

Biophysical characterization of excipient combinations for mAb formulation development

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- Need for and problems with Subcutaneous biologic administration
- Comera SQore™ platform technology
- Identifying and characterizing excipients
 - Computational screening
- New stabilizing excipients
 - Experimental validation
- Case studies on formulation development of mAb A
 - Formulation Buffer screening
 - Viscosity and stability optimization
 - DOE for formulation optimization
- Conclusions

Conversion of IV to SQ Administration



IV

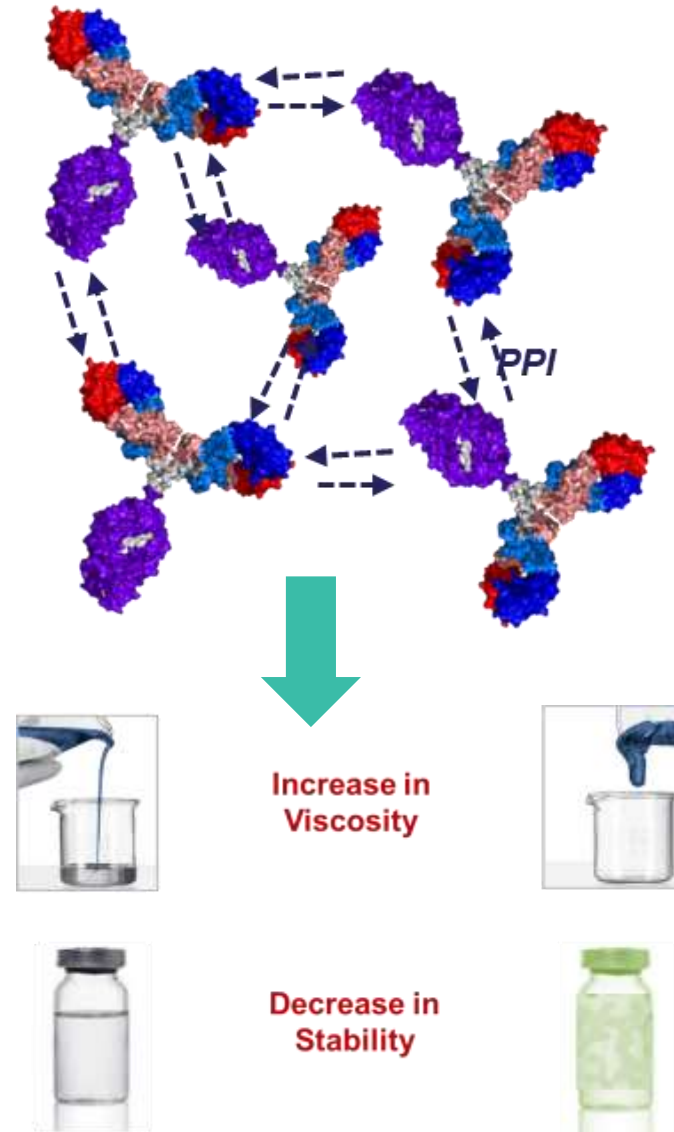
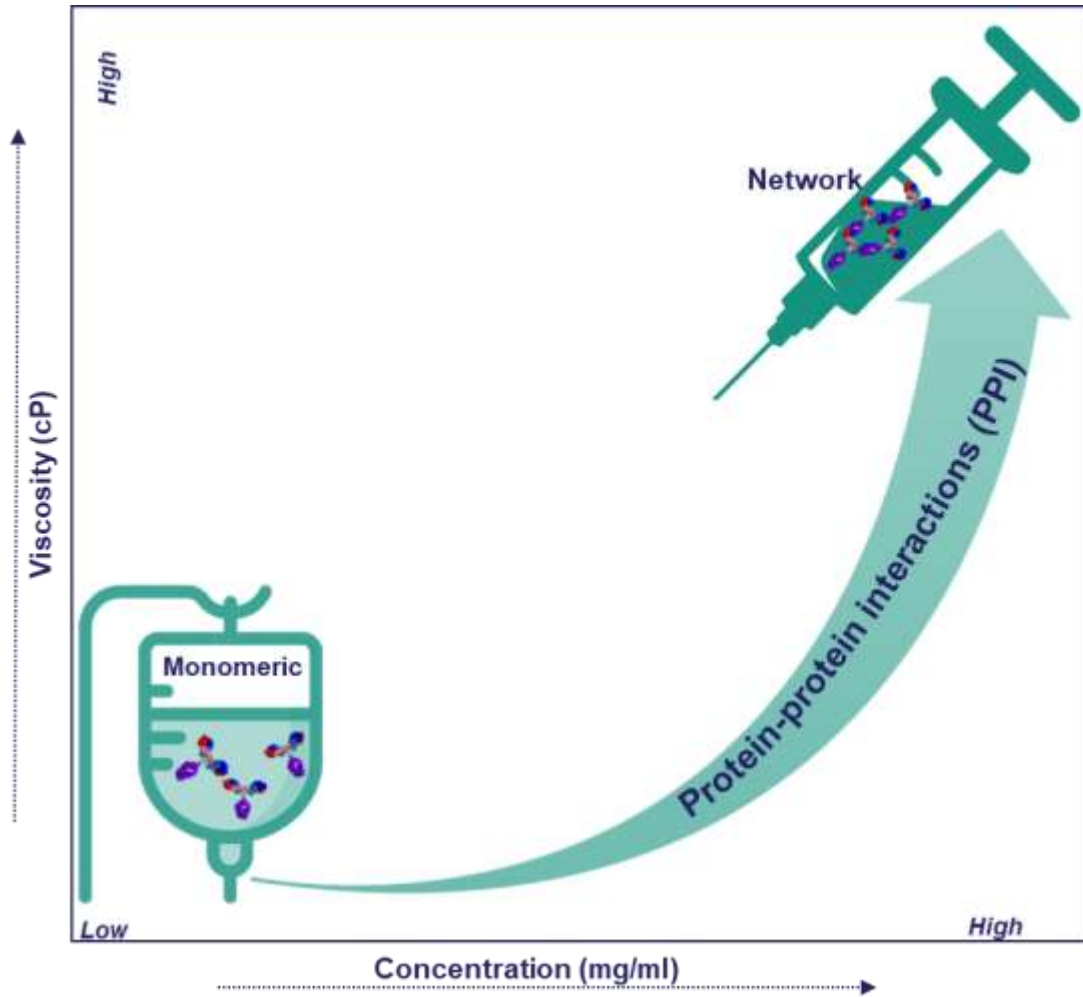
- Pain and discomfort
- Time commitment
- Risk of infection
- Reduced compliance
- Space and nursing time requirements
- Increased costs



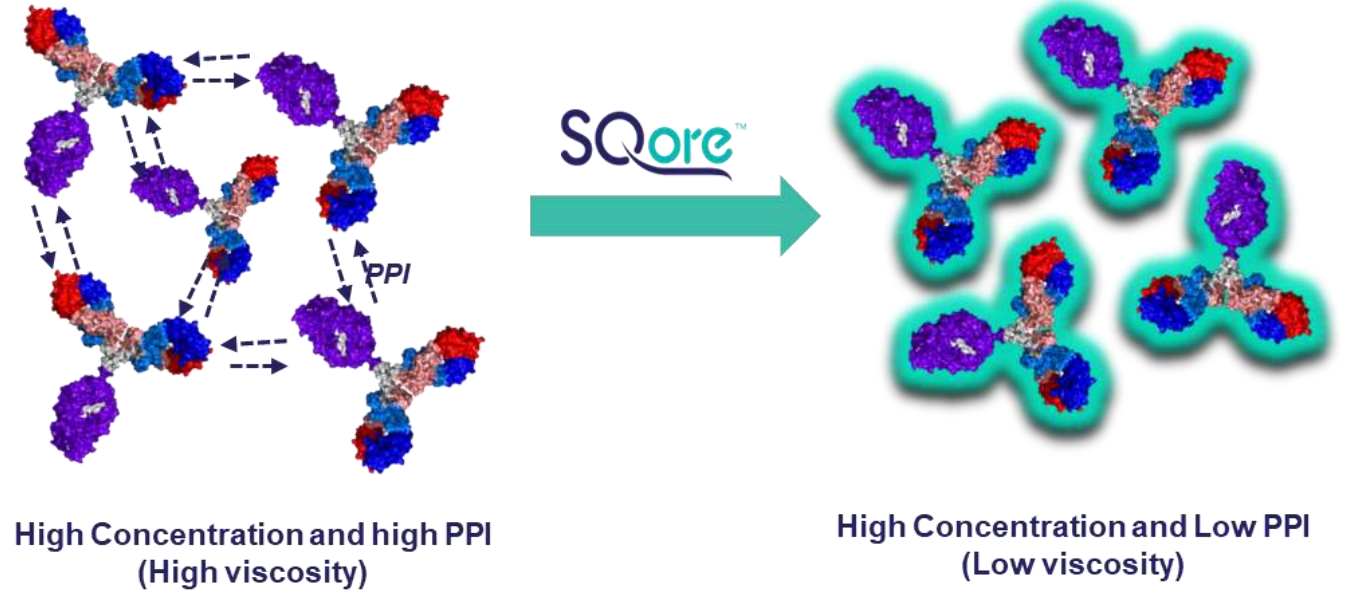
SQ

- Less pain, less time
- Reduced risk of infection
- Potential self-administration
- Higher patient satisfaction
- Improved quality of life
- Reduced cost

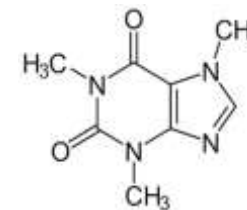
Developing SubQ mAb formulations is challenging



SQore platform helps in IV to SQ Conversion

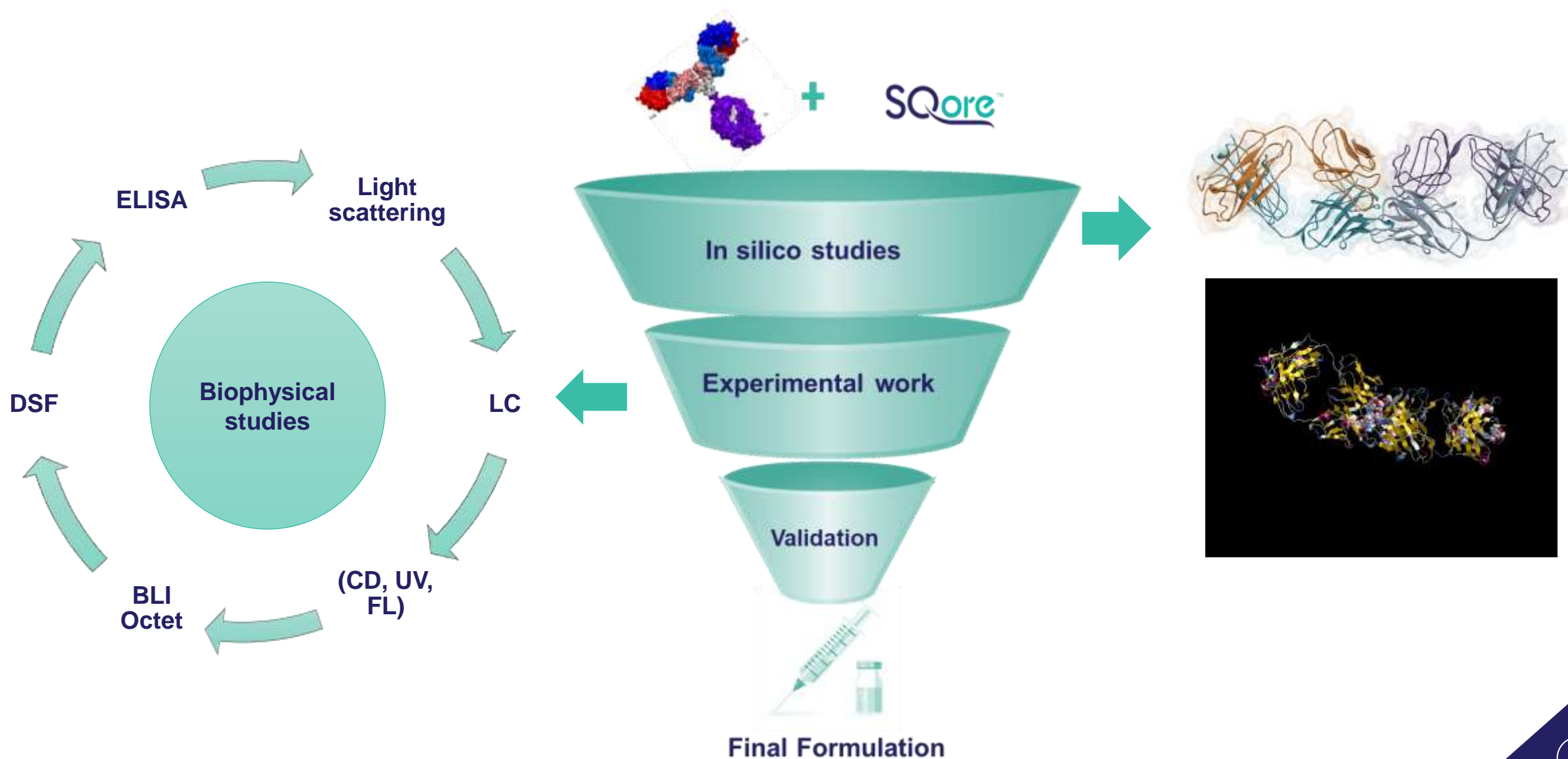


- SQore excipients
 - Viscosity reducers
 - Stabilizers
- They are known chemical structures
- They have well established toxicology profiles



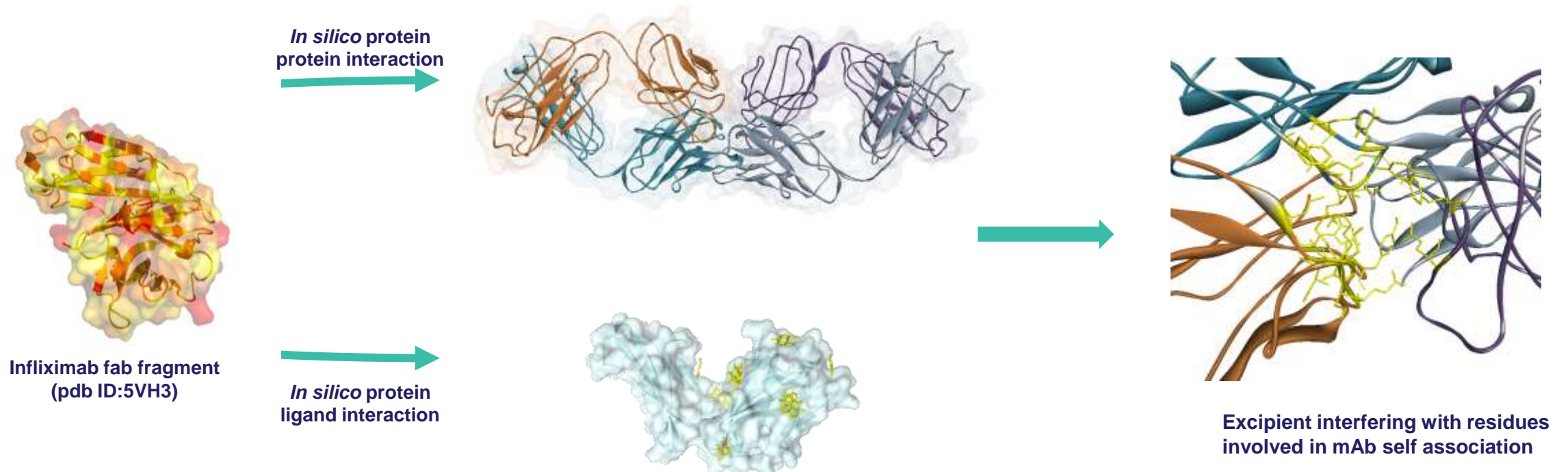
Caffeine (1,3,7-trimethylxanthine)
CAS # [58-08-2]
MW 194.19 g/mol

Developing subQ mAb formulations using SQore platform



Computational studies to identify viscosity hotspots.

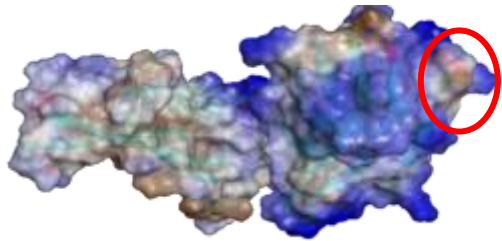
- Protein-protein and protein-excipient blind docking helps identify interaction hotspots and the residues involved.
- Results overlaid with the protein ligand docking to identify excipient binding sites, interfering with mAb self association



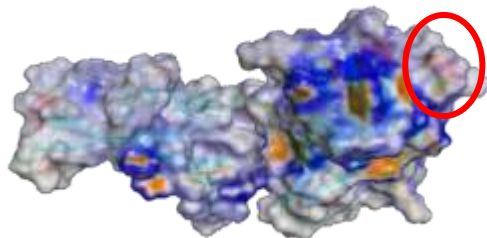
Identifying screening sites and desired pharmacophores

- Computational studies allows
 1. Identifying self interaction hotspots in mAbs
 2. Identifying excipients that decrease self association
 3. Identify excipients that can stabilize the mAb

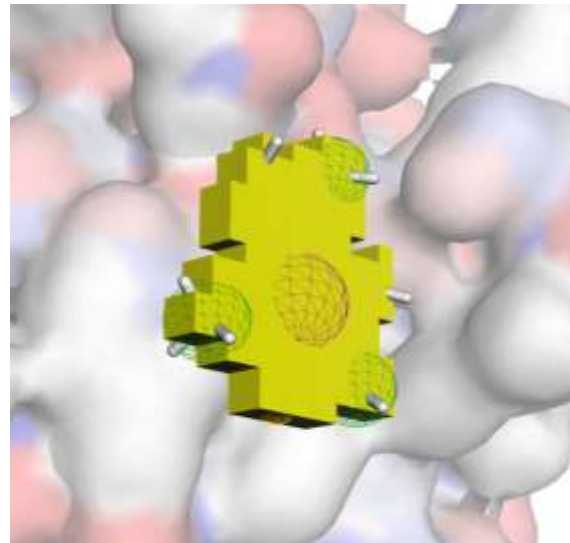
Surface Hydrophobicity



Surface charge



Identifying sites involved with Self interaction



Identify single interaction site and Screen SCore library within the pocket

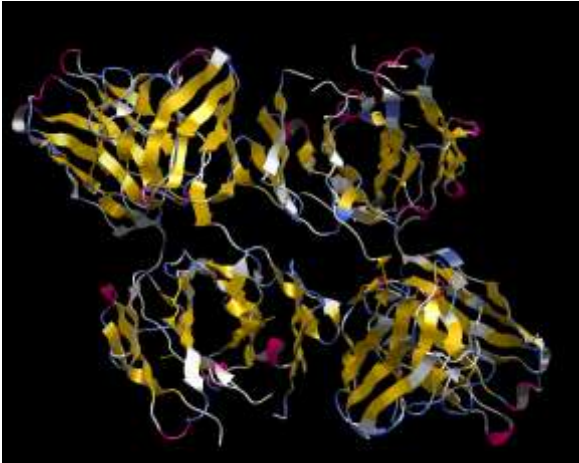


Name	RMSE	Mass	RBinds
MoPort-002-964-480	0.450	364	0
MoPort-039-455-121	0.611	365	2
MoPort-039-455-121	0.613	365	2
MoPort-001-771-998	0.756	374	4
MoPort-001-771-998	0.756	374	4
MoPort-001-771-998	0.766	374	4
MoPort-001-771-998	0.766	374	4
MoPort-001-771-998	0.766	374	4
MoPort-001-771-998	0.766	374	4
MoPort-001-771-998	0.766	374	4
MoPort-001-771-998	0.766	374	4
MoPort-001-771-998	0.766	374	4
MoPort-020-138-470	0.720	376	5
MoPort-046-504-615	0.710	386	5
MoPort-007-857-242	0.739	342	5
MoPort-002-857-242	0.739	342	5
MoPort-002-857-242	0.739	342	5
MoPort-002-857-242	0.739	342	5
MoPort-039-230-797	0.603	343	3
MoPort-039-230-797	0.605	343	3
MoPort-039-230-797	0.609	343	3

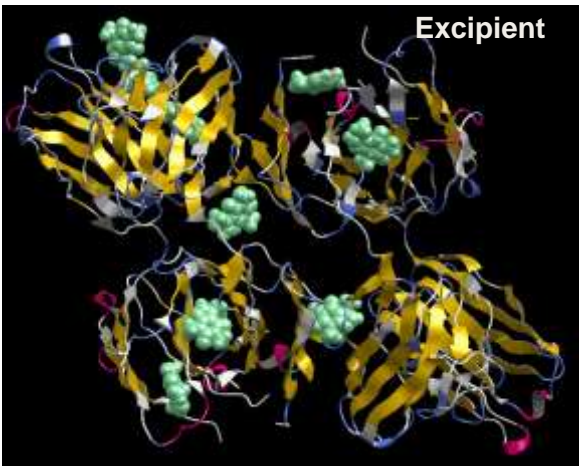
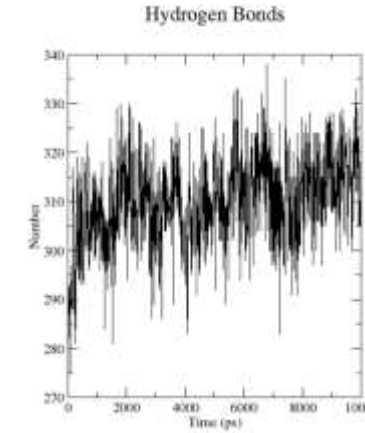
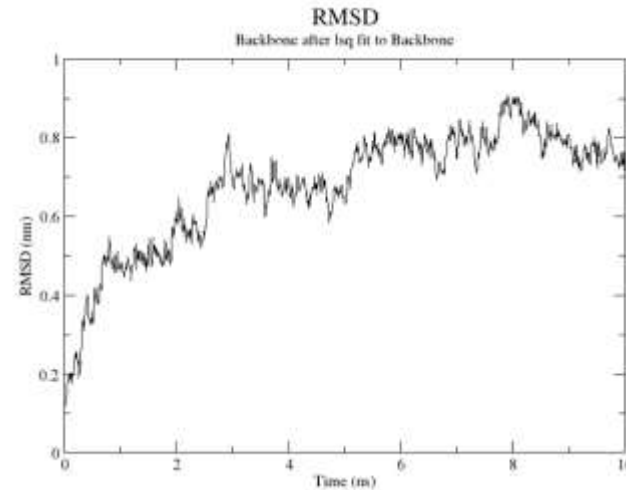
Ranked screening results

MD simulation data of protein excipient interaction

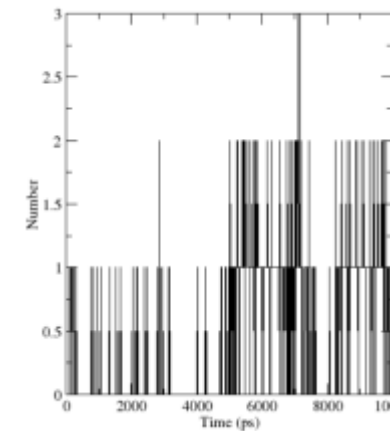
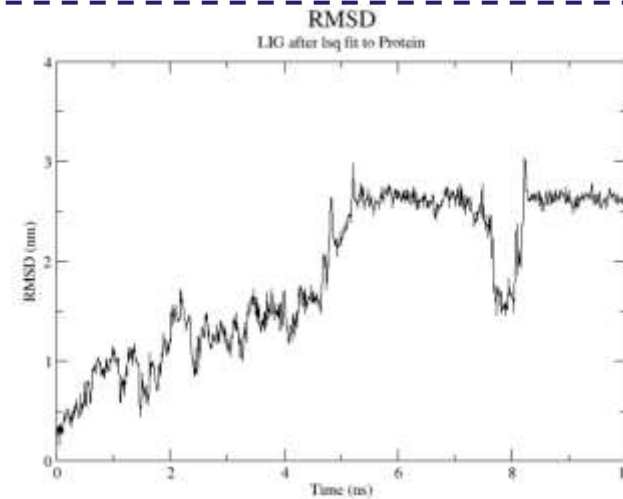
10 ns time scale



Protein →



Ligand →

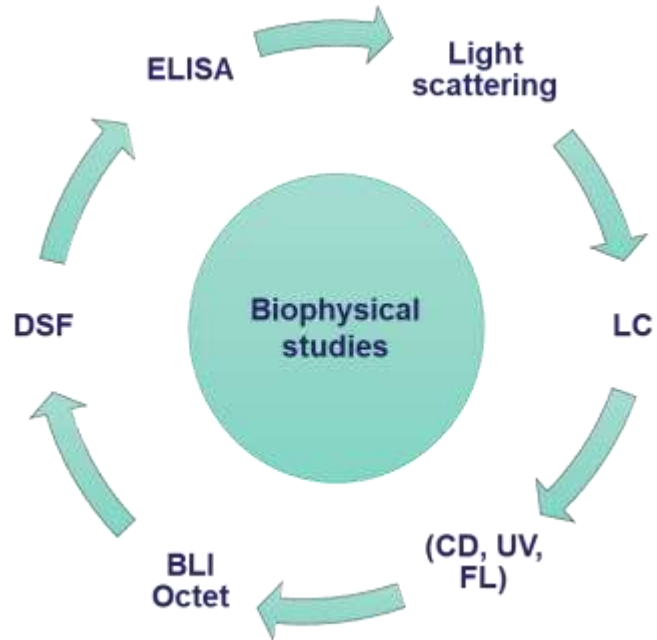


Simulation data allows to identify regions

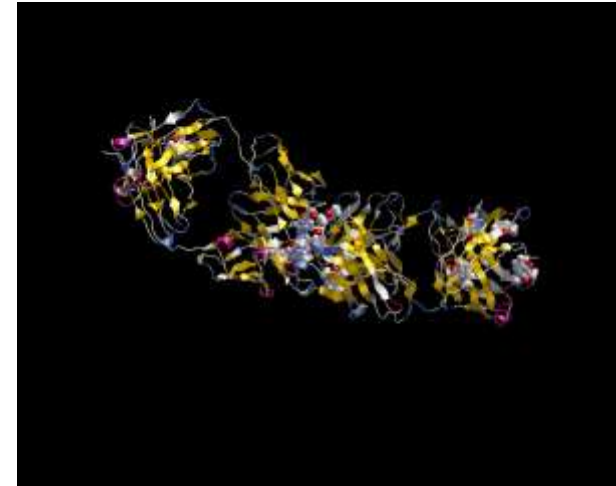
1. Where the excipient binds
2. How the excipient binds
3. Strength of binding
4. Interaction time
5. Residues it can interact with

MD Simulation gives a better predictive power and more reliable analysis of protein-ligand dynamics and improve screening results

Screening and MD simulation with Mab A

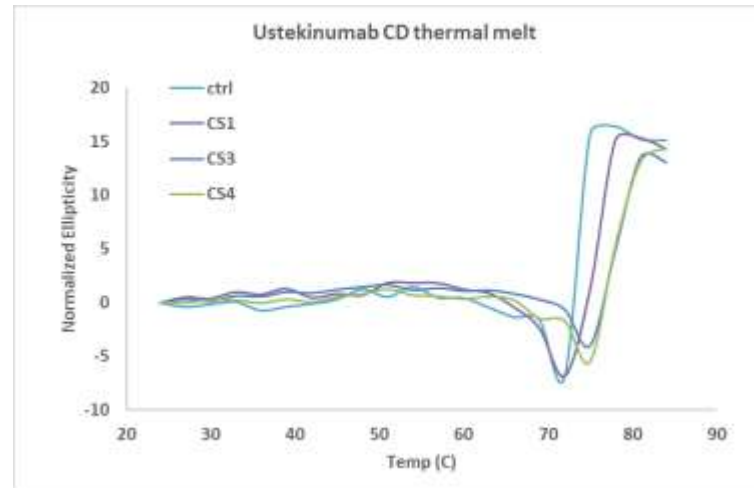
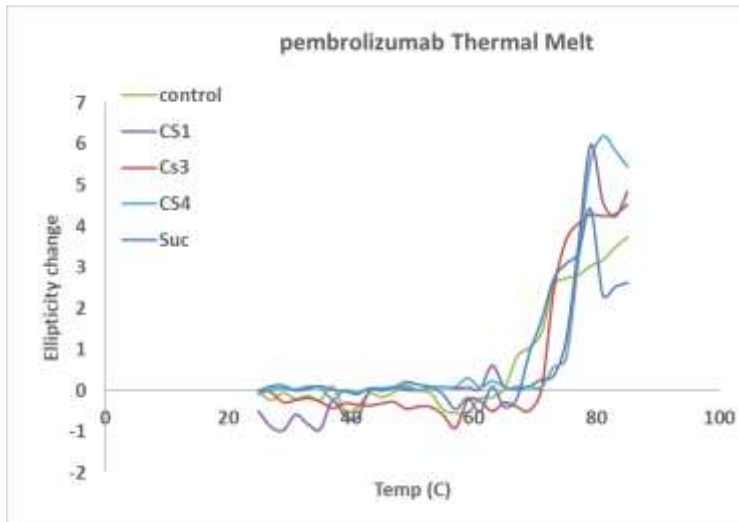
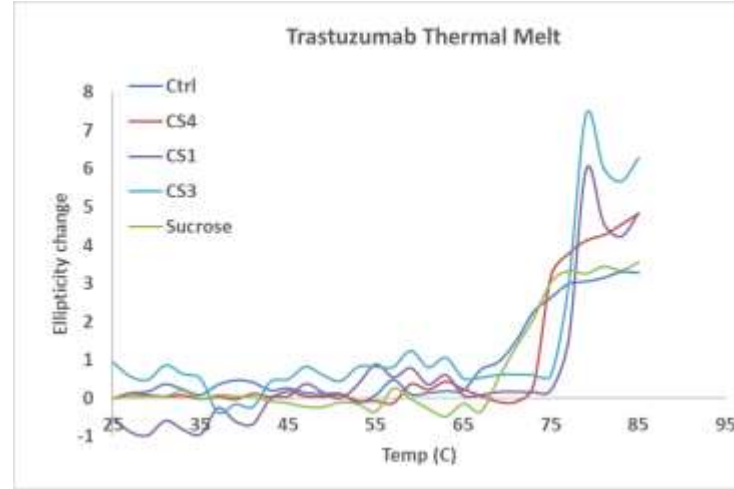
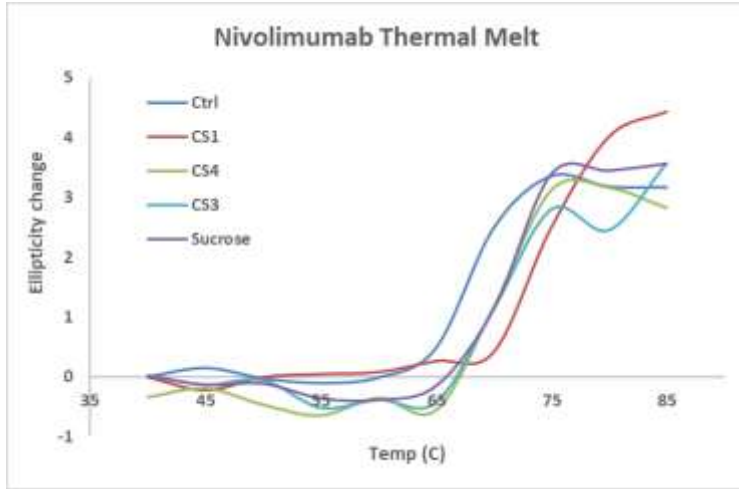


Computational



Excipients	FDA Inactive Ingredient	USP / GMP	Prior injectable use	GRAS
CS1	Yes	Yes	Yes	Yes
CS2	No	Yes	No	Yes
CS3	No	Yes	No	Yes
CS4	Yes	Yes	No	Yes
CS5	Yes	Yes	Yes	Yes

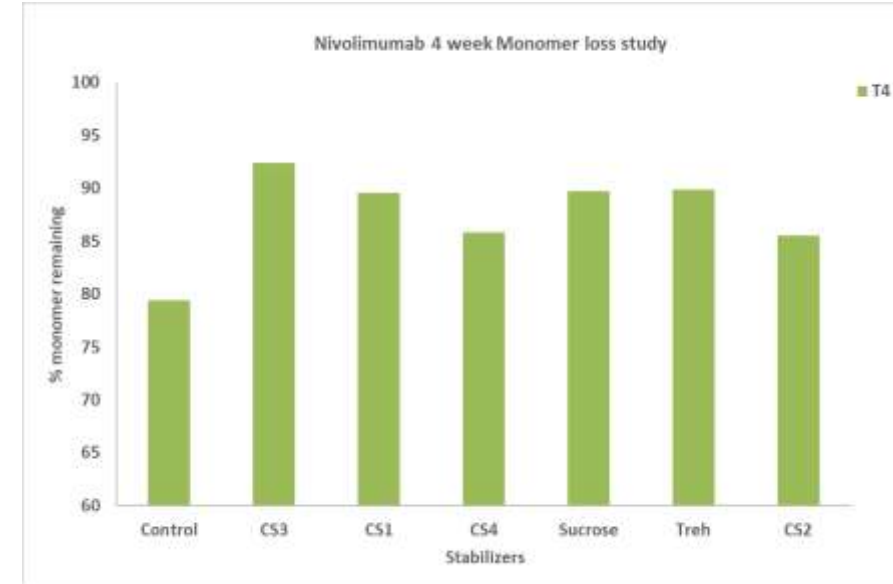
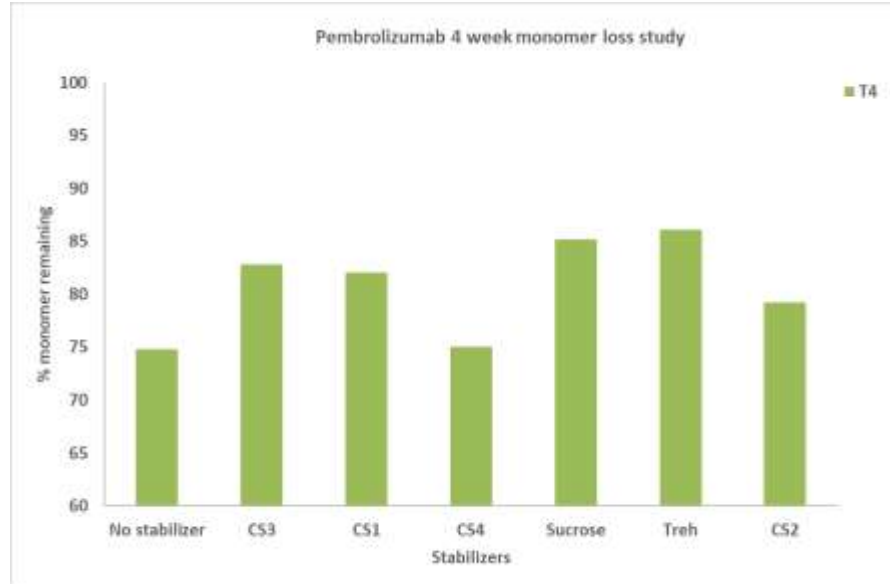
Effect of stabilizers on mAb thermal stability



- Stabilizers validated with CD thermal melt
- mAb conc: 0.2 mg/ml mAb
- Stabilizer conc: 20 mM
- Temp ramp 1C/ min

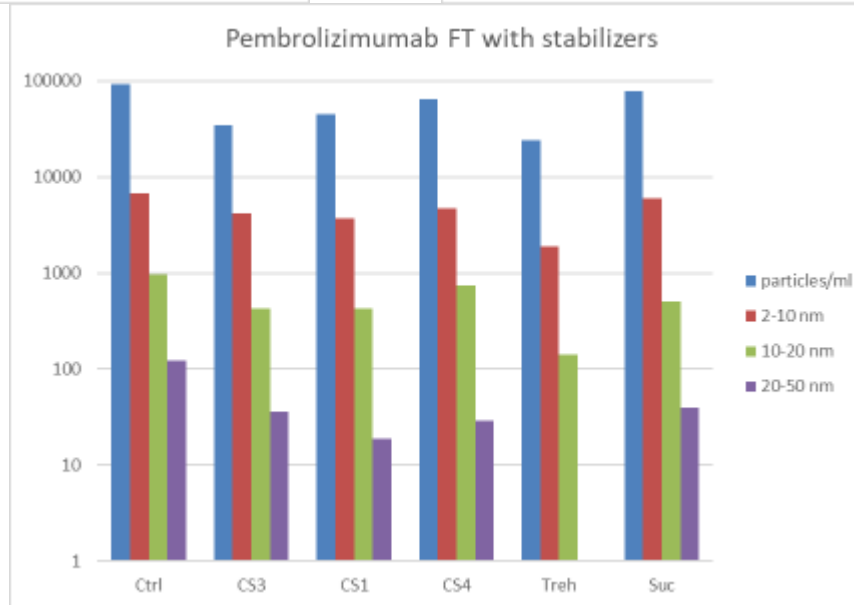
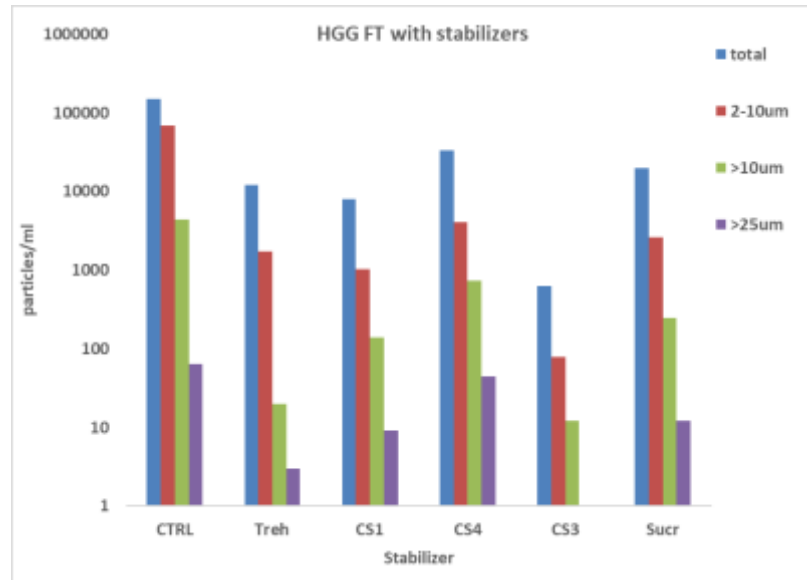
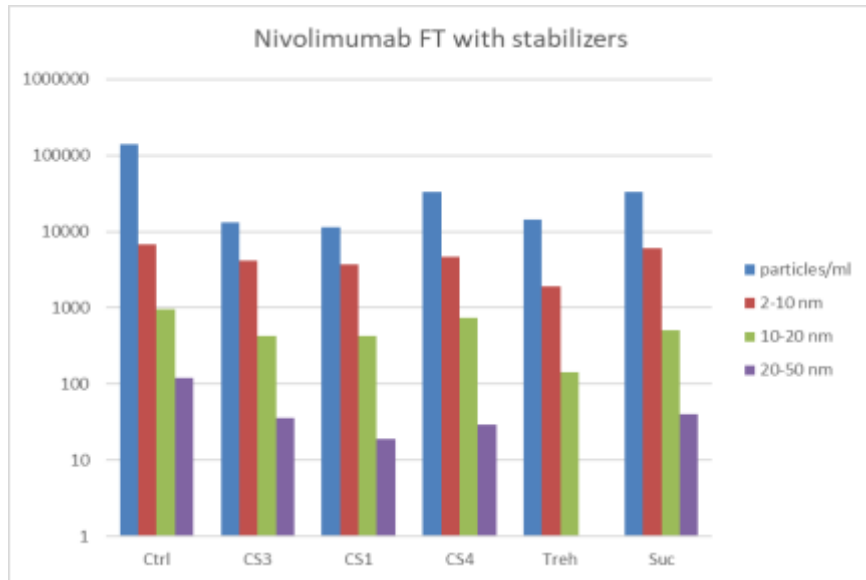
- Novel stabilizers improve the thermal stability by shifting melting temp
- Thus they appear to be similar or better than sucrose in stabilizing mAbs against thermal stress

Effect of stabilizers on Isothermal stability of mAb



- mAbs were formulated with the stabilizers and isothermally incubated at 40C for 4 wk
- 5 mg/ml mAb
- saccharide conc: 0.2M
- All stabilizers were effective in improving thermal stability as compared to no stabilizer control

Effect of stabilizers on Freeze thaw stability of mAbs



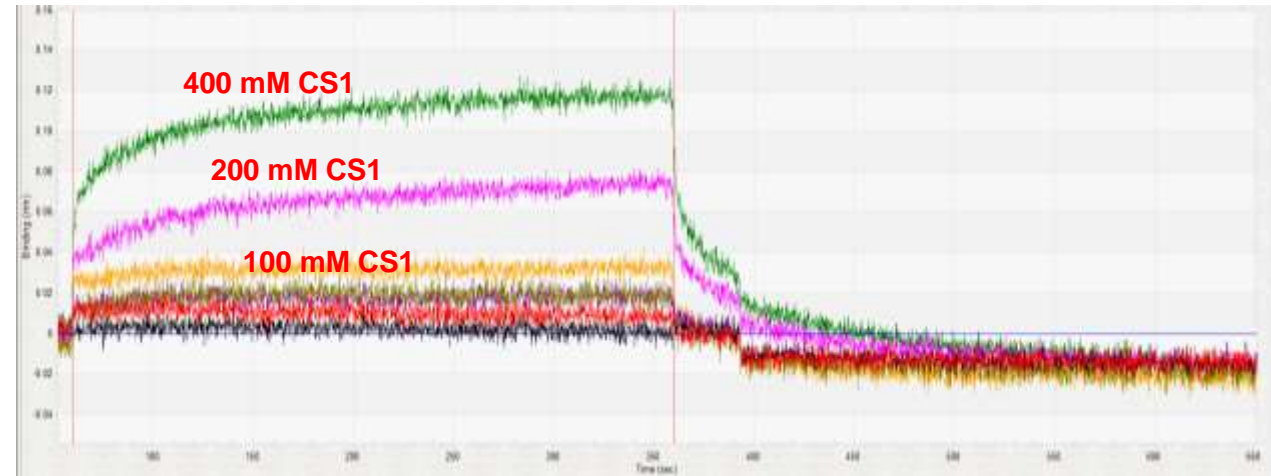
- mAb conc: 10 mg/ml
- saccharide conc: 0.2M
- 10 FT cycles
- Samples analyzed by flowcam

• Stabilizers showed effectiveness in preventing particulate formation due to freeze thaw stress

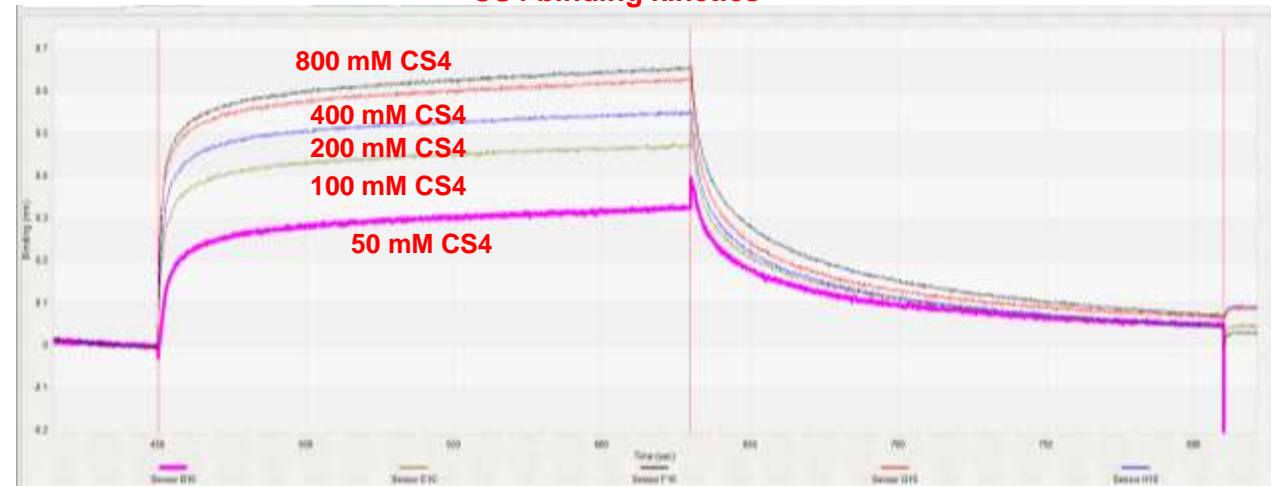
Binding kinetics and mechanism of stabilizers

- Interaction of stabilizers with mAbs was investigated using BLI octet
- Infliximab was biotinylated and loaded onto SSA tips.
- Binding kinetics determined by direct interaction with upto 1M stabilizers
- Kd calculated as 5.7 mM for CS1 and 6.9 for CS4

CS1 binding kinetics



CS4 binding kinetics





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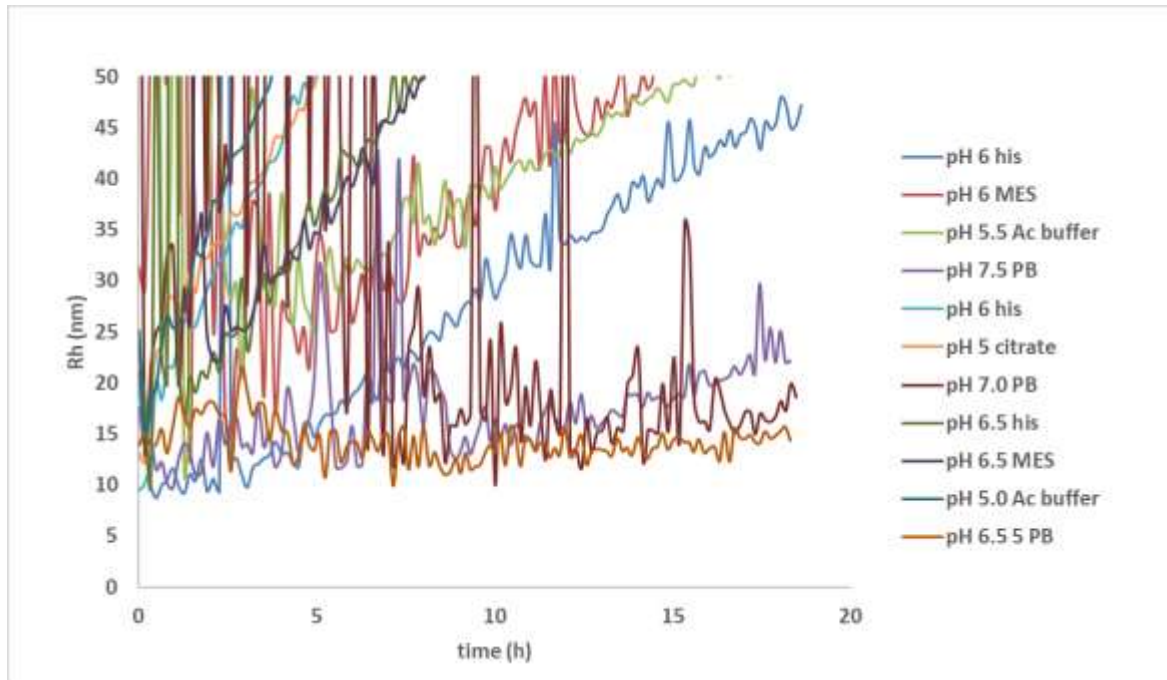


Case Study

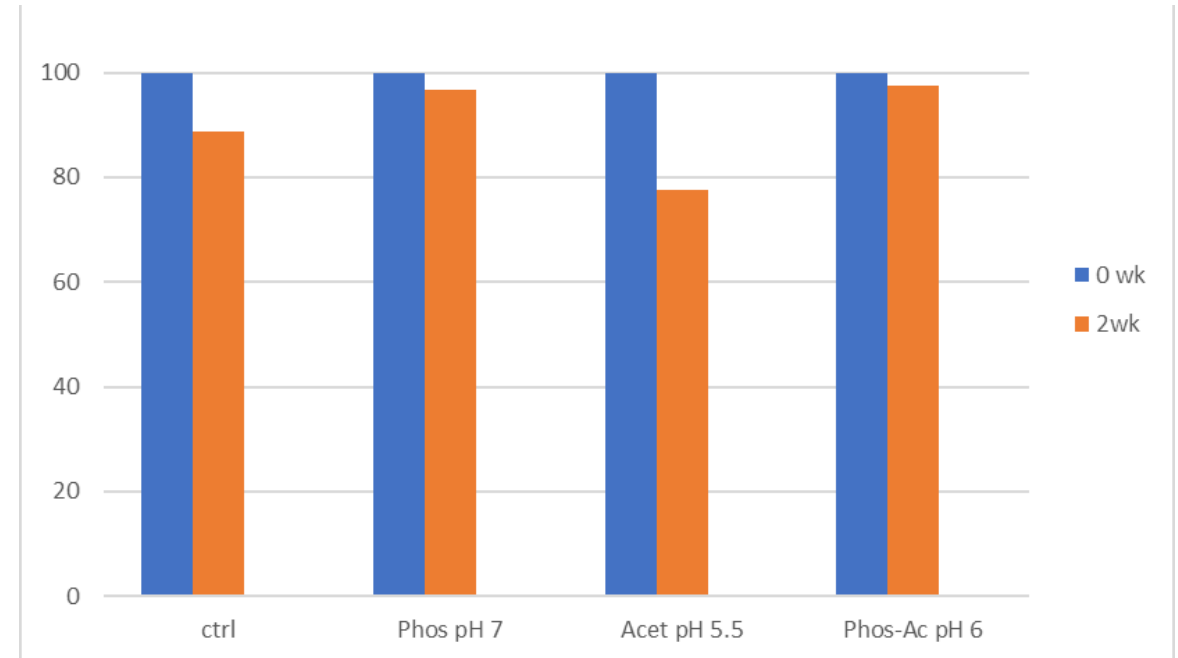
**Developing an optimal
formulation for mAb A using
combination of excipients**

mAb liquid formulation development: Buffer screening

DLS screen



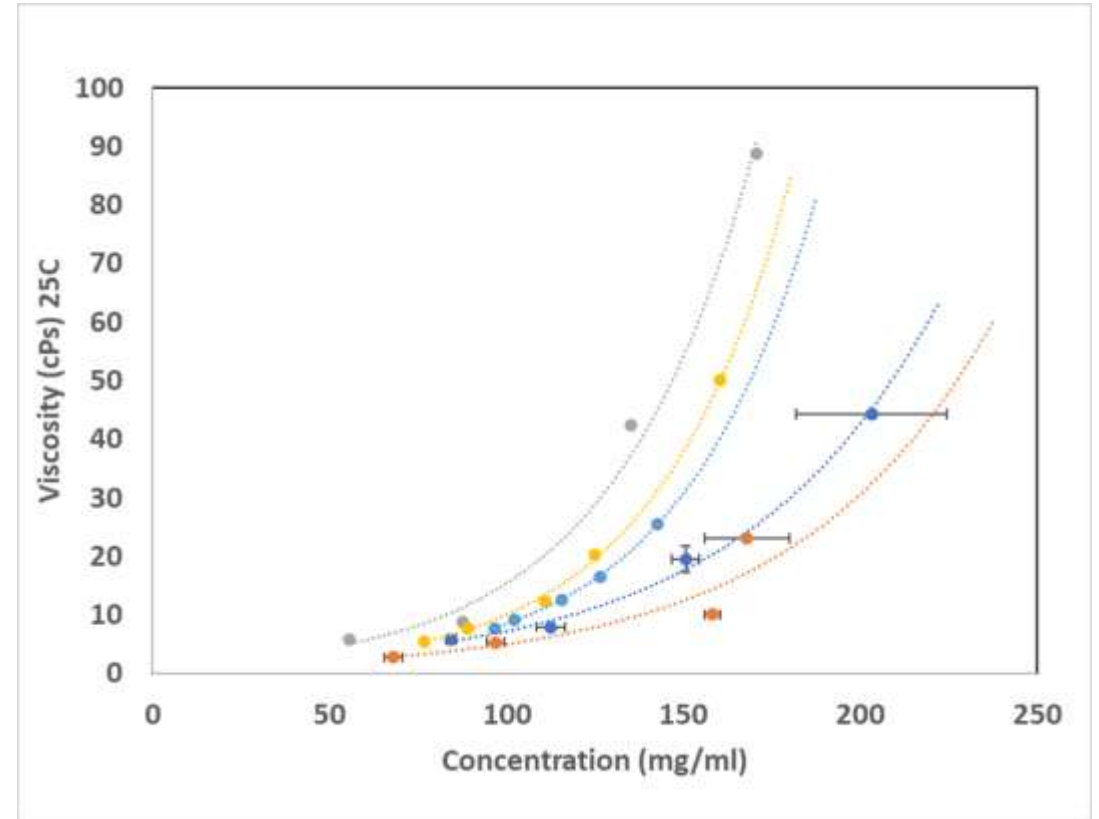
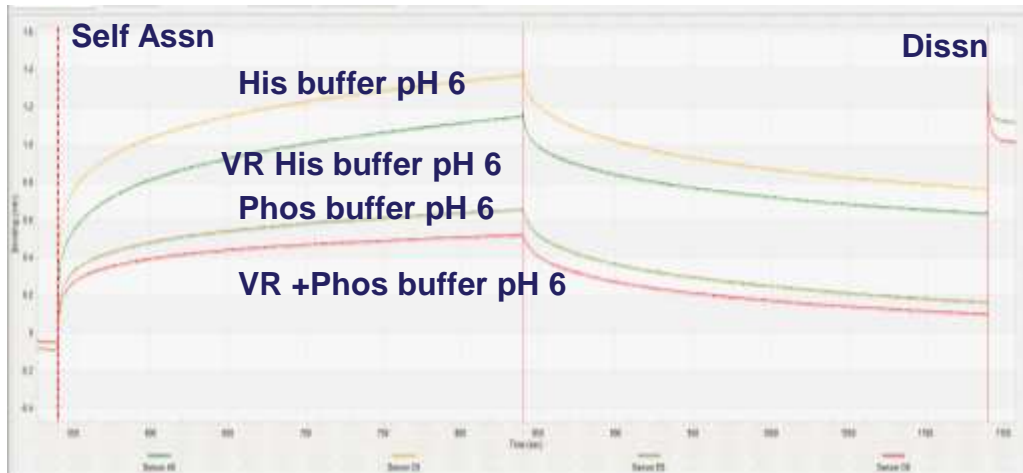
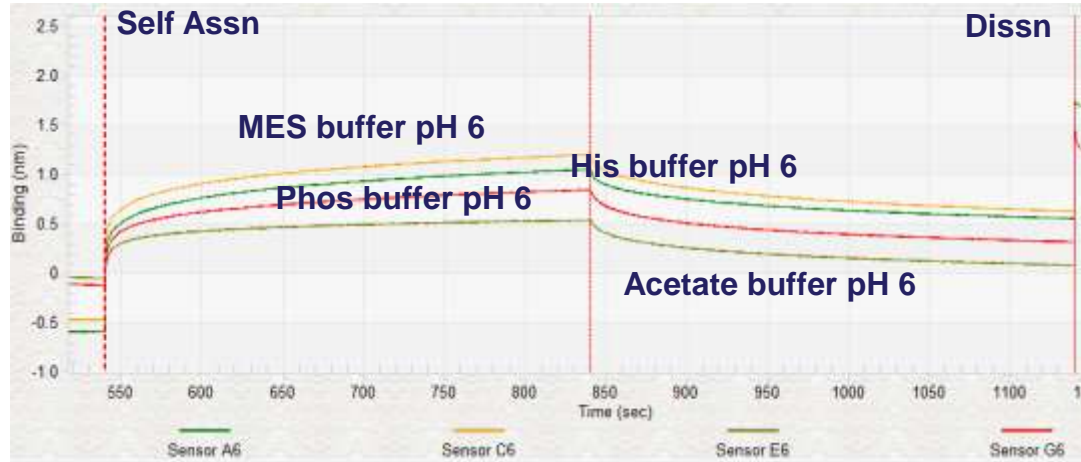
Accelerated stress screen



- DLS and BLI octet screening to identify pH and buffer
- Short Accelerated isothermal hold stress screening for 1-2 week
- Phosphate buffer was observed to improve stability

mAb liquid formulation development: viscosity screen

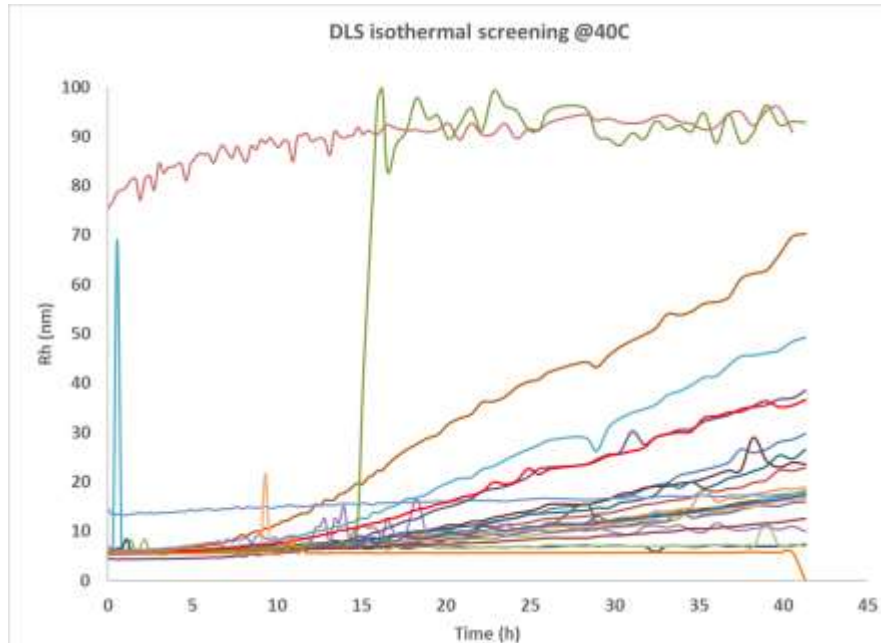
BLI octet screen



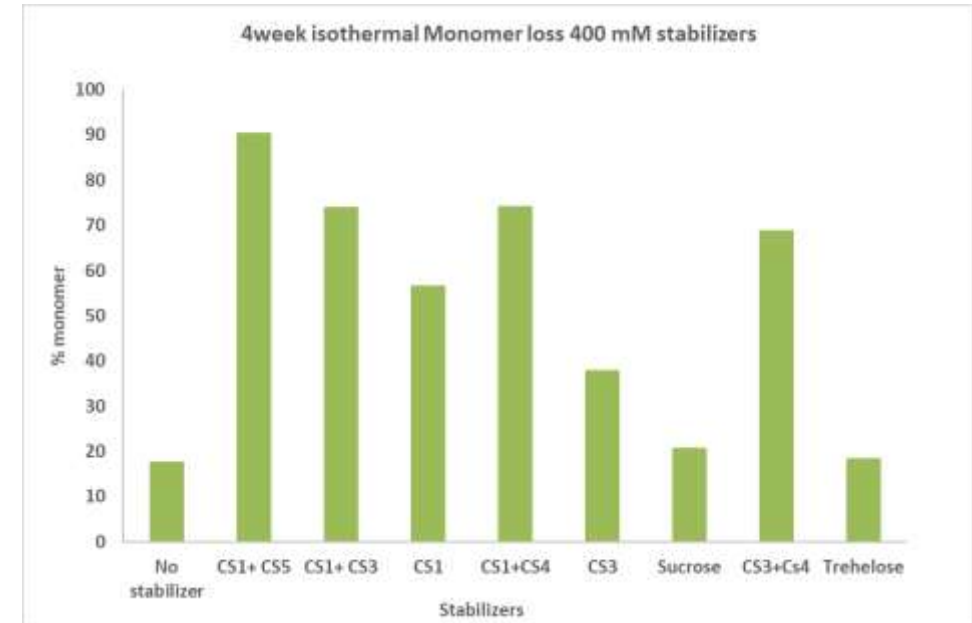
DLS, BLI octet and microvisc help to identify and validate viscosity reducing excipients

mAb liquid formulation development

- DLS screening to identify stabilizing excipients
- Isothermal Accelerated stress screening at 45C

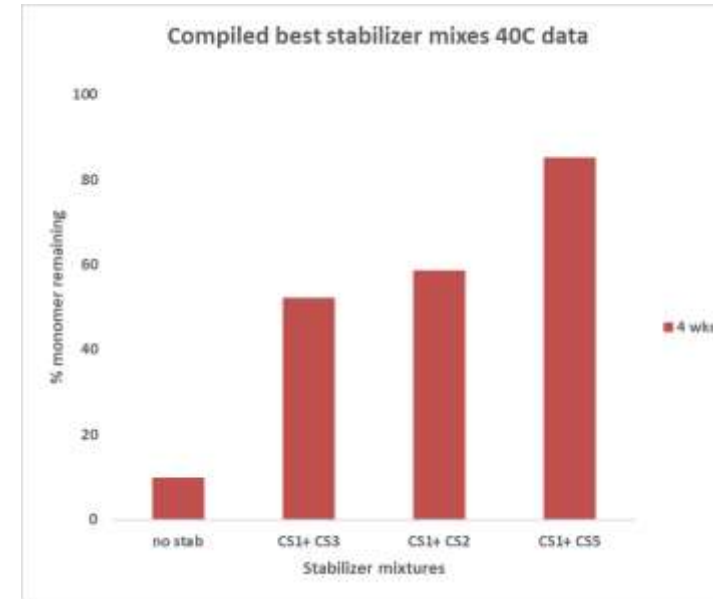
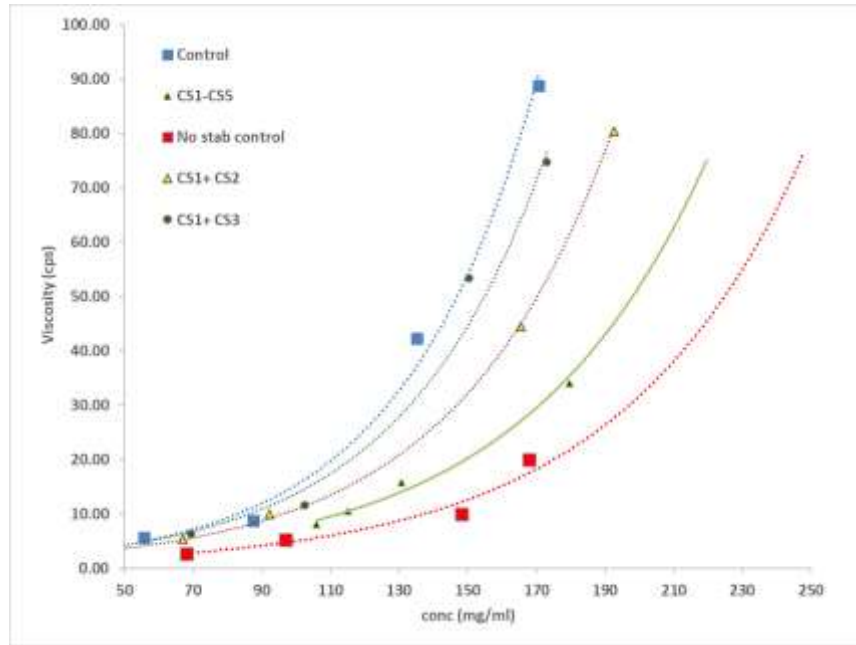


Selected excipients

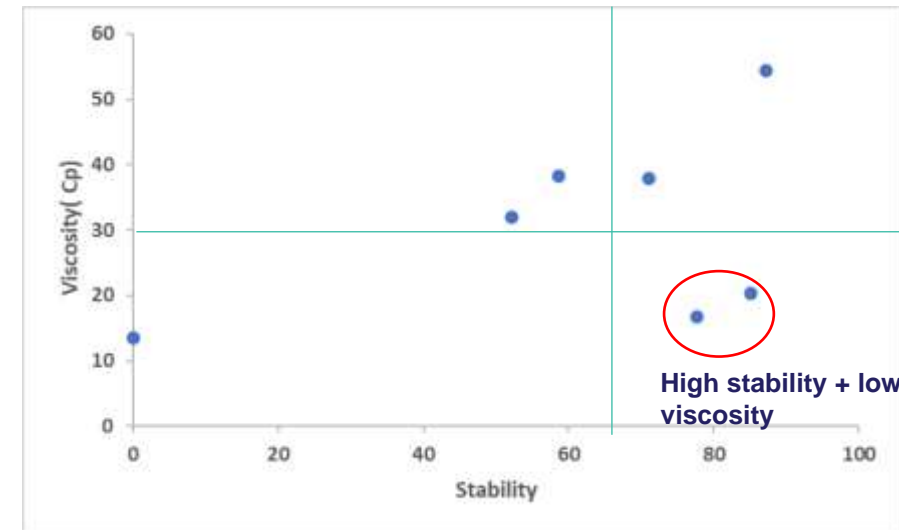


Mixtures were observed to improve stability better than single excipients

mAb liquid formulation development using SQore excipients



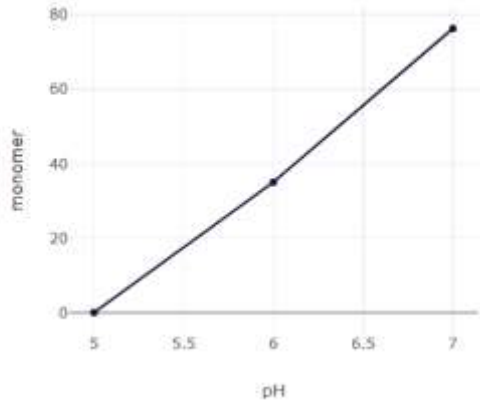
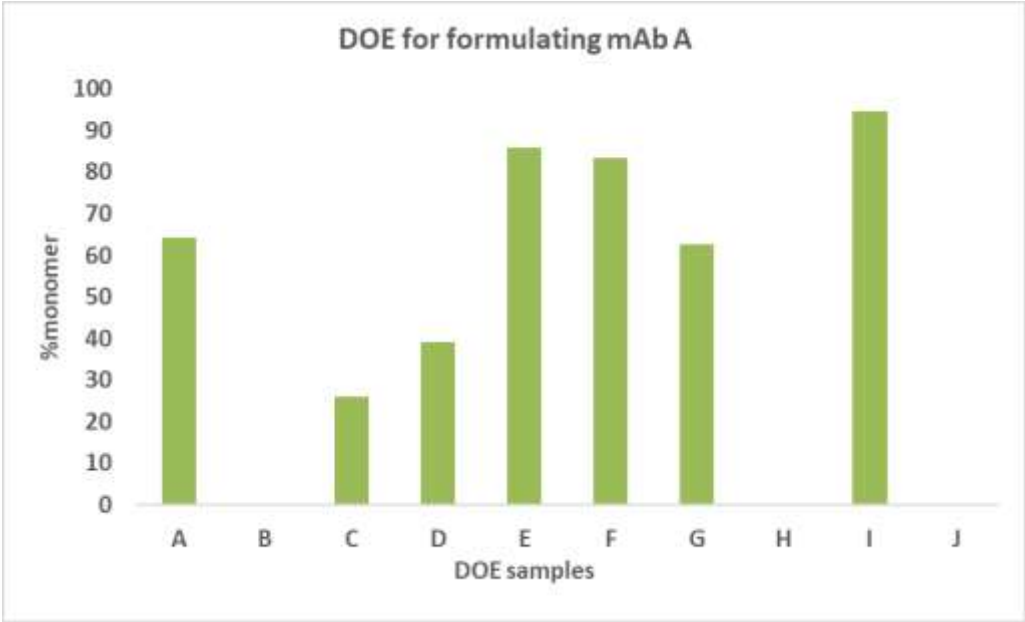
Excipient combination	Monomer stability 40C	Viscosity at 150 mg/ml
CS1+ CS2	52.19	32.05
CS1+ CS3	58.63	38.21
CS1+CS5	85.21	20.25
No stabilizer	20	13.5
No viscosity reducer	87.3	54.38



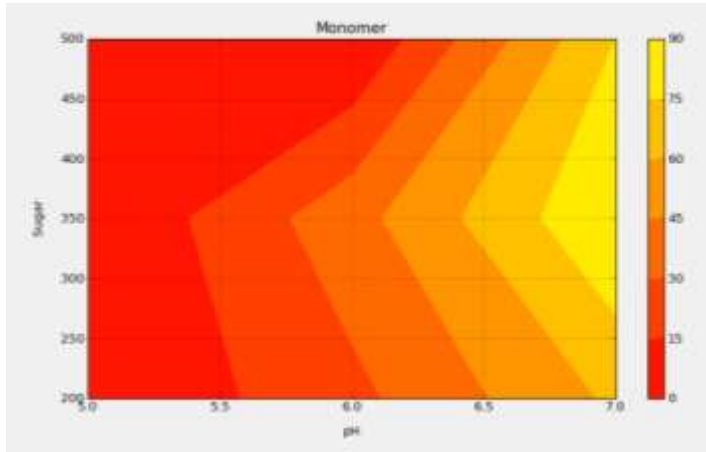
mAb A liquid formulation optimization by DOE

- Isothermal stability studies for optimizing mAb A formulation
- Set up isothermal hold studies at 40C for 4 weeks
 - mAb A: 150 mg/ml
 - Sugars total conc: 200-500 mM

Formulation	pH	Sugars (mM)
A	7	500
B	5	500
C	6	200
D	6	350
E	6.5	500
F	7	350
G	7	200
H	5	350
I	6.5	350
J	5	500



Lower pH detrimental for stability



> 350 mM sugar mix helps stability

- **Recommended Formulation:**
 - mAb A conc (150 mg/ml)
 - 5 mM phosphate buffer, pH 6.5
 - 350 mM sugar mix

Summary and Conclusions

- Comera SQore™ platform provides excipient technology to address viscosity as well as stability issues for highly concentrated protein formulations enabling SQ administration of biopharmaceuticals.
- Comera can utilize computational as well as traditional screening to identify excipients
- Novel stabilizers show similar/improved profile as compared to sucrose or trehalose
- A mixture of stabilizers showed better stability profile as compared to single stabilizer at equivalent conc
- mAb can be easily optimized by DOE to obtain relatively stable low viscosity subQ formulation

Thank you!

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