

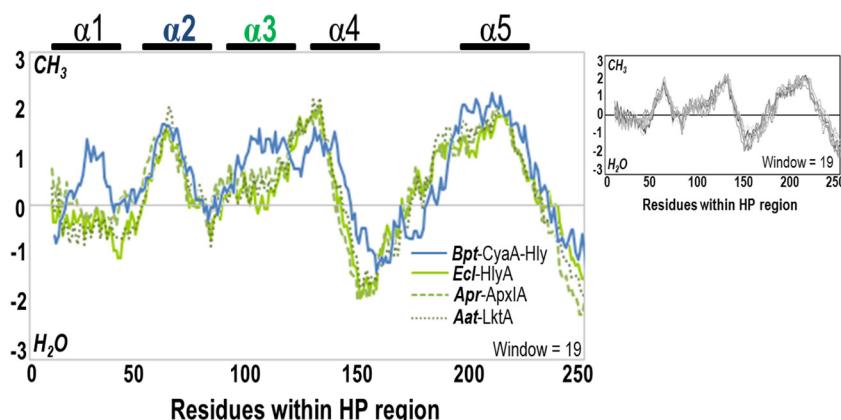
# Supplementary Materials: Functional Contributions of Positive Charges in the Pore-Lining Helix 3 of the *Bordetella pertussis* CyaA-Hemolysin to Hemolytic Activity and Ion-Channel Opening

Chattip Kurehong, Chalermpol Kanchanawarin, Busaba Powthongchin, Panchika Prangkio, Gerd Katzenmeier and Chanan Angsuthanasombat

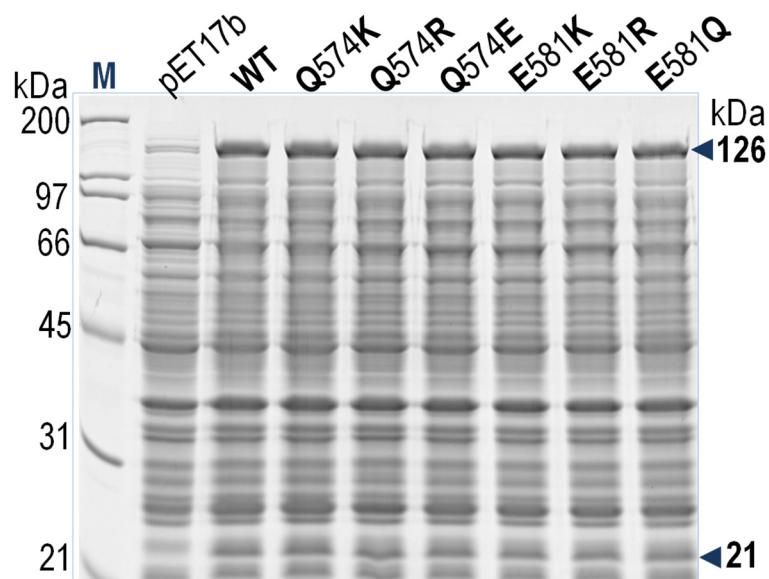
**Table S1.** Complementary primers used in mutagenesis.

Primer <sup>a</sup>	Sequences <sup>b</sup>	Restriction site <sup>c</sup>
Q574K-f	5'-GCG <u>CTGAA</u> ATTGACAGGTGGAACG-3'	
Q574K-r	3'-GGCTCTAG <u>CGC</u> GACTTAACTGTCC-5'	<i>Pst</i> I
Q574R-f	5'-GCG <u>CTGCG</u> CTTGACAGGTGGAACG-3'	
Q574R-r	3'-GGCTCTAG <u>CGC</u> GAC <u>CGA</u> ACTGTCC-5'	<i>Pst</i> I
Q574E-f	5'-GCG <u>CTGGA</u> ATTGACAGGTGGAACG-3'	
Q574E-r	3'-GGCTCTAG <u>CGC</u> GAC <u>CTT</u> AACTGTCC-5'	<i>Pst</i> I
E581K-f	5'-ACGGT <u>CAA</u> ACTGGCTTCTTCCATCG-3'	
E581K-r	3'-TGTCCAC <u>CTT</u> GCCAG <u>TTG</u> ACCGA-5'	<i>Alu</i> I
E581R-f	5'-ACGGT <u>CCG</u> CCTGGCTTCTTCCATCG-3'	
E581R-r	3'-TGTCCAC <u>CTT</u> GCCAG <u>GG</u> ACCGA-5'	<i>Alu</i> I
E581Q-f	5'-ACGGT <u>CCA</u> ACTGGCTTCTTCCATCG-3'	
E581Q-r	3'-TGTCCAC <u>CTT</u> GCCAG <u>GG</u> ACCGA-5'	<i>Alu</i> I

<sup>a</sup> f and r represent forward and reverse primers, respectively. <sup>b</sup> Underlined bases represent the recognition sites introduced for restriction enzyme analysis. Bold letters indicate the substituted nucleotide residues. The mutated residues in introduced restriction sites generate silent mutations. <sup>c</sup> Deleted recognition sites.



**Figure S1.** Hydropathy profile of the hydrophobic (HP) region from CyaA-Hly (blue line) compared with three highly-active RTX cytolsins i.e. HlyA, ApxIA and LtxA (green lines). The hydropobicity scale was plotted versus amino acid sequences (~250 residues) covering the hydrophobic regions with a window size of 19 using Kyte-Doolittle hydropathy index. Five putative helices in the HP region of CyaA-Hly were indicated. Inset: the hydropathy profile of the HP region from all twelve related RTX cytolsins as mentioned earlier in [25].



**Figure S2.** SDS-PAGE (12% gel) of the soluble lysates extracted from *E. coli* harboring different plasmids; pET-17b vector, pCyaAC-PF/H<sub>6</sub> (Wt) and pCyaAC-PF/H<sub>6</sub> with mutations (Q574K, Q574R, Q574E, E581K, E581R and E581Q). Co-expressed with 126 kDa CyaA-Hly is the 21 kDa CyaC acetyltransferase marked by arrow. M is protein standard marker.