```
TmPDIL1Aα   26 EEAAAAEEAA AAPEAVLTLH ADNFDDAIAK HPFILVEFYA PWCGHCKSLA PEYEKAAQLL 85
GmPDIL-1    38 -------EES SEKEFVLTLD HSNFHDTVSK HDFIVVEFYA PWCGHCKKLA PEYEKAASIL 90
                      * : :  * ****.  .**.*:::* * **:***** *******.** *******.:*

TmPDIL1Aα   86 SKHDPAIVLA KVDANDEKNK PLAGKYEVQG FPTLKIFRNG GKNIQEYKGP REAEGIVEYL 145
GmPDIL-1    91 SSHDPPVVLA KIDANEEKNK DLASQYDVRG YPTIKILRNG GKNVQEYKGP READGIVDYL 150
               *.***.:*** *:***:****  **.:*:*:* :**:**:*** ***:****** ***:***:**

TmPDIL1Aα  146 KKQVGPASKE IKAPEDAT-Y LEDGKIHIVG VFTEFSGTEF TNFLELAEKL RSDYDFGHTV 204
GmPDIL1-1  151 KKQSGPASTE IKSADEATAF IGENKVAIVG VFPKFSGEEF DNFSALAEKL RSDYDFGHTL 210
               *** ****.* **:.::** : : :.*: *** **.:*** **  **  ***** *********:

TmPDIL1Aα  205 HANHLPRGDA AVERPLVRLF KPFDELVVDS KDFDVSALEK FIDASSTPKV VTFDKNPDNH 264
GmPDIL-1   211 NAKHLPRGES SVSGPVVRLF KPFDELFVDF QDFNVEALEK FVEESSTPVV TVFNNEPSNH 270
               :*:*****:: :*. *:**** ******.**  :**:*.**** *:: **** * ..*:::*.**

TmPDIL1Aα  265 PYLLKYFQSN APKAMLFLNF STGPFESFKS AYYGAVEEFS GKDVKFLIGD IEASQGAFQY 324
GmPDIL1-1  271 PFVVKFFNSP NAKAMLFINF TAEGAEAIKS KYREAAEQYK QQGVSFLVGD VESSQGAFQY 330
               *:::*:*:*   .*****:** ::   *::**  *  *.*::.  :.*.**:** :*:*******

TmPDIL1Aα  325 FGLKEDQAPL ILIQDSDSKK FLKEQVEAGQ IVAWLKDYFD GKLTPFRKSE PIPEANNEPV 384
GmPDIL-1   331 FGLKEEQVPL IIIQHNDGKK FFKPNLEADH IPTWLKAYKD GHVAPFVKSE PIPETNDEPV 390
               *****:*.** *:**..*.** *:* ::**.: * :*** * * *:::** *** ****:*:***

TmPDIL1Aα  385 KVVVADNIHD VVFKSGKNVL IEFYAPWCGH CKKLAPILDE AAATLQSEED VVIAKIDATA 444
GmPDIL-1   391 KVVVGASLED IVFKSGKNVL LEFYAPWCGH CKQLAPILDE VAISYQNEAD VVIAKLDATA 450
               ****. .:.* :********* :********* **:******* .* : *.* * *****:****

TmPDIL1Aα  445 NDVPGE-FDV QGYPTLYFVT PSGKKVSYEG GRTADEIVDY IKKNKETAGQ AAAAATEKAA 503
GmPDIL-1   451 NDIPSETFDV QGYPTVYFRS ASGKLSQYDG GRTKEDIIEF IEKNRDKPAQ QEQGKDEQEQ 510

               **:*.* *** *****:** : .***  .*:* *** ::*::: *:**::...*    .  *:

TmPDIL1Aα  504 EPAATEPLKDEL 515
GmPDIL-1   511 G-------KDEL 515
                       ****
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Figure S2. Alignment of the amino acid sequences of TaPDIL1Aα and soybean GmPDIL-1. The active center CGHC motifs (shaded in black), conserved arginine (box with straight lines), and glutamic acid (boxes with dotted lines) are indicated. Asterisks indicate the positions that have a single, fully conserved residue. Colon indicates conservation between groups of strongly similar properties. Period indicates conservation between groups of weakly similar properties.