

**Protein-sugar interaction:
Surface Plasmon Resonance (SPR) biosensor
analysis
(Biacore™ technology)**

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Overview

- Presentation of the Biacore™ technology
- Basic principles of SPR
- SPR detection and interaction analysis
- A typical interaction study
- SPR and lectin-carbohydrate interactions
- Examples

The Biacore™ technology



- **Label-free, real time** detection and monitoring of **biomolecular interactions**, based on **SPR**
- Information on a wide range of **interaction parameters**:

Specificity

YES/NO binding response

Concentration

How MUCH?

Affinity

How STRONG? K_D , K_A

Kinetics

How FAST? Rate constants k_a , k_d

Thermodynamics

Affinity and kinetics vs temperature

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Basic Principle of the Biacore™ technology



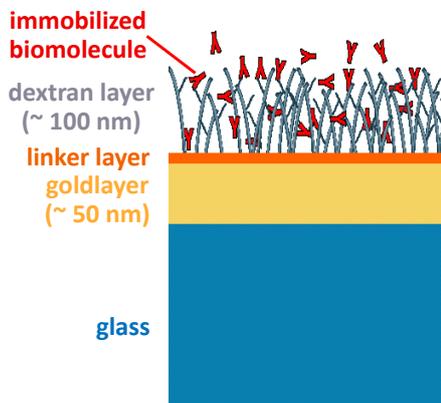
- A binding molecule (**ligand**) is immobilized on a sensor surface
- The target molecule (**analyte**) is passed over the surface in a continuous buffer flow through a microfluidic system
- Analyte binding to the immobilized ligand is detected using SPR



Biacore T200

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The biospecific surface (sensor chip)



The carboxymethylated (CM) dextran matrix (Biacore)

- Hydrophilic
- Easy use for covalent coupling
- High binding capacity
- Low non-specific binding
- Flexible => immobilized ligands can move to a certain extent on the surface
- High chemical resistance

Other matrices

BioRad: alginate

Xantec 3D hydrogel: agarose, alginate, PEG, cellulose, pectin

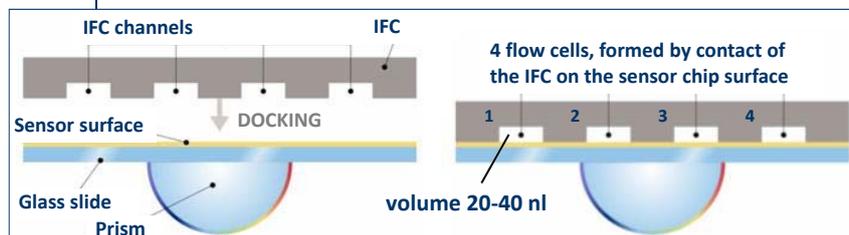
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Liquid handling

Integrated micro Fluidics Cartridge (IFC)



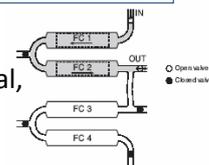
Miniaturized system
Integrated and automated liquid handling



Individual or serial use of the flow cells

Automatic reference signal subtraction from sample signal, using flow cells 1 or 3 as references

Constant analyte concentrations at the sensor surface

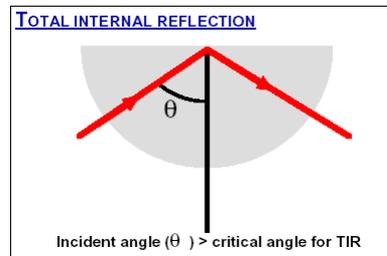
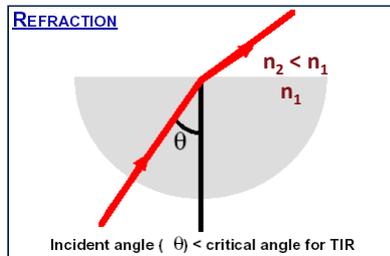


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How does SPR work?



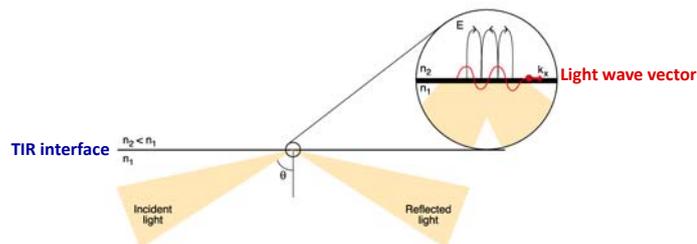
Total internal reflection (TIR)



Light entering the glass semi-circular prism (refractive index $n_1 \sim 1.5$) undergoes **total internal reflection** at the interface with the medium of a lower refractive index (buffer, $n_2 \sim 1.33$) at an angle of incidence above a critical angle (θ)

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Creation of the evanescent field wave

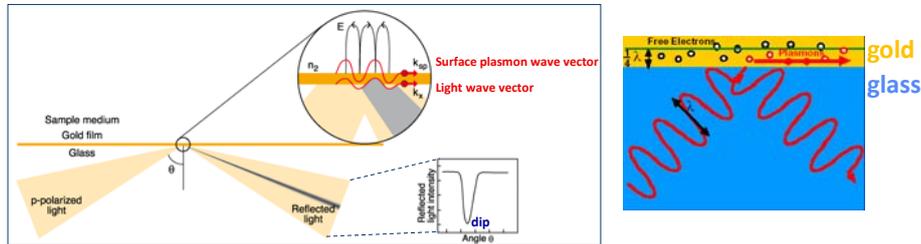


A light electromagnetic component, called **evanescent wave**, enters the low refractive index medium over a short distance from the TIR interface (evanescent field).

The amplitude of this wave decreases exponentially with distance, decaying over a distance of about one wavelength from the surface.

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Surface plasmon resonance (SPR)

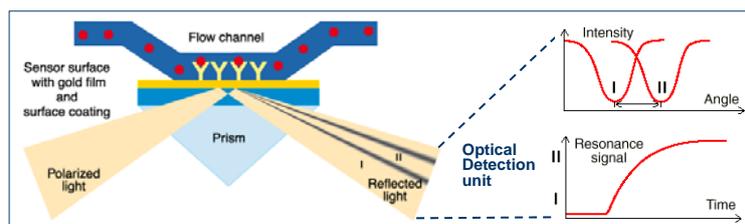


The interposition of a **gold** film at the interface generates a **resonance** phenomenon between free electrons at the metal surface and incident photons, yielding a loss of energy in the reflected light => SPR is seen as a **dip** in the intensity of reflected light at a specific angle of incidence (θ).

The conditions for SPR are sensitive to the **refractive index (RI)** of the medium in which the evanescent wave propagates

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How does BIAcore use SPR to detect biomolecular interactions?



- The detector continuously records the position of reduced light intensity and calculates the SPR angle
- Biomolecular interactions at the sensor surface change the RI within the evanescent wave penetration range
=> the angle of incidence required to create SPR is altered
=> this change is measured as a response signal

$$10^{-6} \text{ RI change} \Leftrightarrow 10^{-4} \text{ deg deviation} \Leftrightarrow 1 \text{ RU (Resonance Unit)} \\ \Leftrightarrow 1 \text{ pg bound/mm}^2 \text{ surface}$$

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SPR detection and interaction analysis



- Importance of the buffer refraction index (DMSO, glycerol)
- RI values for glycoproteins, lipoproteins and nucleic acids of the same order of magnitude => mass detector essentially independent of the nature of the interactants
- SPR observed within a short distance from the gold interface: no quantitative analysis possible for analytes of big size (supramolecular assemblies, microorganisms, cells)
- Soluble analyte not penetrated by incident light => measurements possible on turbid or opaque samples
- Real-time measurement => kinetics (not necessary to reach equilibrium)
- Detection limit: 100-180 Da (Biacore T100-3000)

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A typical interaction study

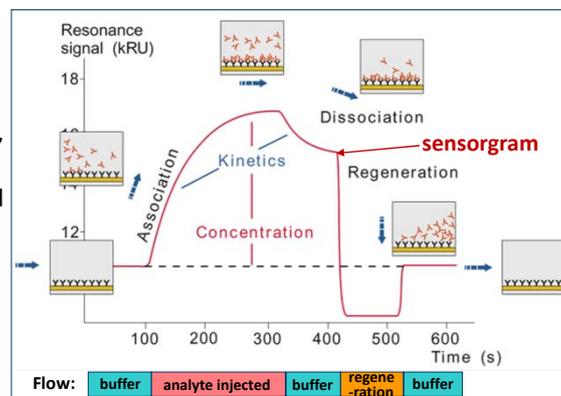


- Immobilization of the ligand on the sensor chip (+ reference surface)
- Injection of the analyte on immobilized ligand and reference surfaces
- Regeneration of the surface
- Data evaluation

Reference surface:

- mock surface (activated/blocked, capture surface without ligand)
- similar but non-interacting ligand (BSA, scrambled peptide)

Flow rate : 1 - 100 μ l/min
Sample volume : 5 - 750 μ l
Temperature : 4 - 40°C

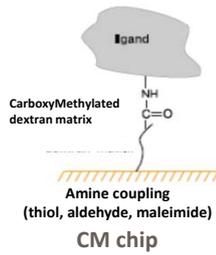


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Immobilization Strategies

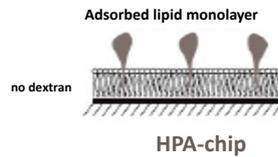


Covalent binding

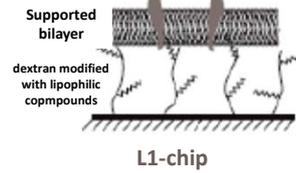


Direct coupling

Membrane-bound proteins



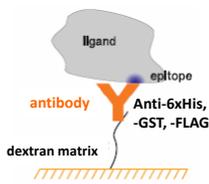
Integral membrane proteins



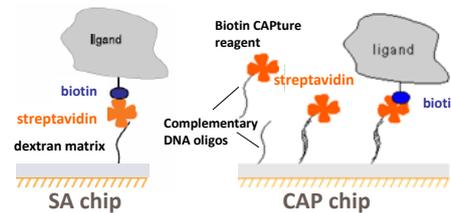
Indirect coupling

Via a capture molecule covalently coupled to a CM chip

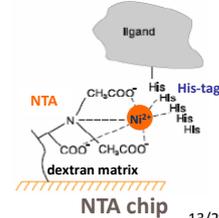
Antibodies



Biotinylated ligands



His-tagged ligand



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Regeneration strategies



- The activity of the immobilized ligand must remain unaffected
- Regeneration solution selected according the nature of the interaction (if known)
=> **specific regeneration** (interaction competitor (**sugar**), EDTA)
- Mild to more stringent conditions applied

Strength	Acidic	Basic	Hydrophobic	ionic
Weak	pH > 2.5 formic acid, HCl 10 mM Gly/HCl	pH < 9 10 mM Hepes/NaOH	pH < 9 50% ethylene glycol	1 M NaCl
Intermediate	pH 2- 2.5 formic acid, HCl, H ₃ PO ₄ 10 mM Gly/HCl	pH 9-10 NaOH 10 mM Gly/NaOH	pH 9-10 50% ethylene glycol	2 M MgCl ₂
Strong	pH < 2 formic acid, HCl, H ₃ PO ₄ 10 mM Gly/HCl	pH > 10 NaOH	pH > 10 25-50% ethylene glycol	4 M MgCl ₂ 6 M GdnCl

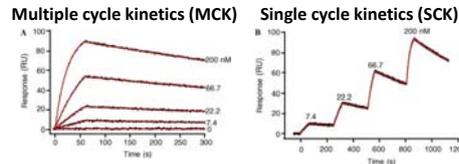
Nucleic acids, heparin: 0.2-0.5% SDS

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Data evaluation (BIAeval software)



- Global fitting of experimental data from several concentrations to a predefined model



- Determination of **kinetic constants** (Langmuir 1:1)
 - association rate constant (k_a) : $10^3 - 10^7 \text{ M}^{-1}\text{s}^{-1}$
 - dissociation rate constant (k_d) : $5 \times 10^{-6} - 0.5 \times 10^{-1} \text{ s}^{-1}$
- Determination of **affinity constant (K_D)**
 - from the kinetic constants: $\text{app } K_D = k_d/k_a$ (50pM -100 μM)
 - from equilibrium analysis (steady state model)
- Evaluation of fitting quality (acceptable statistics: residuals, Chi^2)
- Biological and experimental relevance of the calculated parameters (R_{max})

SPR: principles and use

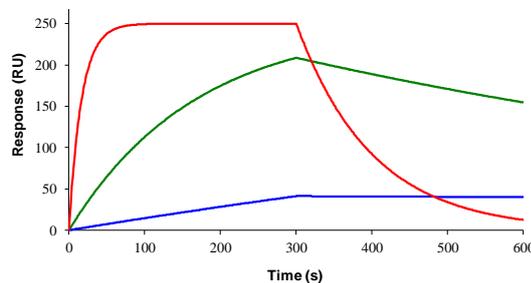
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Relevance of binding kinetics



The same affinity (identical K_D) can be resolved into different kinetic rate constants for different interactions

k_a : driven by **molecular recognition** \neq k_d : driven by **complex stability**



k_a ($\text{M}^{-1}\cdot\text{s}^{-1}$)	k_d (s^{-1})
— 10^5	10^{-3}
— 10^4	10^{-4}
— 10^6	10^{-2}

$$K_D = k_d/k_a = 10^{-8} \text{ M}$$

Kinetic properties are critical to the **therapeutic performance of drugs** and affect multiple functional aspects (pharmacokinetics, dosing)

Rapid kinetics => frequent administration of low dose required to occupy target

Slower kinetics => administration of high dose occupies target for long time

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Some limitations of Biacore™ SPR



- **Kinetics**

- typical k_a values range: 10^3 to 10^7 $M^{-1} s^{-1}$
- typical k_d values range: 10^{-5} to $0.5-1$ s^{-1}

To avoid mass transport (diffusion of the analyte from the bulk to the surface vicinity) limitation: use high flow rate and low immobilized ligand level

- **Affinity**

typical K_D range: 5×10^{-11} - 10^{-4} M

Equilibrium measurements: time to reach equilibrium determined primarily by k_d
=> high affinity interactions ($K_D < 10$ nM) with very slow k_d values unsuitable for equilibrium analysis

- **Small molecules**

<100 Da: difficult to detect

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SPR and lectin-carbohydrate interactions



Carbohydrate-protein interactions in biological systems mostly occur among **multivalent partners**

Affinity: describes the binding of a monovalent ligand to its partner

Avidity: takes into account multivalent interactions between partners

=> apparent enhanced functional affinity

Potency enhancement in multivalent ligands can result from different mechanisms, including clustering, chelation and statistical rebinding effects
=> may be exploited for generation of lectin inhibitors.



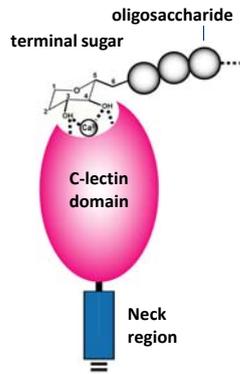
SPR => importance of immobilized partner choice and of ligand surface density

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Avidity in carbohydrate pattern recognition by the innate immune recognition protein mannan-binding lectin (MBL)

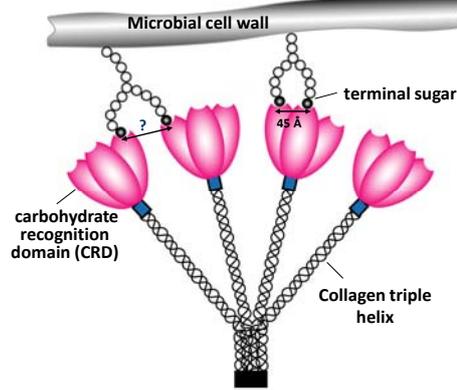


Lectin domain-micropattern interaction



Low affinity ($K_D > 10^{-3}$ M)
1:1 interaction

MBL-macropattern multivalent interaction



High affinity ($K_D \sim 10^{-9}$ M)
Multivalent interaction

Adapted from Hoffmann et al (1999) *Science* 284:1313

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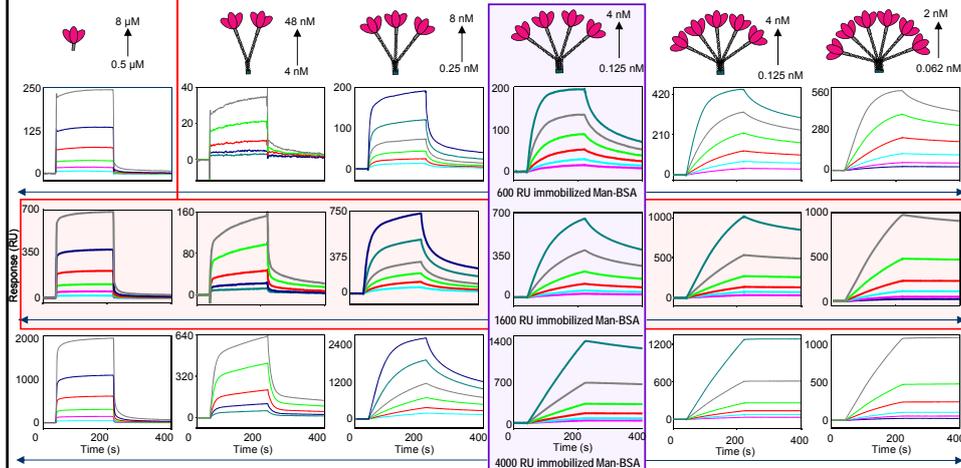
Avidity in the context of SPR analysis MBL-neoglycoconjugate (Man-BSA) interaction



Immobilized glycoconjugate - soluble lectin

Effect of lectin oligomerization

Effect of surface density



SPR: sugar-lectin interactions

Gjelstrup et al (2012) *J Immunol* 188:1292

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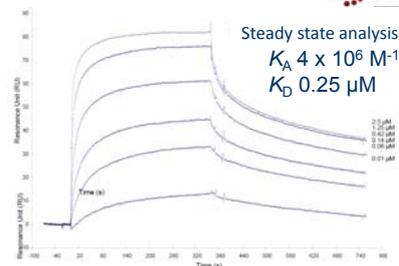
Lectin-carbohydrate interactions



Lectin immobilized - soluble glycoconjugate

- **Direct binding**

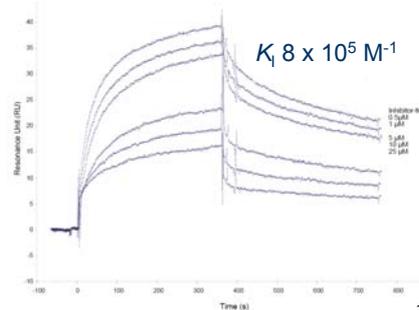
- Immobilized ectodomain of the macrophage mannose receptor
- Soluble glycoprotein (Man-BSA) (0.0125-2.5 μM)



Duverger et al (2010) *Methods Mol. Biol.* 627:157

- **Inhibition study**

- Immobilized ectodomain of the macrophage mannose receptor
- Soluble Man-BSA (0.125 μM) injected in the presence of $(\text{Man}\alpha 2\text{man})_4\text{Lys}_3$ glycocluster (0.5-25 μM)
- Estimation of the lectin-glycocluster affinity from the inhibition of Man-BSA binding to the lectin

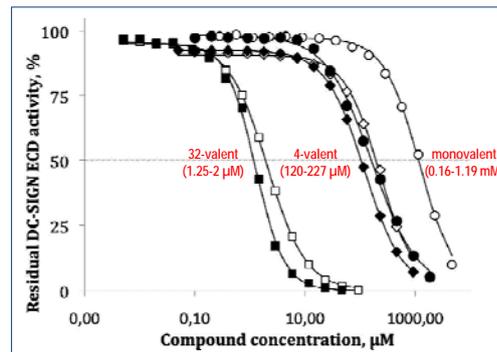
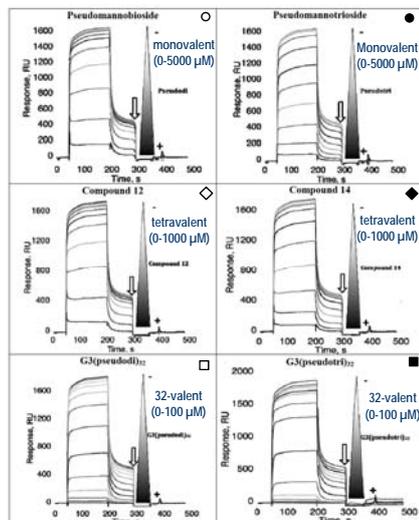


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Inhibitors of lectin-carbohydrate interactions



- Glycoconjugate (BSA-mannotriose) immobilized
- Soluble ectodomain of DC-SIGN receptor (20 μM) injected in the presence of increasing concentrations of multivalent glycomimetics (pseudomanno-bioside and -trioside compounds)
- Steady state response => conversion to lectin residual activity => **IC₅₀ determination**



Strong antiviral activity found for the higher valency compounds with IC_{50} in the nM range => new compounds in anti-viral strategy

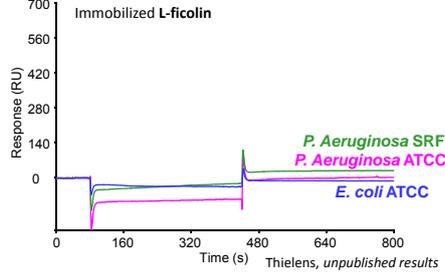
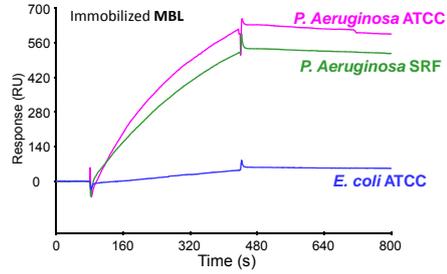
Luczkowiak et al (2011) *Bioconjugate Chem.* 22, 1354

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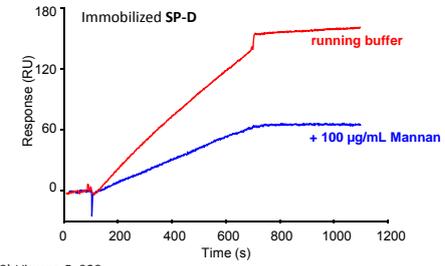
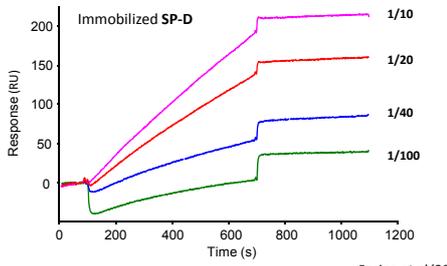
Cell-lectin interaction



Injection of soluble bacteria (10^8 CFU/ml)



Injection of soluble inactivated vaccinia virus (stock: eq 2×10^{10} CFU/ml)



Perino et al (2013) *Viruses*, 5, 928

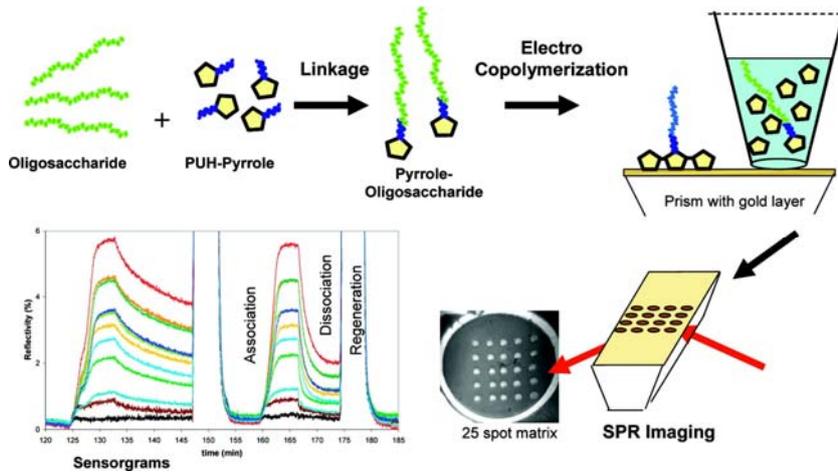
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Screening of lectin-carbohydrate interactions



SPR imaging (SPRi)

Oligosaccharide array for the measurement of glycosaminoglycan (GAG)-protein interactions



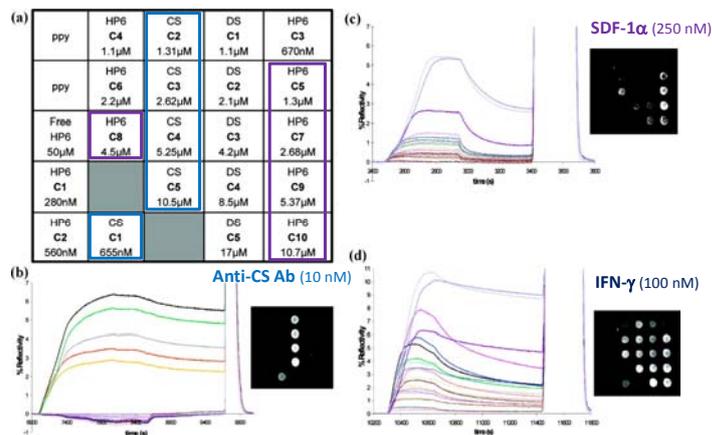
Mercy et al (2008) *Anal. Chem.* 80, 3476

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SPRI of GAG-protein interactions



GAG: negatively charged glycans => regulate the activity of growth factors and cytokines
 - Pyrrole-GAG spotted: 6 kDa heparin (HP6), chondroitin sulfate (CS), dermatan sulfate (DS)
 - Proteins used: stromal derived factor(SDF)-1 α , interferon(IFN)- γ , anti-CS IgM (control)



Mercey et al (2008) Anal. Chem. 80, 3476

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Useful References



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- Duverger E, Lamerant-Fayel N, Frison N, Monsigny M (2010) Carbohydrate-lectin interactions assayed by SPR. *Methods Mol. Biol.* 627: 157-78
- Shinohara Y and Furukawa J-I (2014) *Methods Mol. Biol.* 1200: 185-205
- [Several figures in this presentation were modified from those found in various Biacore® T100 Manuals, Handbooks and Brochures from www.biacore.com. © 2001-2007, Biacore AB]

Acknowledgements

SPR platform: Partnership for Structural Biology (PSB)
 UMS 3518/ISBG (Integrated Structural Biology Grenoble)

SPR experiments: IRPAS (Immune Response to Pathogens & Altered Self) team
 MP (Membrane and Pathogens) team
 SAGAG (Structure and Activity of GlycosAminoGlycans) team

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