Structure and Formation of Antigen-Antibody Complexes

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Immunoglobulin G

- Type of antibody found in human circulation
- Protects body from infection by targeting and binding to antigens
- Different subclasses
  - IgG1, IgG2, IgG3, IgG4
  - Differ in number of disulfide bonds

Streptavidin

- A protein produced by the bacterium Streptomyces avidinii
- Tetrameric
- Extremely high affinity for biotin
Motivation

• Structure of antigen-antibody complexes is important for understanding how they form and their effect in the immune system
  ▪ Goal: to analyze how two subclasses of immunoglobulin G, IgG1 and IgG2, interact with the protein streptavidin and determine the structure of complexes

• A software framework developed at the NCNR lacks experimental data for its docking module
  ▪ Goal: to provide substantial data & results to improve functionality
Size-exclusion chromatography with multiangle light scattering (SEC-MALS)

- Varying concentration ratios, pH to evaluate best conditions for complex formation
- Series of buffer exchanges
Obtain a “pure and monodisperse” complex

Concentration Ratio .50 (strep:IgG1)  Concentration Ratio 5.0 (strep:IgG2)

pH 6.5 buffer
Streptavidin-IgG1 Complex Samples

Streptavidin-IgG2 Complex Samples

pH 6.5 buffer
Effects of Different pH

Aggregation occurs in pH 3.0 buffer
Conclusions from SEC-MALS

- Higher percentage of complex forms in a buffer with a more neutral pH
- 1.0 and 2.0 concentration ratios (strep:IgG) yield most complex
- Aggregation of IgG2 occurs in a more acidic environment
SAXS Profile

- Larger molecules scatter more at low intensity ($q$)
- Complex with 1:1 concentration ratio scatters more than 2:1 complex
Future Work

Performing more small-angle scattering

Testing SASSIE Docking Module

- Software framework designed to create atomistic models of molecular systems and to compare small-angle scattering data from these models directly to experimental data
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