
<table>
<thead>
<tr>
<th>Title</th>
<th>Computational Characterization of Antibody-Excipient Interactions for Rational Excipient Selection Using the Site Identification by Ligand Competitive Saturation-Biologics Approach.</th>
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<td>Jo, S, Xu, A, Curtis, JE, Somani, S, Mackerell, AD</td>
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<tr>
<td>Abstract</td>
<td>Protein therapeutics typically require a concentrated protein formulation, leading to self-association and/or high thermal stability. The SILCS-Biologics approach offers a computational framework to understand these interactions, thereby guiding the rational design of excipients for optimal biologics formulation.</td>
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