Fig. 3. (Zh. I. Andreeva-Kovalevskaya et al.) a) The 3D structure of human defensin hBD2. The molecule consists of a three-strand β-sheet with its flanking α-helix. The structure is stabilized by three disulfide bonds [44]. b) The structure of a pore-forming domain (domain C) of colicin E1. The pore-forming domain is shown in blue, the hydrophobic hairpin in brown, and α-helix linking domain C with other domains in red [47]. c) Crystal structure of Clostridium perfringens perfringolysin O. Localization of amphiphilic transmembrane β-hairpins TMH1 and TMH2 is shown in pink, three loops of domain four in yellow, undecapeptide in red, amino acid residues Y181 and F318 in green, and β5-α1 in light blue. β-Strands β1 and β4 from domain 3 of the β-sheet core and domains 1 to 4 (D1-D4) [70] are indicated. d) The structure of a water-soluble Escherichia coli HlyE monomer. The tail- and head domains and the N- and C-termini are shown [113]. e) Structures of water-soluble monomeric α-hemolysin and a protomer from the heptameric S. aureus α-hemolysin complex. A conformational change occurring in α-hemolysin during pore formation is presented schematically. The main domains are shown in different colors: the pre-stem and stem domains are green, the rim domain is dark red, and the β-sandwich domain is blue. The amino latch is shown in pink, the triangle in yellow-gray [84]. In all figures, the α-carbon skeleton was drawn using Ribbon graphics.

Fig. 4. (Zh. I. Andreeva-Kovalevskaya et al.) a) Schematic illustration of a conformational change occurring in monomeric Clostridium perfringens perfringolysin O during its transition from the pre-pore to conducting pore state. Main domains D1, D2, D3, D4 and localization of some amino acid residues [73] are indicated. b) Stages (α1-α7) of pore formation by S. aureus α-hemolysin. The water-soluble monomer (α1) binds to the membrane through its rim domain (α1*), which is followed by formation of a pre-pore (α7*) that finally turns into a heptameric pore (α7). The main domains are shown in different colors: the pre-stem and stem domains are green, the rim domain is dark red, the β-sandwich domain is blue, the triangle is gray. For convenience, at the heptameric pre-pore (α7*) and heptameric pore (α7) stages only four protamers are shown.