

# PROTEIN CHIPS



# FROM GENOMICS TO PROTEOMICS

**PROTEOME** is the group of protein encoded by the genome.

The study of proteome is known as **PROTEOMICS**

- Proteins from any cell
- Isoforms
- Modified proteins
- Interactions among proteins
- Structural description of proteins
- Structural description of protein complexes
- Moreover: any post-genome thing

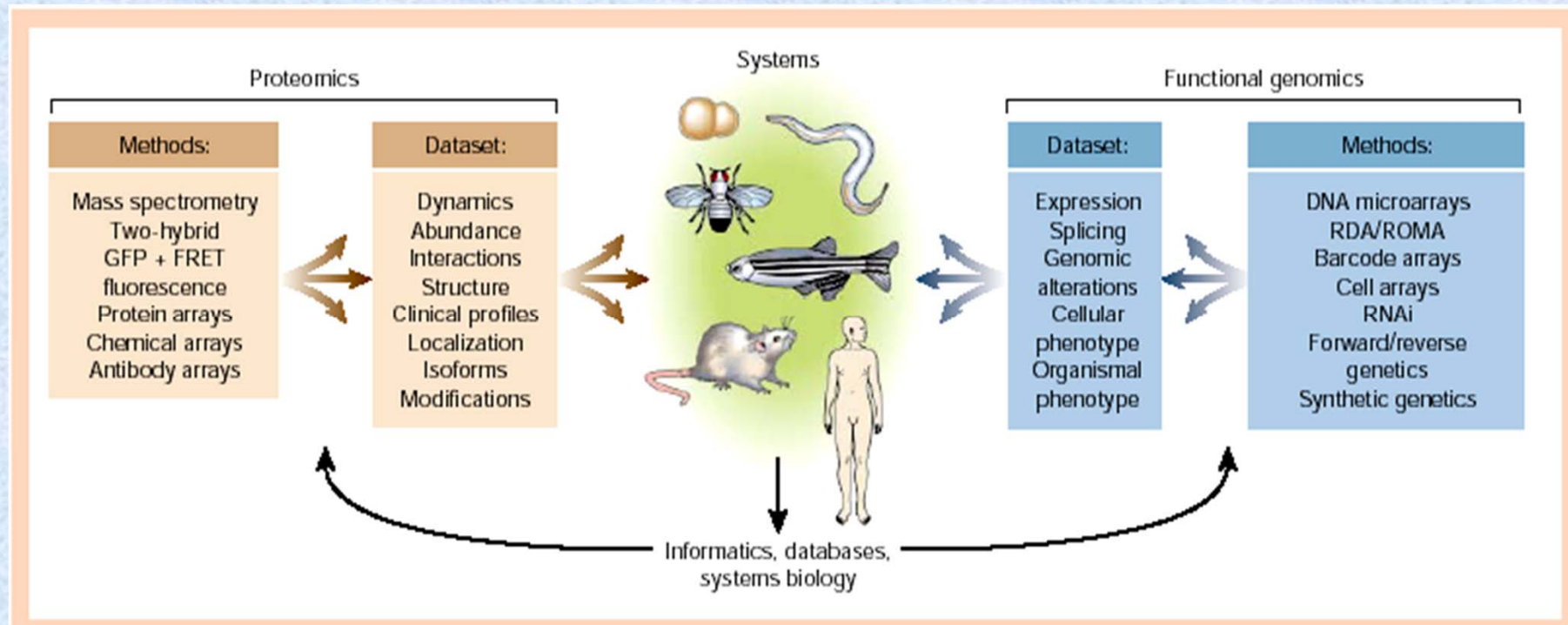


# High-throughput Biochemistry

**Proteomics** (nowadays): Protein biochemistry on a great scale, high precision and performance.

**Objectives:** Full description of cellular function

## Platforms for proteomics and functional genomics





# Proteomics scalability

**Genomics:** High scalability → PCR, automatic sequencers, etc.

**Proteomics:** LOW scalability. Reasons:

- Variable and limited material
- Sample degradation
- Very high dynamic range abundance ( $10^6$ )
- Frequent post-translational modifications
- Temporal and on-going specificity
- Pathological disruptions
- Pharmacological disruptions



# Protein analysis at proteomic scale

If we want to define:

- Identity
- Amount
- Structure
- Function

Of all or a group of proteins  
(within a cellular context)

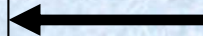
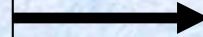
We would be able to:

Generate a group of  
**CLONES** expressing  
individual proteins of all  
or a part of a **PROTEOME**

Followed by:

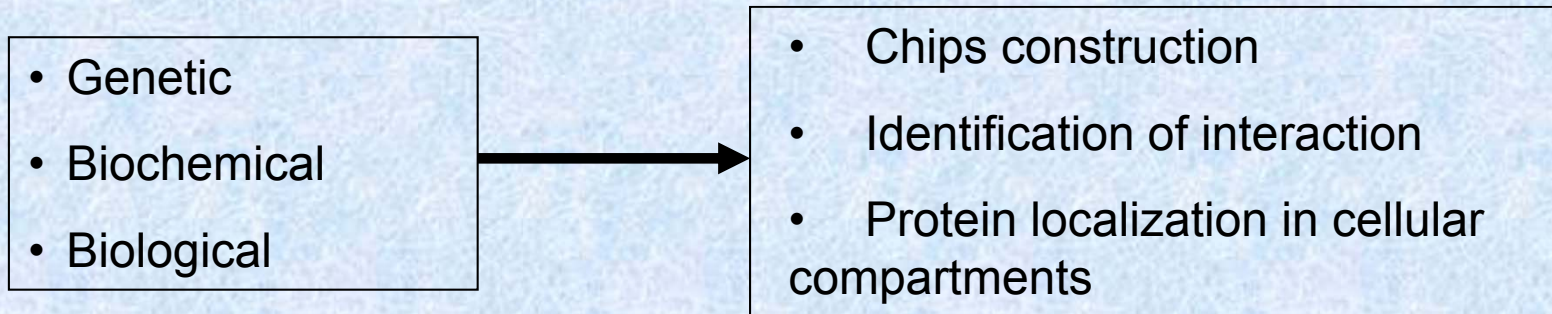
**ANALYSIS**

Proteins in a **READY-TO-USE**  
format





# NECESSARY TECHNIQUES



## 1. Expression and purification of proteins

## 2. Activity tests at proteomic scale

a) Biochemical genomic approximation

b) Microarrays

- Analytic

- Functional



# 1. Expression and protein purification

## ORF Localization

(open reading frame)

### Problems:

- Difficult localization (sometimes)
- Splicing signals
- Polyadenylation

## ORF Clonation

### Problems:

- It is a simplification
- A mRNA is selected and isoforms are discarded
- Post-translational modifications (phosphorilation, glycosylation, methylation, acetylation) should not be considered
- Inadequate for membrane proteins



# ORF Clonation

Requires:

- PCR primers
- Vector insertion

HT synthesis methods:

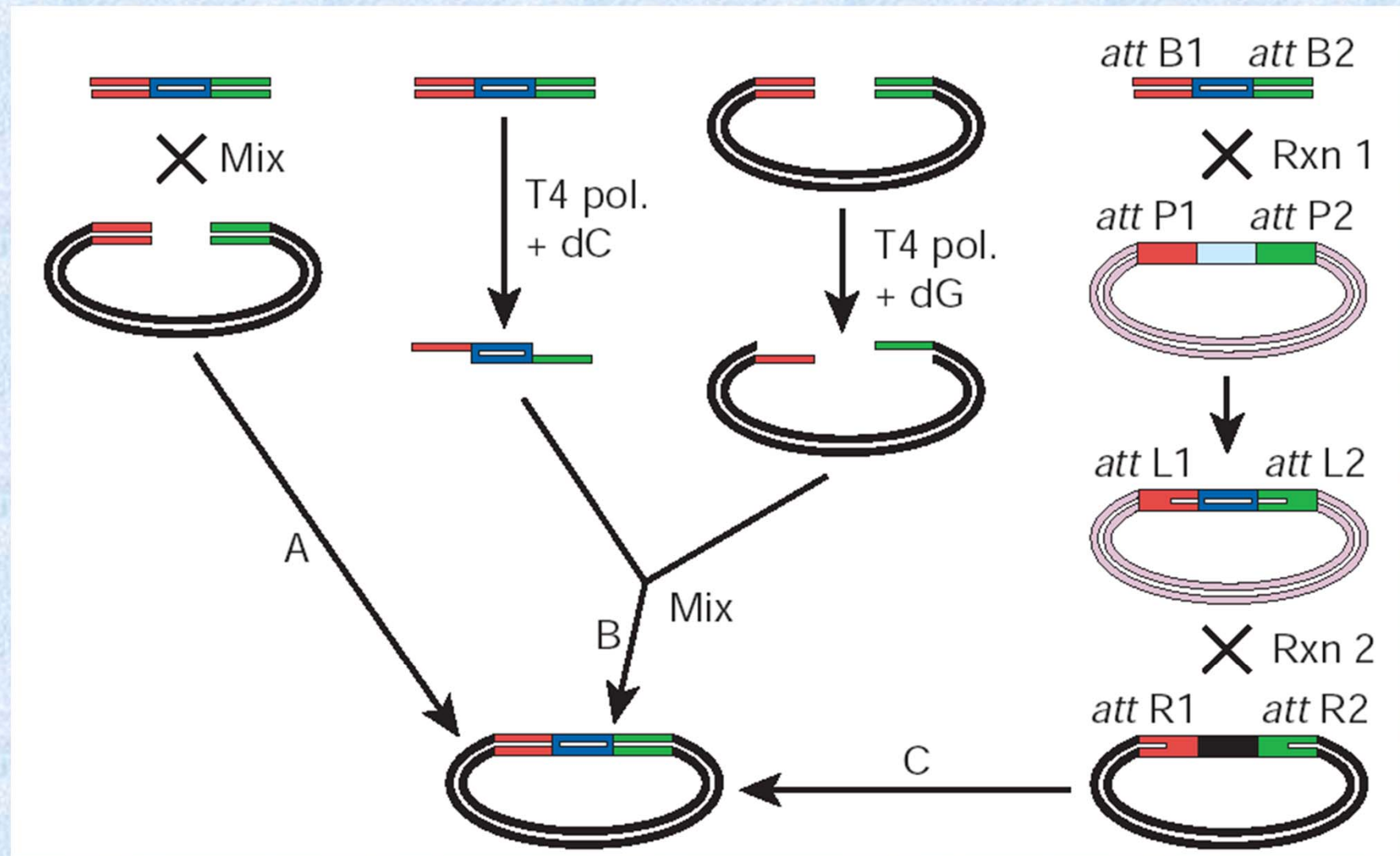
- Automatic synthesis
- Reasonable cost
- Speed and precision

## Vector insertion

- A) Recombination mediated by gap repairing
- B) Ligation independent clonage (T4 polimerase + dCTP or dGTP)
- C) Invitrogen Gateway System (from phage  $\lambda$  integration/split)



# Vector insertion





# Expression

**Homologue systems** → The best (post-translational modifications, interactions with protein pairs, etc)

**Heterologue systems** → Necessary for a great amount of organisms. One alternative is insect cells (similar modifications to mammals)

## Marker incorporation

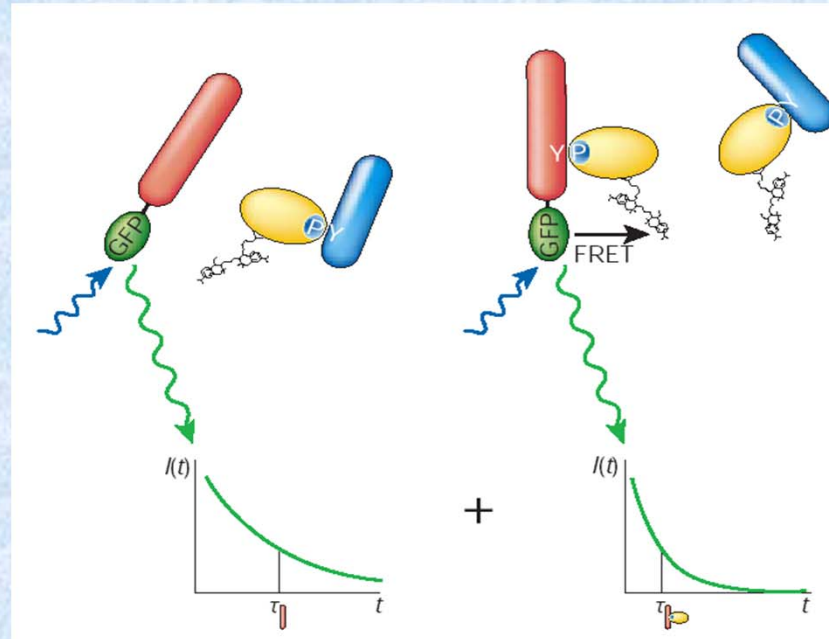
**Peptide or protein fusion to selected proteins**

High **AFINITY** and **SELECTIVITY**  
**ACTIVITY** preservation

- **Glutation-S-transferase** / glutation agarose
- **Hisx6** marker / Ni agarose
- Peptide to **calmoduline** linking / calmoduline agarose
- Protein A /  $\gamma$ -immunoglobuline
- **Protease** sites (trombine, TEV, etc), in addition to the aforementioned
- Maltose binding protein (MBP)
- Epitopes: hemaglutinine, **Myc** and FLAG
- **GFP** derivates. FRET Detection



# FRET GFP detection



## PROTEIN FUSION: GENERAL PROBLEMS

- Each fusion protein requires a different scheme and protocol
- There are proteins which cannot be purified
- There are proteins which become inactive after fusion



## 2. Protein activity at proteomic scale

a) Biochemical genomic approximation

b) Microarrays (Chips)

### a) Biochemical genomic approximation

Use of biochemical analysis in parallel to groups of proteins coming from a proteome. The objective is identifying a protein as responsible of a function.

GST-ORF Clonation → Expression and purification in groups of 96 →

Biochemical assay → Positive groups → Subgroups →

Subgroup assay → Positive (deconvolution)

#### ADVANTAGES:

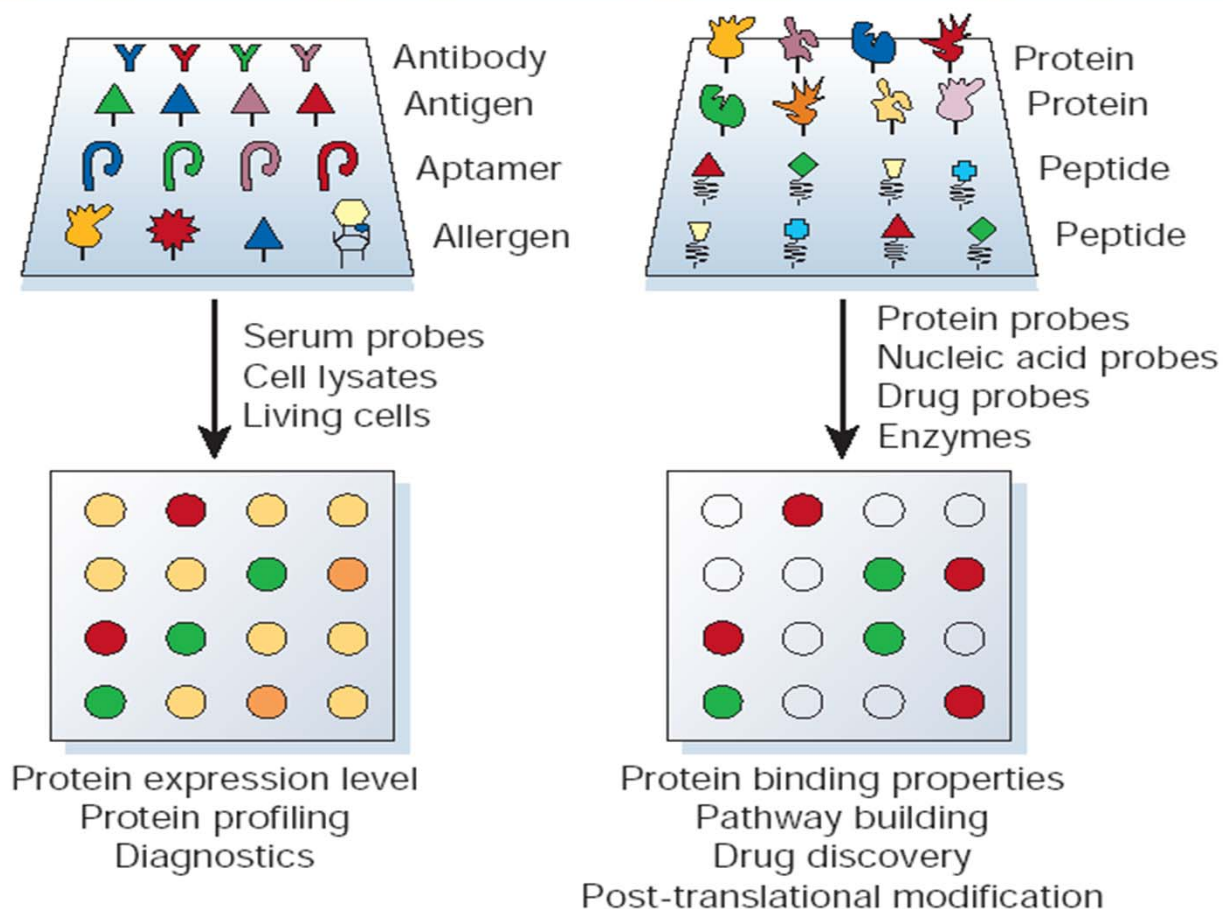
- Speed in function assignation to ORFs.
- Valid for any type of activity assay
- High sensibility
- Allows detection of protein complexes



## b) Microarrays

**Objective:** High performance analysis of genomic function, at a high scale, quick and cheap.

**Methodology:** individual purified proteins are deposited in a surface, generally a glass sheet to analyze its activity





# Comparison with DNA chips

## DNA chips:

- No direct information of genic function
- Easy to make

## Protein chips:

- Direct information of function
- Complex to make, as protein function is dependent of state, like post-translational modifications, interaction with other proteins, subcellular localization, reversible covalent modifications, etc.

# Chips manufacturing

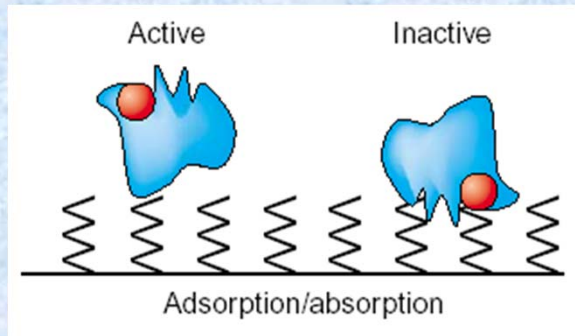
Must **retain** protein function

Must be **compatible** with manufacturing technologies

Must be in a **wet** environment



## Soft substrates



Polystyrene, nitrocellulose or PVDF surfaces are used.

Do not allow high density packing

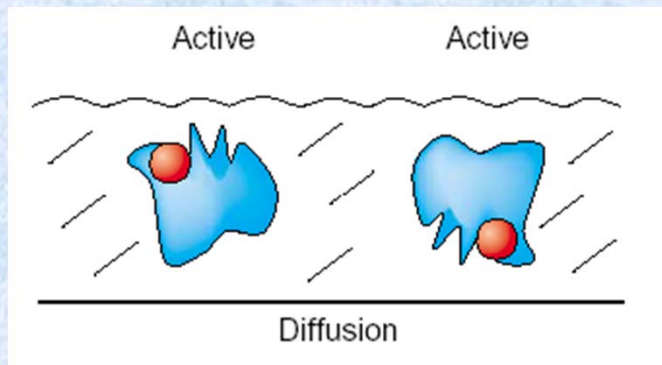
Application points disseminate the surface

Very low signal-noise

Random orientation

## 3D surface structures

- A thin polyacrylamide or agarose layer is prepared on glass
- Proteins are deposited by means of photolithography
- They are immobilised by cross-linking



### Advantages

High immobilization capacity  
Water environment  
Active proteins

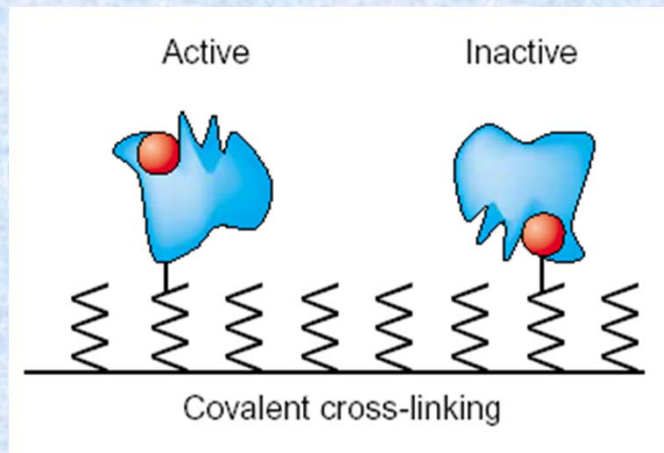
### Disadvantages

Difficult buffer change  
Difficult molecule recovery  
Random orientation



# Nanowells

Glass covered by PDMS  
Nanowells are made, in  
which proteins are deposited  
Proteins are immobilized by  
cross-linking



## Advantages

- High immobilization capacity
- Evaporation reduction
- Cross contamination minimized
- Background noise minimized
- They are open, so they could be treated sequentially with buffers, washes, etc.
- Easy sample recovery

## Disadvantages

Specialized, sophisticated and expensive equipment required  
Random orientation



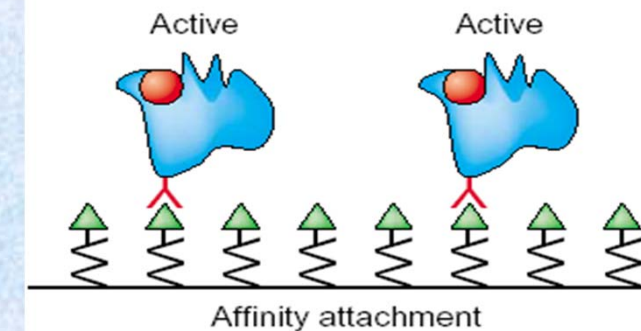
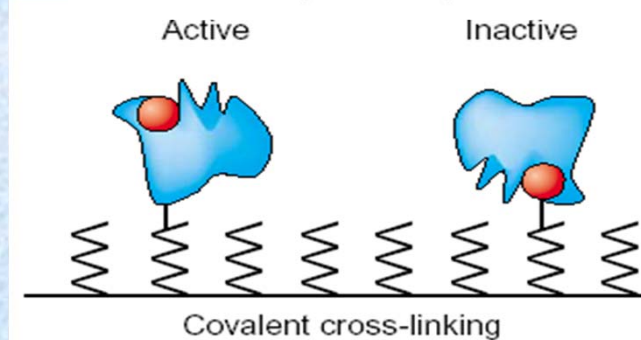
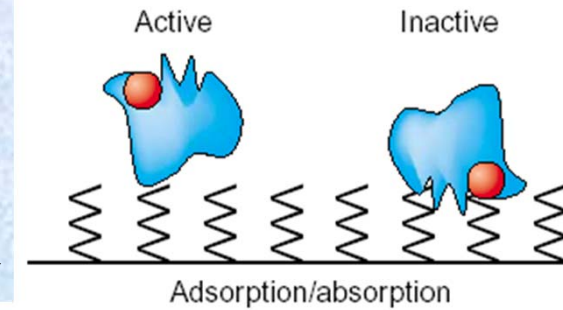
## Glass

Direct protein linking in the glass surface or after chemical modification:

- Poly-L-Lysine (adsorption)
- Aldehyde activation (covalent)
- Epoxy activation (covalent)
- Gold cover (covalent)

Or

- Biotine (afinity)
- Hisx6 (afinity)



### Advantages

- Covalent bond decreases probability of alteration of native conformation
- **Affinity**: correct orientation

### Disadvantages

- NH<sub>2</sub> groups in side chains can modify activity.
- Affinity**: All proteins should be biotinilated or Hisx6 tagged



## Chip types

|                              | Surface   | Advantages   | Disadvantages  |
|------------------------------|---|--|--|
| <b>2D soft substrates</b>    | Polystyrene<br>Nitrocellulose membranes<br>PVDF (Polyvinylidene fluoride)<br>(Adsorption and absorption)  | It does not require protein modifying. High capability of protein retention  | Non-specific linking to protein.<br>Random orientation.<br>Background noise. Low density chips   |
| <b>3D surface structures</b> | Polyacrylamide and agarose (diffusion)  | It does not require protein modifying. High capability of protein retention  | Not commercialised   |
| <b>Nanowells</b>             | PDMS covered glass (polydimethylsiloxane) (cross-linking)   | Strong link and high packing density   | Protein random orientation   |
| <b>Glass</b>                 | Only glass<br>poly-L-Lys cover<br>aldehyde activation<br>Epoxy activation<br>Gold cover<br>Affinity union:<br>Avidin or resin Ni <sup>2+</sup> resin (adsorption, absorption, cross-linking or link affinity) | Idem as 2D<br>Idem as 2D<br>High density chips<br>High density and resolution<br>SPR and MS coupling<br>High density, specific, strong linking | Idem as 2D<br>Idem as 2D<br>Random orientation<br>Random orientation<br>Random orientation<br>Proteins should be biotinylated or His <sub>6</sub> tagged |



# Protein deposit systems

**Low density:** DOT-BLOT systems of 96 wells

**High density:** Robots able to deposit >30000 proteins

- Direct contact with the surface
- Ink-jet technology. Surface not touched
- Electrospray. Decreases spots from 150 to 30  $\mu\text{m}$ .

# Protein detection systems

**Fluorescence** (preferred because)

- Simple
- Safe
- Very sensitive
- Can have very high resolution

Fluorescence detection:

- 1 step: fluorescent molecule
- 2 steps: using an activity marker (f.e. biotine + Fluorescent streptavidin)
- RCA (rolling circle amplification)

**ELISA**

**Radioisotopic marking**

Protein-protein, DNA or drug interaction study



# Protein detection systems (2)

**SELDI-MS**: Mass spectroscopy with laser desorption ionization increased on surface

- No marking needed: direct detection
- Used in chips covered with metallic layers, where laser vaporises proteins and MS reveals the identity of the protein

**AFM**: Atomic Force Microscopy

- Takes advantage of topological changes on the surface to identify captured proteins

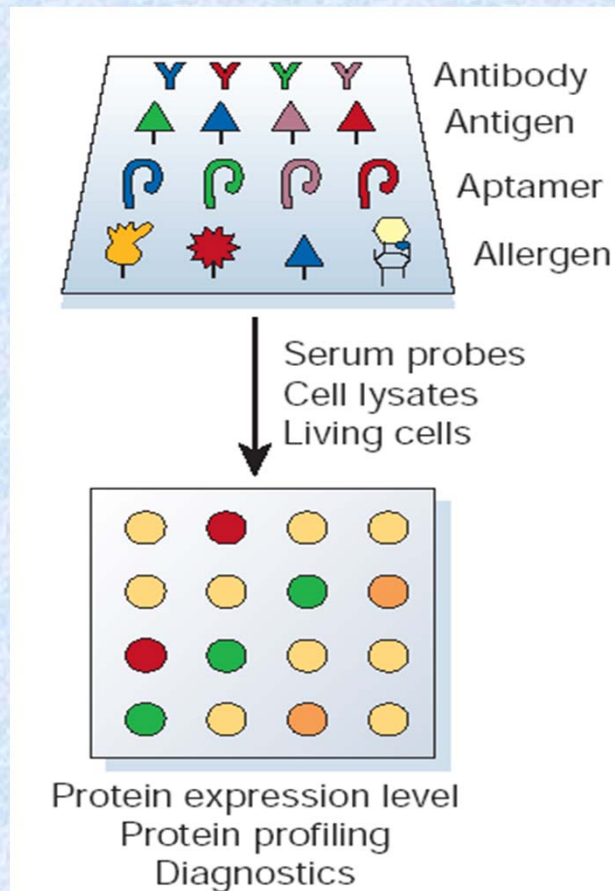
**SPR**: Surface Plasmon Resonance

- Allows detection in real time
- Monitors interaction kinetics (i.e.) antigen-antibody
- Wide range of molecular weights, affinity and linking speed



# Analytic chips

Different ligand types are bound, as antibodies, antigens, DNA or RNA aptamers, carbohydrates and small molecules



Protein samples from **two biological states** are marked separately with **red** and **green** fluorescent agents, mixed and incubated in the chip. **Spots indicate overexpression**

Find out protein expression levels.

Expression profiles

Clinical diagnosis



## Analytic chips: antibodies

- It is the most used
- Antibodies are deposited at high density in the chip
- A cell extract, serum or living cells are deposited on the chip
- The antigen is linked
- Detection with tagged antigen (extract), or with a second antibody

### Disadvantages:

- Having agents recognizing the right protein: antibodies
- Non-specific and expensive polyclonal antibodies
- Very expensive monoclonal antibodies, difficult to produce and time-consuming

### Alternative to production of antibodies or similar

- Ab presentation in phages
- Ribosome presentation
- SELEX (Systematic Evolution of Ligands by Exponential Enrichment)
- mRNA presentation
- Affibody display

Construction of a wide collection of regions with potential **binding activity**



## Analytic chips: allergens or antigens

- Opposite to the previous one
- Antigens are deposited at high density in the chip
- Antibodies are detected (usually serum) on the chip
- Antibody detection

### **Example 1:** Hiller et al.

94 purified allergens linked to glass

Reactivity profiles allergic patient IgE

Small amount of serum

Allergy test as an alternative to skin test

### **Example 2:** Robinson et al.

>300 autoantigens from 8 autoimmune diseases on glass

Small amounts of serum



## Analytic chips: peptides

**Objective:** Detection of epitopes in proteins which define their basic activity.

**Example 1:** Houseman et al

- Immobilization in gold-covered glass of >3000 peptides from 9-mer amino acids
- Localization of c-Src tyrosine kinase substrates
- SPR, fluorescence and phosphorus image detection

**Advantages:**

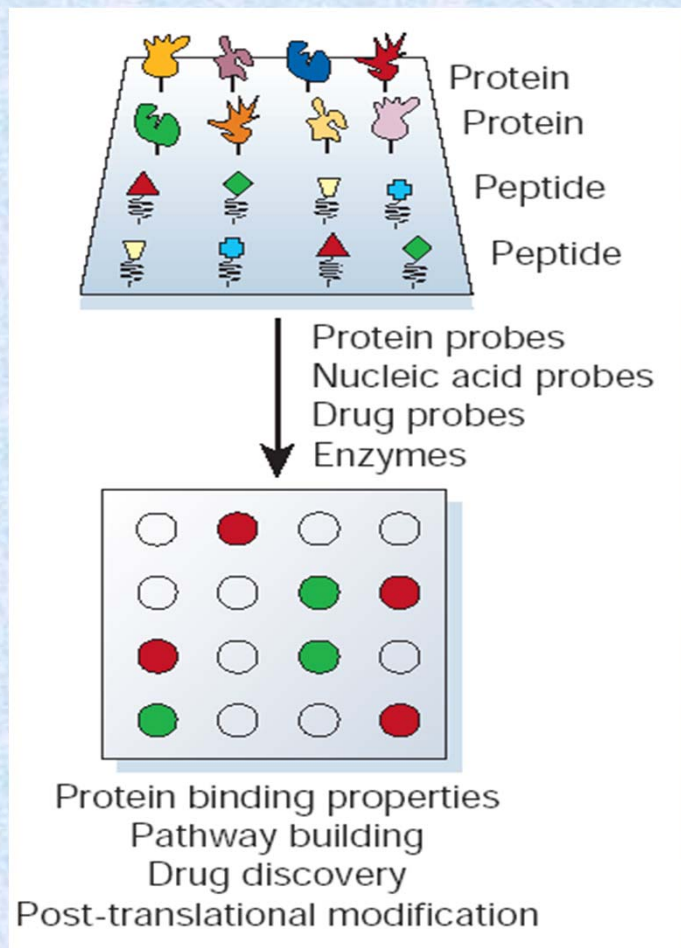
- Shorter peptides
- Peptides more stable than proteins
- Allow high density chip manufacturing
- Peptide synthesis *in situ* using [photolithography](#) or light-directed synthesis (cost-saving and few materials are needed)

## Analytic chips: carbohydrates



# Functional chips

Proteins and peptides coming from an organism's proteome are purified or synthesised individually using high performance methods or high throughput (HT)



Protein samples from **two biological states** are marked separately with **red** and **green** fluorescent agents, mixed and incubated in the chip. **Spots indicate overexpression**

## Allows to analyse:

- Protein activity
- Ligand-binding properties
- Post-translational modifications
- Pharmacological target identification
- Construction of biological networks



# Functional chips: examples

## **Ejemplo 1:** Zhu et al

Interaction analysis of protein families

- 119 kinase proteins and 17 substrates
- Substrates are immobilized in nanowells
- Kinases are incubated with substrates in the presence of ATP\*
- Marked substrates are detected with phosphorus image

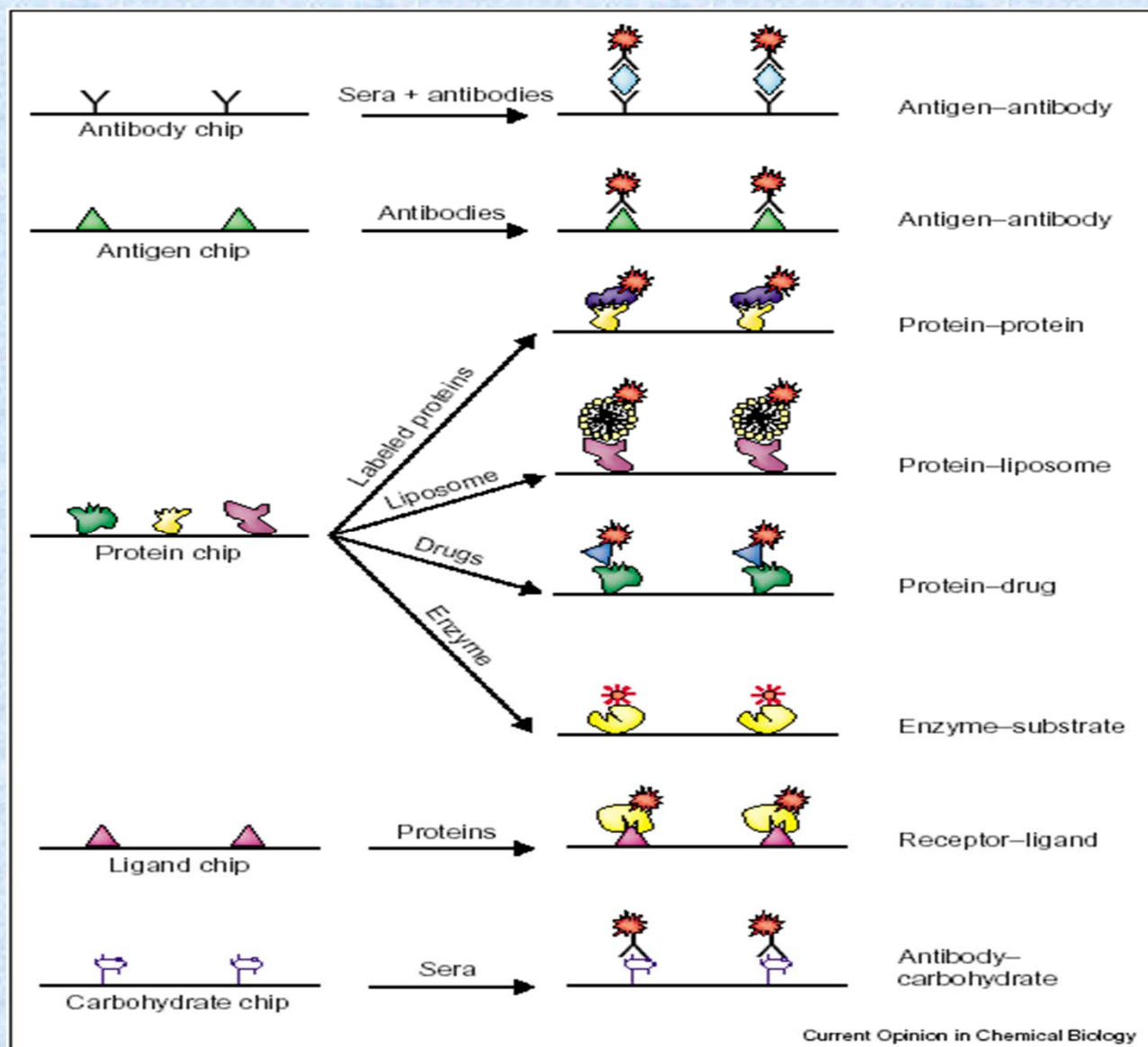
## **Ejemplo 2:** Zhu et al

Analysis of a complete proteome

- 5800 from 6200 yeast ORFs
- Proteins are marked with GST and Hisx6 (both). A performance of 80% functional proteins was obtained
- They are linked to the Ni-NTA-covered chip with His x6
- Tests of calmoduline and phosphoinositides (PIs)
- 6 known interactions were obtained together with 33 new from calmoduline and more than 150 proteins interacting with PIs



# Chip general applications





# Biochemical Genomics vs Chips

## Biochemical Genomics:

- It requires 64 essays to meet yeast genome (groups of 96 proteins)
- Very flexible for most types of biochemical assays
- Particularly useful for enzymatic activity assays

## Disadvantages:

The use of protein pools does not guarantee protein quality

The other 95 proteins can interfere with measurement

No liable measurement of fluorescence linking

Cannot manage multiple positive at the same time

## Protein chips:

Allow checking individual quality of proteins

Immediate ORF identification responsible for specific activities

Identification of multiple positive in one round

High performance analysis from protein activities

Automatation of construction, assay and results reading

## Disadvantages:

6000 strains (yeast) should be cultivated, and 6000 protein purifications

Substrates should be immobilized for fluorescence-linking assays



# Conclusions

- Chips can be a **powerful tool** in high scale biology
- Manufacturing on **glass methodology** is validated for protein analysis from a complete proteome
- Manufacturing methodology is **robotized**, as well as assay's and result reading's
- **Antibody-improved production** as reactive will influence chip improvement as tools for proteome analysis