```
TaPDIL2      29 AVPTSNPDID LEYLIKNAGL DDPTPATTAT DPEDDGAPDF PGLDADYDDE DLFGDDDGPE  88
GmPDIL-2     26 --LTDDEDLG F--------L DEPS------ -----AAPEH G---HYHDDD ANFGDFEEDP  61
                   *.: *:. :        * *:*:            .**:.       :**:   *** :

TaPDIL2      89 EDSSHPSAAD EAHVLLLTAA NFTSVLAARR HVMVEFYAPW CGHCRALAPH YAAAASALAE 148
GmPDIL-2     62 EAYKQP-EVD EKDVVILKEK NFTDTVKSNR FVMVEFYAPW CGHCQALAPE YAAAATELKG 120
                *  .:*  .* * .*::*.   ***..: :.* .********* ****:****. *****: *

TaPDIL2     149 QGVDVALAKV DATEDHDLAQ AHGVQGYPTL LFFIDGVPRD YAGERTKDAI VAWISKKLGP 208
GmPDIL-2    121 E--DVILAKV DATEENELAQ QYDVQGFPTV YFFVDGIHKP YNGQRTKDAI MTWIKKKIGP 178
                :  ** **** ****:::***  :.***:**:  **:**: :  * *:****** ::**.**:**

TaPDIL2     209 AVQNLTTADE AEKIVTGDDV AVLAYLDHLS GAHSDELAAA SRLEDTISFY QTTSPDVAKL 268
GmPDIL-2    179 GIYNLTTVED AQRILTNETK VVLGFLNSLV GPESEELAAA SRLEDDVNFY QTVDPDVAKL 238
                .: ****.:: *::*:*.:.   **.:*: *  *..*:***** ***** :.** **..******

TaPDIL2     269 FHIDPEAKRP SVVLLKKEEE KLTVFDGEFR ASAIAEFVSA NKIPLITTLT QETAPAIFDN 328
GmPDIL-2    239 FHIDPDVKRP ALILVKKEEE KLNHFDGKFE KSEIADFVFS NKLPLVTIFT RESAPSVFEN 298
                *****:.*** :::*:***** **. ***:*.  * **:** : **:**:* :* :*:**::*:*

TaPDIL2     329 PIKKQILLFA VAKESPQFLP IIKETAKSFK GKLLFVFVER DNEEVGEPVA NYFGIAGQET 388
GmPDIL-2    299 PIKKQLLLFA TSNDSEKLIP AFKEAAKSFK GKLIFVYVEM DNEDVGKPVS EYFGISGNAP 358
                *****:**** .:::* :::*  :**:***** ***:**:**  ***:**:**: :****:*: .

TaPDIL2     389 TVLAYTGNED AKKFFFSGEI SLDTIKEFAQ DFLEDKLTPS YKSDPVPESND EDVKVVVGK 448
GmPDIL-2    359 KVLGYTGNDD GKKFVLDGEV TADKIKAFGD DFLEDKLKPF YKSDPVPESND GDVKIVVGN 418
                .**.****:* .***.:.**: : *.** *.: *******.*  ***********  ***:***:

TaPDIL2     449 SLDQIVLDES KDVLLEVYAP WCGHCQSLEP IYNKLAKYLR GIDSLVIAKM DGTNNEHPRA 508
GmPDIL-2    419 NFDEIVLDES KDVLLEIYAP WCGHCQALEP IYDKLAKHLR NIESLVIAKM DGTTNEHPRA 478
                .:*:****** ******:*** ******:*** **:****:** .*:******* ***.******

TaPDIL2     509 KPDGFPTILF YPAGKKSFEP ITFEGDRTVV EMYKFLKKHA AIPFKLKRPD SSAARTDGPG 568
GmPDIL-2    479 KPDGFPTLLF FPAGNKSFDP ITVDTDRTVV AFYKFLKKHA SIPFKLQKPT S---TSDAKG 535
                *******:** :***:***:* **.: *****  :******** :*****::*  *    :*. *

TaPDIL2     569 STAEGEKSSG SNPKDEL 585
GmPDIL-2    536 SSDAKE-SQS SDVKDEL 551
                *:   * *.. *: ****
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Figure S4. **Alignment of the amino acid sequences of TaPDIL2 and soybean GmPDIL-2.** The active center CGHC motifs (shaded in black), conserved arginines (box with straight lines), and glutamic acid (boxes with dotted lines) are indicated. Asterisks indicate 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.