

Physicochemical and Immunological Comparison of CRM197 from Different Manufacturers and Expression Systems

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www.mvsc.ku.edu

Macromolecular and Vaccine Stabilization Center (MVSC) is located in

Department of Pharmaceutical Chemistry in School of Pharmacy at KU:

- Characterization, stabilization and formulation
- Vaccines (live and recombinant purified antigens, adjuvants)
- Biopharmaceuticals (proteins, peptides)

Our Team

Distinguished Professor, PI

Dr. David Volkin



Director, co-PI

Dr. Sangeeta Joshi



Scientific Assistant Directors

Dr. Ozan Kumru

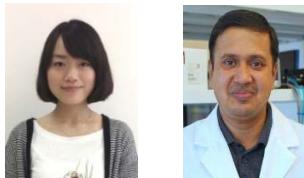


Dr. John Hickey



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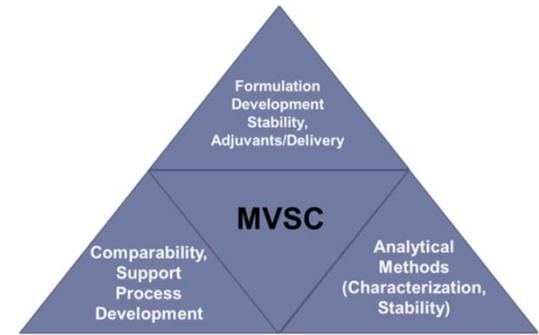


➤ Our group currently has ~25 members (graduate students, post-doctoral fellows, senior scientists, office/lab staff).

- Our research grants and fee-for service contracts include complete analytical characterization and formulation development studies as well as per sample testing.

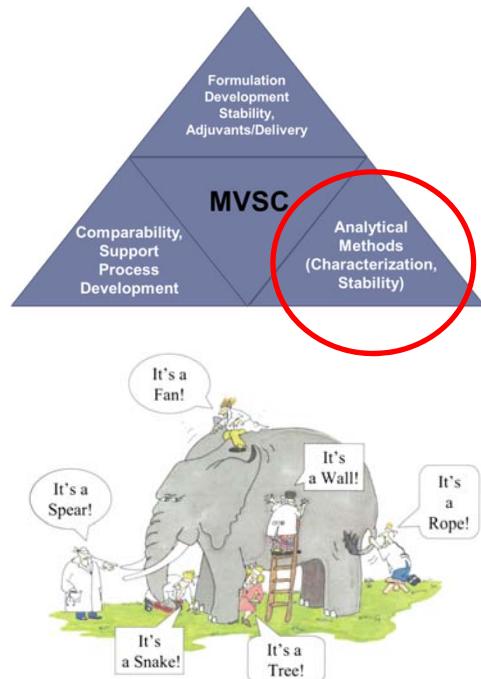
- Our focus is on the science of CMC development.
 - Early-stage Characterize and compare candidates with structural assays, develop stability-indicating assays and identify degradation pathways
 - Translational-stage Characterize, stabilize and formulate biological candidates for first-in-human clinical trials (Phase 1).
 - Late-stage Develop final formulations and perform analytical comparability assessments to support Phase 3 trials.

- Our research goals include developing analytical tools, elucidating degradation mechanisms, improving stability and correlating physicochemical changes with loss of potency



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Analytical Characterization of Vaccines and Biopharmaceuticals



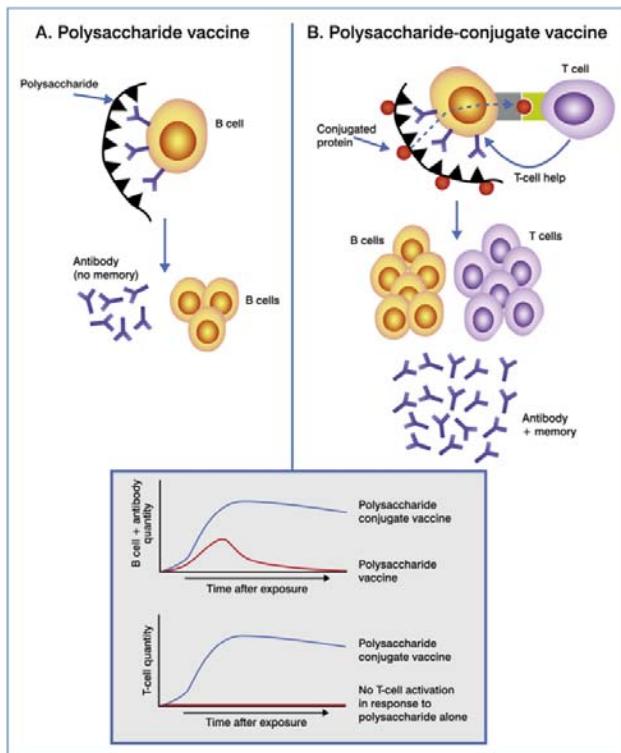
The blind men and the elephant. Poem by John Godfrey Saxe (Cartoon originally copyrighted by the authors; G. Renee Guzlas, artist http://www.nature.com/kj/journal/v62/n5/fig_tab/449326f1.html)

- Requires an overall assessment of results from a family of assays
- Physical, chemical, biological, immunological...
- Key role in vaccine and biopharmaceutical development
 - e.g., process/formulation, testing, comparability, stability

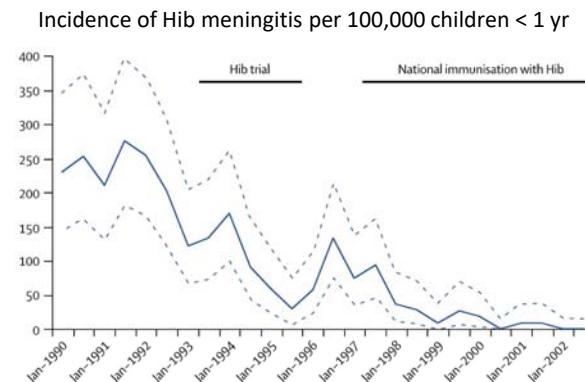
Physical & Chemical Attributes

- Appearance
- Purity
- Primary Structure
- Secondary Structure
- Tertiary Structure
- Overall Conformational Stability
- Characterize Size (Oligomeric State)
- Measure Aggregation/Particles
- Charge Heterogeneity

Carrier Proteins In Polysaccharide-Conjugated Vaccines



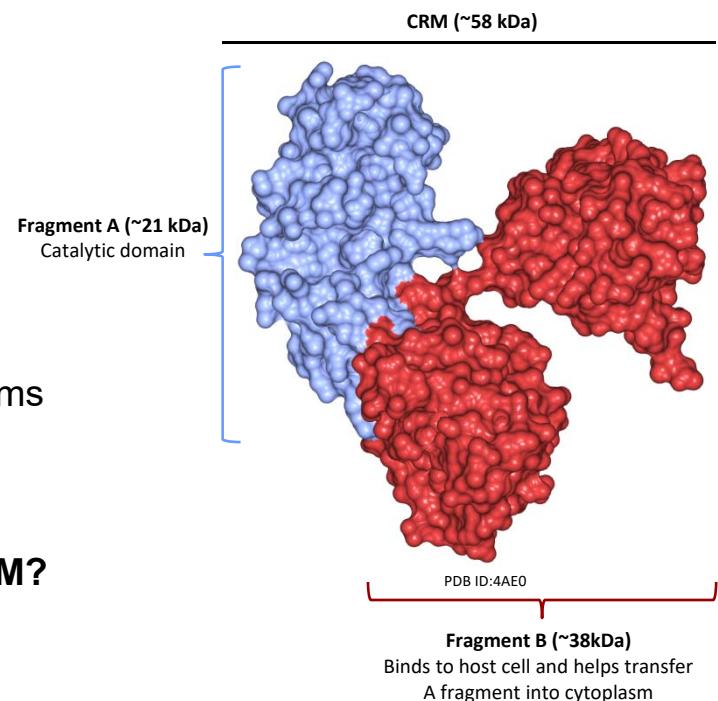
Vaccine	Polysaccharide Source (Organism)	Manufacturer	Carrier Protein
Menveo®	<i>Neisseria meningitidis</i>	Novartis	CRM ₁₉₇
Prevnar®	<i>Streptococcus pneumoniae</i>	Pfizer	CRM ₁₉₇
Prevnar-13®	<i>Streptococcus pneumoniae</i>	Pfizer	CRM ₁₉₇
Hibrix®	<i>Haemophilus influenzae</i>	GlaxoSmithKline	Tetanus Toxoid
ActHIB®	<i>Haemophilus influenzae</i>	Sanofi Pasteur	Tetanus Toxoid
Menhibrix®	<i>Neisseria meningitidis</i> <i>Haemophilus influenzae</i>	GlaxoSmithKline	Tetanus Toxoid
Menactra®	<i>Neisseria meningitidis</i>	Sanofi Pasteur	Diphtheria Toxoid
PedvaxHIB®	<i>Haemophilus influenzae</i>	Merck	OMPC

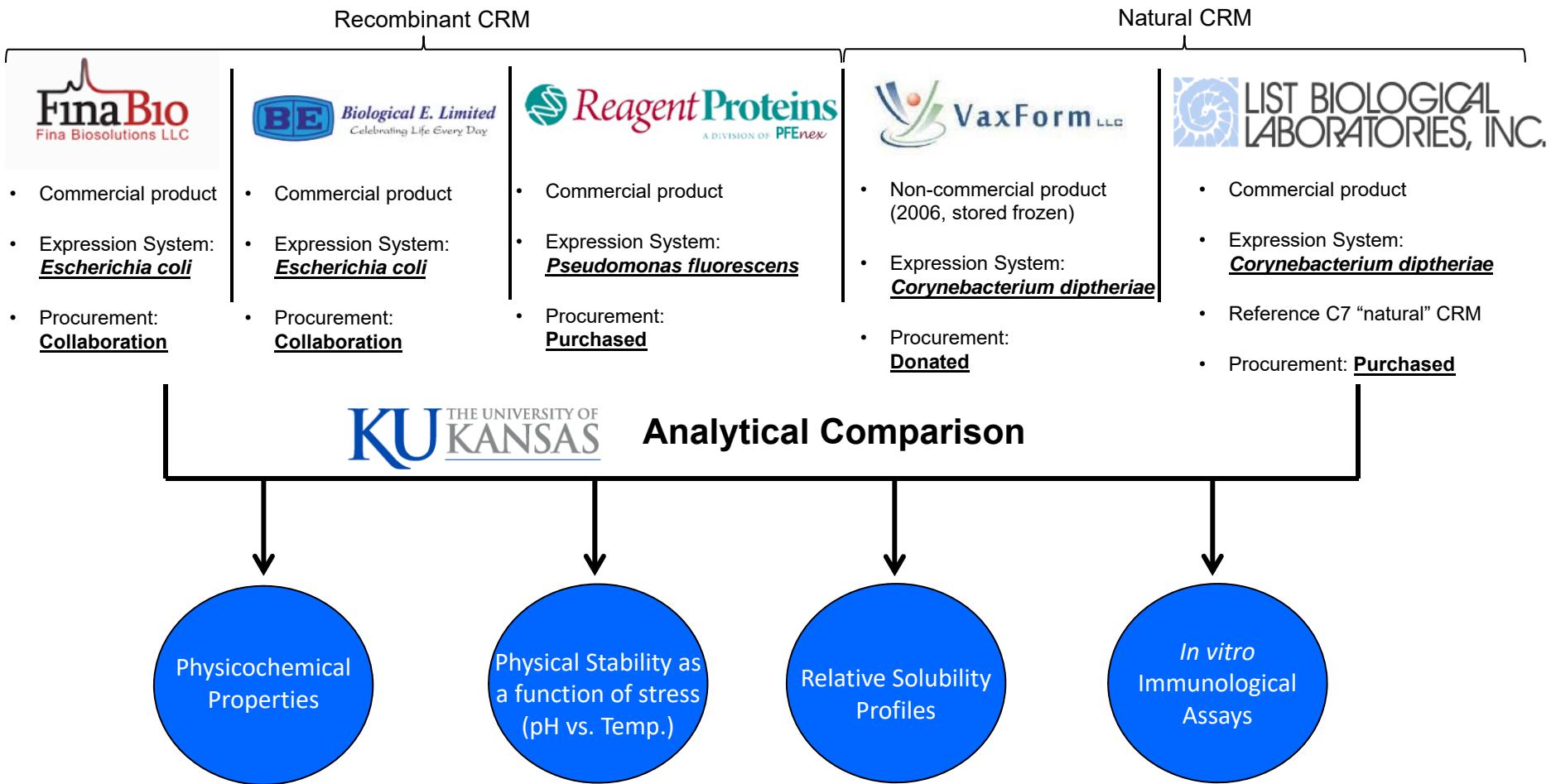


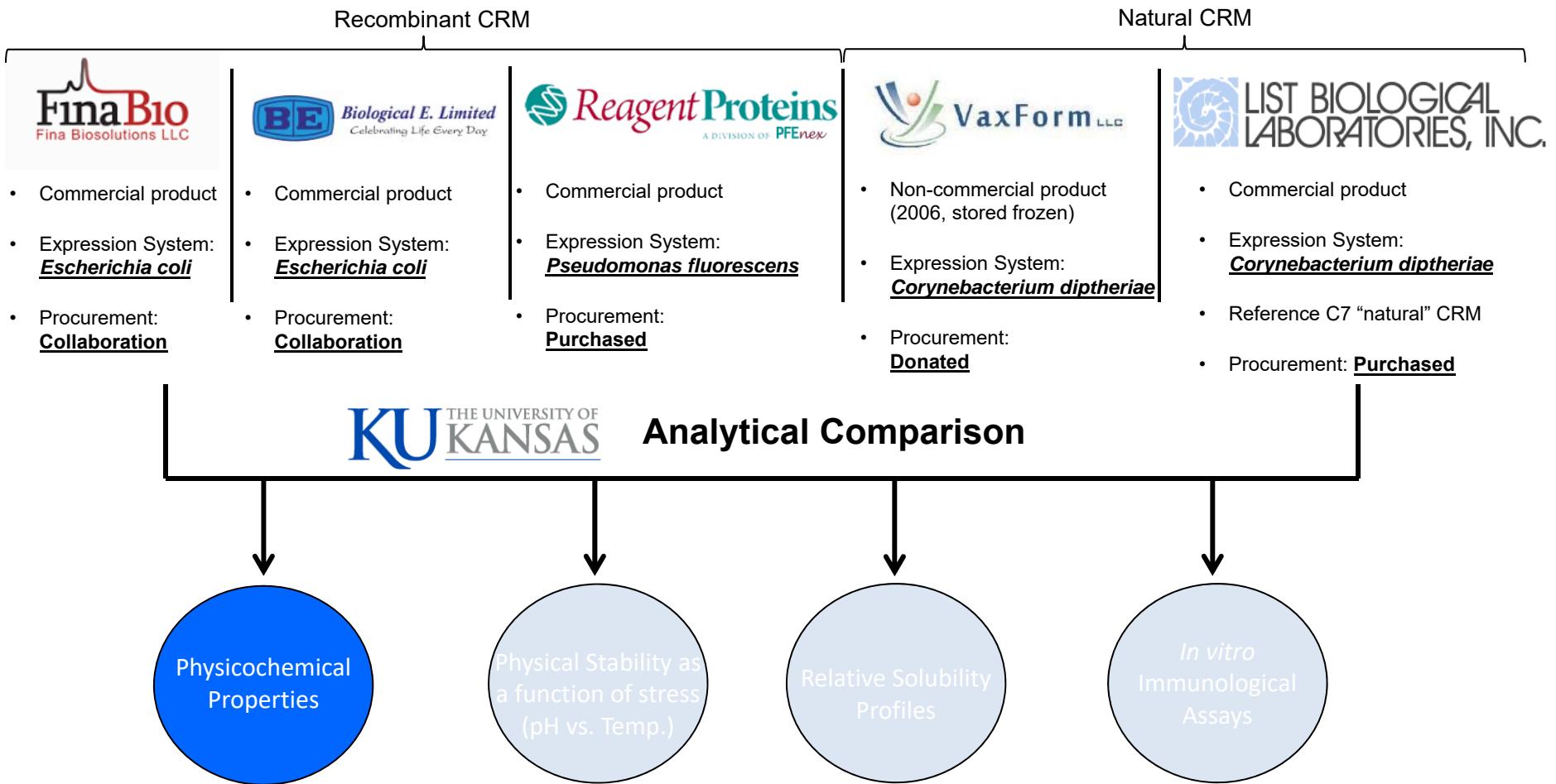
Tetanus Toxoid (TT)	Diphtheria Toxoid (DT)	Cross-Reactive Material 197 (CRM ₁₉₇)	<i>N. meningitidis</i> Outer Membrane Protein (OMP)	Non-Typeable <i>H. influenzae</i> Derived Protein D (PD)
 • Derived from <i>Clostridium tetani</i> • Inactivated with formalin • Purified with ammonium sulfate and filter sterilized prior to conjugation process	 • Derived from <i>Corynebacterium diphtheriae</i> • Detoxified with formaldehyde • Purified by ammonium sulfate fractionation and diafiltration	 • Enzymatically inactive, nontoxic mutant of diphtheria toxin • Requires no formaldehyde detoxification • Obtained at near 100% purity	 • Outer membrane protein complex derived from <i>N. meningitidis</i> serogroup B strain 11	 • Antigenically conserved surface lipoprotein found in all <i>H. influenzae</i> • Used in a nonacylated, antigenically active form

Natural & Recombinant CRM197 (“CRM”)

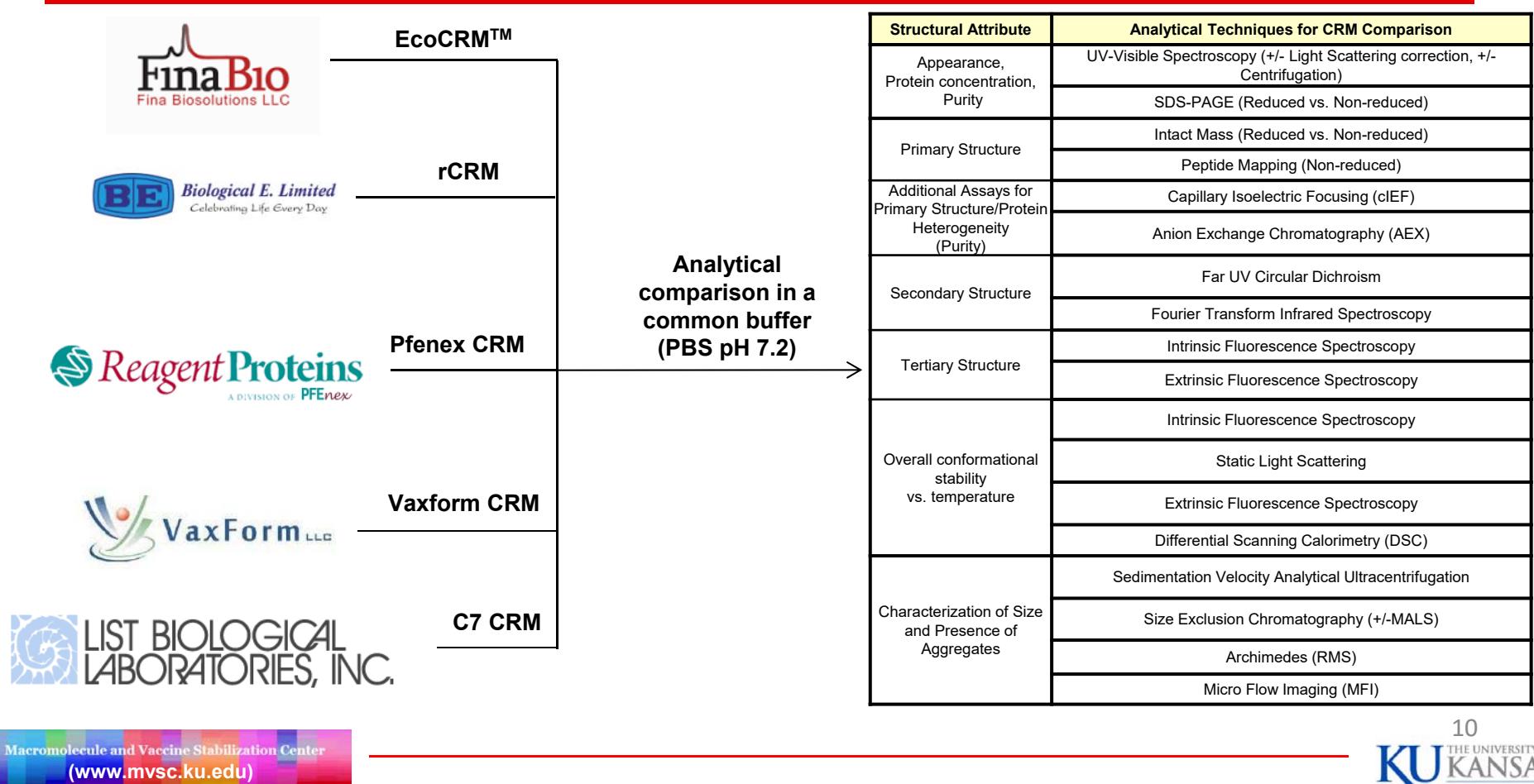
- Produced in *Corynebacterium diphtheriae* (low yield) and requires BSL-2 manufacturing facility
- Natural CRM is commercially available but costly and potential issues obtaining sufficient material for preclinical/clinical studies
- CRM can be produced in recombinant expression systems (*E. coli* and *P. fluorescens*)
- **How does recombinant CRM compare to natural CRM?**



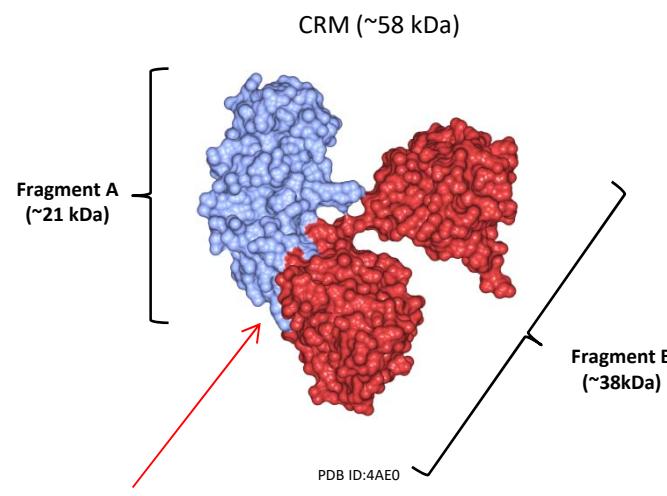




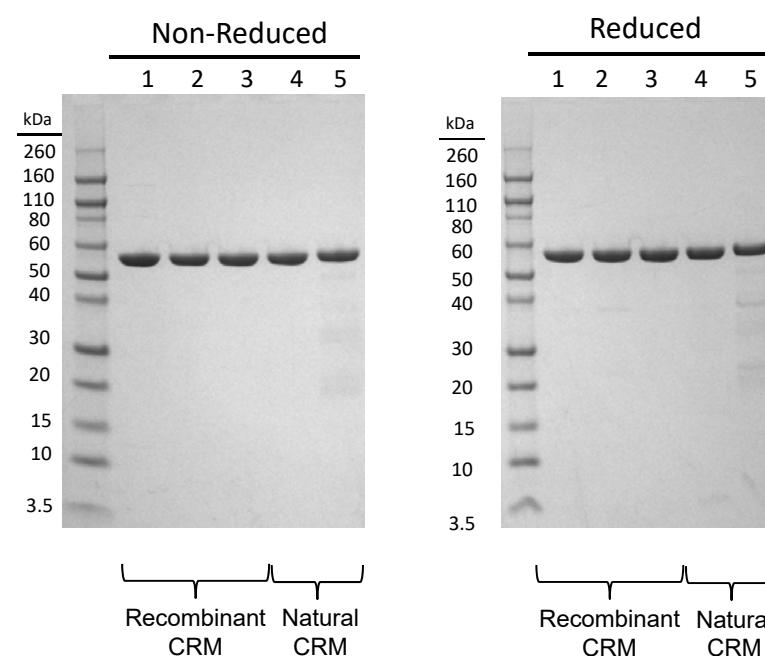
Overview of comparing the physicochemical properties of five CRM samples



Comparison of Purity and Presence of Covalent-Linked Aggregates



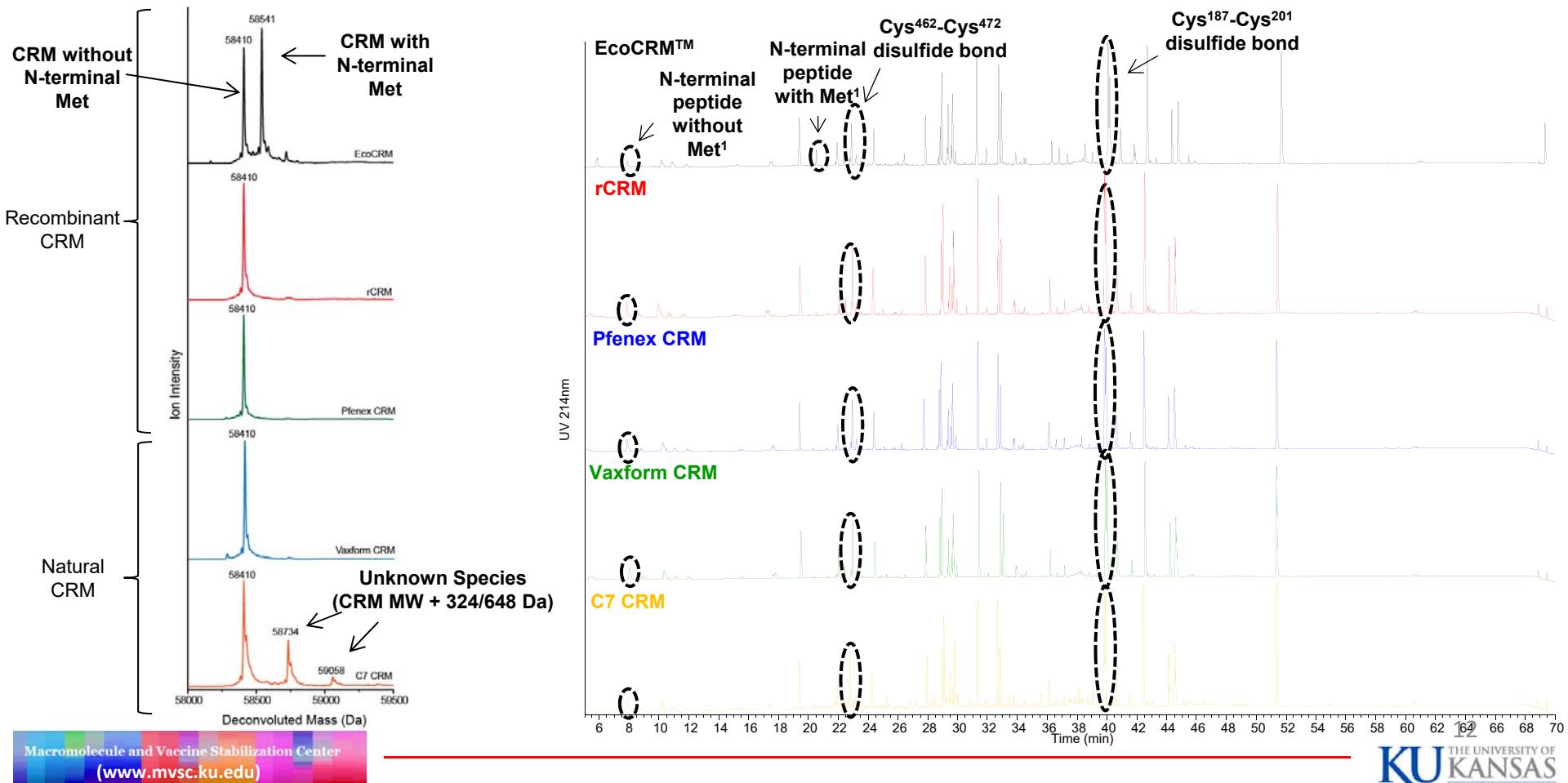
Proenzyme is cleaved by trypsin-like protease in *C. diphtheriae* and fragments A and B are associated through one disulfide bond



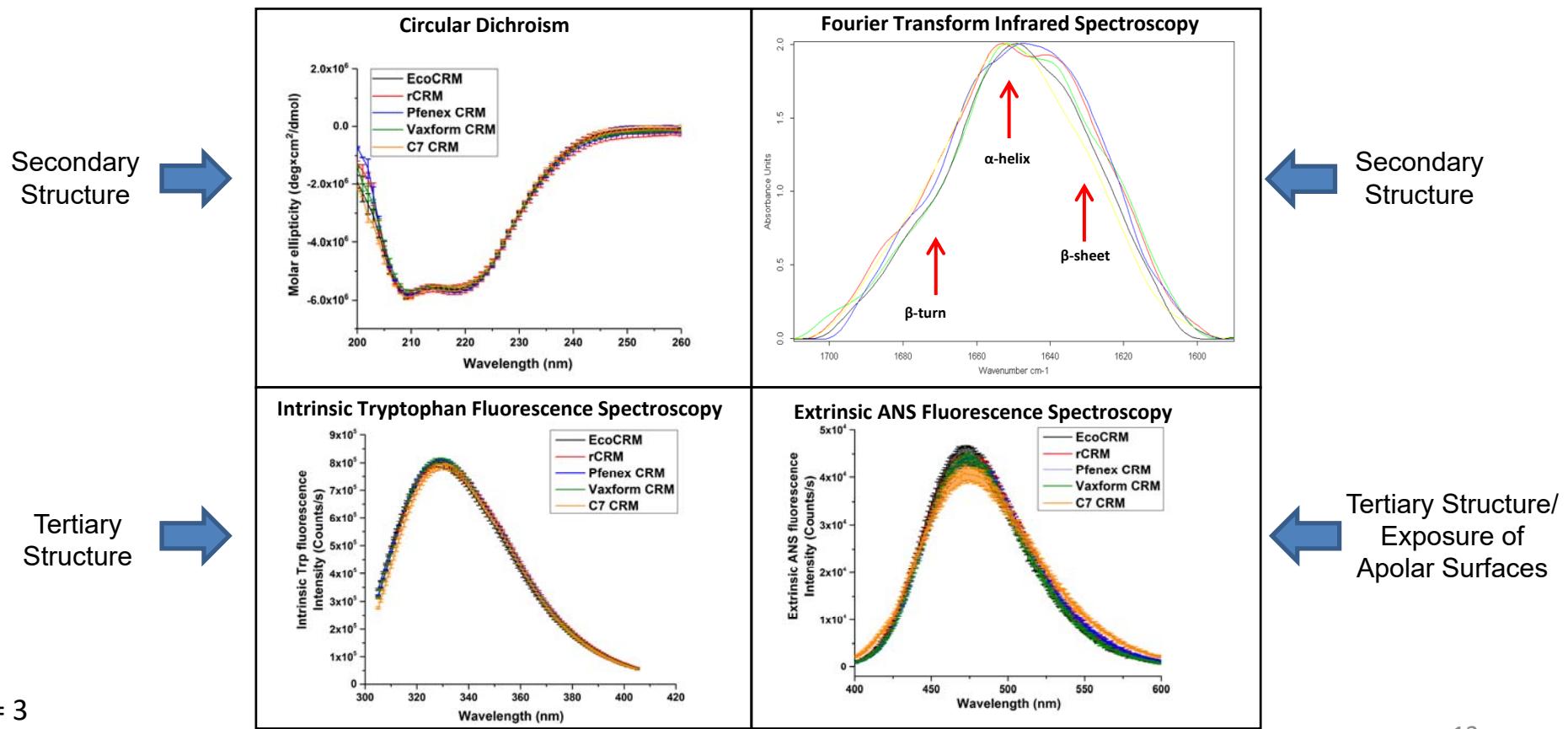
Lane 1) EcoCRM™
 Lane 2) rCRM
 Lane 3) Pfenex CRM
 Lane 4) Vaxform CRM
 Lane 5) C7 CRM

← CRM Monomer (Proenzyme)
 ← B fragment
 ← A fragment

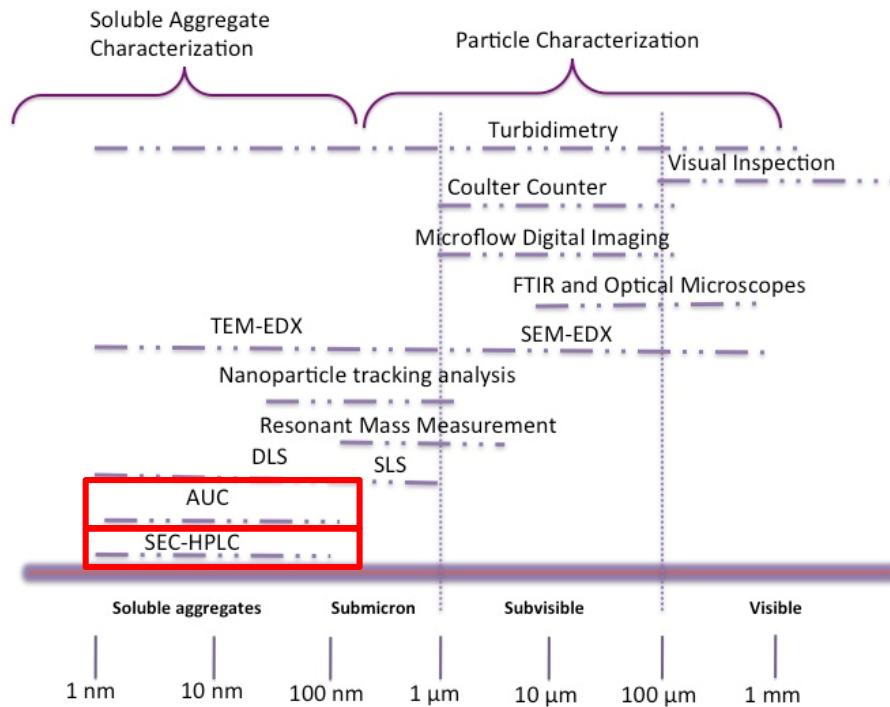
Primary Structure (Intact mass analysis & peptide mapping)



Higher Order Structure Comparison at 10°C

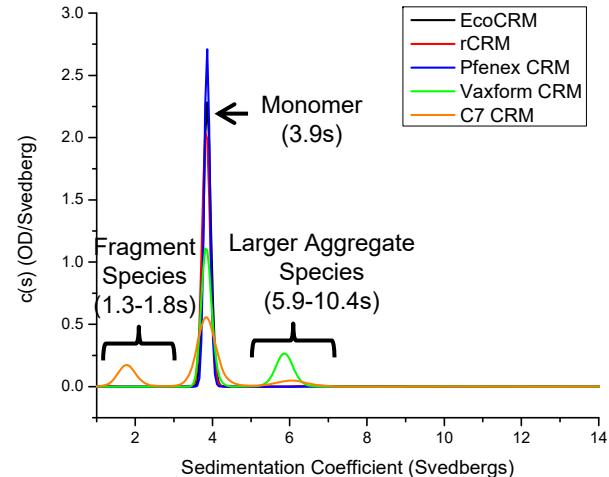


Size Analysis and Quantitation of Soluble Aggregates

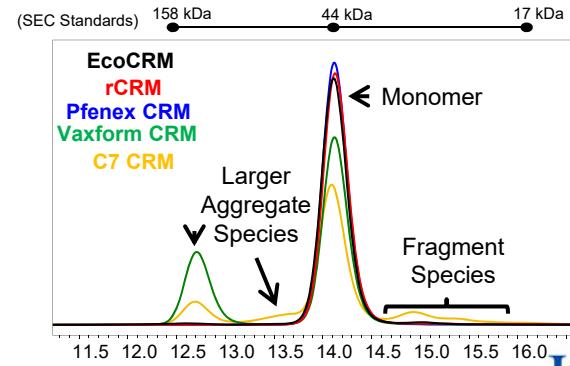


$n = 3$

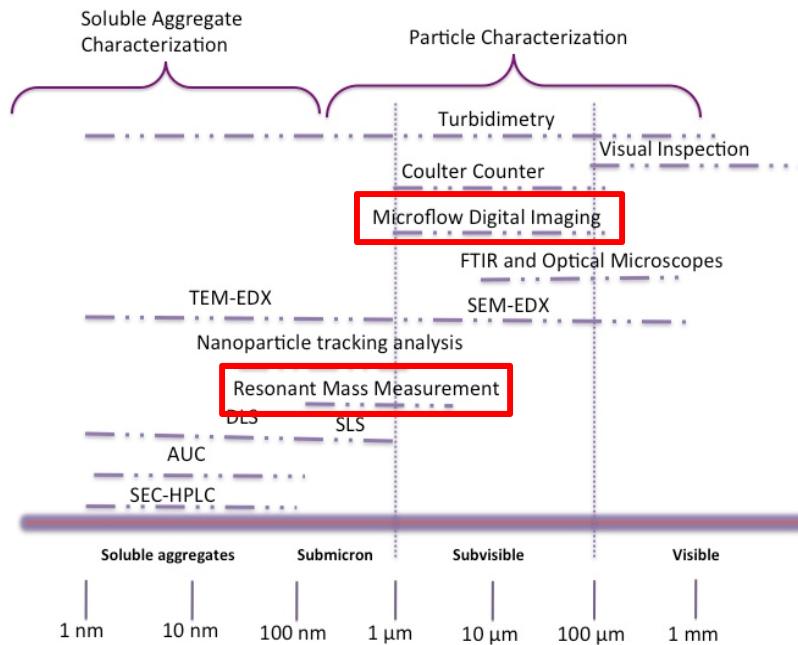
Sedimentation Velocity Analytical Ultracentrifugation (SV-AUC)



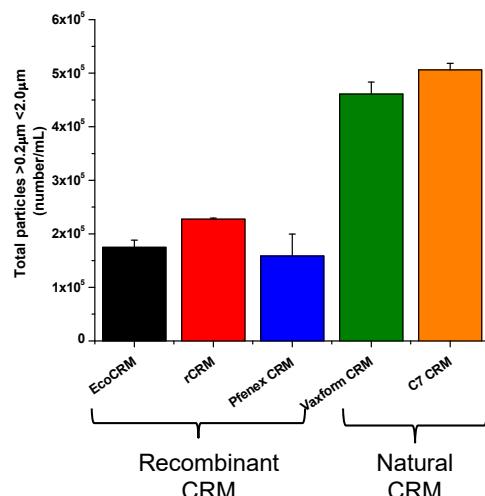
Size Exclusion Chromatography (SE-HPLC)



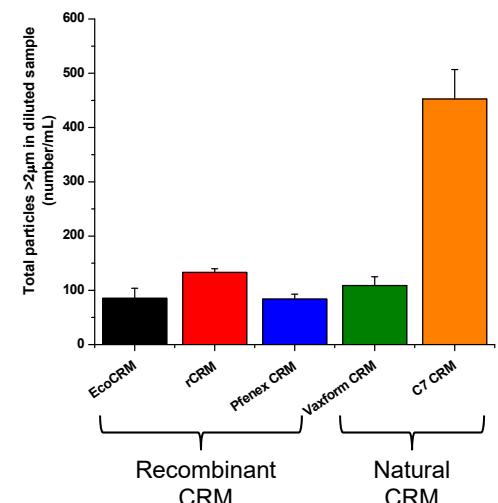
Sub-Micron and Sub-Visible Particle Analysis



Sub-Micron Particle Quantification by Resonance Mass Measurement

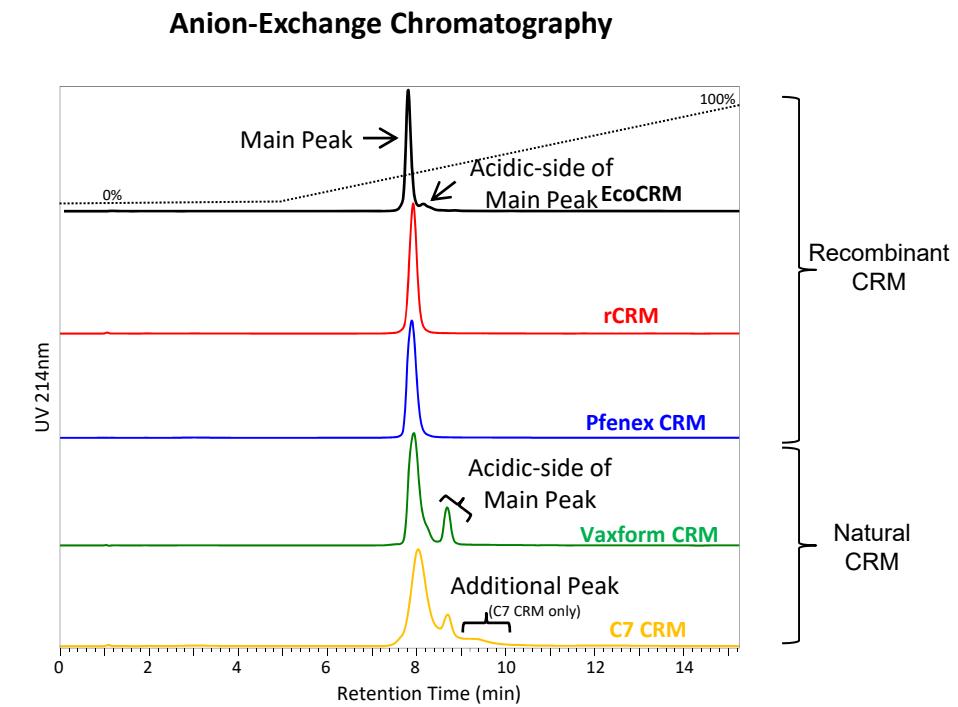
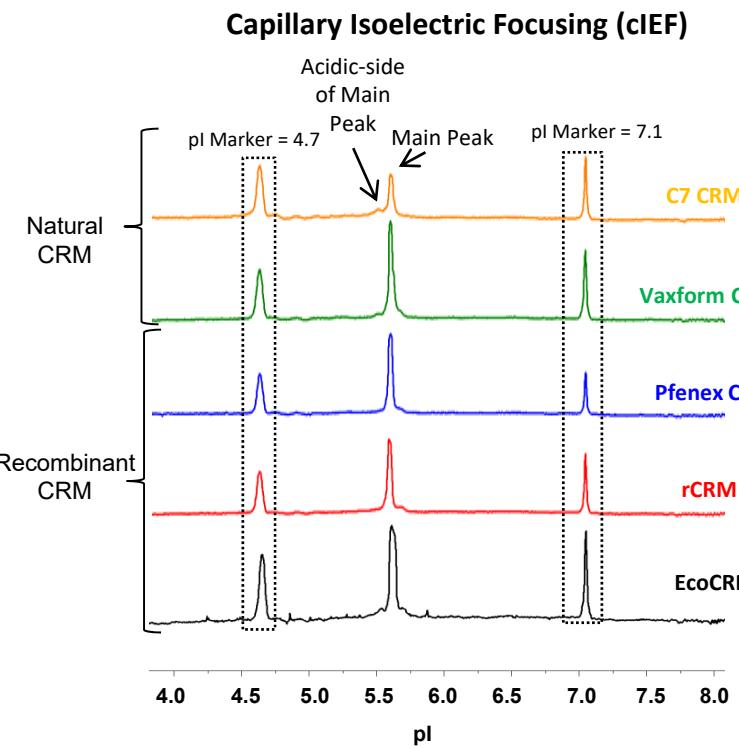


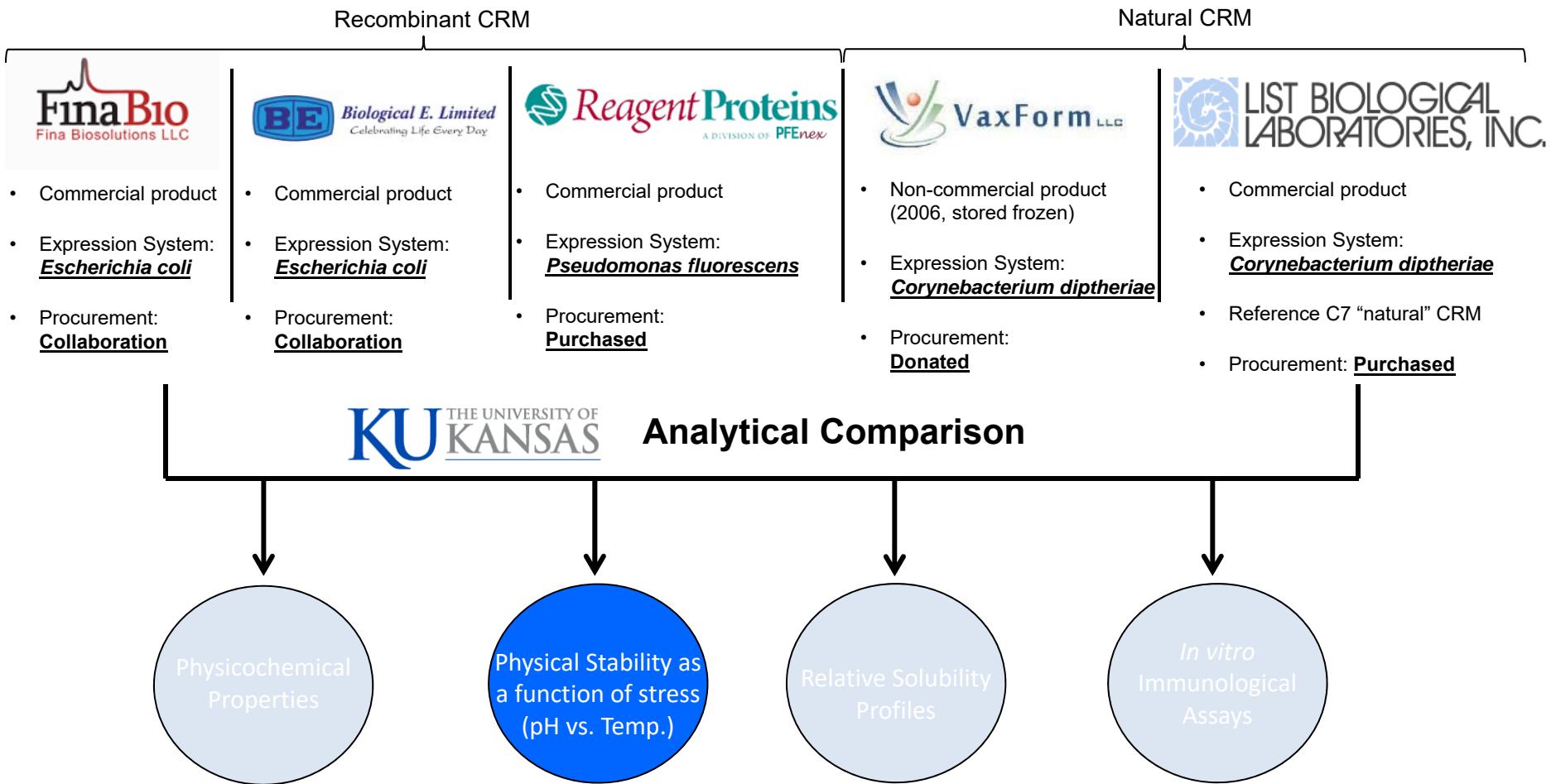
Sub-Visible Particle Quantification by MFI



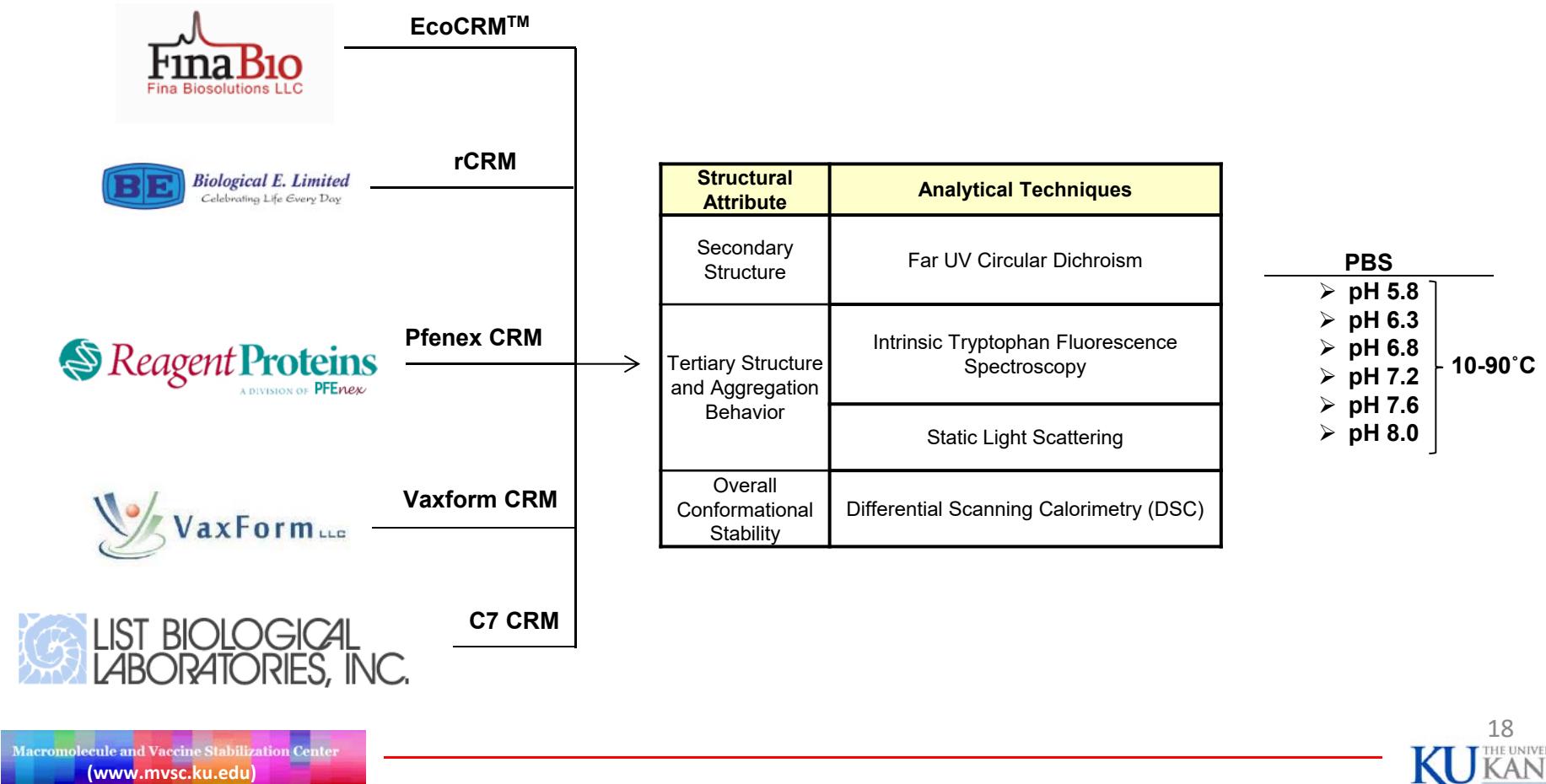
n = 3

Comparison of Protein Charge Heterogeneity



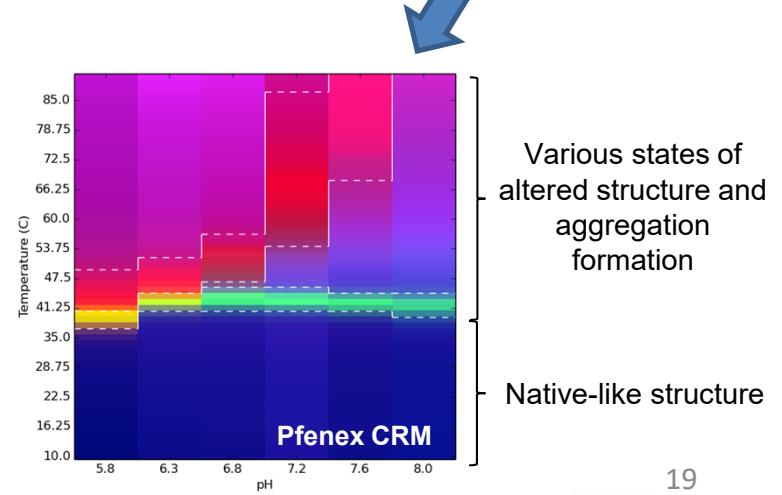
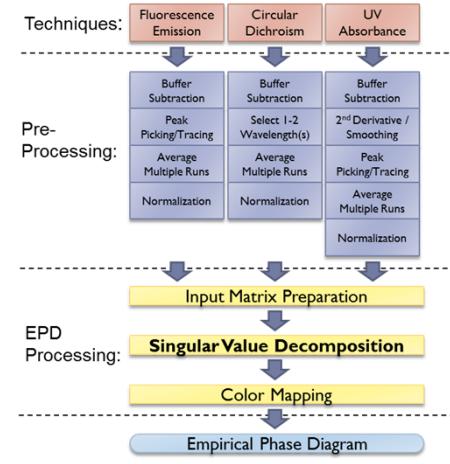
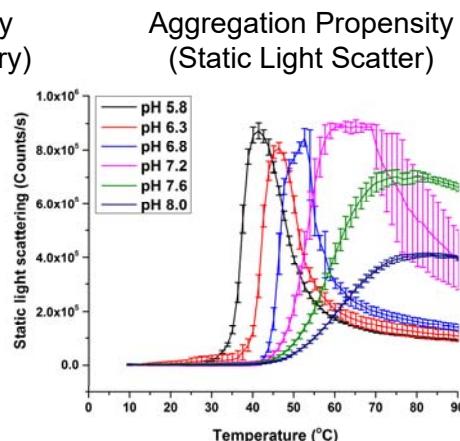
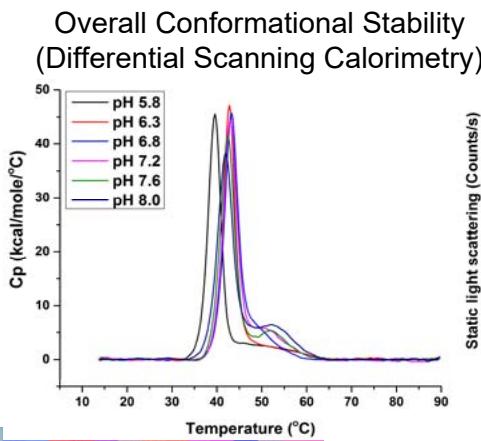
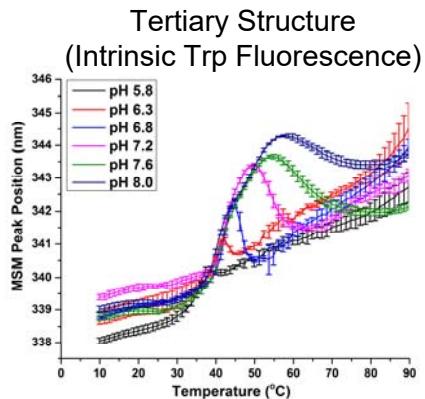
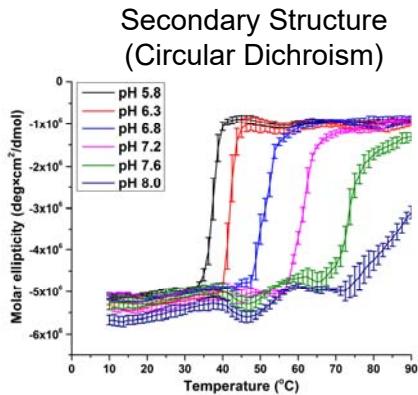


Overview of comparing the physical stability of each CRM molecule as a function of stress (pH & temperature)



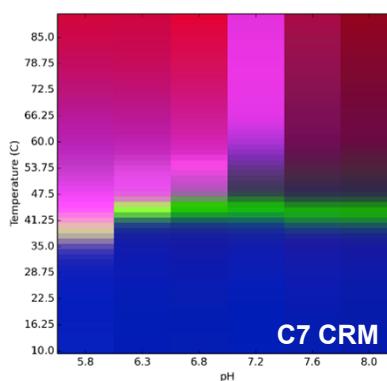
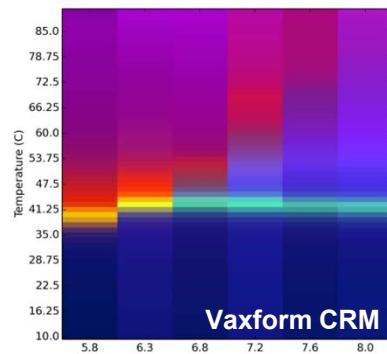
Construction of Empirical Phase Diagrams

Data Visualization: Large Biophysical Stability Data Sets

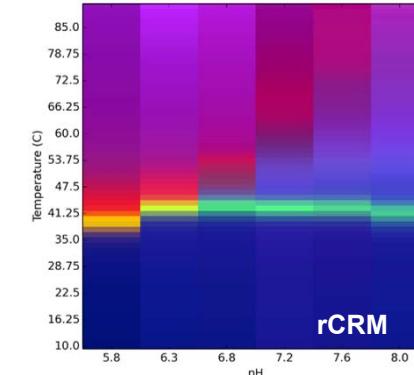
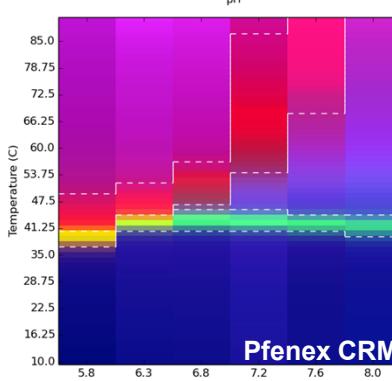
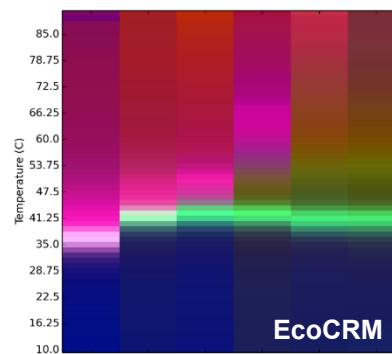


Empirical phase diagram of CRM molecules in PBS

Natural CRM



Recombinant CRM



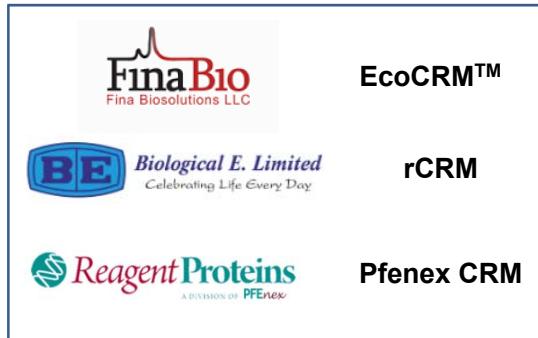
Various states
of altered
structure and
aggregation
formation

Native-like
structure

Source	CRM	Relative area of native-like structure
Recombinant	EcoCRM	~35%
	rCRM	~37%
	Pfenex CRM	~37%
Natural	Vaxform CRM	~37%
	C7 CRM	~36%

Overall comparison of natural and recombinant CRM

Recombinant CRM



Natural CRM



Physicochemical Properties

Physical Stability as
a function of stress
(pH vs. Temp.)

Relative Solubility
Profiles

In vitro
Immunological
Assays

- Overall similar structural integrity and conformational stability but measurable differences were observed
- Similar conformational stability/aggregation propensity as a function of pH (5.8-8.0) and temperature (10-90°C).
- Similar solubility profile in PBS pH 7.2
- Similar *in vitro* immunological reactivity

Acknowledgements



- Prof David Volkin
- Dr. Sangeeta Joshi
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- Dr. Vishal Toprani

Collaborators



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Dr. Andrew Lees



Dr. Akshay Goel
Dr. Ravipratapnarayan Mishra

Funding



Provided Material

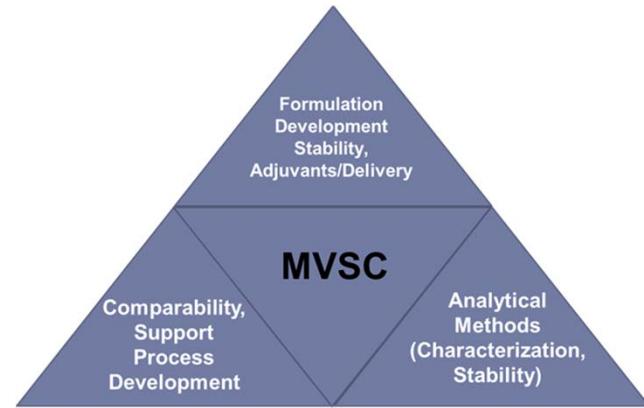


Dr. Garry Morefield

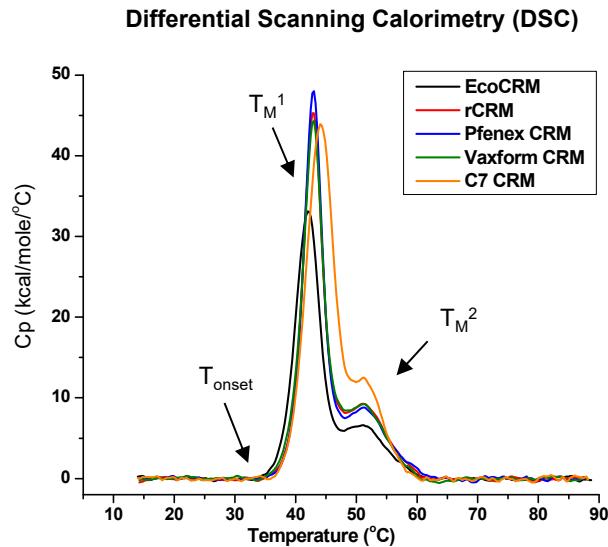
Macromolecule and Vaccine Stabilization Center

Thank you for your attention!

Questions?

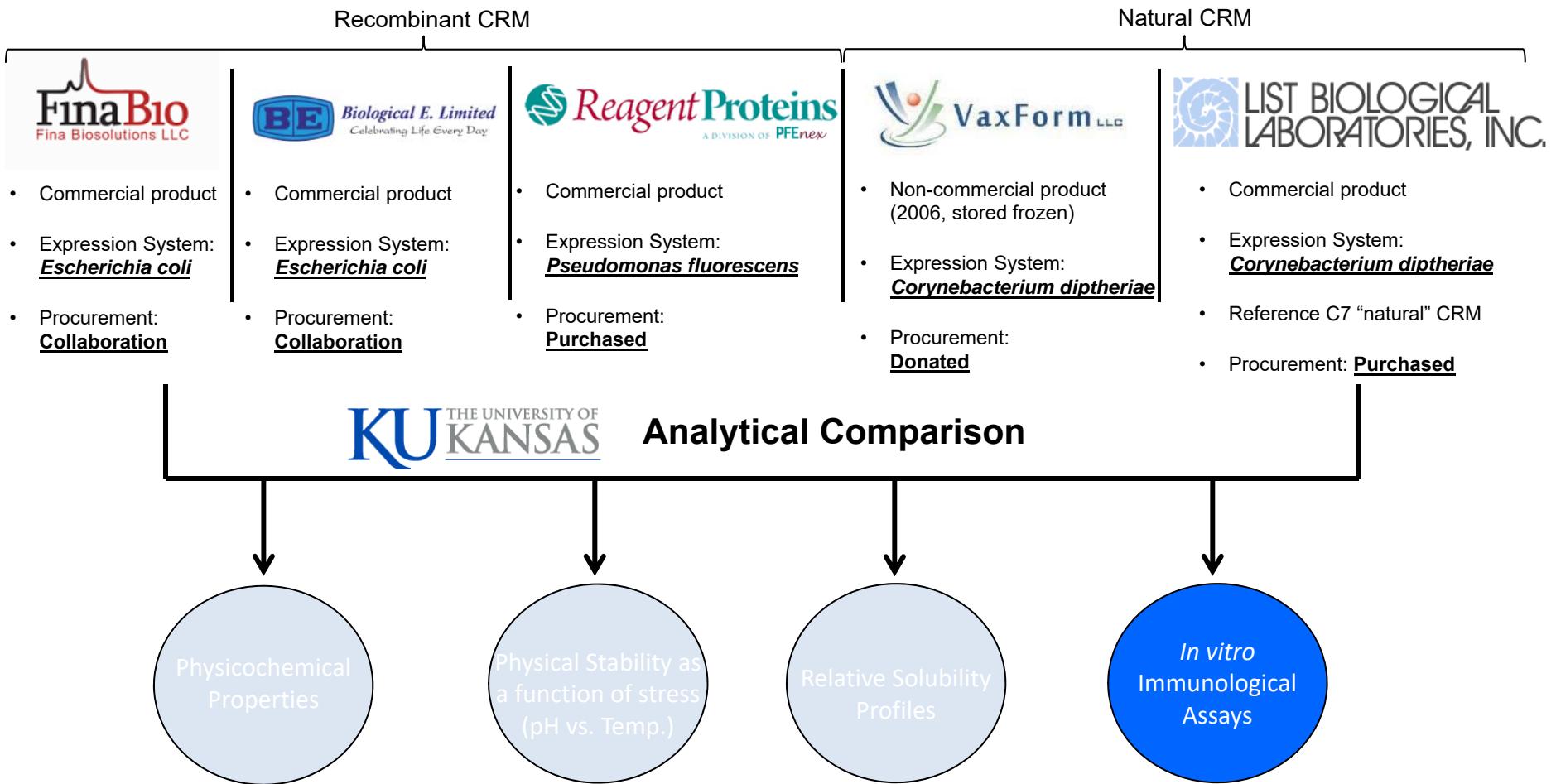


Overall Conformational Stability as a Function of Temperature

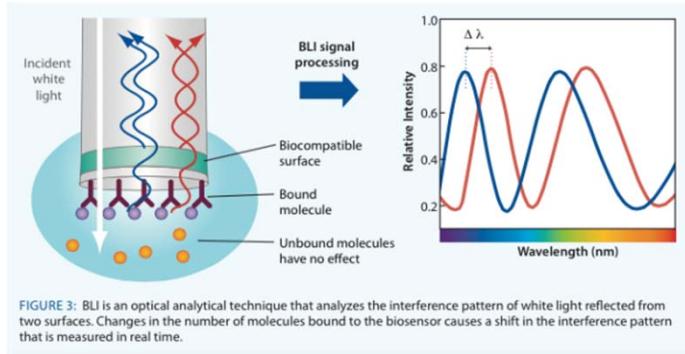


Source	CRM	T _{onset} (°C) Mean ± 3SD	T _{M1} (°C) Mean ± 3SD	T _{M2} (°C) Mean ± 3SD
Recombinant	rCRM	35.0 ± 0.2	42.8 ± 0.1	51.1 ± 0.1
	EcoCRM	32.7 ± 0.3	42.0 ± 0.1	51.3 ± 0.2
	Pfenex CRM	34.8 ± 0.2	42.8 ± 0.1	51.1 ± 0.2
Natural	Vaxform CRM	33.5 ± 0.2	42.8 ± 0.1	51.1 ± 0.3
	C7 CRM	35.2 ± 0.6	44.0 ± 0.1	51.7 ± 0.1

n = 3



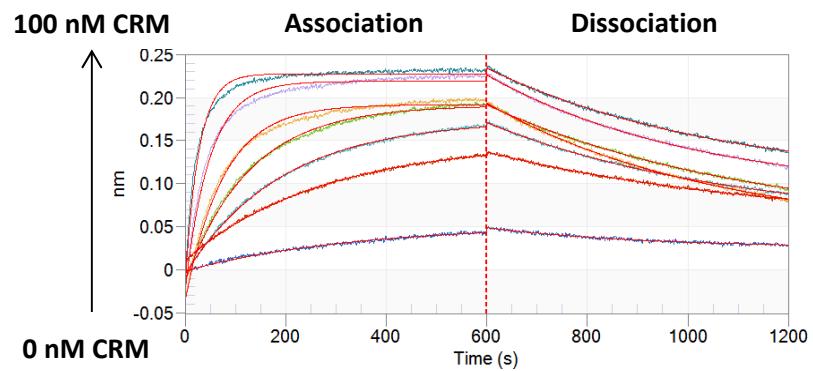
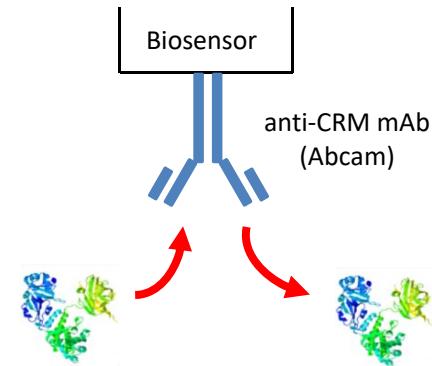
Measuring binding affinity between CRM and mAbs



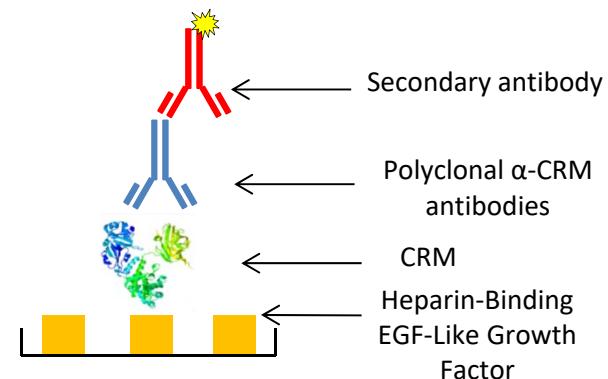
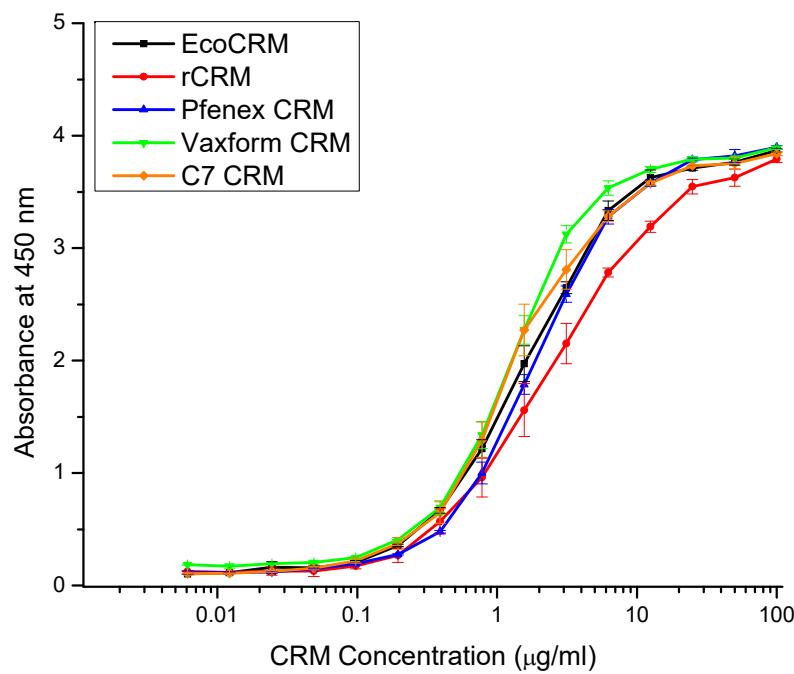
Pall Life Sciences 2013

Source	CRM	K_{on} ($M^{-1} s^{-1}$) Mean \pm 3SD	K_{off} (s^{-1}) Mean \pm 3SD	K_D Mean \pm 3SD
Recombinant	EcoCRM	$4 \pm 1 \times 10^5$	$1 \pm 1 \times 10^{-3}$	$3 \pm 5 \text{ nM}$
	rCRM	$5 \pm 1 \times 10^5$	$1 \pm 1 \times 10^{-3}$	$3 \pm 6 \text{ nM}$
	Pfenex CRM	$5 \pm 2 \times 10^5$	$1 \pm 1 \times 10^{-3}$	$3 \pm 5 \text{ nM}$
Natural	Vaxform CRM	$5 \pm 1 \times 10^5$	$2 \pm 1 \times 10^{-3}$	$3 \pm 3 \text{ nM}$
	C7 CRM	$4 \pm 1 \times 10^5$	$2 \pm 1 \times 10^{-3}$	$5 \pm 6 \text{ nM}$

n = 3

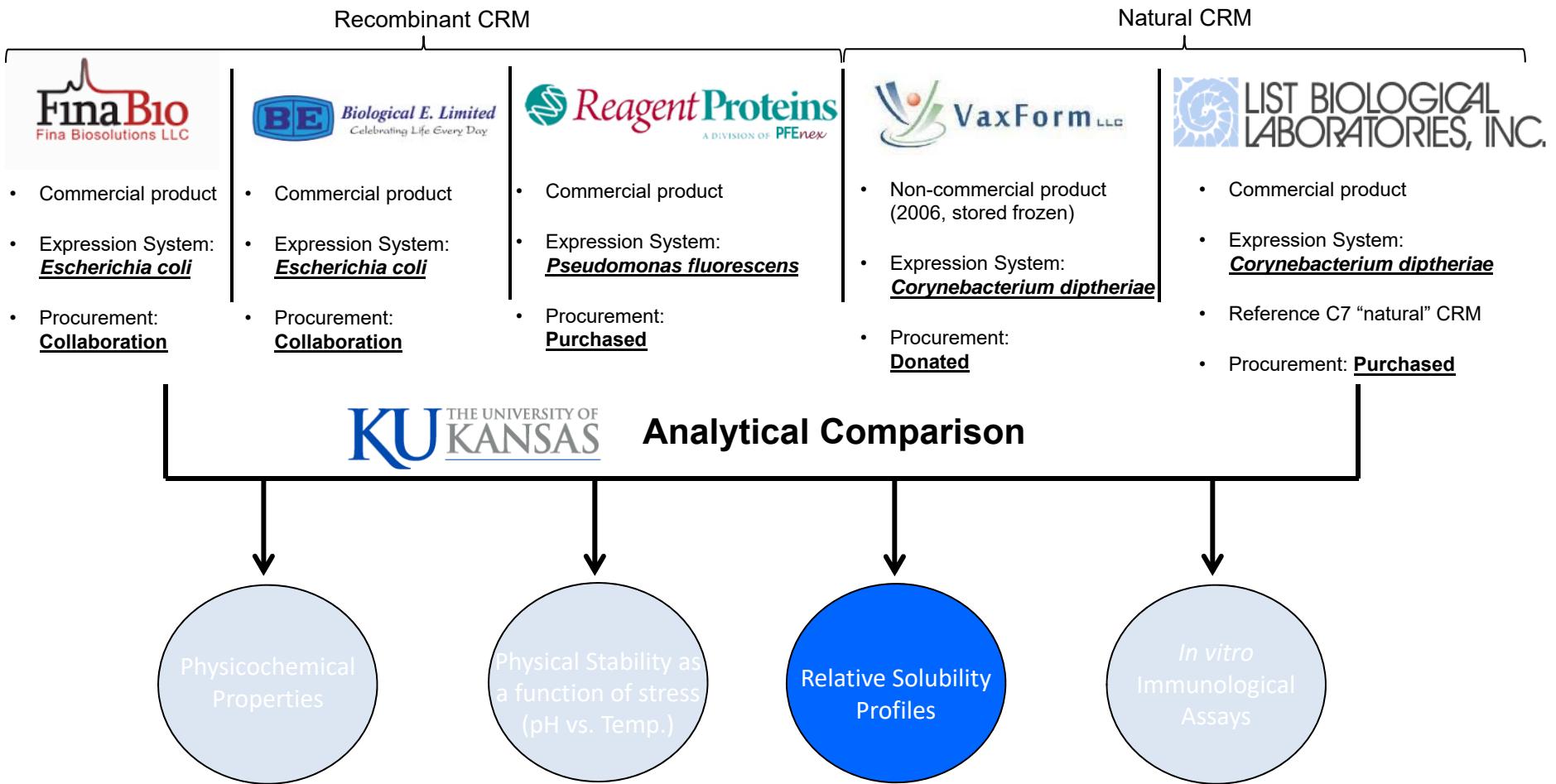


ELISA using polyclonal anti-CRM

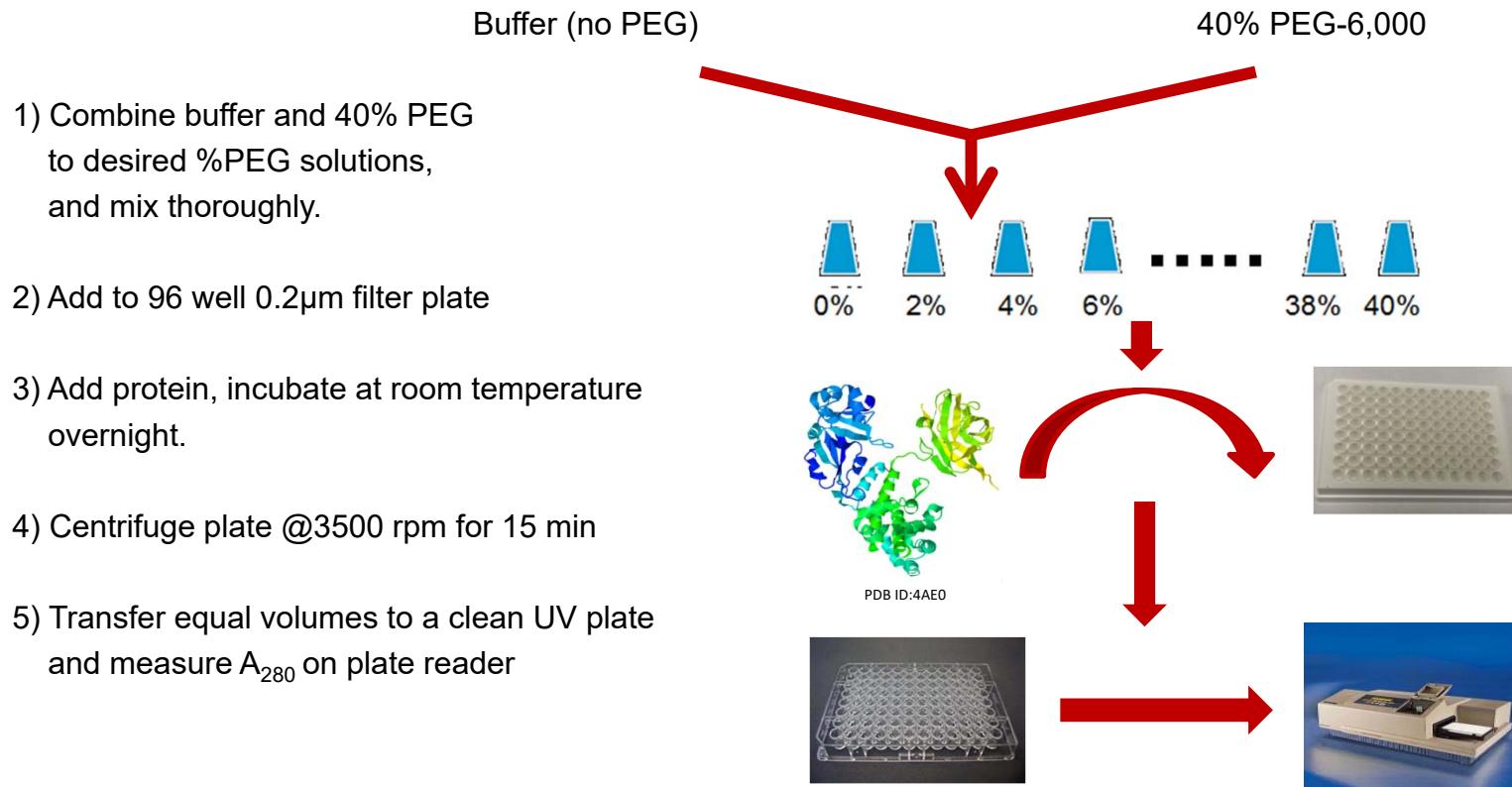


Source	CRM	LogEC ₅₀ Mean \pm 3SD ($\mu\text{g/ml CRM}$)	99% Confidence Interval ($\mu\text{g/ml CRM}$)	R ²
Recombinant	rCRM	2.3 \pm 0.9	1.5 to 3.1	0.97
	EcoCRM	1.6 \pm 0.9	0.9 to 2.3	0.99
	Pfenex CRM	1.8 \pm 0.3	1.4 to 2.2	0.99
Natural	Vaxform CRM	1.3 \pm 0.3	1.1 to 1.5	0.99
	C7 CRM	1.3 \pm 0.3	1.0 to 1.6	0.98

n = 3

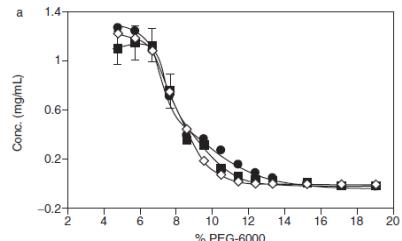


PEG relative solubility of CRM molecules (Overview of PEG assay)



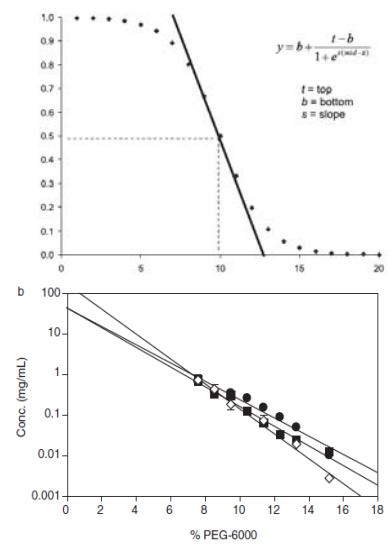
Data analysis from PEG Assay of CRM molecules

Three types of information can be obtained:



1) Overlaying of curves :

- To compare solution conditions for a single molecule
- To compare different molecules under similar solution conditions



2) % $\text{PEG}_{\text{midpt}}$:

is the weight% PEG in solution required to decrease the protein concentration by 50%.

- Quicker way of relative solubility assessments, and for high throughput apparent solubility screening of different molecules.

3) Apparent solubility (thermodynamic activity):

calculated based on assumptions (not shown) and resulting in the equation.

$$\log S_p = \log a_0 - A_{12}[\text{PEG}] \quad \text{where:}$$

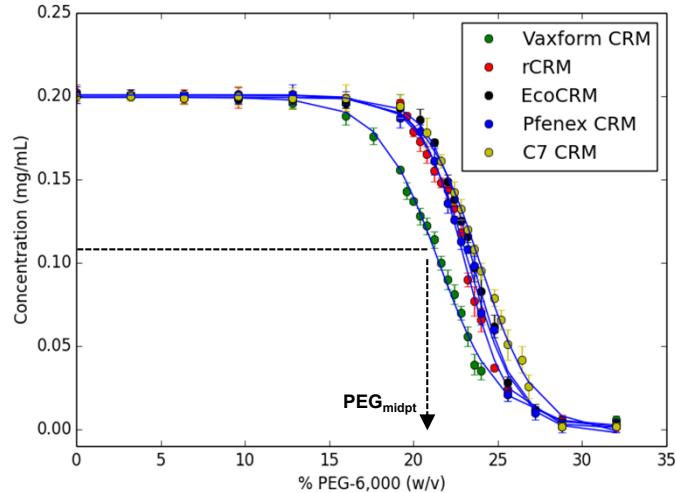
S_p is the concentration of soluble protein in a solution containing PEG-precipitated protein in equilibrium with soluble protein

a_0 is the activity of the protein in a saturated PEG-free environment

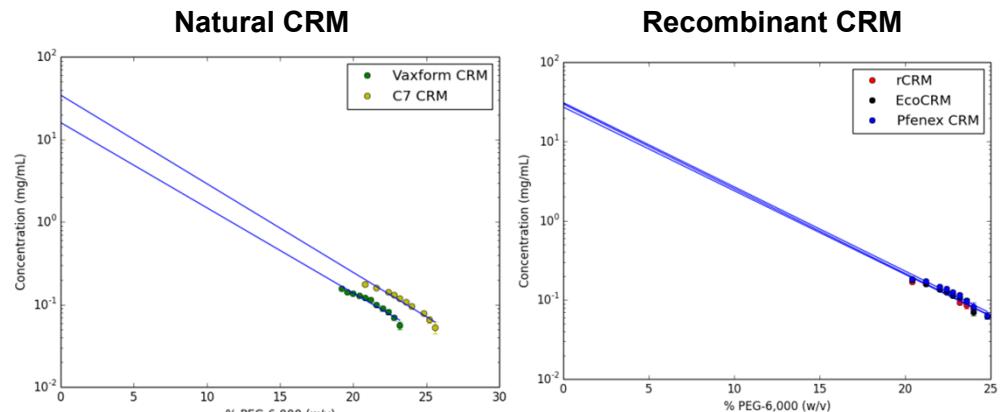
A_{12} is virial coefficient

Relative PEG solubility of CRM molecules in PBS pH 7.2

$\text{PEG}_{\text{midpt}}$: PEG concentration at which 50% of the protein has precipitated out of solution



Apparent Solubility



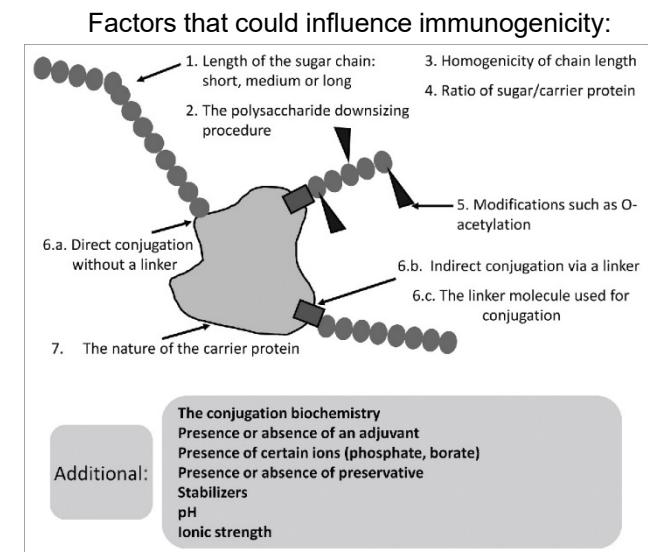
Source	CRM	% $\text{PEG}_{\text{midpt}}$ (w/v) (Mean \pm 3SD)	Apparent Solubility (mg/ml) (Mean \pm 3SD)
Recombinant	rCRM	23.0 ± 0.2	27 ± 9
	EcoCRM™	23.3 ± 0.2	30 ± 12
	Pfenex CRM	23.5 ± 0.1	31 ± 11
Natural	Vaxform CRM	21.5 ± 0.2	16 ± 10
	C7 CRM	24.0 ± 0.2	34 ± 12

n = 3

Pharmaceutical Quality/CMC of CRM

- Can be used to assess comparability, lot-to-lot variability, process changes, etc.

Structural Attribute	Analytical Techniques
Protein Concentration, Purity, and Proenzyme "nicking"	UV-Visible Spectroscopy
	SDS-PAGE (Reduced vs. Non-reduced)
Primary Structure	Intact Mass
	Peptide Mapping
Additional Assays for Primary Structure/Protein Heterogeneity (Purity)	Capillary Isoelectric Focusing (cIEF)
	Anion Exchange Chromatography (AEX)
Secondary Structure	Far UV Circular Dichroism
Tertiary Structure	Intrinsic Fluorescence Spectroscopy
Overall Conformational Stability vs. Temperature	Differential Scanning Calorimetry (DSC)
Characterization of Size and Presence of Aggregates	Size Exclusion Chromatography (+/-MALS)
	Archimedes (RMS)
	Micro Flow Imaging (MFI)



- Critical quality attributes?
- Polysaccharide conjugation and immunogenicity of recombinant vs. natural CRM?