

Spatial-Charge-Map (SCM): A High-Throughput Method for Antibody Screening Based on their Viscosity

Technology #15981

Applications

This technology is a computer program that predicts the viscosity of antibody solutions with applications in biologic drug development.

Problem Addressed

Antibodies are the most common class of biologic drugs, but they have very high R&D costs. Antibody drugs require highly concentrated formulations, which can result in highly viscous solutions that are challenging to handle both in manufacturing processes and in end user injections. Currently, it is difficult to predict antibody viscosity. These challenges are only discovered late in drug development after there has been significant R&D investment. This invention is a new way of predicting antibody viscosity early in the drug development process, which will allow pharmaceutical companies to save R&D money by prioritizing low viscosity antibody candidates.

Technology

This technology uses a high-throughput computer model to predict the viscosity of concentrated antibody solutions. The computer model, called special charge map (SCM), uses electrostatics-based modeling to predict the strength of the antibody-antibody interactions that lead to viscous solutions. The SCM program predicts the 3D structures of the Fv antibody domain, calculates the partial charge of each exposed atom in the structure, then generates an SCM score of the resulting Fv domain. As a proof of principle, the inventors demonstrated that high SCM scores correlated with high viscosity in antibody formulations from three major pharmaceutical companies. The SCM computer program could be used to eliminate highly viscous candidates early in the R&D process, or could be used to rationally engineer less-viscous versions of established antibody therapeutics.

Advantages

- Quantitative, high-throughput prediction of antibody viscosity
- Saves R&D money by eliminating highly viscous candidates early in development
- Facilitates rational engineering of less-viscous versions of established antibody drugs

Intellectual Property

IP Type: Granted US Patent

IP Title: Computer-implemented methods of determining protein viscosity

IP Number: 10,762,980

Categories For This Invention:

Computer Sciences & Information Technology

Simulation & Modeling

Life Sciences

Clinical Applications

Research Tools

Antibody (Research Tools)

Protein & Protein Chemistry

Therapeutics

Antibody (Therapeutics)

Protein

Inventors:

Bernhardt Trout

Bernhard Helk

Neeraj Agrawal

Publications:

Computational Tool for the Early Screening of Monoclonal Antibodies for their Viscosities

MABs

October 15, 2015. 8(1)

External Links:

Trout Research Group

<http://troutgroup.mit.edu/>