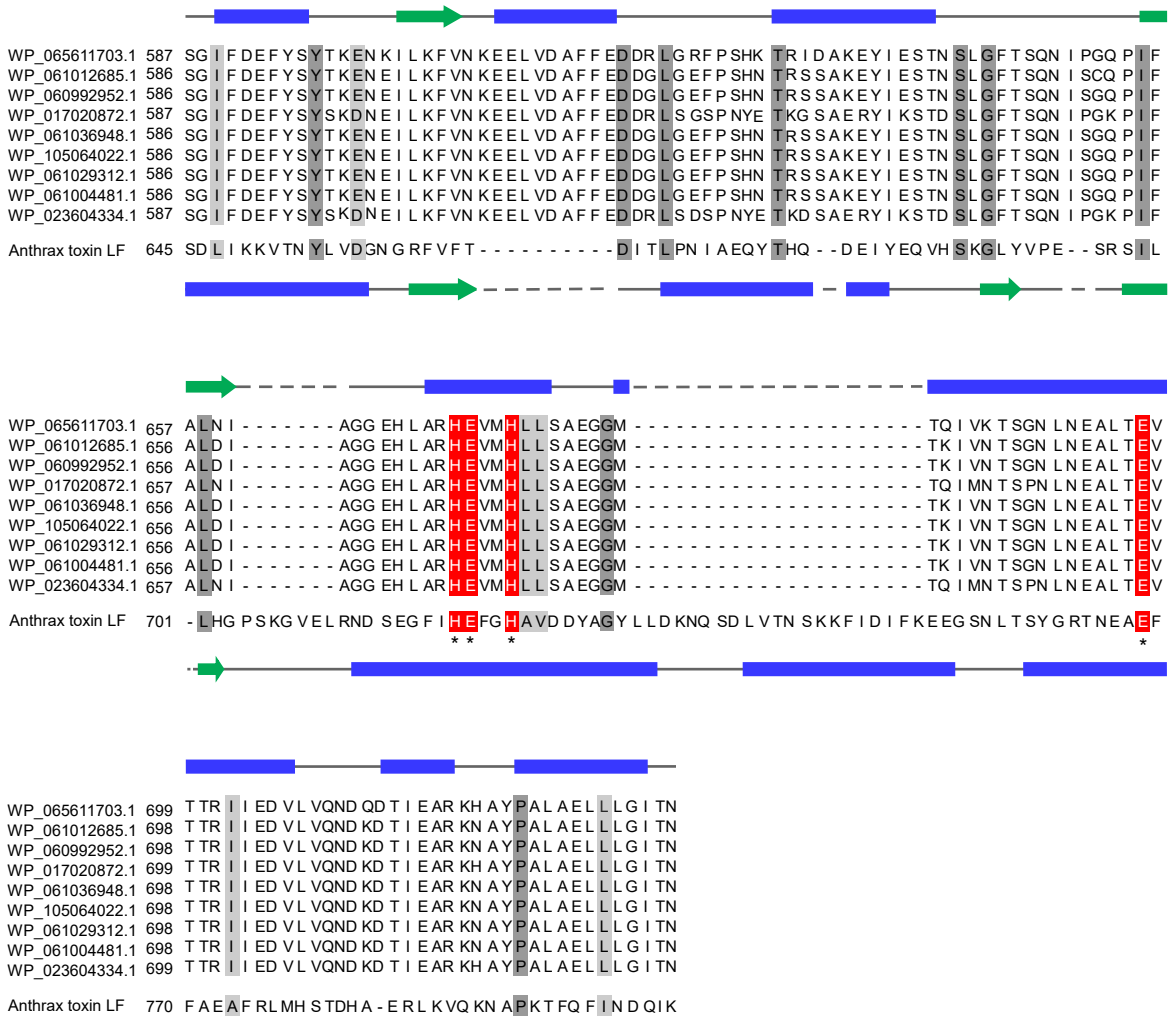
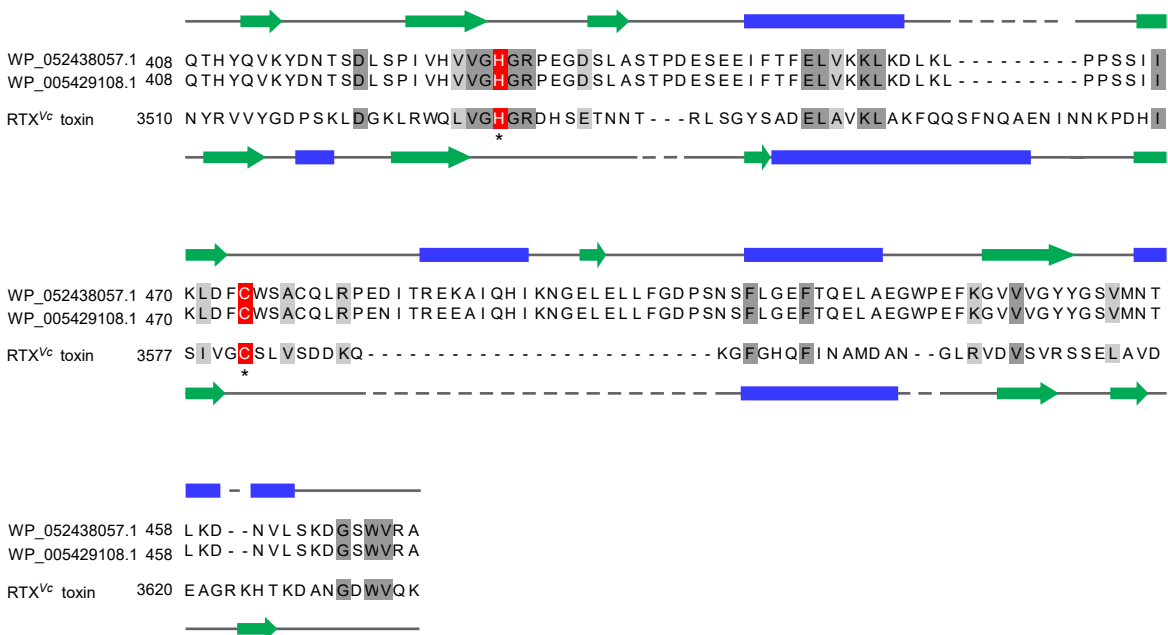
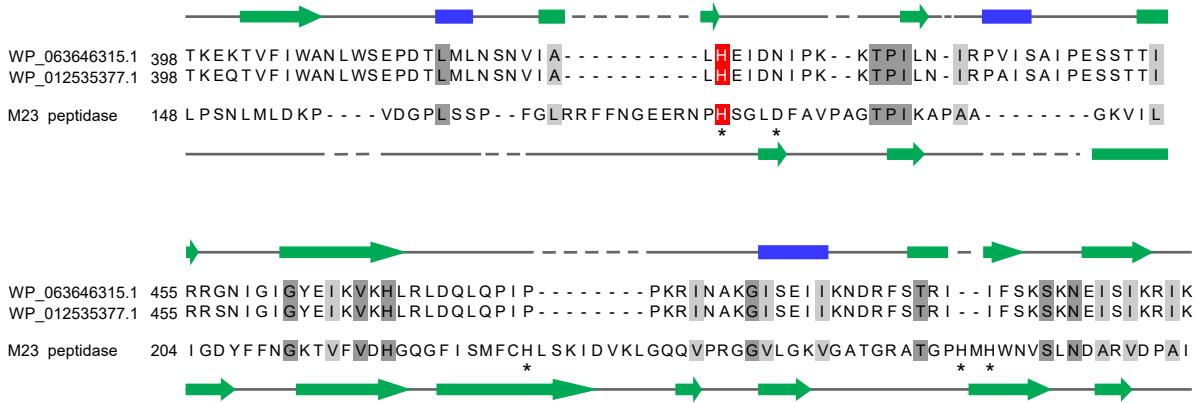
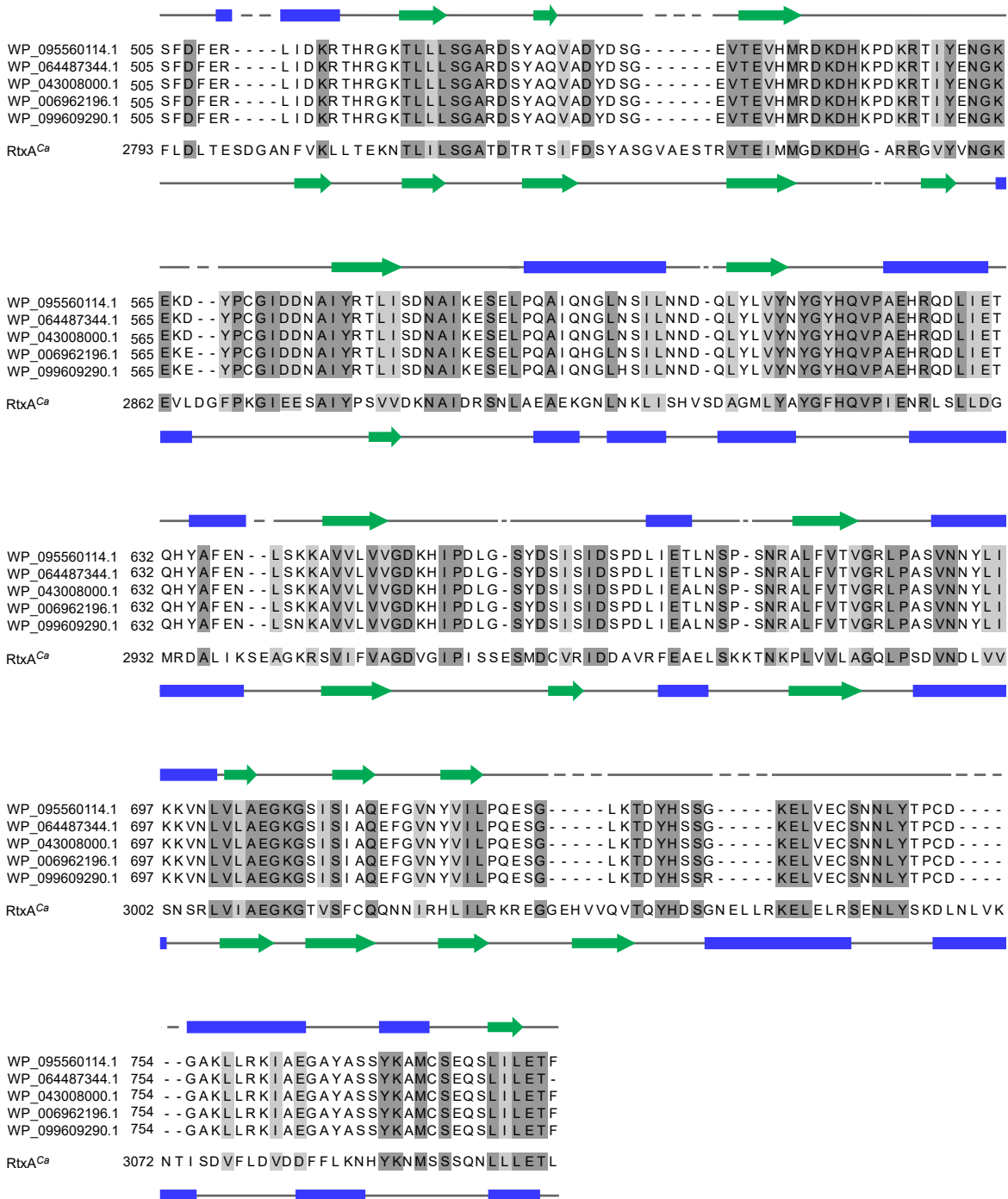


a**b**

c



d



e

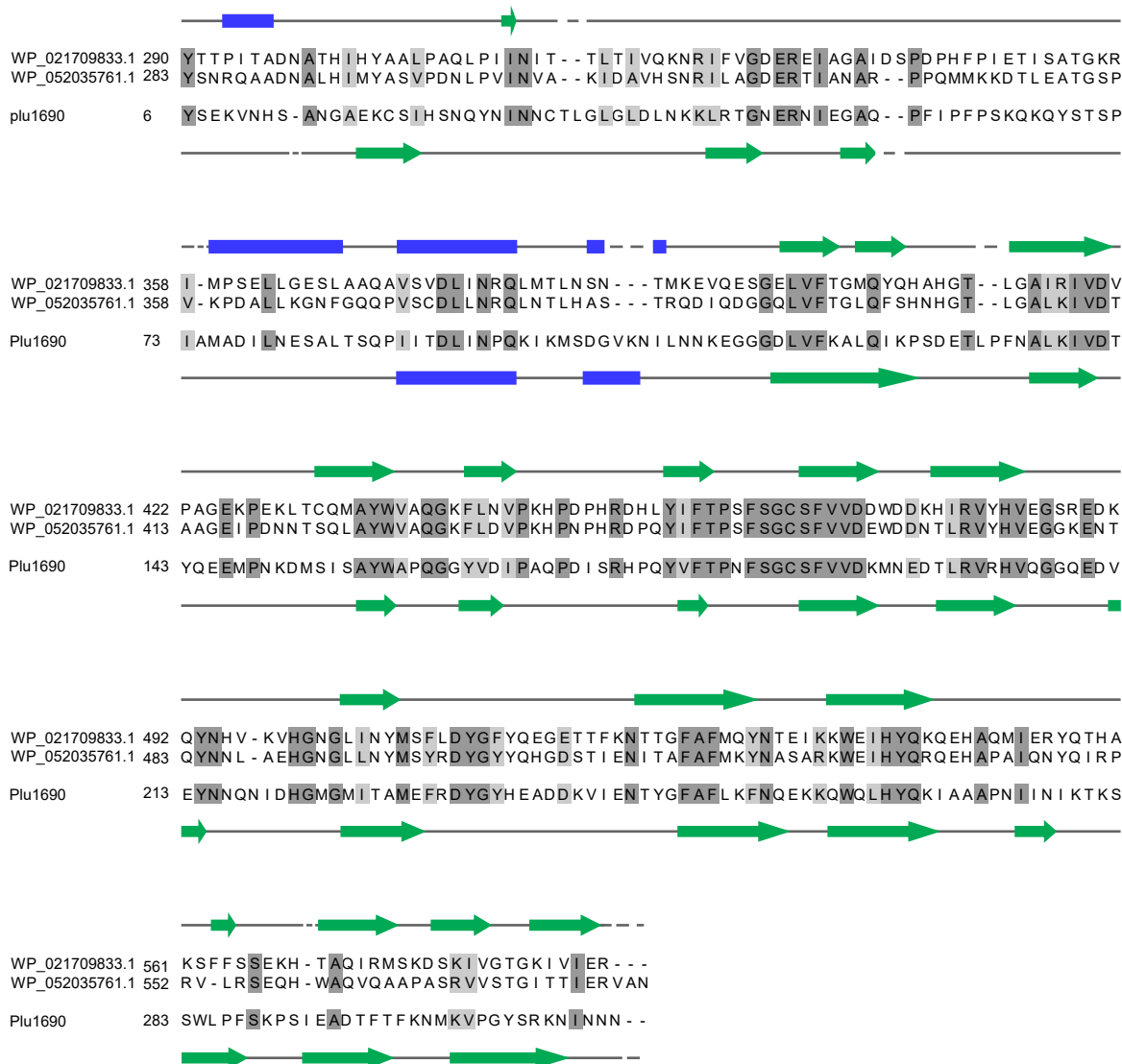


Figure S1. C-terminal domains of predicted virulence MIX-effectors are homologous to other virulence toxins. (a-e) Multiple sequence alignments of predicted virulence MIX-effectors and their homologous toxins with the start positions indicated. MIX-effector C-termini of clusters 27 (a), 55 (b), 53 (c), 38 (d), and 58 (e) are shown above the sequence of the virulence homologs: *Bacillus anthracis* anthrax toxin lethal factor (WP_001022097.1; PDB: 5d1u) (a), *Vibrio cholerae* RtxA toxin cysteine protease domain (NP_231094.1; PDB: 3gcd) (b), *Pseudomonas* M23 family peptidase (WP_003092745.1; PDB: 2hsi) (c), *Chromobacterium amazonense* RtxA (WP_083340985.1) (d), and *Photorhabdus* Plu1690 (CAE13983.1) (e). Catalytic residues of virulence homologs are denoted by an asterisk. Catalytic residues that are conserved in MIX-effectors are in red. Other identical residues are in dark gray, whereas residues that share similar chemical properties are in light gray. The predicted secondary structure (Jpred4) of the MIX-effector sequences are depicted above the alignments, whereas secondary structures of homologous sequences were taken from PDB-deposited structures for (a-c) or predicted (Jpred4). Green arrows represent beta sheets and blue rectangles represent alpha helices. Gaps in sequences are denoted in the secondary structures by dashed lines. Alignments were performed using HHpred (a-c) or Clustal Omega (d-e).