_SRK28           KTISVRTYV.VA..DHPISSSDGT.KISGIN--LVLLN-QSNITV.STNLTGA-VR--SPVVAE.LPN..FVLRNSKTNGHDV
9. Al_SRK01           KKIPERTYV.VA..DTPLSNSVGT.KISDGN--LVILD-HSNIPI.STN-TKGDVR--SPIVAE.LDT..LVIRYFNNN-SQE
10. Al_SRK25          KNVSEKTYV.VA..DKPLSNSIGI.KITNAN--LVLLN-HYDTPV.STNLTGA-VR--SPVVAE.HDN..FVLRDSKTNASDR
11. Ah_SRK13          KEIPKRTYV.VA..DNPLSNSTGT.KISDNN--LVLVD-QFNTLV.STNVTGA-VR--SLVVAE.LAN..LVLRDSKINETDG
12. Ah_SRK43          KTILQRTYV.VA..DKPLINPIGT.KISNTN--LVLLD-SSDTLV.STNLTERDVI--SPVVAQ.LDN..FVLRYSNKDVQSE
13. Bo_SRK12          KKLPYRTYI.VA..DNPLSNSTGT.KISGSN--LVILG-HSNKSV.STNLTRGNER--SPVVAE.LAN..FVMRDSNNNDASK
14. Br_SRK54          KKVYFRTYV.VA..DNPLSRSIGT.RISNMN--LVLLD-HSNKSV.STNLTRGNER--SPVVAE.LAN..FVMRDSNNNDASG
15. Br_SRK60          KKVSQKTYA.VA..DNPLSNSIGT.KISGNN--LVLLG-QSNNTV.STNLTRENVR--SPVIAE.LPN..FVMRYSNNKDSSG
16. At_ARK1           KIIPIRTYV.VA..DNPLSSSNGT.KISGNN--LVIFD-QSDRPV.STNITGGDVR--SPVAAE.LDN..FLLRDSNNR----
17. At_ARK3           KAISKRTYV.VA..DTPLSSSIGT.KISDSN--LVVLD-QSDTPV.STNLTGGDVR--SPLVAE.LDN..FVLRDSKNSAPDG

                         170       180       190       200       210       220       230       240
Consensus             XXWXSFXXPXBXLJXXMXJGXXXXXXXXXXXJXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRXXXXXXXXX

1. La_Lal2_a1-1       FQ.Q..DY.TDF.LPG.KL.WDRTKNLNKT-LTSWASLTEPTSGSYVFAIENW-TVSHGLLYSN----GQLEF.TG-PLY---
2. La_Lal2_a2         SL.Q..DY.TDT.LPG.KL.LDRTKNLNKT-LTAWASLYDPSSGSYVFKIENW-KVSHGLLYDT----GQIDS.TG-PSY---
3. La_Lal2_a4         FL.Q..DY.TDT.LPG.KL.WDRTKNLNKT-LTSWASLYDPSSGNYDFEIENW-KVSHGLITNT----GQPEF.TD-LSY---
4. Al_Lal2            YL.Q..DF.TDT.LPG.KL.WDRRTNHTKS-LISWNSSDDPSSGRYVYKIDTL-KPSQGLIIFG---DDLPVS.PG-PSY---
5. Carubv10025960m    FL.E..DS.TDT.LPG.KL.WDRRTNVNTTSLRSWKSLYDPSYGDYKFQVEIW-ELSQGFIWKN--EDMYLQS.IGLSNH---
6. Bra010990          IL.G..DY.SNV.IPG.VL.YYPGLDYIRT-IT-YDDIFHEGGTETGYEHYIW-GSS-----------GTKIC.ID-PIYTTK
7. Al_SRK14           LL.Q..DY.TDT.LPH.KL.LDLKTGNNRL-LTSWKNSFDPSSGYISYKLETL-GLPEFFMWRN----EVPIF.SG-PWDGTR
8. Ah_SRK28           FM.Q..DN.TDT.LPH.KL.LDLKTGNNRF-LTSWKNAYDPSSGYLSYKLEMQ-GLPEFLMLRG----GGPVF.SG-PWDGFR
9. Al_SRK01           FL.Q..DF.TDT.LPE.KL.WDRKTGLNRF-LRSYKSSNDPTSGSFSYKLETG-VYSEFFMLAK----NSPVY.TG-PWNGIQ
10. Al_SRK25          FL.Q..DF.TNT.LPQ.KL.WDHKRGLNRF-LTCWKNSFDPSSGDYMFRLDTQ-GLPEFFGLKN----FLEVY.TG-PWDGHR
11. Ah_SRK13          FL.Q..DF.TDT.LPE.KL.WDLKTGVNKF-LRSWKSPYDPSSGDFSYKLETR-EFPEFFLSWS----NSPVY.SG-PWEGFR
12. Ah_SRK43          FL.Q..HF.TDT.LPQ.KI.LDRKTEFNRF-LRSWRSADDPASGDYSFKLKTR-GVPEFFIWVK---QNTRMY.SG-PWNGIR
13. Bo_SRK12          FS.Q..DY.TDT.LPE.KL.YNLKKGLNRF-LVSWRSSDDPSSGDYSYKLEPR-RLPEFYLLQG----DVREH.SG-PWNGIR
14. Br_SRK54          FL.Q..DF.TDT.LPE.KL.YDLKTGLNRF-LTAWRNSDDPSSGDYSYKLENR-ELPEFYLLKS----GFQVH.SG-PWNGVR
15. Br_SRK60          FL.Q..DF.TDT.LPE.KL.YDFKTGRNRF-LTSWRSYDDPSSGKFTYELDIQTGLPEFILINRFLNQRVVMQ.SG-PWNGIE
16. At_ARK1           LL.Q..DF.TDT.LAE.KL.WDQKTGFNRI-LRSWKTTDDPSSGEFSTKLETS-EFPEFYICSK----ESILY.SG-PWNGMR
17. At_ARK3           VL.Q..DF.TDT.LPE.KL.WDAKTGFNRF-IRSWKSPDDPSSGDFSFKLETE-GFPEIFLWNR----ESRMY.SG-PWNGIR

                      250       260       270       280       290       300       310       320       330
Consensus             XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCBXXXXCXXX

1. La_Lal2_a1-1       -------------RNIVNITETEDEISHSLNITPNVSSTSLLQLTTAGTLQLTEFI--GGERHFLFLFPLD-R.DFYNK.GE-
2. La_Lal2_a2         -------------SNIVNITETEEEISHSLNITTNVGSISLLQMMYTGSLQLLEFI--GGERHILFHFPDG-T.DFYNT.GY-
3. La_Lal2_a4         -------------SNLVNIAETEEEISHSLNITTNVSSISILQLTSAGALRLTELI--GGEKRTLFYFPND-R.DYYNS.GE-
4. Al_Lal2            -------------RKLFNITETDNEITHSLGISTENV--SLLTLSFLGSLELMAW---TGEWNVVWHFPRN-L.DSYGA.GQ-
5. Carubv10025960m    -------------DRIFNITESSEEATCTLAMSSNASLHSALRMTFTGSLQLF------VERNLVWSIPFD-Q.DVYDA.GF-
6. Bra010990          -------------AMIQ--TRTTNSYTYSLRRNTTTSYYASLKMSDTGFLIWSEWTRRDRKLKDLVIAPSD-I.DKYTT.GSG
7. Al_SRK14           LSGIPEMQRWKDINISYNFTENKEEVAFTFRVTTPNV-YSRLIMNSEGFLQLSRWNPTLSEWNVFWRSSTS-D.NGYQS.TP-
8. Ah_SRK28           FSGIPEMQNWKFAYIVYNFTENKEDVAFTYRVTTPNF-YAKLTMRFEGFLELSTWDPDMLEWNVFWVSSTA-D.NIYMG.TA-
9. Al_SRK01           FIGMPEMRKSD--YVIYNFTENNEEVSLTFLMTSQNT-YSRLKLSDKGEFERFTWIPTSSQWSLSWSSPKD-Q.DVYDL.GP-
10. Al_SRK25          FSGIPEMQQWD--DIVYNFTENSEEVAYTFRLTDQTL-YSRFTINSVGQLERFTWSPTQQEWNMFWSMPHE-E.DVYGT.GP-
11. Ah_SRK13          FSGMPEMQQWT--NIISNFTENREEIAYTFRDTDQNI-YSRLTMSSSGYLQRFKWISNGEDWNQHWYAPKD-R.DMYKK.GP-
12. Ah_SRK43          FSGMPEMLEFD--YMVYNFTENREEIVYTFLMTNHSI-YSRLTMTPAGYLQQSTWFPTEEEAS--WVSPNE-Q.DTYRI.GP-
13. Bo_SRK12          FSGILEDQKLS--YMVYNFTENSEEVAYTFRMTNNSF-YSRLTLSSTGYFERLTWAPSSVIWNVFWSSPANPQ.DMYRM.GP-
14. Br_SRK54          FSGIPENQKLS--YMVYNFTENSEEVAYTFRMTNNSF-YSRLKVSSDGYLQRLTLIPISIAWNLFWSSPVDIR.DMFRV.GP-
15. Br_SRK60          FSGIPEVQGLN--YMVYNYTENSEEIAYSFQMTNQSI-YSRLTVSDY-TLNRFTRIPPSWGWSLFWSLPTD-V.DSLYF.GS-
16. At_ARK1           FSSVPGTIQVD--YMVYNFTASKEEVTYSYRINKTNL-YSRLYLNSAGLLQRLTWFETTQSWKQLWYSPKD-L.DNYKV.GN-
17. At_ARK3           FSGVPEMQPFE--YMVFNFTTSKEEVTYSFRITKSDV-YSRLSISSSGLLQRFTWIETAQNWNQFWYAPKD-Q.DEYKE.GV-
```



```
                            340       350       360       370       380       390       400       410
Consensus            XXXXCXXXXXXXXXCXCXXGFXXXXXXXXXXXXXXXXXXXXXXXCXRXXXXXXCXXXXXFXXXXXXXXPXTXXXXXXXXXXXXXXXXCX
1. La_Lal2_a1-1      -NSY.ITNET---.V.IA..QP-----GGQYAVGLTKSKPR.L.KSNLS.-LEKE.KKIRNVKL.D.QY-AIADTKVGLEE.E
2. La_Lal2_a2        -NTY.NTSSN---.E.IP..QP-----GGQYAWGLTKSKPR.V.NLQLS.-QERE.KKIRNMKL.D.EY-AIVDTKVGLEE.E
3. La_Lal2_a4        -NSY.NTSNN---.E.MA..QW-----GGQYAWGLTKSRQI.V.KSQLS.-HEKE.KKIRNMKL.D.EY-AIVDIKVGLEE.E
4. Al_Lal2           -NSY.NIVNEKTK.N.IQ..QG-----DQQHAWDLLDSEKR.L.KTQLS.DSKAE.KQLKKMDF.D.KT-SIVDTTVGSEE.R
5. Carubv10025960m   -NSY.AISSSKLH.I.LP..H------------QLPDSKTG.V.RSQLS.PERVD.TLMNNMKL.S.EG-TIVDSRAGIEE.R
6. Bra010990         TNTY.SMNPLKS-.E.FP..RPQTDSERNQDSYALH---GH.V.KSPLA.SDDDG.QLLKNMKL.E.DNWTISYEGVGLEE.K
7. Al_SRK14          -YSY.DTNTTPN-.N.IK..AP-----QNPQEGALDNTNTE.V.KTQLS.-DGDG.FWLRNMKP.D.SG-AIVDKRIGLKE.E
8. Ah_SRK28          -NSF.DTNTSPN-.N.IK..EP-----RNPQGGALENRSTE.V.KTQLN.-NGDG.FWLRNMKL.D.SG-AIVDKRIGLKE.E
9. Al_SRK01          -YSY.DINTSPI-.H.IQ..EP-----KFPE-WKLIDVAGG.V.RTPLN.-GKDR.LPLKQMKL.D.KT-VIVDRKIGMKD.K
10. Al_SRK25         -YAY.DMSKSPA-.N.IK..QP-----LNQQEWESGDESGR.R.KTRLN.-RGDG.FKLMNMKL.D.TA-AMVDKRIGLKE.E
11. Ah_SRK13         -YGI.DTNSSPE-.N.IK..QP-----RNLQEWSLRDGSKG.V.KTRLS.-SEDA.FWLKNMKL.D.TT-AIVDRRLGVKE.R
12. Ah_SRK43         -YGY.DMITSPI-.N.IK..TP-----RYSEAWKLKDGASG.V.KTPVS.NGKDE.VQLKNMKL.D.TS-AVVDKRIGLNE.R
13. Bo_SRK12         -YSY.DVNTSPS-.N.IQ..DP-----RNLQQWALRISLRG.K.RTLLS.-NGDG.TRMKNMKL.E.TM-AIVDRSIGLKE.E
14. Br_SRK54         -YAY.DGNTSPL-.N.IQ..DP-----WNLQQWDIGEPAGG.V.RTLLS.-SDDG.TKMKKMKL.D.RL-AIVDRSIGLKE.E
15. Br_SRK60         -YSY.DLNTSPY-.N.IR..VP-----KNRQRWDLRDGSHG.V.TTQMS.-SGDG.LRLNNMNL.D.KT-ASVDRTIDVKK.E
16. At_ARK1          -FGY.DSNSLPN-.Y.IK..KP-----VNEQAWDLRDGSAG.M.KTRLS.DGRDG.TRLKRMKL.D.TA-TIVDREIGLKV.K
17. At_ARK3          -YGY.DSNTSPV-.N.IK..KP-----RNPQVWGLRDGSDG.V.KTLLS.GGGDG.VRLKKMKL.D.TT-ASVDRGIGVKE.E
                     S_locus_glycop (PF00954)                        PAN_AP (SM00473)

                         420       430       440       450       460       470       480       490
Consensus            XXCXXXCXCTXXXXXXXXXXXXXCVXWXXXXXXXXRXXXXXXXXBLXXXXXXXXXXXXXXXXXXXXXXXXIIXXXXGXXXXXXXX
1. La_Lal2_a1-1      KR.LMN.N..AFANTDMGNGESG..M.TGDLIDV.SYNTDEGQD.YVKLPADDL----RGKRNVNIKT..GSII.GLGLLGL-
2. La_Lal2_a2        KR.LMN.N..AFANIDMRNGGSD..M.TGDLLDM.SYNNTEGQD.YVKLPAEDL----GGKKNINT--..GSVI.GLGLFSL-
3. La_Lal2_a4        KR.LKN.N..AFAITDMGNGGSG..M.TGDLIDL.SYMTE-GQD.YVKLPADDL----GGKRNINIKP..GSII.GLGLLGLV
4. Al_Lal2           KS.LTN.N..AFANTEW-----G..R.TSDLIDL.SYNTE-GVD.YIKLATADL----G----VNKKT..GSIV.GCLLLVLS
5. Carubv10025960m   AR.ATN.T..AFASTDIRNGESG..M.NGDLVDV.SESSNRGQD.YVKHAVPDL----G----LNRKT..GSTV.GCLLLVLS
6. Bra010990         ER.LTT.N..AFANTDMPTGVRS..M.TVSLEDT.RNR---GQN.YVKLAALDM----GSNQNKKKR-..GFTV.AIVLLLLI
7. Al_SRK14          ER.IKE.N..AFSNMNIQDGGKG..I.TKELADI.RYADG-GQD.YVRLAAVDLVTEKANNNSGKTRT..GLSV.AIALIFLS
8. Ah_SRK28          ER.IEN.N..AFANTNIQNGGSG..L.TRELADI.RYVDA-GQD.YVRLAAVDLVTEKGNNNSRKTRT..GLSV.ATALIVLS
9. Al_SRK01          KR.LND.N..AYANTDI--GGTG..M.IGELLDI.NYAVG-SQD.YVRLAASEL----GKEKNINGK-..GLIV.VSVVLFLS
10. Al_SRK25         KK.KND.N..AYAS--ILNGGRG..I.IGEFRDI.KYAAA-GQD.YIRLAAADI----RERRNISGK-..ILIV.ISLMLVMS
11. Ah_SRK13         EK.LND.N..AFANADIR--GSG..I.TGDLVDI.SYPNG-GQD.CVRLAAAEL-----EERNIRGK-..GLCV.ISLILFLS
12. Ah_SRK43         ER.LND.N..AFANINIQNRGSG..V.TRELLDI.NYPAA-GQD.YVKIAAADY----GDERNQRGK-..GLTV.VSLMVLLS
13. Bo_SRK12         KR.LSD.N..AFANADIRNGGTG..I.TGNLADM.NYVAD-GQD.YVRLAVADL----VKKSNANGK-..SLIV.VSVLLLLI
14. Br_SRK54         KR.LSD.N..AFANADIRNGGTG..I.TGHLQDI.TYYDE-GQD.YVRLAADDL----VKKKNANWK-..SLIV.VSVVLLLL
15. Br_SRK60         EK.LSD.N..SFATADVRNGGLG..F.TGDLVEI.KQAVV-GQD.YVRLNAADLDFSSGEKRDRTGT-..GWSI.VSVMLILS
16. At_ARK1          ER.LED.N..AFANADIRNGGSG..I.TREILDM.NYAKG-GQD.YVRLAAAEL----EDKRIKNEK-..GSSI.VSILLLLS
17. At_ARK3          QK.LRD.N..AFANTDIRGSGSG..T.TGELFDI.NYAKG-GQD.YVRLAATDL----EDKRNRSAK-..GSSI.VSVLLLLS
                     PAN_AP (SM00473)                                                   transmembrane domain

                      500       510       520       530    ●  540       550       560       570       580
Consensus            XXXXXXXXWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXATXXFXXXXXXXGXG
1. La_Lal2_a1-1      ----VCY-.LVITRNRSKTNSPSDSS-------------------------QVFEDWGSICMDYDVIAT..GN.SDSNTL.K.
2. La_Lal2_a2        ----LCY-.LVITRNRSRSNSQETSQ--------------------------TIEDWGSICMDYDVIAT..EN.SDSNTL.K.
3. La_Lal2_a4        I---LCY-.LVITRNRSKSNSPSITEPP------------------SSDSSKVFEDWGSICMDYDVIAT..EN.SDSNTL.K.
4. Al_Lal2           FII-LCL-.IR-RKKRARAIAAANVSQE-RNRDLTI---------------NTTEDWGSKHMDFDVIST..NH.SELNKL.K.
5. Carubv10025960m   III-LCF-.LK-KKNLAKLNYLGNVSKE-TNQDLII---------------KRDEDWGSKVIDFEVIAA..NN.SDNNKL.K.
6. Bra010990         VVVTFCCC.KR-YNRTEVDTVTPTEN----------------VSR-SAPEEETTGSLTSLFMEFDVIAQ..NN.SD--EI.S.
7. Al_SRK14          FTI-FFL-.RRHKKAREIAQYTECGQRV---------------GR-QNLLETDEDDLKLPLMEYDVVAM..DD.AITNKL.E.
8. Ah_SRK28          FTI-FFF-.RKHKQARGIALYTECGQTG---------------GRLNLLDTTDDDDLKLPLMEYDVVAM..ND.SISNKL.E.
9. Al_SRK01          FIT-FCF-.KW-KQKQARASAAPNVNPE-RSPDILMDGMVIPSDI-HLSTENITDDLLLPSTDFEVIVR..NN.SVSNKL.E.
10. Al_SRK25         FIM-YCF-.KR-KHKRTRARATASTI-E-RIQGFLTNGYQVVSRRRQLFEENKIEDLELPLTEFEAVVI..GN.SESNIL.R.
11. Ah_SRK13         FCM-ICF-.KR-KQKRLIALAAPIVYHE-RNAELLMNGMVISSRR-RLSGENITEDLELPLVELDAVVM..EN.SNANKV.Q.
12. Ah_SRK43         FII-FCL-.KR-KQMLARATATPTVLQE-RNQDLLMIGVVISSRR-HLSEENITEDLELPSMELKAVVM..EN.SDCNKL.Q.
13. Bo_SRK12         M---FCL-.KR-KQNREKSSAASIANRQ-RNQNLPMNGIVLSSKR-QLSGENKIEELELPLIELEAIVK..EN.SNSNKI.Q.
14. Br_SRK54         LLIGFCL-.KR-KQNRAKAMATSIVNQQ-RNQNVLMNTMTQSDKR-QLSRENKADEFELPLIELEAVVK..EN.SNCNEL.R.
15. Br_SRK60         VIV-FCF-.RR-RQKQAKADATPIVGNQ-----VLMNEVVLPRKKIHFSGEDEVENLELSLMEFEAVVT..EH.SDFNKV.K.
16. At_ARK1          FVI-FHF-.KR-KQKRSITIQTPNVDQV-RSQDSLINDVVVSRRG-YTSKEKKSEYLELPLLELEALAT..NN.SNDNKL.Q.
17. At_ARK3          FII-FFL-.KR-KQKRSILIETPIVDHQLRSRDLLMNEVVISSRR-HISRENNTDDLELPLMEFEEVAM..NN.SNANKL.Q.
                     transmembrane dom...DUF3660                                           kinase domain (P...

                             590       600       610       620       630       640       650       660
Consensus            GXXXVYKGXXXXGXXXAVKXXXXXXXXXXXXXXXXEXXXIXXXQHXNXXXJXXXXXXXXXXXXXXLXYEXXXXXSLBXXJXXXXX
1. La_Lal2_a1-1      .FGT....QLPD.HKI...KMTADSKGGLTGLGN.INL.AKV..S.LIRLLGFCSTSHPDHNL.V..YVENS..DTYIFDTTG
2. La_Lal2_a2        .FGT....QLPD.QYI...KMTEMSQGGVEGFAN.MKL.ARV..S.LIRLLGFCST--ADHRL.V..YIENS..DTYIFDTTE
3. La_Lal2_a4        .HGT....QLPD.HKI...KMTADSKGGLTGLGN.INL.AKV..S.LIRLLGSCSTSRPDHNL.V..YVENS..DTYIFDTTG
4. Al_Lal2           .FGI....RLCD.QEI...RLSKMSPIGVEGFTV.AKL.ALV..V.VIRLIGFCSN--ADEKI.V..FLENS..DTYLFDSTR
5. Carubv10025960m   .FGI....QLSH.QEI...RLSEMTPKGVEGFAI.TKL.AML..T.LVRLVGFCSN--ADEKI.V..FLENS..DRYLFDTTR
6. Bra010990         .FAK....RLLD.RDI...RLYKLTTHAIQGFWN.VNL.AVL..T.LVRLIGFVDD--PDTKI.V..YLPRS..NTYIYDTTR
7. Al_SRK14          .FGT....RLID.EEI...KLSDVSTQGTNEFRT.MIL.AKL..I.LVRLLGCFAD--ADDKI.V..YLENL..DYYIFDETK
8. Ah_SRK28          .FGT....RLID.EEI...KLSDVSTQGTNEFRT.MIL.AKL..I.LVRLLGCFAD--EDDKI.V..YLENL..DYYIFDETK
9. Al_SRK01          .FGI....RLHN.KEF...RLSDLSHQGSDEFKT.VKV.SRL..I.LVRILGCCAS--GKEKM.I..YLENS..DRHLFDKTR
10. Al_SRK25         .FGM....RLPD.QDT...RLSEVSAQGTTEFMN.VRL.ARL..I.LVRLLSCCIY--ADEKI.I..YLENG..DSHLFKINQ
11. Ah_SRK13         .FGI....RLLD.QEI...RLSKTSLQGTNEFKN.VRL.AKL..I.LVRLLGCCVE--VDEKM.I..YLENL..DSYIFDKNR
12. Ah_SRK43         .FGI....RLLD.QEI...RLSETSDQGVHEFKN.LRL.ARL..I.LVRLLGCCVD--EGEKM.I..YMENL..DSHLFDKTR
13. Bo_SRK12         .FGI....ILLD.QEI...RLSKTSVQGVDEFMN.VTL.ARL..V.LVQILGCCID--ADEKM.I..YLENL..DSYLFGKTR
14. Br_SRK54         .FGI....-MLD.QEV...RLSKTSLQGIDEFMN.VRL.ARL..I.LVRILGCCIE--ADEKI.I..YLENS..DYFLFGKKR
15. Br_SRK60         .FGV....RLVD.QEI...RLSEMSAQGTDEFMN.VRL.AKL..N.LVRLLGCCVY--EGEKI.I..YLENL..DSHLFDETR
16. At_ARK1          .FGI....RLLD.KEI...RLSKMSSQGTDEFMN.VRL.AKL..I.LVRLLGCCVD--KGEKM.I..YLENL..DSHLFDQTR
17. At_ARK3          .FGI....KLLD.QEM...RLSKTSVQGTDEFKN.VKL.ARL..I.LVRLLACCVD--AGEKM.I..YLENL..DSHLFDKSR
                     kinase domain (PF00069)
```

```
                        670       680       690       700       710       720       730       740
Consensus            XXXLBWXXRXXIXXGXXXGJXYLHXDSRXXXIHXDLKXXNXLLXXXMXPXISDFGXAXXXXXXXXXXXXXXXXGTXGYXXPXX

1. La_Lal2_a1-1      QYA.D.EM.FE.IK.IVR.LI...Q...FRI..L...PN.I..DKD.I.K.....L.QTLERNATKGFVETAV..F..IA.EL
2. La_Lal2_a2        QYV.N.EK.FE.IK.IVK.LI...Q...FRI..L...PN.I..DKD.I.K.....L.KILEGNATEGRAPTAV..L..ID.NY
3. La_Lal2_a4        QYV.N.EK.FE.IK.IVR.LI...Q...FRI..L...PN.I..DKK.I.K.....L.QTLEGNATIGFARTAV..F..IA.EL
4. Al_Lal2           GSV.N.DT.FD.AK.IIR.LV...Q...FRI..L...PS.I..GKD.V.K.....M.RILGGDETEAHVTTVT..F..IA.EY
5. Carubv10025960m   GSL.N.EY.MK.TL.IVR.LV...H...FRI..L...PA.V..DKD.S.K.....M.KILGGDETEAHVTTVK..F..IA.EY
6. Bra010990         SDV.D.NK.MD.AK.IAR.LL...Q...VRI..L...LS.V..CDQ.I.R.....T.KRLDGEDTEVVASSAT..Y..MA.EY
7. Al_SRK14          SSD.N.QT.FN.IN.IAR.LL...K...CKV..R...TS.I..DKD.I.K.....L.RIFARDEEEATTRRIV..Y..MA.EY
8. Ah_SRK28          SSE.N.QT.FN.IN.IAR.LL...K...CKV..R...TS.I..DKD.I.K.....L.RIFARDEEEATTRRIV..Y..MA.EY
9. Al_SRK01          SSN.N.QR.FD.TN.IAR.IL...H...CRI..R...AS.I..DKN.I.K.....M.RIFSDDVNEAITRRIV..Y..MS.EY
10. Al_SRK25         SSK.N.QK.FN.IN.IAR.LL...Q...FKI..R...AS.V..DKN.T.K.....M.RIFERDETEANTRKVV..Y..MS.EY
11. Ah_SRK13         SWK.N.QM.FN.TN.IAR.LL...Q...CRI..R...AS.V..DKD.T.K.....M.RIFGREETEANTKKVV..Y..MS.EY
12. Ah_SRK43         SCK.N.QM.FD.TT.IAR.IL...Q...CRI..R...AS.V..DKD.T.K.....M.RIFGREETEANTRKVV..Y..MS.EY
13. Bo_SRK12         RSK.N.KE.FD.TN.VAR.LL...Q...FRI..R...VS.I..DRN.V.K.....M.RIFARDETEANTMKVV..Y..MS.EY
14. Br_SRK54         SSN.N.KD.FA.TN.VAR.LL...Q...FRI..R...PG.I..DKY.I.K.....M.RIFARDETQVRTDNAV..Y..MS.EY
15. Br_SRK60         SCM.N.QM.FD.IN.IAR.LL...Q...FRI..R...AS.V..DKD.T.K.....M.RIFGQDETEADTRKVV..Y..MS.EY
16. At_ARK1          SSN.N.QK.FD.IN.IAR.LL...Q...CRI..R...AS.V..DKN.T.K.....M.RIFGREETEANTRRVV..Y..MS.EY
17. At_ARK3          NSK.N.QM.FD.IN.IAR.LL...Q...FRI..R...AS.I..DKY.T.K.....M.RIFGRDETEANTRKVV..Y..MS.EY
                     kinase domain (PF00069)

                      750       760       770       780       790       800       810       820       830
Consensus            XXXXXXSXKXDVXSFGVXXLEXXXXXXXXXXXXXXXXXXXXXXXWXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXZXXXCXXX

1. La_Lal2_a1-1      RNDNVY.V.S..Y....ML..IVSGKKNMEYFKNFDGTSLLRYI.DSWSKGKVLEIV.PVLKDSSLSS---LQEEEIRR.VQI
2. La_Lal2_a2        SKHNIY.A.S..Y....LL..IVSGKRNMDFLNSFDGTSLLTHI.NSWSKGEVLEIV.PVLKIASLTS---LQAEEILK.VHI
3. La_Lal2_a4        RNDNVY.V.S..Y....ML..IVSGKKNMEFIKNFDGTSLLRII.DSWSKGEVLEIV.PVLKDSSLSS---LQEEEIRR.VQI
4. Al_Lal2           RSDGVL.V.S..F....ML..IISGKRNIDFLHLNDGSTLLSYM.NHWSQGNGLEIV.PAIKDSSSSS------QQILR.VQI
5. Carubv10025960m   RNDGTI.V.S..F....MV..IVSGKRNIDFLNLDDGSTLLSYI.QRWSEGNGLEIV.PAIKDSSSSV---FP--QVLR.IQI
6. Bra010990         AIDGVC.V.A..F....LL..MVSGINAREFYWKNDYKSFVGFM.NLWLQGKVLDIV.PYFTSSSSSS-SSYQPEEALR.IQI
7. Al_SRK14          AMDGVY.E.S..F....VI..IVTGKKNRGFTSSDLDTNLLSYV.RNMEEGTGYKLL.PNMMDSSSQA---FKLDEILR.ITI
8. Ah_SRK28          AMDGVY.E.S..F....VI..IVTGKKNRGFTSSDLDTNLLSYV.RNMEEGTGYKLL.PNMIDSSSQA---FKLDEILR.ITI
9. Al_SRK01          AMDGIY.E.S..F....ML..IVTGMKNRGFFNSDLDSNLLSYV.RNMEEEKGLAVA.PNIIDSSSLS-PTFRPDEVLR.IKI
10. Al_SRK25         AMDGIF.V.S..F....LV..IISGKRNRGFYNSNQDNNLLSYT.DNWKEGEGLKIV.PIIIDSSSSF-SMFRPYEVLR.IQI
11. Ah_SRK13         AMDGVF.M.S..F....LL..IISGKRNKGFYNSDNDLNLLGCV.RNWTEGKGLEIV.PIILESSSST---VILQEILK.MQI
12. Ah_SRK43         AMDGIF.M.S..F....LL..IISGKRNKGFYNSNGDLNLLGFV.RNWKEGKWTEII.PAIIDSSSSSLSDFQPQEVLR.IQV
13. Bo_SRK12         AMGGIF.E.S..F....MV..IITGKRNRGFY----EDNLLSYA.RNWKGGRALEIV.PVIVNSFSPLSSTFQLQEVLK.IQI
14. Br_SRK54         AMYGVI.E.T..F....IV..IVIGKRNRGFYQVNPENNLPSYA.THWAEGRALEIV.PVILDSLSSLPSTFKPKEVLK.IQI
15. Br_SRK60         AMNGTF.M.S..F....LL..IISGKRNKGFCDSDSNLNLLGCV.RNWKEGQGLEIV.RVIIDSSSPT---FRPREILR.LQI
16. At_ARK1          AMDGIF.M.S..F....LL..IISGKRNKGFYNSNRDLNLLGFV.RHWKEGNELEIV.PINIDSLSSK---FPTHEILR.IQI
17. At_ARK3          AMDGIF.M.S..F....LL..IISSKRNKGFYNSDRDLNLLGCV.RNWKEGKGLEII.PIITDSSST----FRQHEILR.IQI
                     kinase domain (PF00069)

                                                            ●                            ▼
                             840       850       860       870       880       890       900 904
Consensus            XLXCXXXXXEXRPXMXXXXXXLXXXXXXXXXXXXPXXXXXXXXXXXXXXXXXXXXXXXXXTXXXXXXXXXXXR*

1. La_Lal2_a1-1      G.L.VHESP.D..T.TLILSL.GKEVDFIDRPKP.----------AETEWTGIKGEASTS.APPIAST-MGA..
2. La_Lal2_a2        G.L.VHELP.D..T.SLVGSL.GKEVDFIDRPKP.----------AEIGSKEAKGEASTV.SPQITFS-MDA..
3. La_Lal2_a4        G.L.VHESP.D..T.TLVLSL.GKEVDFIDRPKP.----------AETEWTGIKGEASTS.APPIGST-MGA..
4. Al_Lal2           G.M.VQELP.D..T.SSVGLM.GRETEAIPQPKS.--------VETGSSSGGQQ-ESESG.VPEITLF-IEG..
5. Carubv10025960m   G.L.VQPLP.D..T.SAVGLM.AREAEVIPLPRS.--------VEIGSSSRGGQEESVSG.VPDITMF-IEC..
6. Bra010990         G.L.VQAHR.D..P.ASIILM.GSQNELISLPKP.ADLL----LLQDP-------QGESF.ASVATG*
7. Al_SRK14          G.T.VQEYA.D..M.SWVVSM.GSNTD-IPKPKP.GYCLA---ISSDPWTS---------.TIEYTTTEVEP..
8. Ah_SRK28          G.T.VQEYA.D..M.SWVVSM.GSDTD-IPKPKP.GYCLA---ISSDPWTS---------.TIEYTTTEVEP..
9. Al_SRK01          A.L.VQEYA.D..T.LSVVSM.GSETAEIPKAKA.GYCVGRSLHDTDFSSS------LTW.FG-FAFSDIEP..
10. Al_SRK25         G.L.VQERA.D..K.SSVVLM.GSEKGDIPQPKP.GYCVGRSSLETDSSSSTQR-GDESL.VNQITLSVING..
11. Ah_SRK13         G.L.VQERA.D..R.SSVVAM.GSETAVVPQPKL.GYCVGRSPLETDSSRSKQH-DDESW.VNEITLSVIDA..
12. Ah_SRK43         G.L.VQERA.E..T.SSVVVM.GSETAAIPHPKP.GYCVGRNLLETVSSSS-----DESC.VNQITISIMDA..
13. Bo_SRK12         G.L.VQELA.N..T.SSVVWM.GNEATEIPQPKS.G-CVKRSPYELDPSSSRQRDDDESW.VNQYTCSVIDA..
14. Br_SRK54         G.L.IQERA.H..T.SSVVWM.GSEATEIPQPKP.VYCLIASYYANNPSSSRQFDDDESW.VNKYTCSVIDA..
15. Br_SRK60         G.L.VQERV.D..M.SSVVLM.GSETALIPQPKQ.GYCVSQSSLETYSSWSKLR-DDENW.VNQITMSIIDA..
16. At_ARK1          G.L.VQERA.D..V.SSVMVM.GSETTAIPQPKR.GFCIGRSPLEADSSSSTQR-DDEC-.VNQITLSVIDA.
17. At_ARK3          G.L.VQERA.D..T.SLVILM.GSESTTIPQPKA.GYCLERSLLDTDSSSSKQR-DDESW.VNQITVSVLDA.
                     kinase domain (PF00069)  DUF3403 (PF11883)
```