Electronic Supplementary Material (ESI) for Analytical Methods

Supporting information for

Selection, identification and application of a DNA aptamer against *Staphylococcus aureus* enterotoxin A

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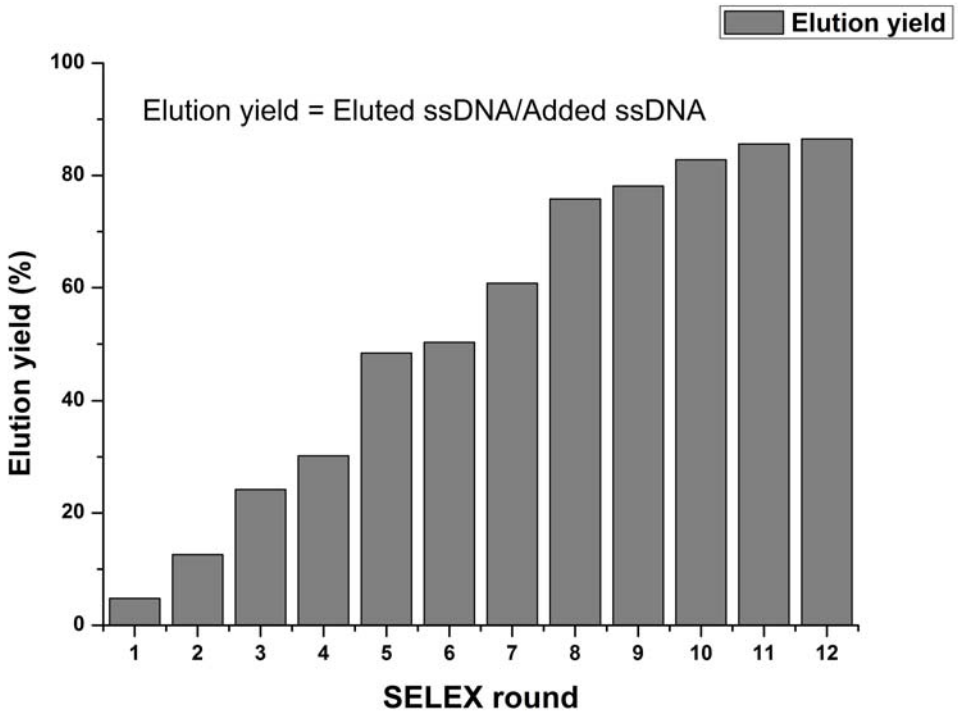

Fig. S1. Monitoring the progression of the selection approach by evaluating the elution yield of each ssDNA pool bound to the target exotoxin. The rounds of 4, 5, 7, 8, 10 and 11 were negative-selection using bare magnetic beads. The rounds of 6, 9 and 12 were counter-selection using SEC1-coated magnetic beads instead.

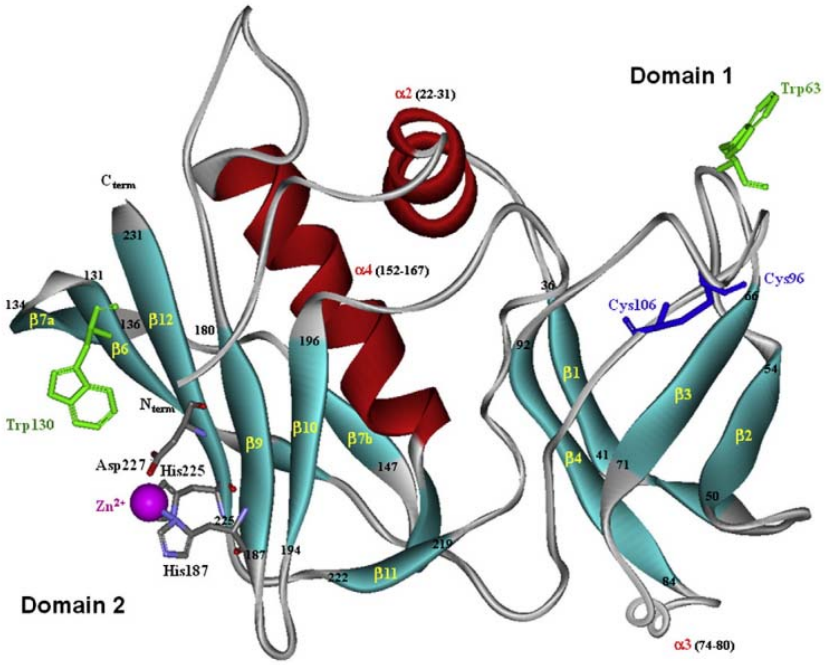

Fig. S2. Ribbon-type representation of the crystal structure of staphylococcal enterotoxin A (code pdb: 1SXT; Schad et al.[1]) drawn using Weblab ViewerPro (version 3.7, Molecular Simulation Inc.). The β-strands and α-helices are drawn in blue (or light grey) and red (or dark grey), respectively. The secondary structural elements along the SEA sequence are indicated. The primary amino acid residues belonging to the Zn^{2+} binding site (His187, His225 and Asp227), the disulfide bridge (Cys96–Cys106) and the tryptophan residues (Trp63 and Trp130) are indicated.

1. l. Z. E.M.Schad, V.N.Zaitsev, *The EMBO Journal*, 1995, **14**, 3292-3301.