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Field-Flow Fractionation (FFF) in Protein Purification and Characterization

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- What is Field-Flow Fractionation?
- Asymmetrical flowFFF- Analytical advantages
- FFF-MALS an informative combination
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- FFF SEC in comparison
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- Sedimentation FFF in glycosylation analysis a method under development

FIELD-FLOW FRACTIONATION: An Alternative to Chromatography ideal for Characterization of Colloids and Macromolecules



Flow field: elution time t_r prop. to size

Sedimentation field: *t*_r prop. to mass

Asymmetrical Flow FFF channel with downstream central injection (DCI) and trapezoidal outline



Upper block non-permeable for the crossflow (but permeable for light!)

Wahlund, Giddings Anal. Chem. 1987; Wahlund, Litzén J. Chromatogr. 1989; Litzén, Wahlund Anal. Chem. 1991

Illustration of the tapered trapezoidal asymmetrical flow FFF channel



Asymmetrical Flow FFF



FFF – and multiangle light scattering (FFF - MALS)

Provides directly (without calibration) the molar mass and radius distributions

From $I_{scattered}$ and θ the molar mass and rootmean-square radius of the sample can be directly determined $\theta = 0^{\circ}$



FFF - MALS - RI



Channel thickness 100-300 μ m, length ~ 30 cm, width ~ 2 cm.

The *Eclipse 2*: Accommodating needs of the pharmaceutical industry



- High degree of integration with Wyatt detectors and Agilent 1100 get the AF4 system accepted
- IQ/OQ available for the complete system

The Eclipse is manufactured in Germany by Wyatt Technology Europe

Oligometric aggregates of the 52kDa protein α 1-antitrypsin



Field-Flow Fractionation Handbook (2000); Courtesy of Mikael Nilsson, Technical Analytical Chemistry, Lund University, Sweden; (1997)

Standard proteins containing aggregates



The carrier was 0.025 M phosphate buffer at pH 6.5. Vin = 7.9 mL/min; Vout = 0.5 mL/min; Vc = 7.4 mL/min. Temperature: 25 °C. Channel thickness: 122 µm. Ultrafiltration membrane: Hoechst NADIR UF10-C regenerated cellulose.

Field-Flow Fractionation Handbook (2002); Courtesy of Mikael Nilsson, Technical Analytical Chemistry, Lund University, (1997)

Protein aggregates analysed by

flow FFF-TALS-RI

Eluent outlet from asymmetrical flow field-flow fractionator coupled on-line to a flow-through triangle laser light scattering (TALS) detector and a refractive index (RI) (or UV) detector. Protein: <u>ferritin</u> (440 kDa); flowrate: 1.28 ml/min



Measurement on BSA

molar mass vs. time/volume

BSA 1mgmL 60uL 490um 3zu1 04[5Runs].vaf



Courtesy Dr. Christoph Johann, Wyatt Technology Europe.

AF4 AND SEC Analysis of two Monoclonal Antibodies



SEC: TSK Column, G 3000 SW. Flow rate: 1.0 mL/min.

Reproduced from: Litzén, Walter, Krischollek and Wahlund, **Anal. Biochem.** <u>212</u> (1993) 469-480.

RECENT HIGH PROFILE USE OF AF4



Architecture of transmitter transport





J.R. Silveira et al., Nature 437 (2005) 257-261

The SdFFF system



 $R=t^0 / \ te \approx 6 \ \lambda$





Homogenous: $\lambda_{SFFF} = kT/[m(\Delta \rho/\rho_p) Gw] = 6kT/[d^3\Delta \rho \pi Gw]$

Layered: $\lambda_{SFFF} = kT/[m_A(1-\rho_{car}/\rho_A) + m_B(1-\rho_{car}/\rho_B) + + +]Gw$

Aim:

The Nanoparticle Microarray Platform for Glycoprotein Mapping



Side view; Different colors represent different lectins

Quantification of mass uptake per particle



Fromell et al. Colloids and Surfaces B. Biointerfaces, (2005) 46, 84-91.

Glycoprotein binding to latex-ConA



1.3-5 ng protein/sample

| Row | Sample | Intensity |
|-----|---------------|----------------|
| 1 | HSA | 171 ± 108 |
| 2 | Ovalbumin | 1301 ± 540 |
| 3 | Fetuin | 714 ± 144 |
| 4 | Thyroglobulin | 1311 ± 468 |
| 5 | Man-BSA | 3765 ± 1157 |
| | | |

SUMMARY

- Field-Flow Fractionation takes place in unobstructed channels with minimal shear stress on sample components
- Migration is well described by existing theoretical models
- The working field strength is selected by the operator for optimal resolution of a given sample
- FFF-LS provides real-time evidence for mass/size selectivity, especially suited for detection of aggregates
- Through sedFFF analysis of lectin-decorated particles and their interactions with glycoproteins we can gather information on glycosylation patterns