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TaPDIL5A 23 LYSAGSPVHQ LNPNNFK-KV LNANGVVLVFF FAPWCGHCK QLTPIWEKAA GVLKGVATVA 81
αGmPDIM 29 LYGASSPVLQ LTPSNFKSKV LNSNGVVLVFF FAPWCGHCQ ALTPIWEKAA TVLKGVVTVA 88
      *.**.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.*
      **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.*

TaPDIL5A 83 ALDADAHKEL AQQYGIRGFP TIKVFLPGKP PVDYEGARFDV KPIVNFALSQ VKGLLRDRLD 141
GmPDIM 89 AIDADAHPSL AQEYGIRGFP TIKVFAPGKP PVDYQGARRDA KPIAEFALQQ VKALLKDRLS 148
      *:*:**.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.*
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TaPDIL5A 142 GKTSGGSSGK TSGGSSEKKN EPNESVELNS SNFDELVVKS KDLWIVLFFFA PWCGHCKKLA 201
GmPDIM 149 GKATGGSSDK T----- ETSSSVELNS GNFDLVIKS KELWIVLFFFA PWCGHCKKLA 199
      **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.*
      **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.*

TaPDIL5A 202 PEWKRAAKNL KGQVKLGHVD CSDSKLSMSK YKVEGFPTIL VFGADKESPF PYQGARAAASA 261
GmPDIM 200 PEWKKASNSL KGKVKLGHVD CDAEKLSMSR FKVQGFPTIL VFGADKDSPI PYEGARATALA 259
      **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.*
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TaPDIL5A 262 IEPFALEQLE ANAAPPEVSE LTSADVMEEK CASAAICFVS FLPDILDSKA EGRNKYLELL 321
GmPDIM 260 IESFALEQLE TNVAPPEVTE LHSPDVLEEK CGSAAICFVA FLPDILDSKA EGRNIYLQQL 319
      **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.*
      **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.*

TaPDIL5A 322 LSVAEKFKKS PYSFVWAGAG KQADLEKQVG VGGYGYPAMV ALNVKKGAYA PLRSAFELAE 381
GmPDIM 320 LSVAEKFKRS PYSYVWVAAG NQPDLKENVG VGGYGYPALV ALNLKKAVYA PLKSAFELDQ 379
      **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.*
      **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.*

TaPDIL5A 382 ITEFVKEAGR GGKGNLPLEG APTVVESEPW DGKDGEVIEE DEFSLEELMA DSSAPNDEL 440
GmPDIM 380 IIEFVKEAGR GGKGNLPLQG TPTIVKTEPW DGKDGEIEE DEFSLEELMG EDASSKDEL 439
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      * **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.* **.***.*

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**Figure S7. Alignment of amino acid sequences of TaPDIL5A and soybean GmPDIM.** 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 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.