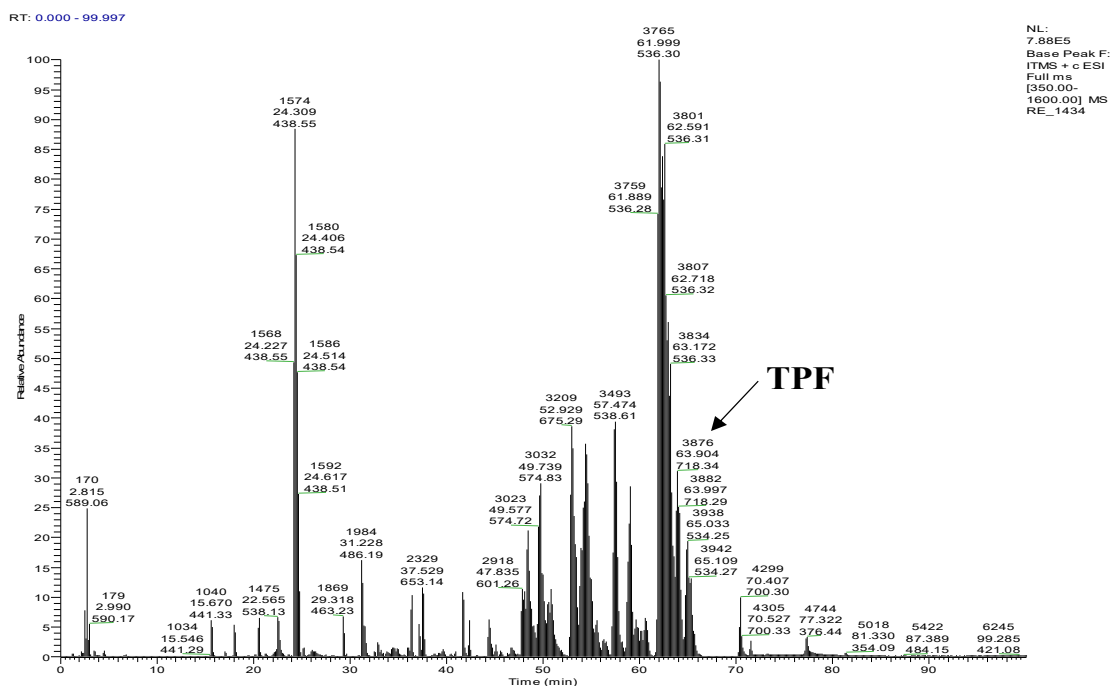


M F T L K K S L L L I F F L G T I
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 · N F S L C E Q E R N A D E E Q R R
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 · D E P E E R D V E V Q K R F L P
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 CTCTGCTCGG TCTCCTTTCT CTACAACTTC ATGTTTTTGC AAAAGATGGT
 L I A G L F G K I F G K *
 151CTTATCGCAG GCCTGTTTCGG TAAAATTTTC GGAAAATAAC CAAAAATGT
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 CGATTTACGT GTAGTCTACA GAATTTTTTTT TTATTTATTT TGAGAAATGC
 301TCAACTCTAA AAAAAAAAAA AAAAAAAAAA

Figure S1. Nucleotide sequence of the cDNA cloned from the skin secretion of *Pelophylax fukienensis* and its predicted peptide sequence. The putative signal peptide and temporin-PF (TPF) are indicated by single underline and double underlines, respectively.



ITMS, CID, z=+1, Mono m/z=1435.56000 Da, MH+=1435.56000 Da, Match Tol.=0.8 Da

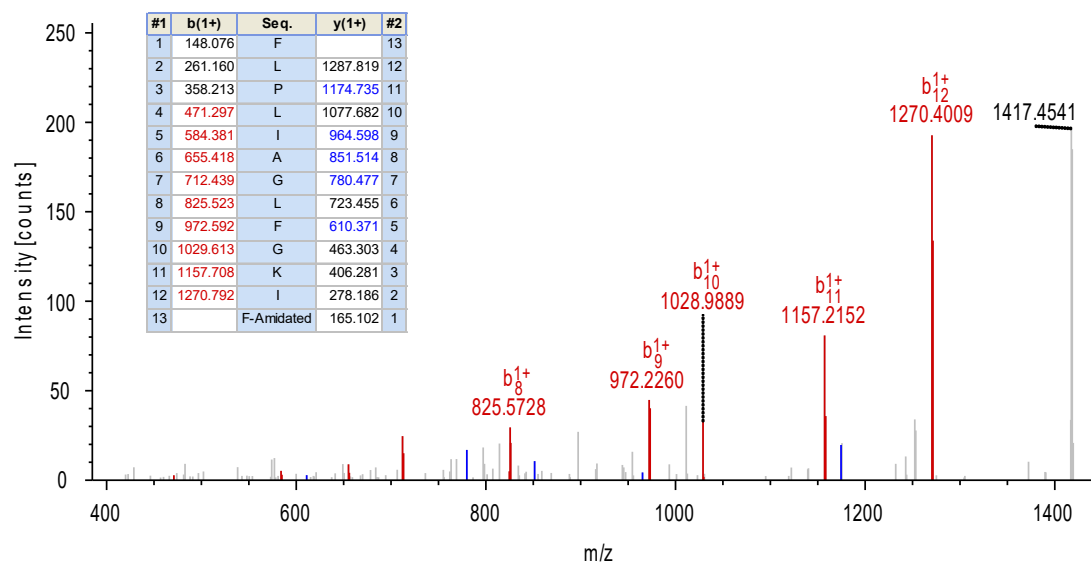


Figure S2. Identification of TPF derived from the skin secretion of *Pelophylax fukienensis*: (A) RP-HPLC chromatogram of skin secretion of *P. fukienensis* monitored at 214 nm. The arrow indicates the retention time of QUB-1434. (B) Annotated MS/MS spectrum of QUB-1434. Predicted b- and y-ions arising from collision induced dissociation of the mono-charged (1435.56 m/z, [M+H]⁺) precursor ion. The observed b- and y-ions are indicated in red and blue typefaces.

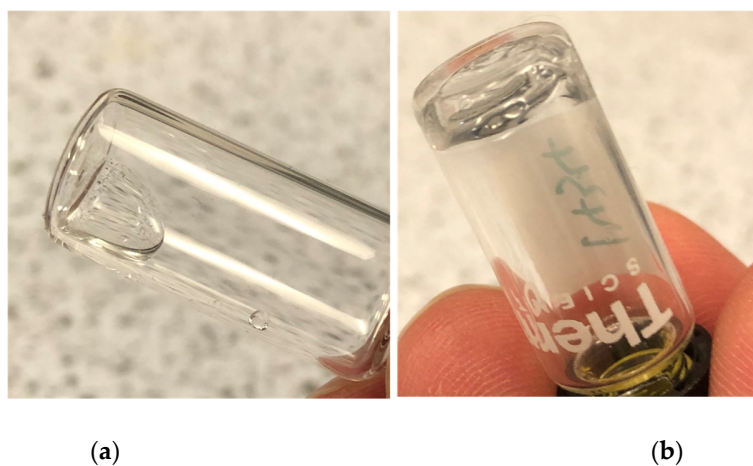


Figure S3. The fluidity of (a) PBS and (b) 10 mg/ml TPF in PBS. The peptide is dissolved in PBS and formed hydrogel-like morphology.

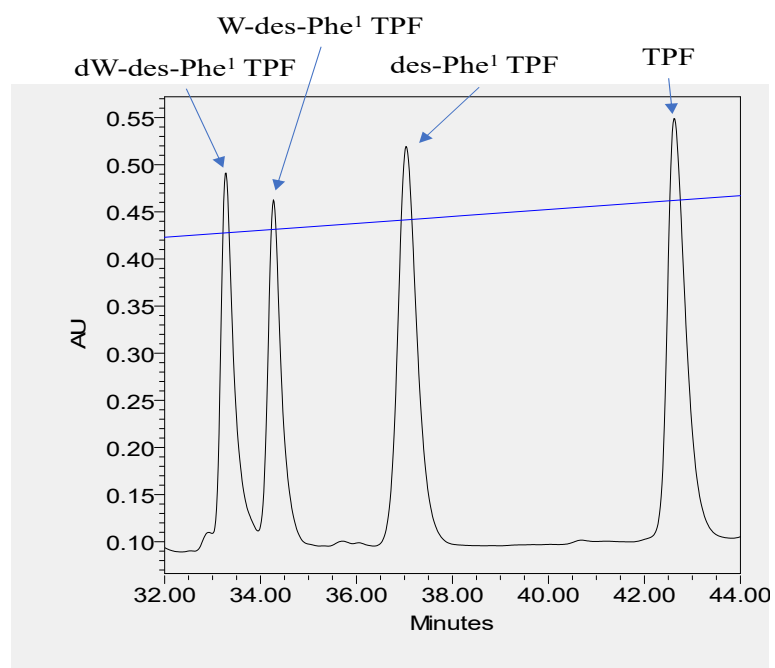


Figure S4. The chromatogram of the mixture of TPF analogues. The retention time of each peptide is indicated by arrow. The gradient of mobile phase is presented by a blue line.

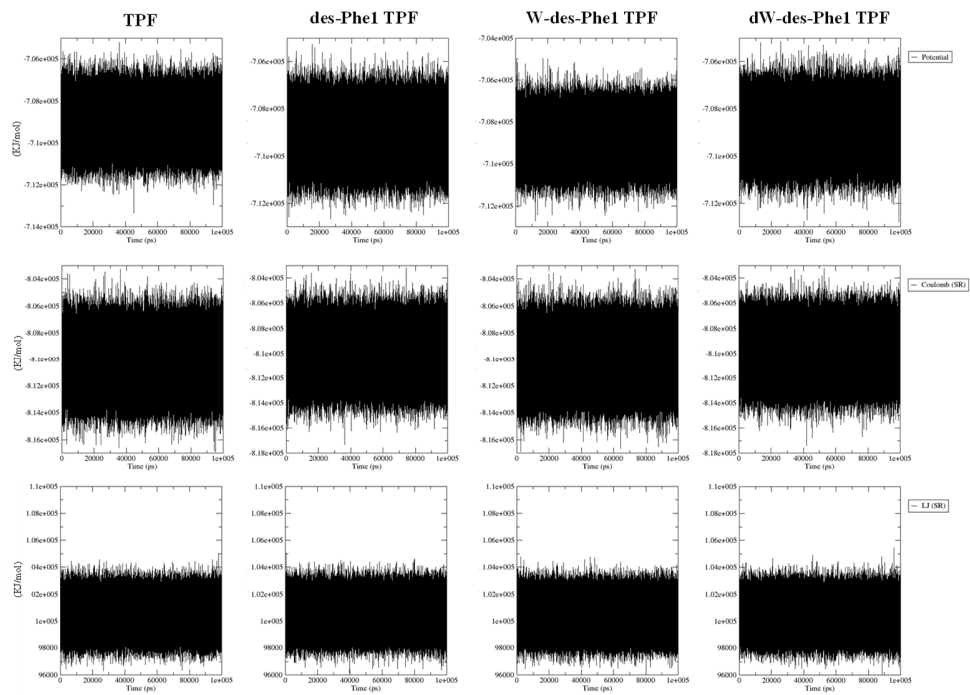
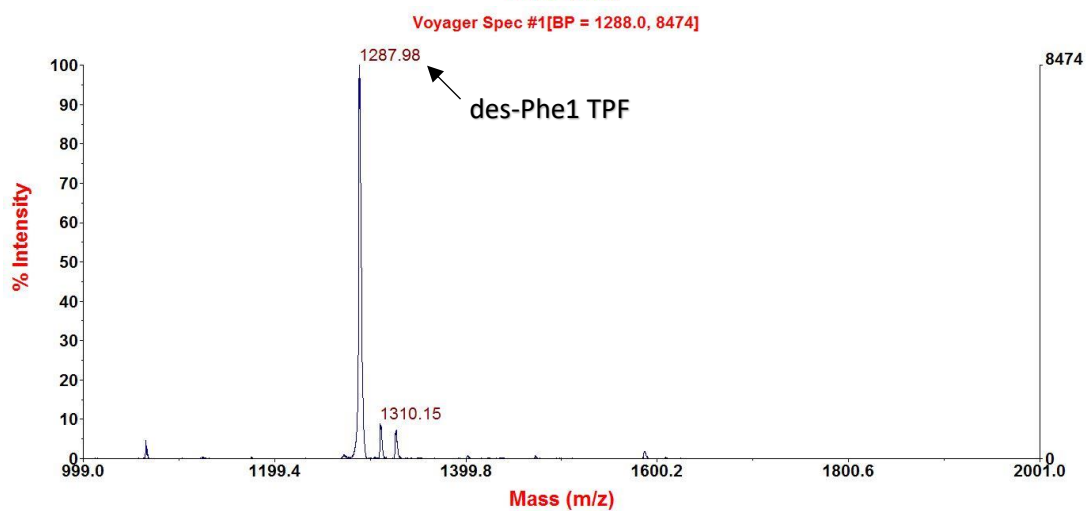
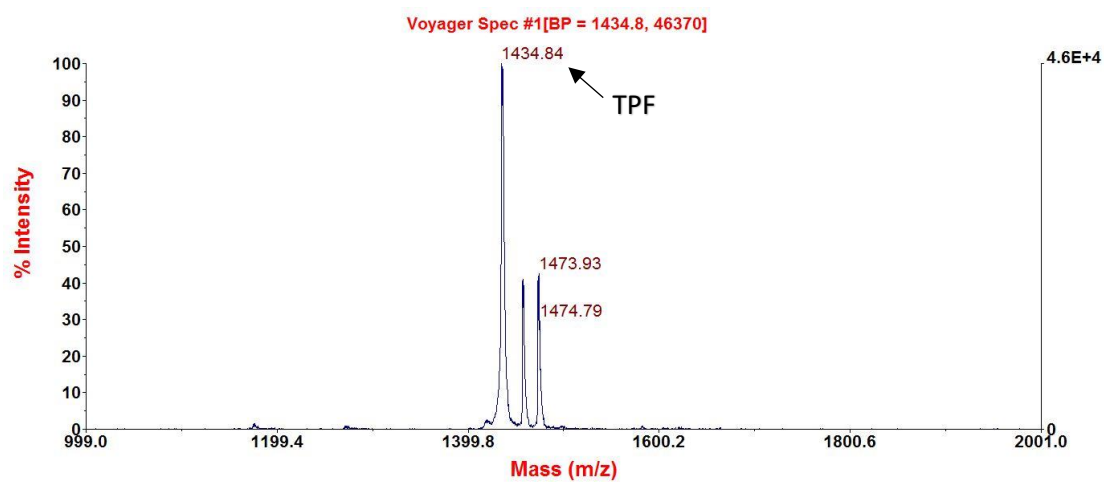


Figure S5. The energy analysis of TPF and the analogues monomer during 100 ns MD simulation.



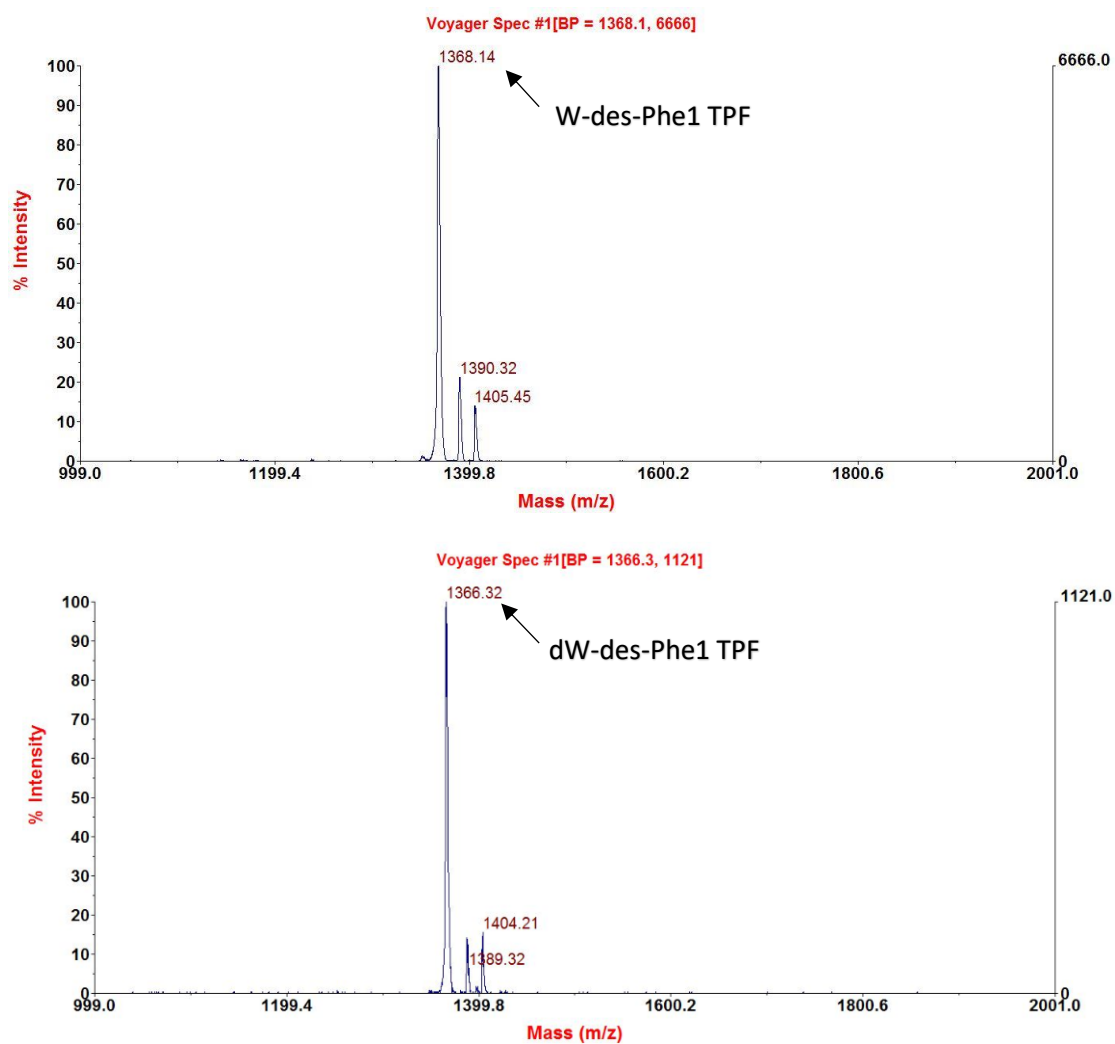


Figure S6. Mass of TPF and its analogues identified by matrix-assisted laser desorption ionization, time-of-flight mass spectrometry.

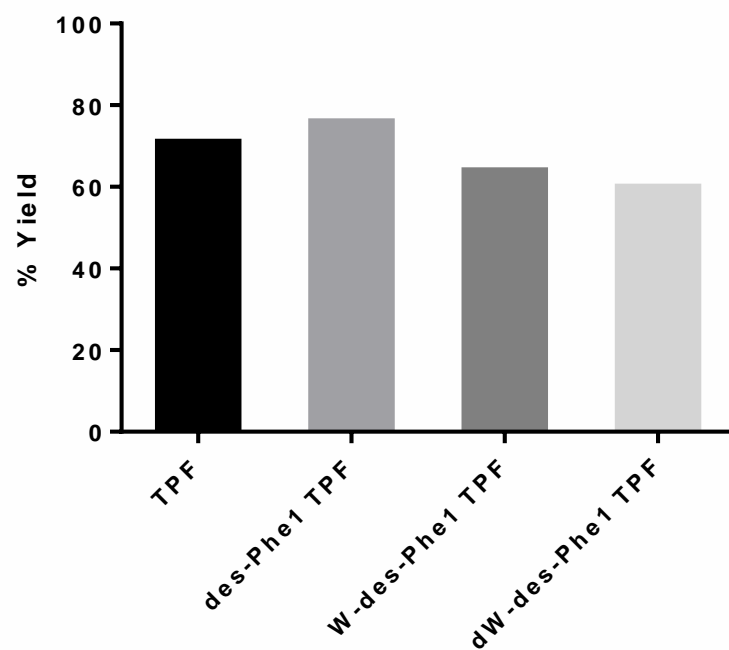


Figure S7. Synthetic yield of TPF and its analogues. The yield of TPF, des-Phe1 TPF, W-des-Phe1 TPF and dW-des-Phe1 TPF were 71%, 76%, 64% and 60%, respectively.