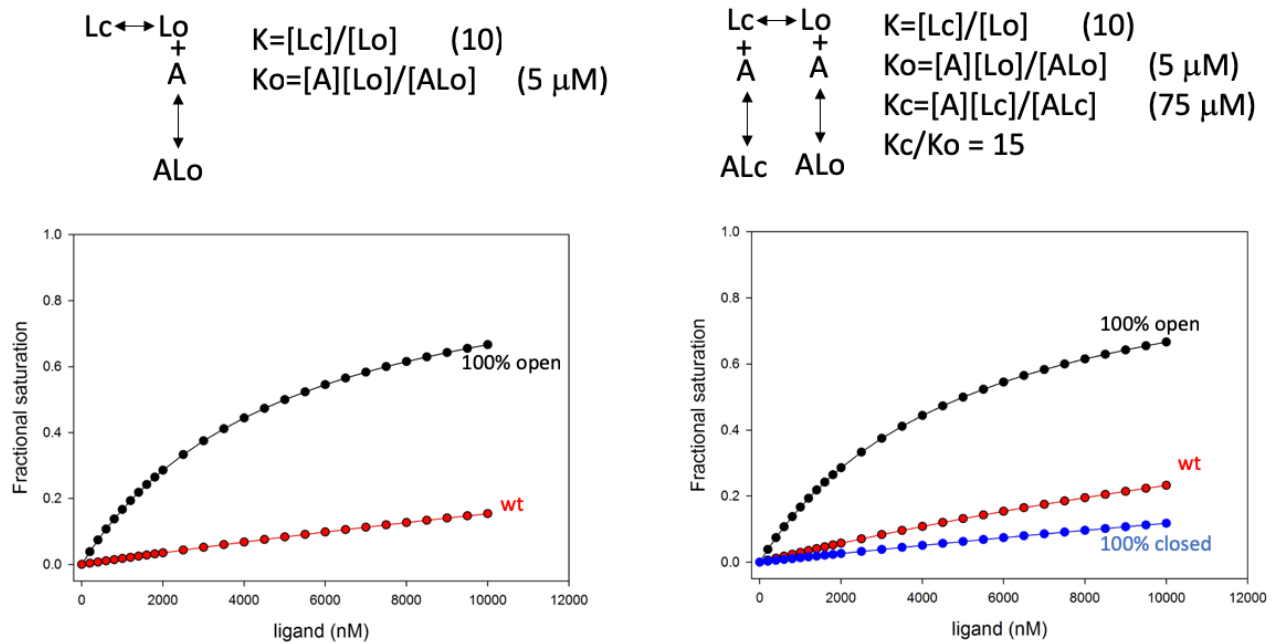


# Discovery and characterization of two novel subpopulations of aPS/PT antibodies in patients at high risk of thrombosis

Mathivanan Chinnaraj<sup>1</sup>, William Planer<sup>1</sup>, Vittorio Pengo<sup>2</sup>, and Nicola Pozzi<sup>1\*</sup>

<sup>1</sup>Edward A. Doisy Department of Biochemistry and Molecular Biology, Saint Louis University School of Medicine, St. Louis, MO 63104, <sup>2</sup>Division of Cardiac, Thoracic, and Vascular Sciences, University of Padova, Padova, Italy.



**Figure S1.** Calculated expected values of competition for proTWT (wt, red), prothrombin 100% closed (blue) and prothrombin 100% open (black). The ligand (L) exists in equilibrium between closed (Lc) and open (Lo) states defined by the isomerization constant K (10-fold bias toward the closed state in proTWT). In scheme 1 (left), the simplest scenario, the antibody (A) interacts with the open form (Lo) to form the reversible complex ALo. This reaction is defined by the dissociation constant Ko. In scheme B (right), a more realistic scenario, the antibody (A) interacts with both closed (Lo) and open (Lo) forms with different dissociation constants, Kc and Ko. Both models are fully consistent with the experimental data in figure 2 supporting a conformational-dependent mechanism of ligand recognition for aPS/PT.