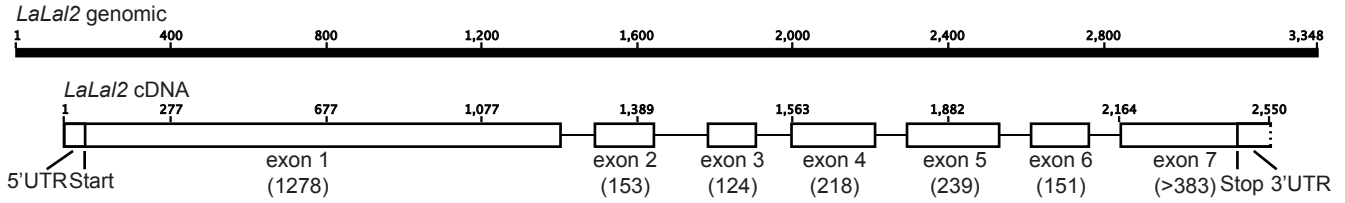


**A**



**B**

1 10 20 30 40 50 60 70 80 90 100  
 MXTXNSYTFPFXLFLXXSFXXXXXINGFSLTAREXV**KLSEXRRXIXSPXEIFEXGLFKXATXXXXXDGWYLGWYKXLPXXVWVIANRDXXLSNSTATLKK**

a1 .T.L.....Q....LV..GVSL.....S.....YK.S.V..G....L....A..RWTFDM.....R..TL.....YP.....I  
 a2 .T.H.....P....VI...ILRM.....S.....DT.N.V..G....M....A..SLTDI.....Q..RI.....SH.....M  
 a4 .M.D.....P....VV..VLSK.....P.....DK.S.I..D...L....-..RLSGI.....R..AT.....HP.....I

110 120 130 140 150 160 170 180 190 200  
**SNXNLFLEXDQSGXXVWXTNXINXINXEEXXVAELLDNGNFVLXSNXKXXWQSFDPYPTDXLLPGMKLGXDRTKNLNKTLTWASLXXPXSGYXXFXIENW**

a1 .N...D.D...LP..N..V..Q..I..PS.....R..S..FQ.....F.....W.....S...TE.T..S.V.A...  
 a2 .T...H.D...RT..N..L..Q...-..TL.....K..G..SL.....T.....L.....A...YD.S..V.K...  
 a4 .T...D.E...PP..K..L..H...-..PL.....R..R..FL.....T.....W.....S...YD.S..N..D.E...

210 220 230 240 250 260 270 280 290 300  
 XVSHGLJXX**XGQXXRXTXXXYXNVNIXETEXEISHSLNITXNVXSXSJLQXXXGXLLXEXIGGEXXLFXPXXXCDXYNXCGXNYCXTXXXCXXXG**

a1 T....LYSN..LEF..GPL.R.I...T...D.....P..S.T.L..LTTA.T.Q.T.F...RHF..L..LDR..F..K..E.S..I.NET.V.IA..  
 a2 K....LYDT..IDS..GPS.S.I...T...E.....T..G.I.L..MMYT.S.Q..L.F...RHI..H..DGT..F..T..Y.T..N.SSN.E.IP..  
 a4 K....ITNT..PEF..DLS.S.L..A...E.....T..S.I.I..LTS.A.A.R.T.L...KRT..Y..NDR..Y..S..E.S..N.SNN.E.MA..

310 320 330 340 350 360 370 380 390 400  
**FOXGGQYAXGLTKSXXXCRXXXLS**CXEXEFKKIRNXKLPDTZYAI**XDXXVGLBECEKRCIXNCNTAFAXXDMXNGXSXCVMWTFGDLJDXRSYXXEGQDI**

a1 .P....V....KPR.L.KSN..L.K.....V.....Q...A.T.....M.....NT..G..E.G.....I.V...NTD...  
 a2 .P....W....KPR.V.NLQ...Q.R.....M.....E..V.T.....M.....NI..R..G.D.....L.M...NNT...  
 a4 .W....W....RQI.V.KSQ...H.K.....M.....E..V.I.....K.....IT..G..G.G.....I.L...-MT...

410 420 430 440 450 460 470 480 490 500 510  
**YVKLPAXDLXGKXNXXIXIGSXIGGLGLXXLXXCYWLVI**TNRNSXXNSXXXXXXXXXXXXXXXXXEDWGSICMDYDVIATATXN**ESDSNTLGKGGXGTVYK**

a1 .....D..R.R.V.IKT...I.....LG--V.....KT..P-----SDS.QVF.....G.....F.....  
 a2 .....E..G..K.I--T...V.....FS--L.....RS-----QET.QTI.....E.....F.....  
 a4 .....D..G..R.I.IKP...I.....LG.VIL.....KS..PSITEPPSSDS.KVF.....E.....H.....

520 530 540 550 560 570 580 590 600 610  
**GQLPDGXXI**AVK**MTXXSXG**GXXGXNEXXLI**AXVQHSNLRLLLGXCSTXX**DXHLLVY**EXENS**SLDTYDFDTT**XOYXLBWEXRFEI**IKGIVXGLIY**LHQD**

a1 .....HK.....AD.K..LT.LG..IN...K.....F..SHP..N...V.....G..A.D..M.....R.....  
 a2 .....QY.....EM.Q..VE.FA..MK...R.....F..A--R.....I.....E..V..N..K.....K.....  
 a4 .....HK.....AD.K..LT.LG..IN...K.....S..SRP..N...V.....G..V..N..K.....R.....

620 630 640 650 660 670 680 690 700 710  
**SRFRIIHLDLKPNNILLDKXMI**PKISDFGL**AXXLE**XNATXG**XXX**TAVGTXGYI**XPXXXXXXNYXKSDVY**SFGVX**LLEIVSGKXN**MX**XXXX**FDG**TSL**XXI**W**

a1 .....D.....QT..R...K.FVE...F...A.ELRND.V.V.....M.....K..EYFKN.....RY..  
 a2 .....D.....KI..G...E.RAP...L...D.NYSKH.I.A.....L.....R..DFLNS.....TH..  
 a4 .....K.....QT..G...I.FAR...F...A.ELRND.V.V.....M.....K..EFIKN.....RI..

720 730 740 750 760 770 780 790 800 810  
**BSWSK**G**XVLEIVDPV**LKXX**SLXSLQ**XEI**XXCVX**IGLLC**VHEXPEDRPT**M**XLX**S**LLGKEVDF**TD**RPKPPA**EX**XXXXX**KG**EAST**XT**XPX**IX**XXXX**MX**AR**

a1 D....K.....DS..S..E..RR..Q.....S.....T.I.L.....TEWTGI.....S.A.P.AST.G..  
 a2 N....E.....IA..T..A..LK..H.....L.....S.VG.....IGSKEA.....V.S.Q.TFS.D..  
 a4 D....E.....DS..S..E..RR..Q.....S.....T.VL.....TEWTGI.....S.A.P.GST.G..

■ signal peptide      ■ S-locus glycoprotein      ■ transmembrane domain  
 ■ B-lectin Smart      ■ PAN\_APPLE      ■ Kinase domain  
 ■ B-lectin PFam