

A computational investigation of folding free energy surfaces and structural characterization of Staphylococcal Protein A

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What is Staphylococcal **Protein A?**

- SpA is a component of the cell wall of **Purification of Monoclonal** the bacteria S. aureus.
- The significance of SpA is its high affinity and exceptional specificity to antibodies IgG.
- SpA has 5 homologous domains that can bind to the Fc fragment of IgG.



AlphaFold Predicted Structure of Full-Length **Protein A**



SpA Binds to the Fc fragment of Antibody



Monoclonal Antibody Targets the Antigen Unique To Or Overexpressed By Tumor Cell





However, we currently lacked a detailed structural and thermodynamic characterization of the full-length protein A.

While well-studied, the ⇔

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Due to its affinity to IgG, **Protein A is utilized in the** Antibodies IgG

Protein A in Affinity Chromatography Purification of Monoclonal Antibodies IgG

individual domains are detailed structural and a thermodynamic characterization of the full-length SpA has been elusive, due to predominant intrinsic disorder between the folded domains.

Therefore, performed we advanced-sampling molecular dynamic simulations of full-length

SpA to investigate the folding free energy surfaces and the behaviors of the flexible regions of SpA.

1. Simulation 1: We run the simulation of the full-length SpA to analyze the behavior of SpA as a whole.

2. Simulation 2: We restrained the folded domains for the duration of simulation to observe the behavior of the flexible regions.









Fig 5. Radius of gyration and E2E of SpA in Simulation 2