

**Additional file 1. Characteristics of RTA<sub>DHF</sub> and RTA<sub>IHF</sub>.** (A) Wild-type RTA, RTA<sub>DHF</sub> and RTA<sub>IHF</sub> predicted ribbon models. Models were prepared by Geno3D server [36], proteins were visualized in the PyMOL [64]. The C-terminal hydrophobic region (Val245-Val256) of ricin A-chain in all models is shown in green. (B) Combined fragments of the backbone models of wild-type ricin A-chain (marked in red, hydrophobic region in green), DHF ricin A-chain (marked in turquoise) and IHF ricin A-chain (marked in pink). In the foreground hydrophobic regions are presented, sticks are indicated. (C) Electrostatic surface models for structures presented in (A). Color code is indicated (local PyMOL scale).

