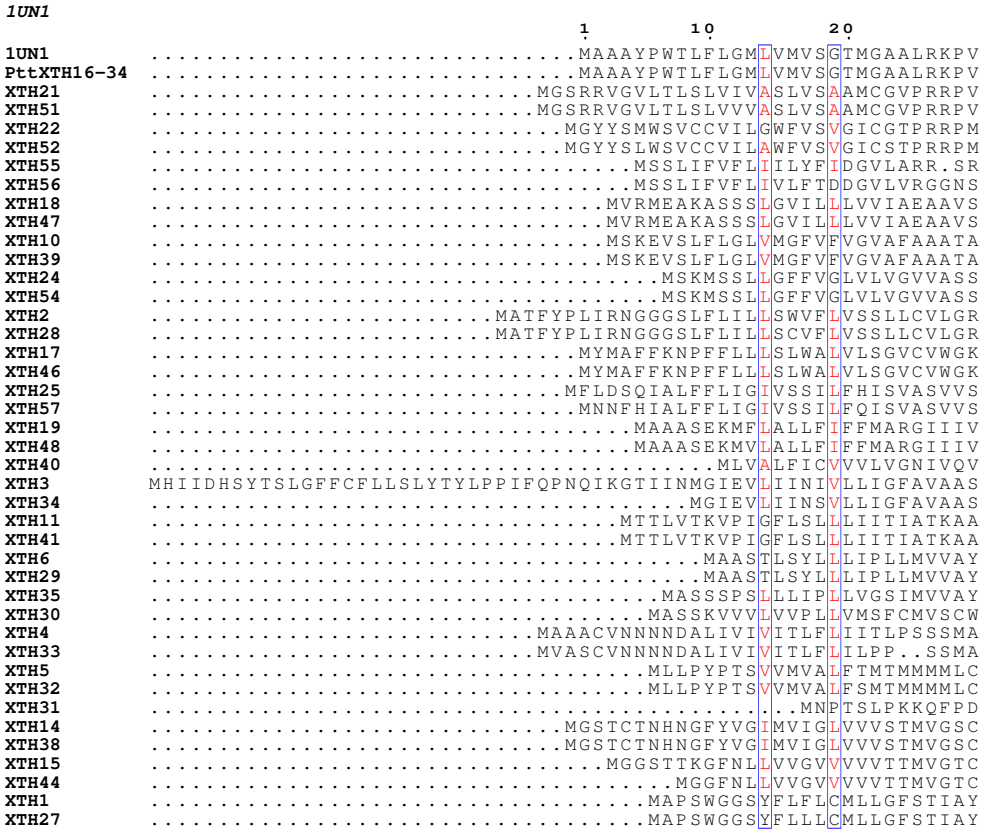
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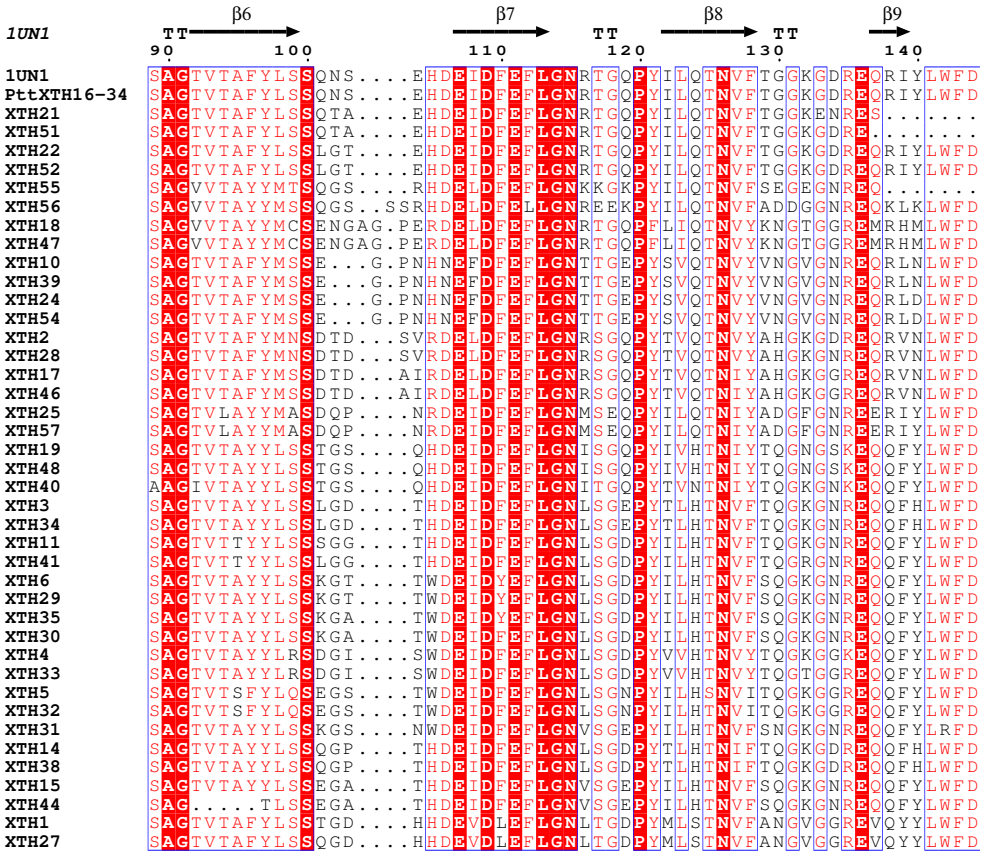
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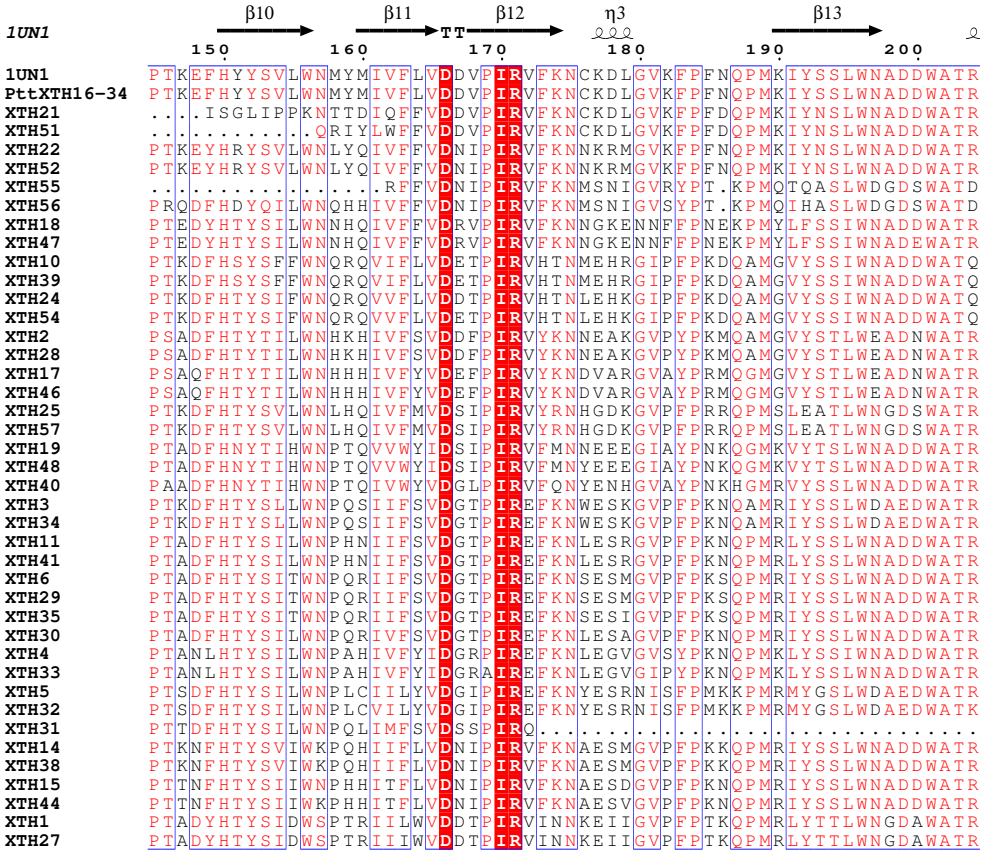
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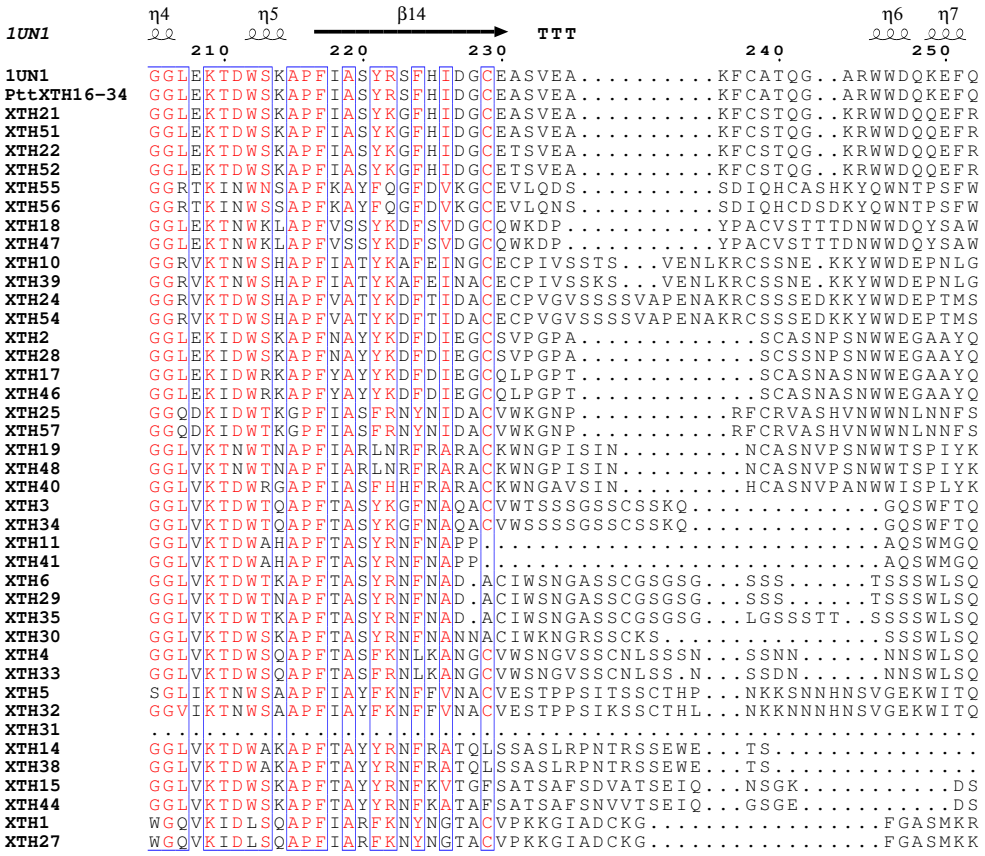
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α2 β15 η8 α3
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260 270 280 290
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1UN1

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XTH1          ............................................................
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1UN1

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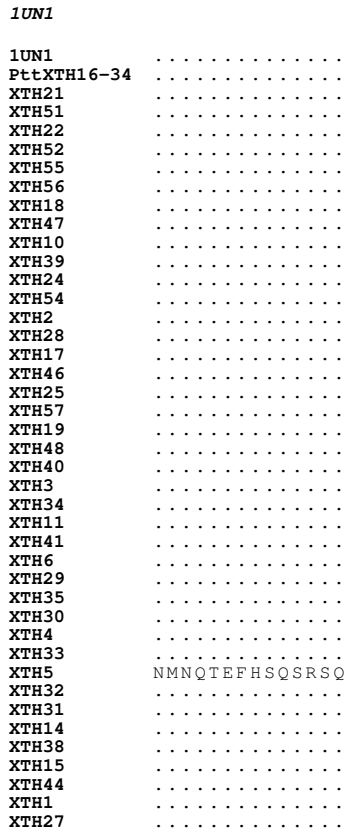

Supplementary Files 5 The multiple alignment of amino acid sequences among 58 AhXTHs in peanut and 1UN1

Amino acid sequences from 58 AhXTHs in peanut were aligned using PttXET16-34 (1UN1) as a referent sequence by MEGA X, and their secondary structures were predicted using ESPript. The conserved residues were shown in blue frames.