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TaPDIL2          1 MAAMPMPRSL LLILLLATPL LILPLAAAAV PTSNPDIDLE YLIKNAGLDD PTPATTATDP  60
TaPDIL2-1        1 MAAMPMPRSL LLILLLATPL LILPLAAAAV PTSNPDIDLE YLIKNAGLDD PTPATTATDP  60
                   ********** ********** ********** ********** ********** **********

TaPDIL2         61 EDDGAPDFPG LDADYDDEDL FGDDDGPEED SSHPSAADEA HVLLLTAANF TSVLAARRHV 120
TaPDIL2-1       61 EDDGAPDFPG LDADYDDEDL FGDDDGPEED SSHPSAADEA HVLLLTAANF TSVLAARRHV 120
                   ********** ********** ********** ********** ********** **********

TaPDIL2        121 MVEFYAPWCG HCRALAPHYA AAASALAEQG VDVALAKVDA TEDHDLAQAH GVQGYPTLLF 180
TaPDIL2-1      121 MVEFYAPWCG HCRALAPHYA AAASALAEQG VDVALAKVDA TEDHDLAQAH GVQGYPTLLF 180
                   ********** ********** ********** ********** ********** **********

TaPDIL2        181 FIDGVPRDYA GERTKDAIVA WISKKLGPAV QNLTTADEAE KIVTGDDVAV LAYLDHLSGA 240
TaPDIL2-1      181 FIDGVPRDYA GERTKDAIVA WISKKLGPAV QNLTTADEAE KIVTGDDVAV LAYLDHLSGA 240
                   ********** ********** ********** ********** ********** **********

TaPDIL2        241 HSDELAAASR LEDTISFYQT TSPDVAKLFH IDPEAKRPSV VLLKKEEEKL TVFDGEFRAS 300
TaPDIL2-1      241 HSDELAAASR LEDTISFYQT TSPDVAKLFH IDPEAKRPSV VLLKKEEEKL TVFDGEFRAS 300
                   ********** ********** ********** ********** ********** **********

TaPDIL2        301 AIAEFVSANK IPLITTLTQE TAPAIFDNPI KKQILLFAVA KESPQFLPII KETAKSFKGK 360
TaPDIL2-1      301 AIAEFVSANK IPLITTLTQE TAPAIFDNPI KKQILLFAVA KGSPQFLPII KETAKSFKGK 360
                   ********** ********** ********** ********** * ******** **********

TaPDIL2        361 LLFVFVERDN EEVGEPVANY FGIAGQETTV LAYTGNEDAK KFFFSGEISL DTIKEFAQDF 420
TaPDIL2-1      361 LLFVFVERDN EEVGEPVANY FGIAGQETTV LAYTGNEDAK KFFFSGEISL DTIKEFAQDF 420
                   ********** ********** ********** ********** ********** **********

TaPDIL2        421 LEDKLTPSYK SDPVPESNDE DVKVVVGKSL DQIVLDESKD VLLEVYAPWC GHCQSLEPIY 480
TaPDIL2-1      421 LEDKLTPSYK SDPVPESNDE DVKVVVGKSL DQIVLDESKD VLLEVYAPWC GHCQSLEPIY 480
                   ********** ********** ********** ********** ********** **********

TaPDIL2        481 NKLAKYLRGI DSLVIAKMDG TNNEHPRAKP DGFPTILFYP AGKKSFEPIT FEGDRTVVEM 540
TaPDIL2-1      481 NKLAKYLRGI DSLVIAKMDG TNNEHPRAKP DGFPTILFYP AGKKSFEPIT FEGDRTVVEM 540
                   ********** ********** ********** ********** ********** **********

TaPDIL2        541 YKFLKKHAAI PFKLKRPDSS AARTD---GP GSTAEGEKSS GSNPKDEL 585
TaPDIL2-1      541 YKFLKKHAAI PFKLKRPDSS AARTDGADGS GSTTEGEKSS GSNPKDEL 588
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Figure S3. Alignment of the amino acid sequences of TaPDIL2 and TaPDIL2-1*. The putative signal peptide (underlined), active center CGHC motifs (shaded in black), N-glycosylation consensus asparagine (shaded in gray), conserved arginine (box with straight lines), and glutamic acid (boxes with dotted lines) are indicated. *GenBank accession number: AK07151