



Supplemental Figure 5A. Homology model of 3D structure of FLS2 kinase domain generated using SWISS-MODEL.

FLS2 residues 860-1161 were modelled based on PDB template 2QKW_B (tomato Pto kinase), the top selection by SWISS-MODEL (Arnold, et al. 2006) at the time of the modeling. 3D-Jury results suggested multiple similar-scoring models, including 2QKW-B, 3TL8_A (Arabidopsis BAK1) and 1B6C_B (cytoplasmic domain of Type I TGF- β receptor). Top of model is rotated 90o toward viewer on a horizontal axis in the right image. Rainbow coloring transition is from amino- (blue) to carboxy- (red) termini. Amino acid side chains are represented only for S938 and D997 (red), and T867, S909 and S1084 (purple), which are located in the left image as depicted in the cartoon below that image. Cartoon also emphasizes catalytic cleft of the protein kinase.

Arnold K., Bordoli L., Kopp J., and Schwede T. (2006). The SWISS-MODEL Workspace: A web-based environment for protein structure homology modelling. *Bioinformatics*, 22, 195-201.

Supplemental Figure 5B

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1  mkllsktfli  ltlthffffgi  alakqsfepe  iealksfkng  isndplgvls  dwtiigslrh
61  cnwtgitcds  tghvsvsll  ekqlegvlsp  aianltylqv  ldltsnsftg  kipaeigklt
121  elnqlilyln  yfsgsipsgi  welknifyld  lrnllsgdv  peeicktssl  vligfdynnl
181  tgkipeclgd  lvhlqmfvaa  gnhtgsvip  sigtlanltd  ldlsqnqltg  kiprdfgnll
241  nlqslvltten  llegdipaei  gncsslvqle  lydnqltgki  paelgnlvql  qalriyknkl
301  tssipsslfr  ltqlthlgls  enhlvgpise  eigfleslev  ltlhsnnftg  efpqsitnlr
361  nltvltvgfn  nisgelpadl  gltlnlrnls  ahdnlltgp  pssisnctgl  kllldlshnqm
421  tgeiprgfgr  mnltfisigr  nhftgeipdd  ifncsnletl  svadnntgt  lkpligklqk
481  lrilqvsyng  ltgpiPREIG  nlkdlnilyl  hsnftgrip  remsnltllq  glrmysndle
541  gpipemfdm  kllsvldlsn  nkfsgqipal  fsklesltyl  slqgnkfngs  ipaslkslsl
601  lntfdisdnl  ltgtipgell  aslknmqlyl  nfnlltgt  ipkelgklem  vgeidlsnnl
661  fsgsiprslq  acknvftldf  sqnllsghip  devfqgmdmi  islslsrnsf  sgeipqsfgn
721  mthlvsllds  snnltgeipe  slanlstlkh  lklasnnlkg  hvpesgvfkn  inasdlmgnt
781  dlcgskkplk  pctikqkssh  fskrtrvili  ilgsaaalll  vlllvliitc  ckkkekkien
                                     I                               II
841  sseSlpdlD  salklkrfep  keleqatdsF  nsaniigsss  lstvykgqlE  dgtviavkvl
          909 III                               IV                               938  V
901  nlkefsaeS  kwfyteaktl  sqlKhrnlvk  ilgfaweSgk  tKalvlpfme  ngnledtihg
          VIa                               VIb                               VII
961  saapigslLe  kidlcvhias  gidylhsgyg  fPivhcdlcp  anilldsdRv  ahvsdfgtar
          VIII                               IX
1021  ilgfredgst  taStsafegt  igylapefay  mrkvttKadv  fsfgiimmel  mtkqrptsln
          1084  X                               XI
1081  dedsqdMtlr  qlveksigng  rkgmrvldm  elgdsivsLk  qeeaiEdflk  lclfctssrp
1141  edrpdmneil  thlmklrgka  nsfredrned  rev

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Supplemental Figure 5B. Annotated amino acid sequence of full-length FLS2 (At5g46330). Blue residues indicate transmembrane domain that separates predicted extracellular N-terminus from predicted intracellular C-terminus. Each kinase subdomain (indicated with Roman numerals) starts with a capital amino acid letter. Red residues are the three phosphorylation sites identified *in vitro*, for which amino acid number is also shown.