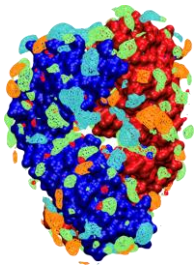
SILCSBIO

SilcsBio offers software and services to unlock the full potential of computer-aided drug design. New developments enable a leading-edge approach to analyze protein-excipient/buffer and protein-protein interactions at an atomic level and give insight on excipient formulation for biologic therapeutics including antibodies and other proteins.

The Problem

The formulation of biologics has become a major bottleneck in bringing these novel therapies to market. Biologics are formulated to maintain their activity during long-term storage and subsequent administration. Maintaining their 3D conformations and preventing protein aggregation is an important challenge in their development. Experiments to identify the optimal combinations of excipients, buffers, and surfactants are low throughput and require high concentrations of protein – which is limited and costly. Failure to determine the optimal formulation results in decreased product performance; impacting patient treatment and in some cases requiring the costly re-engineering of the therapeutic protein.



FragMaps on CNTO607 mAb variable domain

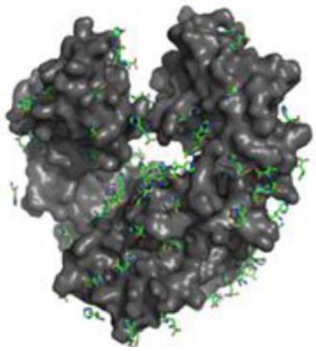
SilcsBio Innovation

SilcsBio is developing a novel **formulation design technology in silico** to inform the selection of desired excipient/buffer combinations. With the help of the established SILCS platform, SilcsBio's technology **3D maps the protein of interest (FragMap) and its functional group affinity pattern,** providing data to enhance stability and prevent aggregation.

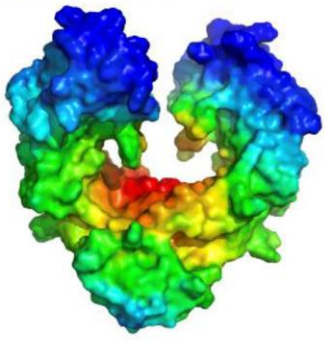
Benefits

- The SILCS technology allows **screening of 100's** of excipients and buffers as well as protein-protein interaction (PPI) **within a day**, minimizing the need for experimental screening.
- Rational selection of excipient/buffer combinations in silico guided by SilcsBio's approach will **lower costs and timelines** in developing novel biologics
- improved formulations to **better maintain the stability** of biologics during storage and delivery.

PPI and excipient binding data are combined to score various excipients



Excipient docking to FragMaps binding site prediction



Protein-protein docking for PPI prediction

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MORE INFO

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Yu, W, Jo, S, Lakkaraju, SK, Weber, DJ, MacKerell, AD. Proteins. 2019; 87: 289 -301. https://doi.org/10.1002/prot.25650