

# Structure and Formation of Antigen-Antibody Complexes

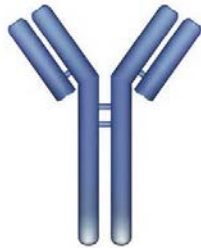
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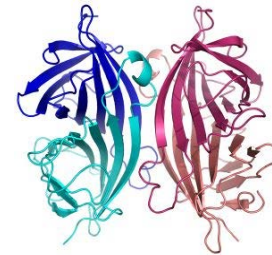
## Immunoglobulin G

- 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

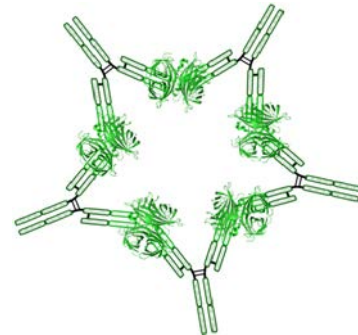
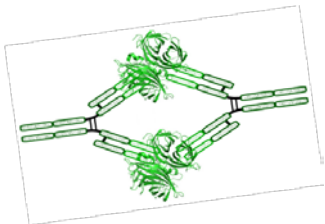
- A protein produced by the bacterium *Streptomyces avidinii*
- Tetrameric
- Extremely high affinity for biotin





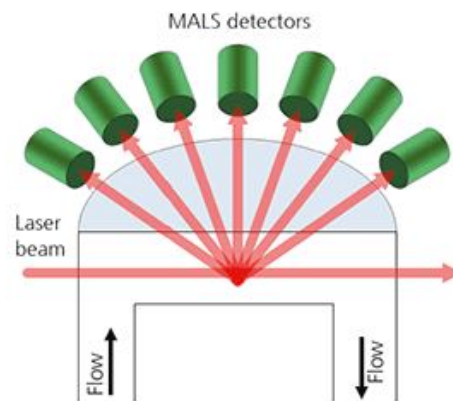
# Motivation

- 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)

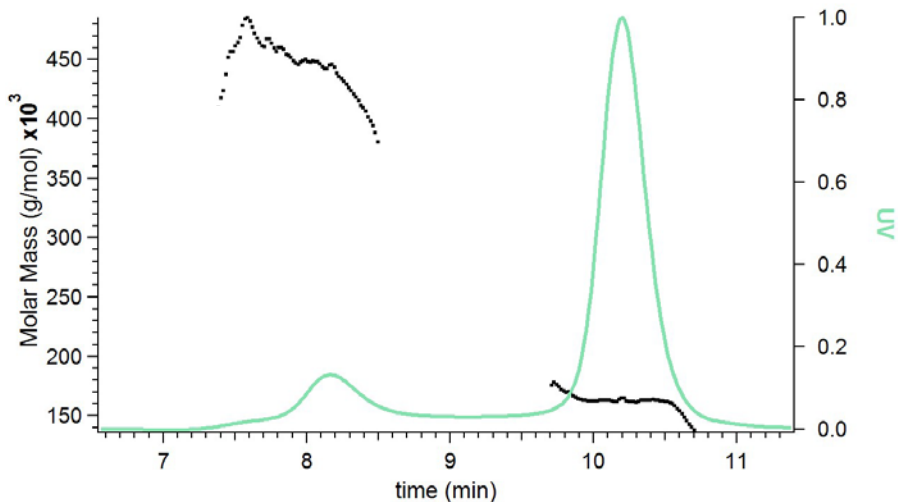
- Varying concentration ratios, pH to evaluate best conditions for complex formation
- Series of buffer exchanges





# Obtain a “pure and monodisperse” complex

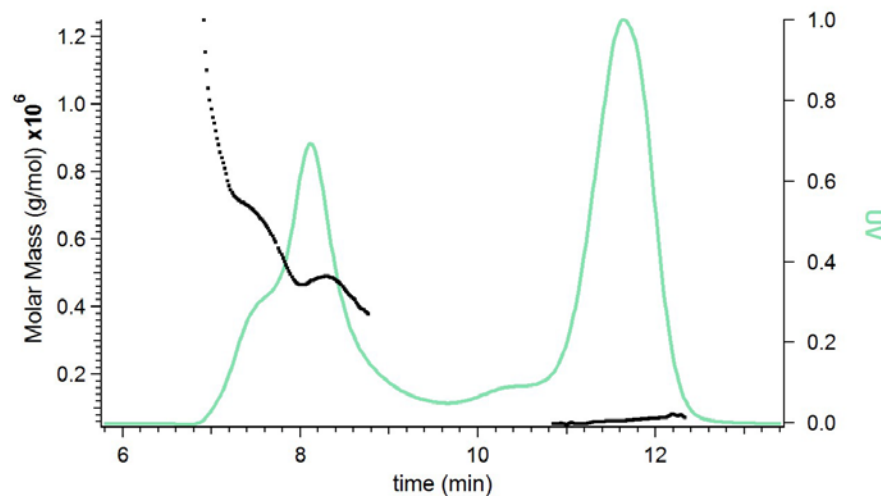
### Results Fitting



Concentration Ratio .50 (strep:IgG1)

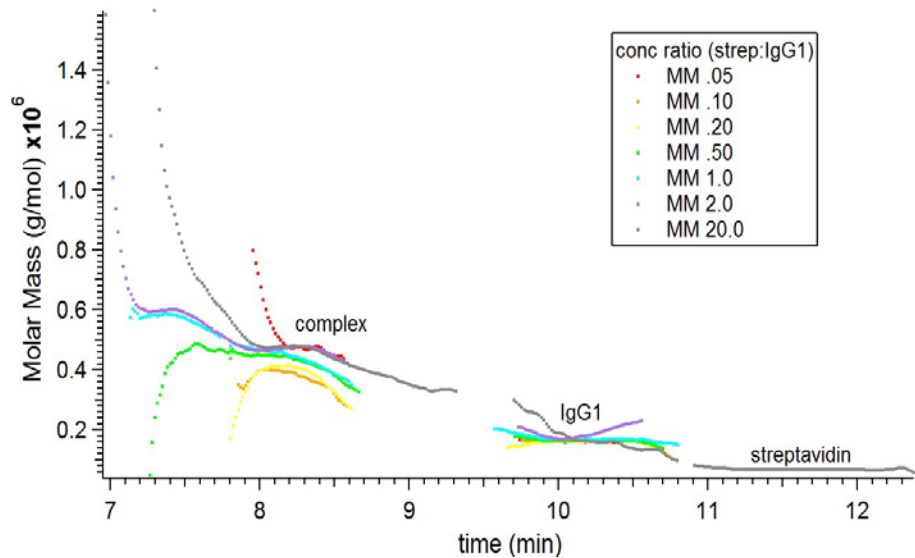
pH 6.5 buffer

### Results Fitting

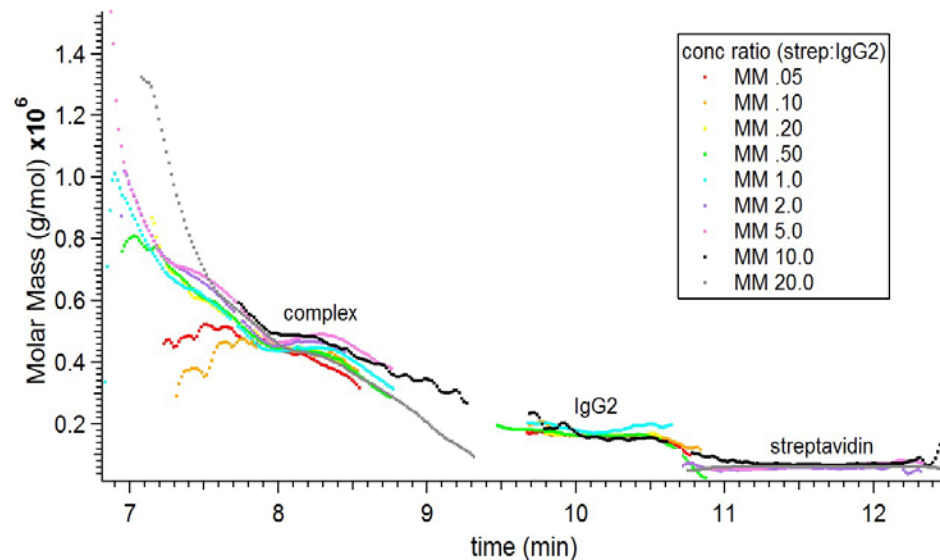


Concentration Ratio 5.0 (strep:IgG2)

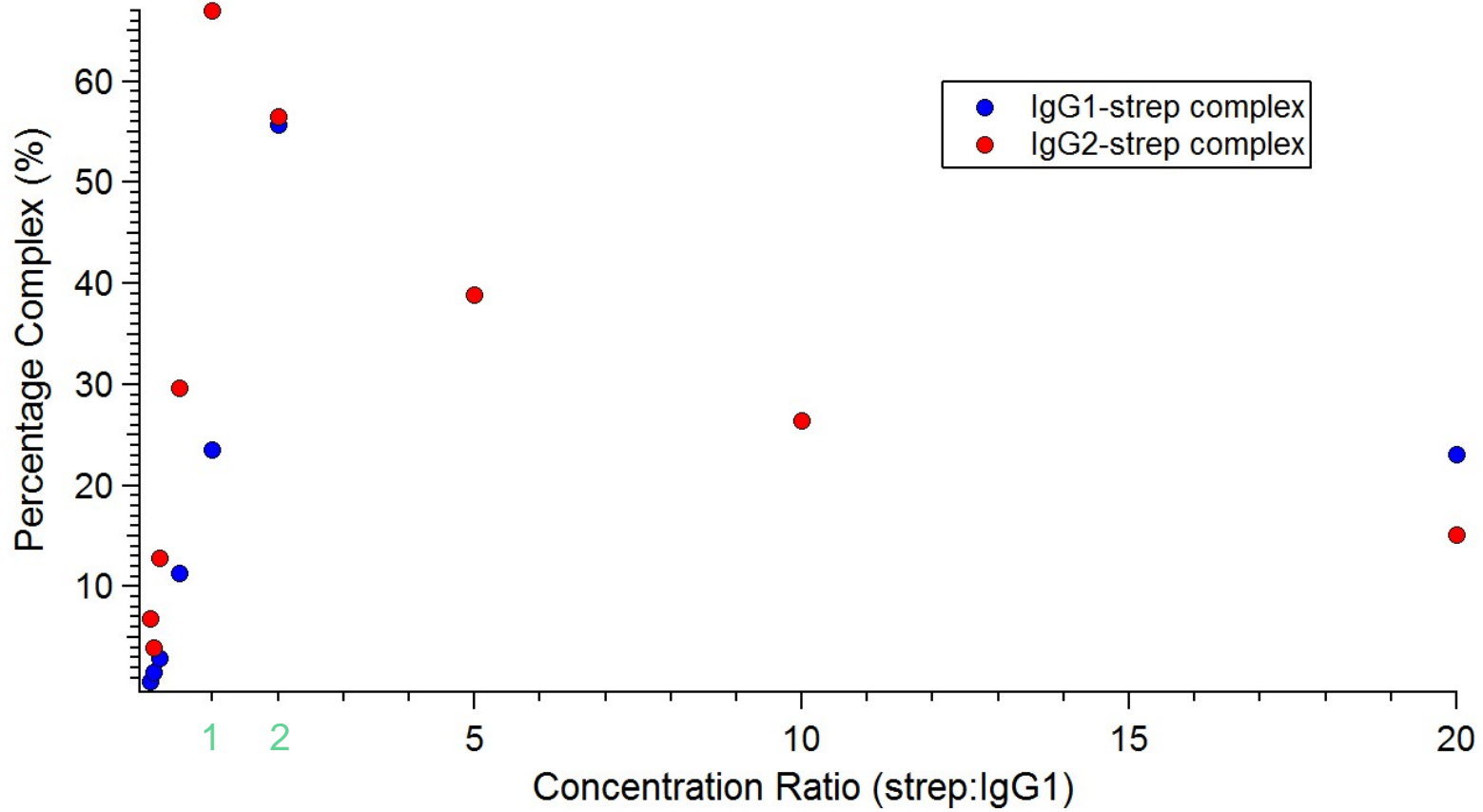
## Streptavidin-IgG1 Complex Samples



## Streptavidin-IgG2 Complex Samples



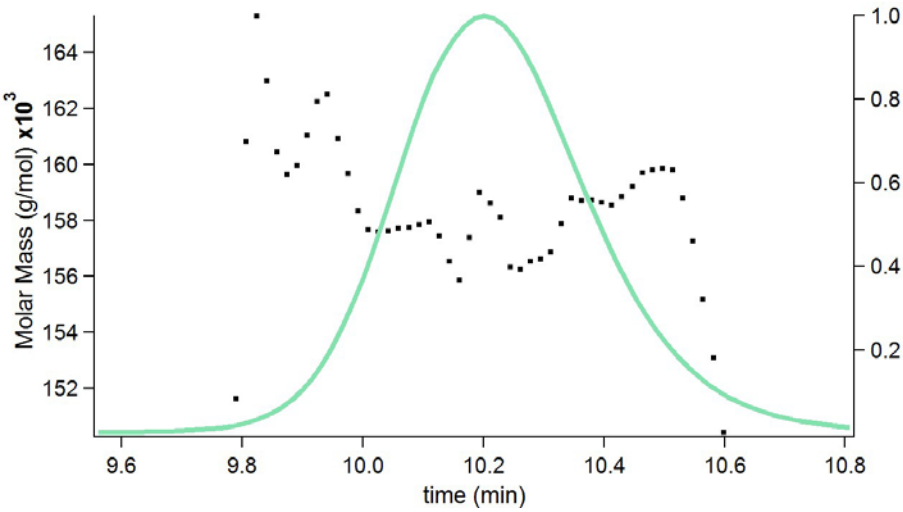
pH 6.5 buffer





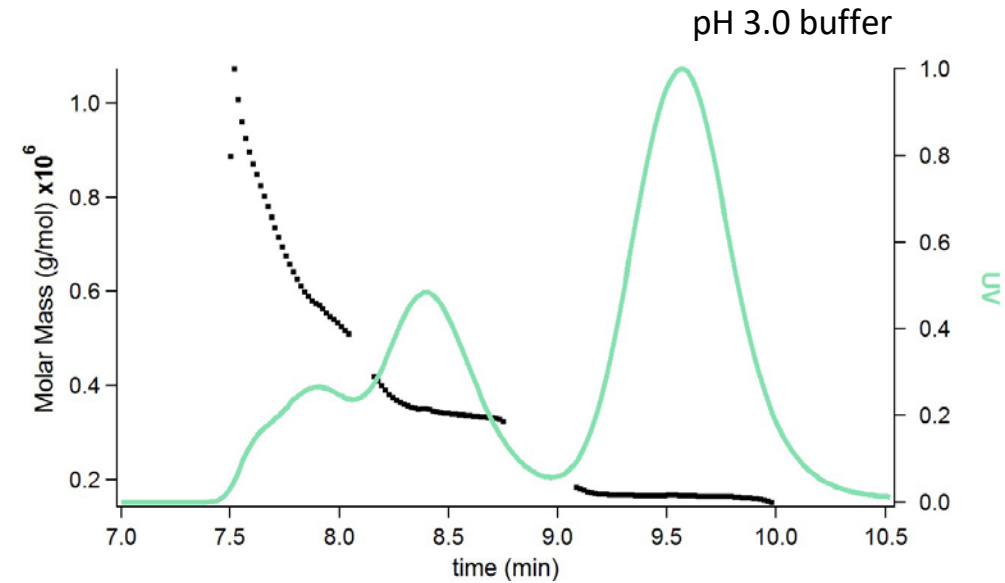
# Effects of Different pH

pH 6.5 buffer



Aggregation occurs  
in pH 3.0 buffer

IgG2 Individual Sample

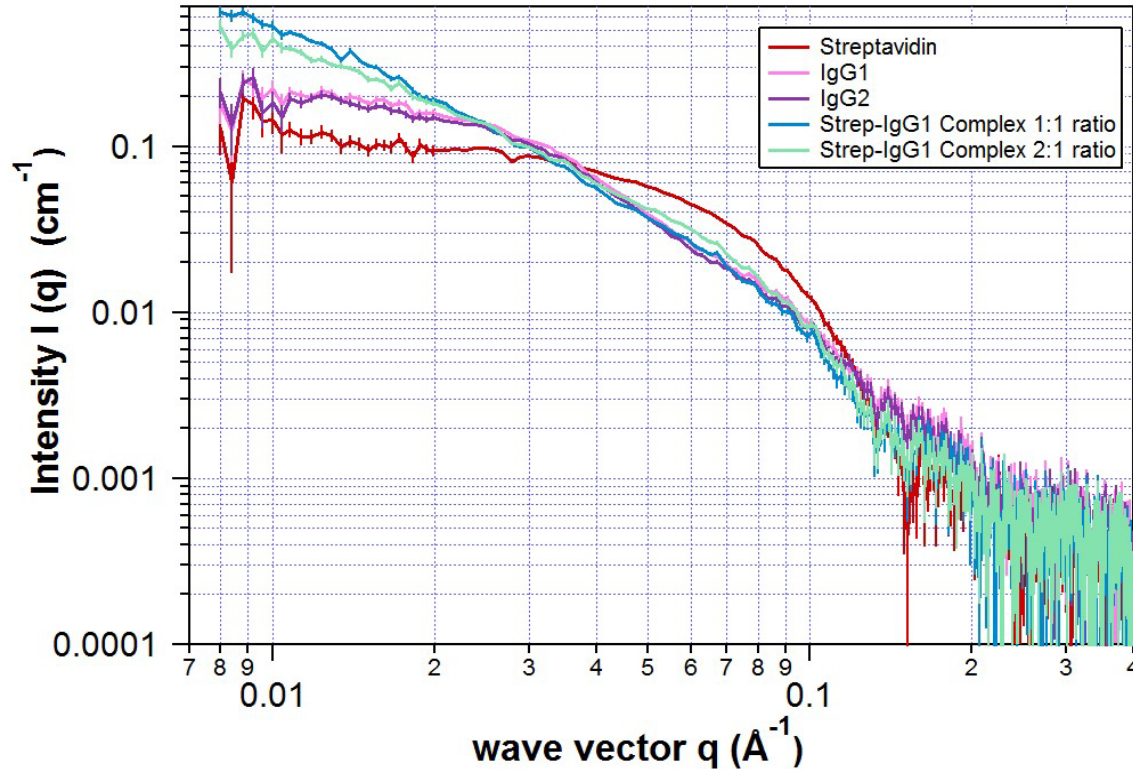




# Conclusions from SEC-MALS

- 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



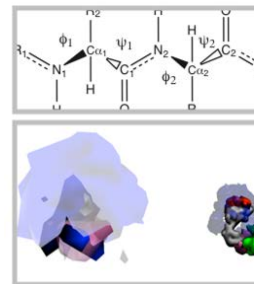
# Future Work

Performing more small-angle scattering

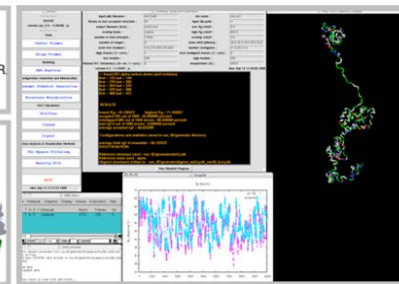
Testing SASSIE Docking Module

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

SASSIE



NCNR



# Acknowledgements

- Monica Castellanos
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