```
                                                                                  η1        α1      β1
2UWA
                    1         10        20        30        40        50
2UWA      .........MPPNILSIFLHLLPILMFSSSCLGQGPPSPGYYPSSQITSLGFDQGYTNLW
TmNXG1    .........MPPNILSIFLHLLPILMFSSSCLGQGPPSPGYYPSSQITSLGFDQGYTNLW
XTH8      .......MMKALLLFLFAISSSLFMEPCYSSSGYWPPSPGYWPSHKFRSMNFYKGFRNLW
XTH9      .MFTTMLPSSPLSFFFFFFLLVLSFMICASAQ..GPPSPGYYPGSKISPISFDQGFRNLW
XTH20     ...............MALFVFAILMLMAPSSNAEWPPSPGYWPSSKFKTMNFYKGFRNLW
XTH23     ..MPSLLSSSLLQMPPLLFSLILSLMLCGIIADESPPSPGYYPSSQVSSVAFDQAYRNLW
XTH37     .......MMKALLLFLFAISSSLFMEPCYSSSGYWPPSPGYWPSHKFRSMNFYKGFRNLW
XTH49     ......MMMKALLLFLFAISSSLFMEPCYSSSGYWPPSPGYWPSHKFRSMNFYKGFRNLW
XTH50     ......................MLMAPSSNAEWPPSPGYWPSSKFKTMNFYK......
XTH53     ..MPSLLSSSLLQMLPLLFSLIISLMLCGIIADESPPSPGYYPSSQVSSVAFDQAYRNLW
XTH7      ................................MADPVLHPDTTNPLHHHQTQPLKEIAIDY
XTH12     ....MALIWQLKLLFSPLLIILLAN.VVSSRTRPFTAPTVTPLTNSFPRVPIDPNFSNAF
XTH13     ....................MGLGGGLVTFFLCLLFFAAPSASSTNLLPIIPFDEGYAPLF
XTH16     MDHNNTLRRFGEIIPKTHRNHNFLLSLFLFFFFFFFFFFSSHAAFDLATIPFNDGYSPLF
XTH26     ..................MGGCHLCFLFLCLSSAMVVVSGSSSMNNNLPIIAFEDGYTPLF
XTH36     ................................MADPVLHPDTTNPLHHHQTQPLKEIAIDY
XTH42     ....MALIWQLNLLFSPLIIICLLSNVVSSRTRPFTAPTVTPLTNSFPRVPIDPAFSNAF
XTH43     ....................MGLGGGLVTFFLCLLFFAAPSASSTNLLPIIPFDEGYAPLF
XTH45     MDHNNTLRRFGEIIPKTHRNHNFLLSLFLFFFFFFFFFFSSHAAFDLATIPFNDGYSPLF
XTH58     ..................MGGCHVCFLFLCLSSAMVVVSGSSSMNNNLPIIAFEDGYTPLF

                η2  β2        β3                  β4                  β5
2UWA            T.T                                          TT
                60                  70        80        90        100
2UWA      GPQHQRVDQ.G.SLTIWLDSTSGSGFKSINRYRSGYFGANIKLQSGYTAGVITSFYLSNN
TmNXG1    GPQHQRVDQ.G.SLTIWLDSTSGSGFKSINRYRSGYFGANIKLQSGYTAGVITSFYLSNN
XTH8      GPQHQALDNNN.ALTIWLDRTSGSGFKSVRPFRSGYFGASIKLHPGYTAGVITAFYLSNN
XTH9      GPQHQRLEQG..TLSIWLDSNSGSGFKSLHSYQSGYFSAAIKLQPGYTAGVITTLYLSNN
XTH20     GPQHQRIEQN..ALTIWLDRTSGSGFKSVAPFRSGYFGASIKLQPGYTAGVITAFYLSNN
XTH23     GPQHQRLDQSG.SLTIWLDSYSGSGFKSIRPYRSGYFGAAIKLQSGYTAG......LSNN
XTH37     GPQHQALDNNN.ALTIWLDRTSGSGFKSVRPFRSGYFGASIKLHPGYTAGVITAFYLSNN
XTH49     GPQHQALDNNN.ALTIWLDRTSGSGFKSVRPFRSGYFGASIKLHPGYTAGVITAFYLSNN
XTH50     ..............................GSGFKSVAPFRSGYFGASIKLQPGYTAGVITAFYLSNN
XTH53     GPQHQRLDQSG.SLTIWLDSYSGSGFKSIRPYRSGYFGAAIKLQSGYTAG......LSNN
XTH7      TPEACSHCPNSNTITLTFDHRGGARWRTTTRFHYGTFSSLIQCPKGNTNGLNFNLYLSSL
XTH12     GASNIKLLANGTMATLALDKLSGSGLVSKSSYYYGFFSAAIKLPAGISSGVVVAFYLSNA
XTH13     GDNNLVIHRDGKTVHLSLDERTGSGFVSHDLYLHGYFRASIKLPADYTAGVVVAFYMSNG
XTH16     GDSNVVRSDDGNGVNLLLDRFTGSGFISSSMYKYGFFSANIKLPSNYTAGICVAFYTSNG
XTH26     GDNNLIIHNDGKLVHLTLDQGTGSGFVSHELYLHGYFSAKIKLPADYTAGVVVAFYMSNG
XTH36     TPEACSHCPNSNTITLTFDHRGGARWRTTTRFHYGTFSSLIQCPKGNTNGLNFNLYLSSL
XTH42     GASNVKLLANGTMATLALDKLSGSGLVSKSSYYYGFFSAAIKLPAGISSGVVVAFYLSNA
XTH43     GDNNLVIHRDGKTVHLSLDERTGSGFVSHDLYLHGYFSASIKLPADYTAGVVVAFYMSNG
XTH45     GDSNVVRSDDGNGVNLLLDRFTGSGFISSSMYKYGFFSANIKLPSNYTAGICVAFYTSNG
XTH58     GDNNLIIHNDGKLVHLTLDQRTGSGFVSHELYLHGYFSAKIKLPADYTAG.....MSNG

                    β6                  β7                  β8
2UWA                      TT                                      TT
110                 120       130       140       150       160
2UWA      QDYPGKHDEIDIEFLGTIPGKPYTLQTNVFIEGSGDYN.IIGREMRIHLWFDPTQDYHNY
TmNXG1    QDYPGKHDEIDIEFLGTIPGKPYTLQTNVFIEGSGDYN.IIGREMRIHLWFDPTQDYHNY
XTH8      EAHPGFHDEVDIEFLGTTFGKPYTLQTNVYIRGSGDG.TIIGREMKFHLWFDPTKDFHHY
XTH9      QDHPGNHDEIDIEFLGTTPDKPYVLQTNVYIRGTGD.GNIVGREMRFHLWFDPTQDFHIY
XTH20     EAHPGFHDEVDIEFLGTTFGKPYTLQTNVYIRGSGDG.QIIGREMKFHLWFDPTKDFHHY
XTH23     QDYPGDHDEVDIEFLGTIPDKQYVLQTNVFMRGSGDKNNVIGREMRFHLWFDPTQDFHHY
XTH37     EAHPGFHDEVDIEFLGTTFGKPYTLQTNVYIRGSGDG.TIIGREMKFHLWFDPTKDFHHY
XTH49     EAHPGFHDEVDIEFLGTTFGKPYTLQTNVYIRGSGDG.TIIGREMKFHLWFDPTKDFHHY
XTH50     EAHPGFHDEVDIEFLGTTFGKPYTLQTNVYIRGSGDG.QIIGREMKFHLWFDPTKDFHHY
XTH53     QDYPGDHDEVDIEFLGTIPGKQYVLQTNVFMRGSGDKNNVIGREMRFHLWFDPTQDFHHY
XTH7      E.GEKSQDEIDFEFLGKDR...TIVQTNYFSGGNGNK.....EKIHHLGFDASDGFHEY
XTH12     DKFPHNHDEIDIELLGHDKRNDWVIQTNVYANGSVST....GREEKFYFWFDPTKQYHYY
XTH13     DMFQNNHDEIDFEFLGNIRGKDWRIQTNVYGNGSTSI....GREERYGLWFDPAEDFHQY
XTH16     DVFEKTHDELDFEFLGNLAGKPWRFQTNLYGNGSTHR....GREERYRLWFDPTKEYHRY
XTH26     DMFKKNHDEIDFEFLGNIRGRDWRMQTNFYGNGSTNT....GREERYDLWFDPSQDFHQY
XTH36     E.GEKSQDEIDFEFLGKDR...TIVQTNYFSGGNGNK.....EKIHHLGFDASDGFHEY
XTH42     DKFPHNHDEIDIELLGHDKRNDWVIQTNVYANGSVST....GREEKFYFWFDPTKQYHYY
XTH43     DMFQNNHDEIDFEFLGNIRGKDWRIQTNVYGNGSTSI....GREERYGLWFDPAEDFHQY
XTH45     DVFEKTHDELDFEFLGNLAGKPWRFQTNLYGNGSTHR....GREERYRLWFDPTKEYHRY
XTH58     DMFKKNHDEIDFEFLGNIRGRDWRMQTNFYGNGSTNT....GREERYDLWFDPSQDFHQY

          β9        β10       β11       η3        β12       η4        η5
2UWA                TT
170       180       190       200       210       220
2UWA      AIYWTPSEIIFFVDDVPIRRYPRKSDA..TFPLRPLWVYGSVWDASSWATENGKYKADYR
TmNXG1    AIYWTPSEIIFFVDDVPIRRYPRKSDA..TFPLRPLWVYGSVWDASSWATENGKYKADYR
XTH8      AILWSPK.....................EIIPMWVYGSIWDASSWATEDGKYKADYR
XTH9      AILWKPSETIFFVDDVPIRRYPRKGDA..TYPNRPMYVYGSIWDASSWATEDGKYKANYK
XTH20     AILWSPKEIIFFVDDVPIRRYPRKSAE..TFPMRPMWLYGSIWDASSWATEDGKYKADYR
XTH23     AILWTPTDIIFLVDDVPIRNYPRKNDA..TFPERAMYVYGSIWDASSWATENGKYKADYK
XTH37     AILWSPK.....................EIIPMWVYGSIWDASSWATEDGKYKADYR
XTH49     AILWSPK.....................EIIPMWVYGSIWDASSWATEDGKYKADYR
XTH50     AILWTPKEIIFFVDDVPIRRYPRKSAE..TFPMRPMWLYGSIWDASSWATEDGKYKADYR
XTH53     AILWTPTDIIFLVDDVPIRNYPRKNDA..TFPERAMYVYGSIWDASSWATENGKYKADYK
XTH7      VIKWSYDVIEWLIDGKVVRREEKKEGKG..FPQKPMFLYASIWDASCIDNGRWAGKYDGS
XTH12     SILWNSYHTVFLVDNIPVREFIH....GSVFPSKPMSVYATIWDGSEWATHGGKYPVDYK
XTH13     SILWTDSQIIFYVDNVPIREIKRTESMGGDFPSKPMTLYATIWDASDWATNGGKYRVNYK
XTH16     SILWTAKNVFFYIDEVPIREVLRSAEMGADYPSKPMSLYATIWDASNWATSGGKYKVNYK
XTH26     SILWTDSKIIFYIDNVPIREVKRTESMGGDFPSKPMTLYATIWDASDWATDGGKYRVNYK
XTH36     VIKWSCDVIEWLIDGKVVRREEKKEGKG..FPQKPMFLYASIWDASCIANGMWAGKYDGS
XTH42     SILWNSYHTVFLVDNIPVREFIH....GTVFPSKPMSVYATIWDGSEWATHGGKYPVDYK
XTH43     SILWTDSQIIFYVDNVPIREIKRTESMGGDFPSKPMTLYATIWDASDWATNGGKYRVNYK
XTH45     SILWTAKNVFFYIDEVPIREVLRSAEMGADYPSKPMSLYATIWDASNWATSGGKYKVNYK
XTH58     SILWTDS.....KIIEVKRTESMGGDFPSKPMTLYATIWDASDWATDGGKYRVNYK
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                    β13                                                                α2
2UWA                ---------->TT   TT                                   ------------
                    230       240       250                       260       270
2UWA     YQPFVGKYEDFKLGSCTVEAA.SSCNPASV.........SP..YGQLSQQQVAAMEWVQK
TmNXG1   YQPFVGKYEDFKLGSCTVEAA.SSCNPASV.........SP..YGQLSQQQVAAMEWVQK
XTH8     YQPFVARYTNFKASGCSAYAS.RWCHPVSA.........SPYRSGGLTRQQYWAMRWVQR
XTH9     YQPFIGRYKNFKLQGCTINESPSSCKPPSA.........SPSGYGSLSLQQISAMQWVQN
XTH20    YQPFVARYTNFKASGCTAYAP.RWCHAVSA.........SPYRSGELSRQQYSAMRWVQM
XTH23    YQPFIGRYKDFKLQGCTTQSS.SSCQPPSP.........SPPGYNSLSPQQYNAMQWVQN
XTH37    YQPFVARYTNFKASGCSAYAS.RWCHPVSA.........SPYRSGGLTRQQYWAMRWVQR
XTH49    YQPFVARYTNFKASGCSAYAS.RWCHPVSA.........SPYRSGGLTRQQYWAMRWVQR
XTH50    YQPFVARYTNFKASGCTAYAP.RWCHAVSA.........SPYRSGGLSRQQYSAMRWVQT
XTH53    YQPFIGRYKDFKLQGCTTQSS.SSCQPPSP.........SPPGYNSLSPQQYNAMQWVQN
XTH7     DAPYVCLYKDIHVPTSTAVK...................................
XTH12    YAPFVVSFSEMQLAGCTSDPLACSKSTPSS....GVDPVNGPQFTKLSPQQMAALDWARK
XTH13    YAPYVAEFSDLVLHGCAVDPIEH.EAKCD......NAQTSKAVPTGVTPAQRIKMENFRK
XTH16    YAPFVAEFKDLVLKGCSVDPIEESTVAGRSICSDQHADLEAQDYAAVTPRRRLAMRRFRQ
XTH26    YAPYVAEFSNFVMHGCGVDPIDENVAMCN......NAQNSKAN...IIPKHKIKMENFRN
XTH36    DAPYVCLYKDIHVPTSTAVK...................................
XTH42    YAPFVVSFSEMQLTGCTSDPLACSKSTPSS....GVDPVNGPQFTKLSPQQLAALDWARK
XTH43    YAPYVAEFSDLVLHGCAVDPIEH.EAKCD......NAQTSKAVPTGVTPAQRIKMENFRK
XTH45    YAPFVAEFKDLVLKGCSVDPIEESTVAGRSICSDQHADLEAQDYAAVTPRRRLAMRRFRQ
XTH58    YAPYVAEFSNFVMHGCGVDPIDENVAMCN......NAQNSKAN...IIPKHKIKMENFRN
                          1         1
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                    β14   η6      η7
2UWA                ---->   TT    TT
                    280       290
2UWA     NYMVYNYCDDPTRDHTLTPEC.........................................
TmNXG1   NYMVYNYCDDPTRDHTLTPEC.........................................
XTH8     HHMVYNYCQDPKRDHRLTPECWGKKKENNEKRMRSRGYVIVHIYASYFIILLLTVSSETF
XTH9     HYLVYYYCHDPKRDHTLTPEC.........................................
XTH20    YHMVYNYCQDSKRDHRLTPECWS.......................................
XTH23    NYLVYDYCRDPTRDHTLTPEC.........................................
XTH37    HHMVYNYCQDPKRDHRLTPECWGKKKENNEKRMRSRGYVIVHIYASYFIILLLTVSSETF
XTH49    HHMVYNYCQDPKRDHRLTPECWG.......................................
XTH50    YHMVYNYCQDSKRDHRLTPECWS.......................................
XTH53    NYLVYDYCRDPNRDHTLTPEC.........................................
XTH7     ..............................................................
XTH12    KLMFYSYCTDKNRYKVMPPECH........................................
XTH13    KHMTYSYCYDKVRYKVPPTECVINPQEAERLRKFDPVTFGGGRRRHG...KRHYRSRGSQ
XTH16    RYMYYSYCYDTLRYPNPLPECDIIPSEKQRFKETGRLKFGGSHRRQSRRKGRTTTPVDDT
XTH26    NHMTYSYCYDRARYQVPPPECVISLQEAEALRKLDPATFGGGRRHRGGGKRRHHQSKGRK
XTH36    ..............................................................
XTH42    KLMFYSYCTDKNRYKVMPPECH........................................
XTH43    KHMTYSYCYDKVRYKVPPTECLINPQEAERLRKFDPVTFGGGRRRHG...KRHYRSRGSQ
XTH45    RYMYYSYCYDTLRYPNPLPECDIIPSEKQRFKETGRLKFGGSHRRQSRRKGRTTTPVDDT
XTH58    NHMTYSYCYDRARYQVPPPECVISLQEAEALRKLDPATFGDGRRHRGGGKRRHHQSKGRK
                  2         2
```

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2UWA

2UWA     ................
TmNXG1   ................
XTH8     QLVSFISFTPRNLQVQN
XTH9     ................
XTH20    ................
XTH23    ................
XTH37    QLVSFISFTPRNLQVQN
XTH49    ................
XTH50    ................
XTH53    ................
XTH7     ................
XTH12    ................
XTH13    AEEAAAF.........
XTH16    DQGDM...........
XTH26    AEDASF..........
XTH36    ................
XTH42    ................
XTH43    AEEAAAF.........
XTH45    DQGDM...........
XTH58    AEDASF..........
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Supplementary Files 6 The multiple alignment of amino acid sequences among 58 AhXTHs in peanut and 2UWA

Amino acid sequences from 58 AhXTHs in peanut were aligned using TmNXG1(2UWA) as a referent sequence by MEGA X, and their secondary structures were predicted using ESPript. The conserved residues were shown in blue frames.