Supplementary Materials: BmP02 Atypically Delays Kv4.2 Inactivation: Implication for a Unique Interaction Between Scorpion Toxin and Potassium Channel

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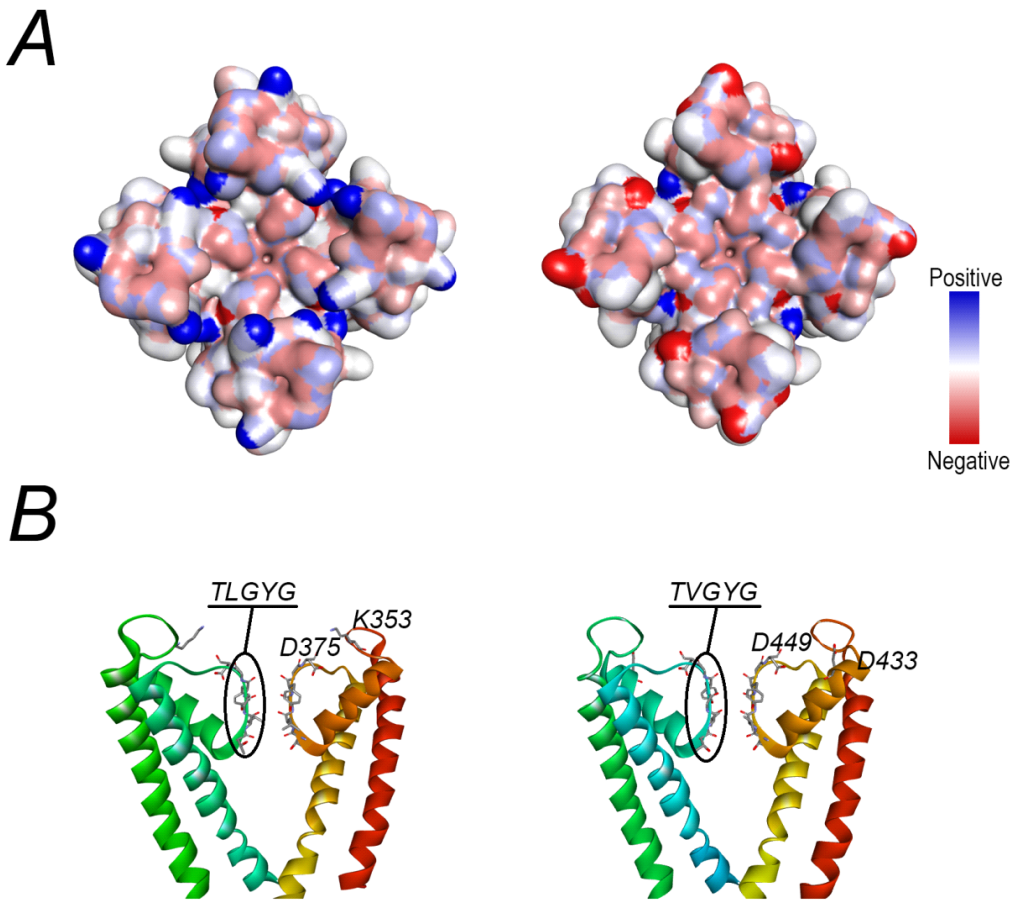

Figure S1. Homology modeling of Kv4.2 and Kv1.3 using the structure of KcsA (PDB: 1BL8) as template. (**A**) A vertical view of Kv4.2 (left) and Kv1.3 (right). The positively charged groups are shown in blue and the negatively charged groups are in red; (**B**) An insight into the structure of Kv4.2 (left) and Kv1.3 (right). Residues in the selectivity filter and a Asp nearby are highlighted. K_{353} in Kv4.2 and D433 (the corresponding residue of A_{359} in Kv4.2) in Kv1.3 are also highlighted.

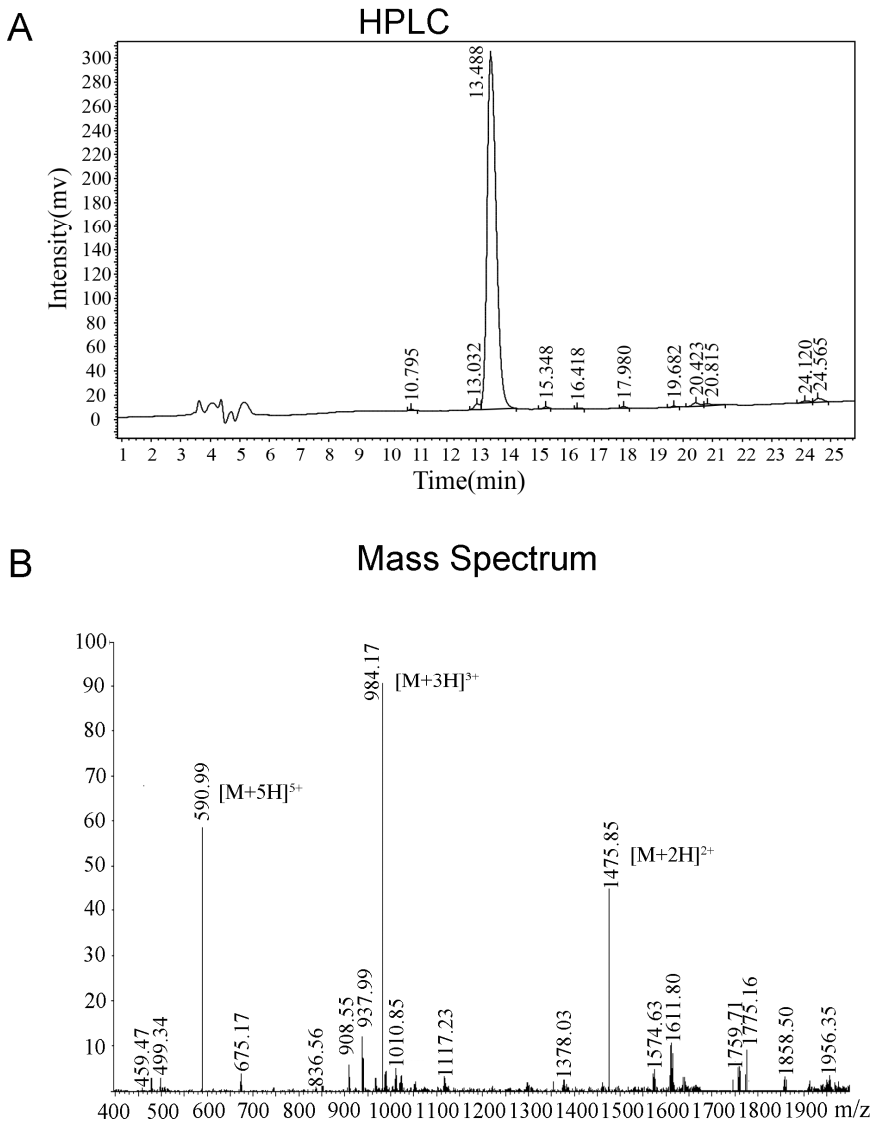

Figure S2. The purity and the molecular weights of synthetic BmP02. (**A**) Purity of synthetic BmP02 was determined by High Performance Liquid Chromatography (HPLC); (**B**) Molecular weights of the peptides were determined by mass spectrum (MS).

Table S1. The primers used in the construction of mutants. The mutated sites are underlined. S: sense, A: anti-sense.

Name	Mutated Sides	Primer
Kv4.2M1	$A_{359}D$	S:5′-CAGCATCCCTGACGCCTTCTGGTATACCATCGT A:5′-GGTATACCAGAAGGCGTCAGGGATGCTGGTGAA
Kv4.2M2	$K_{347}A/K_{353}G$	S:5′-GCGGGGTCTTCGGCTAGCGGGTTCACCAGCATCCCT A:5′-CCCGCTAGCCGAAGACCCCGCCTCTGCGTAGAACAT
Kv4.2M3	$K_{347}A/K_{353}G/A_{359}D$	S:5′-GCGGGGTCTTCGGCTAGCGGGTTCACCAGCATCCCTGACGCCTTCTGGTA TACCATCGT A:5′-GTCAGGGATGCTGGTGAACCCGCTAGCCGAAGACCCCGCCTCTGCGTAG AACATAACTG