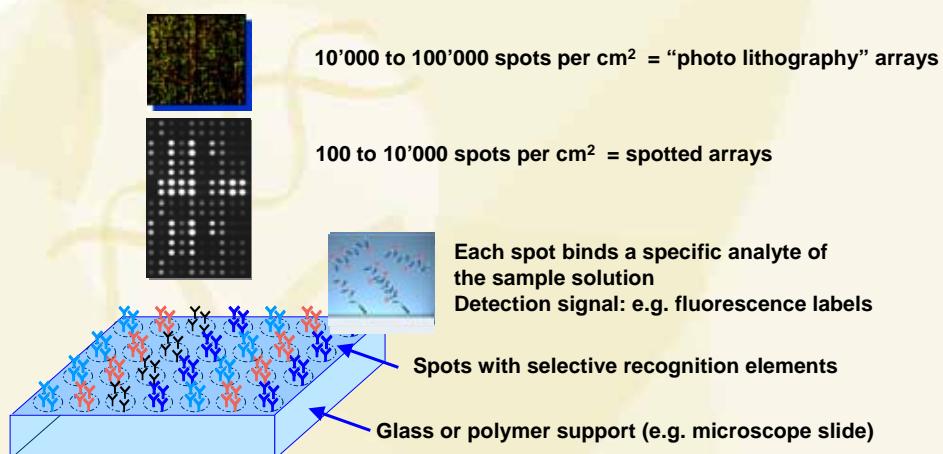


## Planar Waveguides: How Nano Layers Enable to Detect Zepto Moles of Macro Molecules in Pico Liter Spots on Micro Arrays

Dr. Markus Ehrat  
Zeptosens – A Division of Bayer Schweiz AG

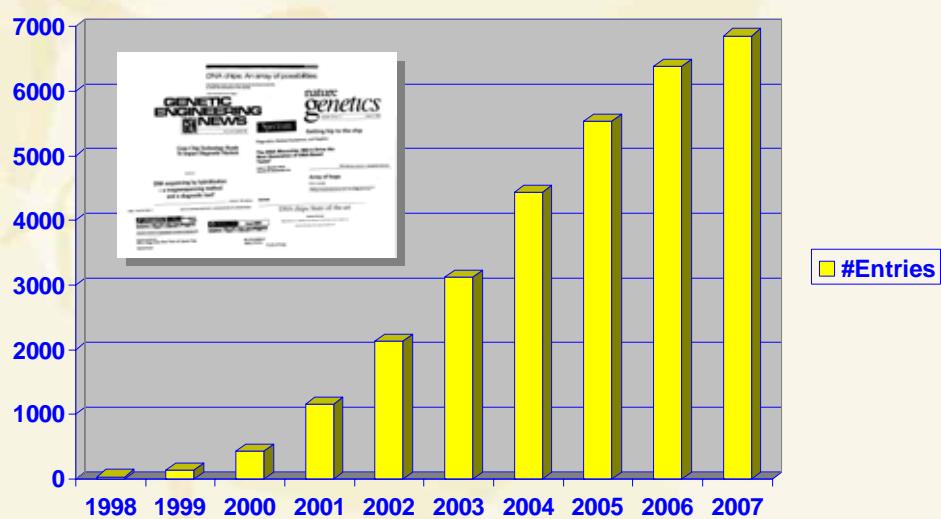
SSOM Meeting  
March 16 /17 2009  
Engelberg

## What are Biochemical Microarrays?



**Microarrays -  
A powerful technology to measure  
thousands of samples and  
thousands of analytes  
- genes or proteins -,  
in a short period of time**

**Entries in PubMed Database, Search Term „Microarray“**



### Information Obtained from 200 µL of Sample

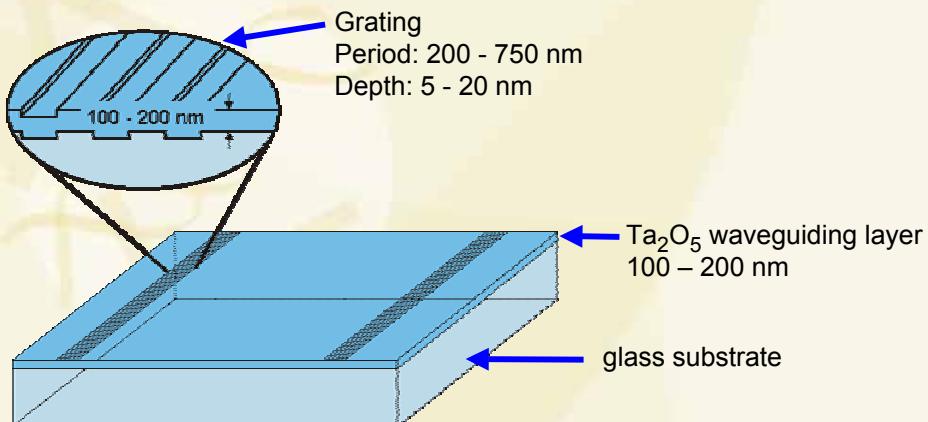
	Detection area (mm <sup>2</sup> )		Information per cm <sup>2</sup> *
96 well plate	40		1
1536 well plate	2.5		16
150 µm spot microarray	1.7 x 10 <sup>-2</sup>		4500
15 µm spot microarray	1.7 x 10 <sup>-4</sup>		450'000
1.5 µm spot microarray	1.7 x 10 <sup>-6</sup>		45'000'000

\* Sample solution of 200 µL

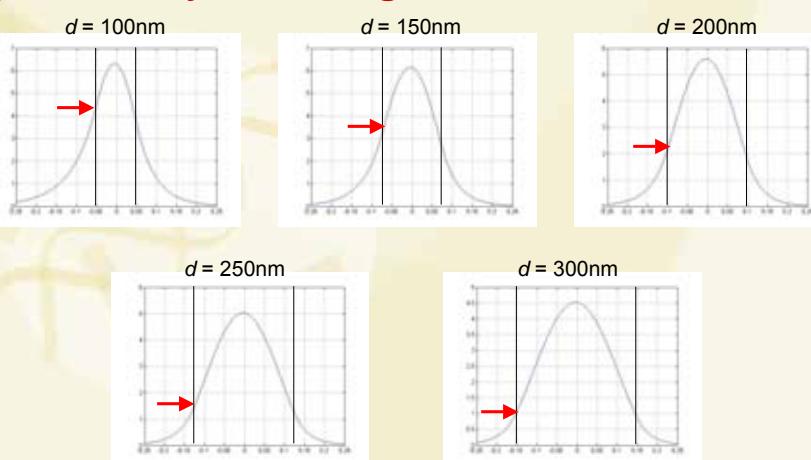
**Microarrays -  
Small detection areas  
Nanoliters of sample volumes:**

**Require high detection sensitivity**

## Thin Film Planar Waveguide (PWG) Chip Design



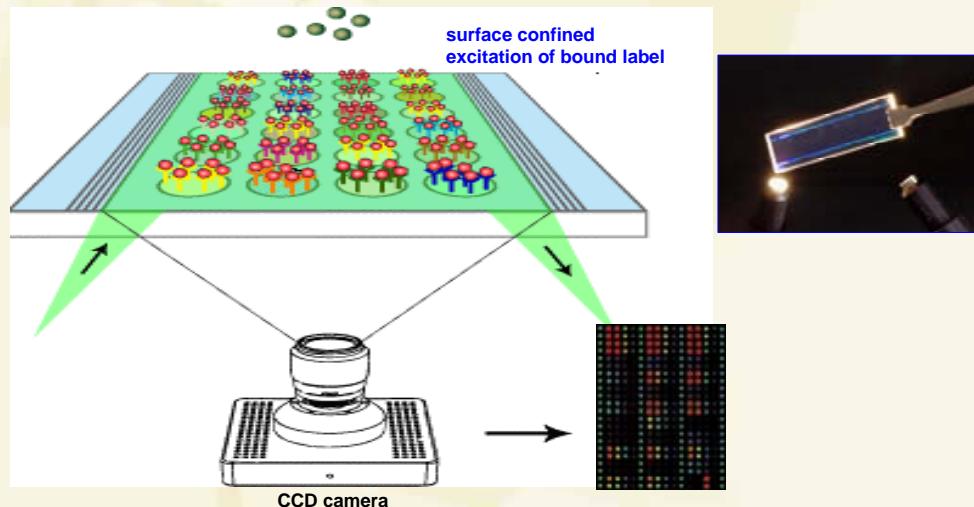
## Light Intensity vs. Waveguide Thickness



Parameters:

$$n_{\text{sub}} = 1.52, n_{\text{sup}} = 1.335, n_{\text{PWG}} = 2.15, m = 0, \lambda = 635 \text{ nm}$$

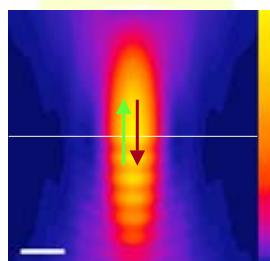
## Planar Waveguide Principle - High Sensitivity Fluorescence Microarray Detection



## Advantages of Fluorescence Excitation on PWG

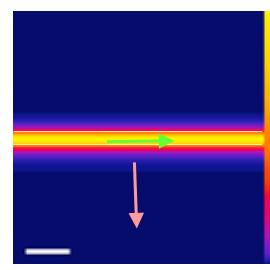
### Conventional excitation

sample  
solution  
  
support



background problems  
  
Confocal excitation:  
Focus depth ~ 2µm

### ZeptoREADER™ - Evanescence excitation



~ no background  
  
Evanescence excitation:  
Depth ~ 100nm

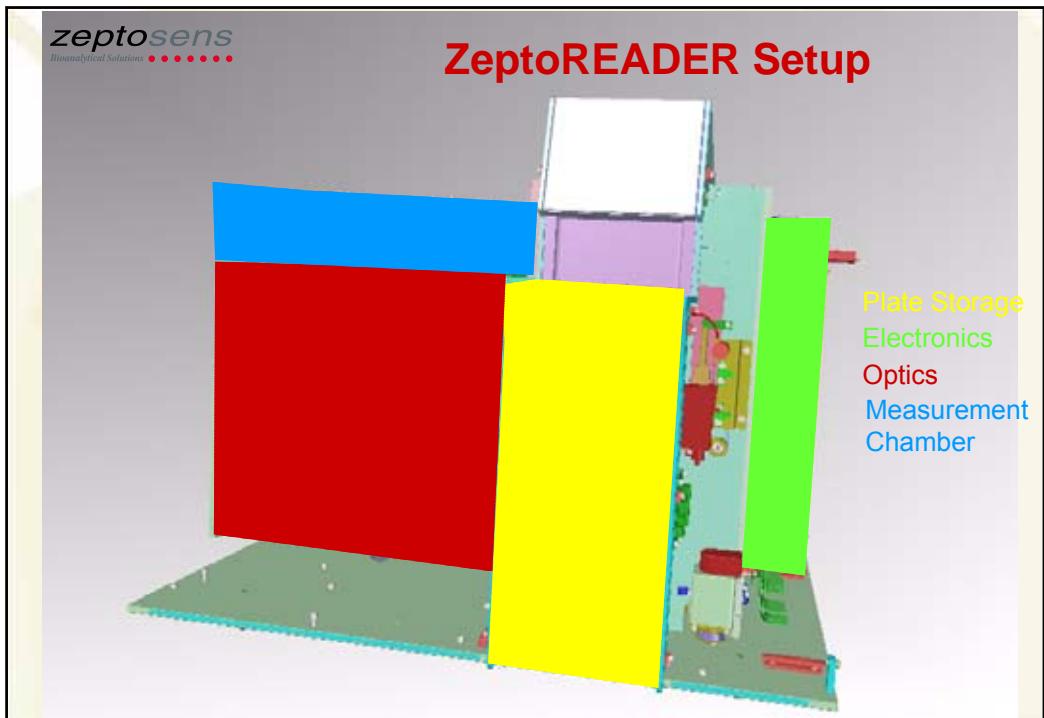
- Separation of excitation and detection directions
- Ultimate sensitivity
- Fast time to result
- Less sample preparation
- Direct measurement in blood or serum

**zeptosens**  
Bioanalytical Solutions •••••

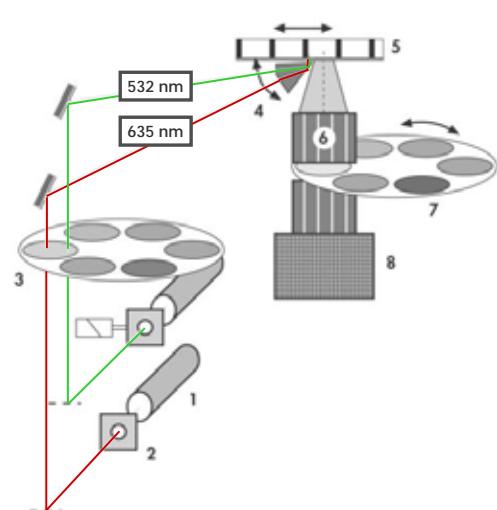
### ZeptoREADER – PWG Inside



- **Ultra sensitive:**  
Planar wave guide technology based evanescent field fluorescence excitation
- **Exceptionally fast:**  
Over 120'000 data points in 6 hours
- **Increase efficiency:**  
Extended walk away time using 60 slides integrated autoloader
- **Absolutely reliable:**  
Swiss designed and manufactured for highest quality and precision possible

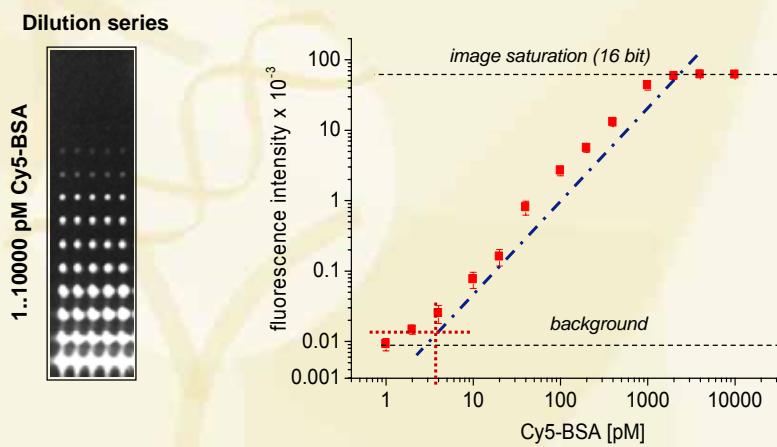


## Optical Scheme of the ZeptoREADER™

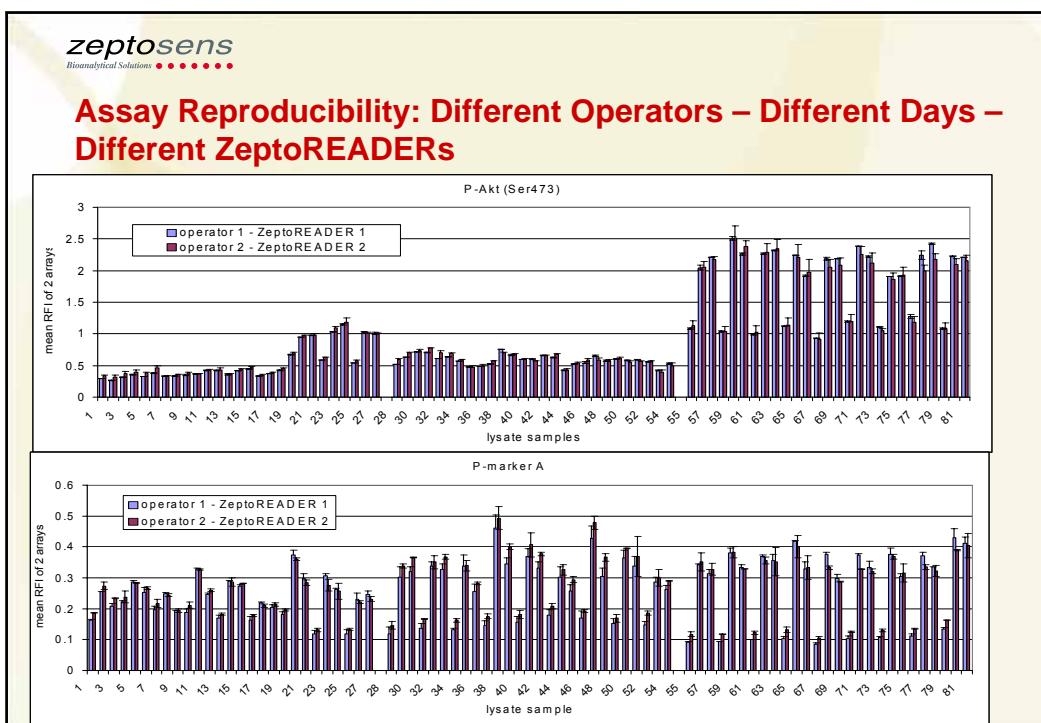
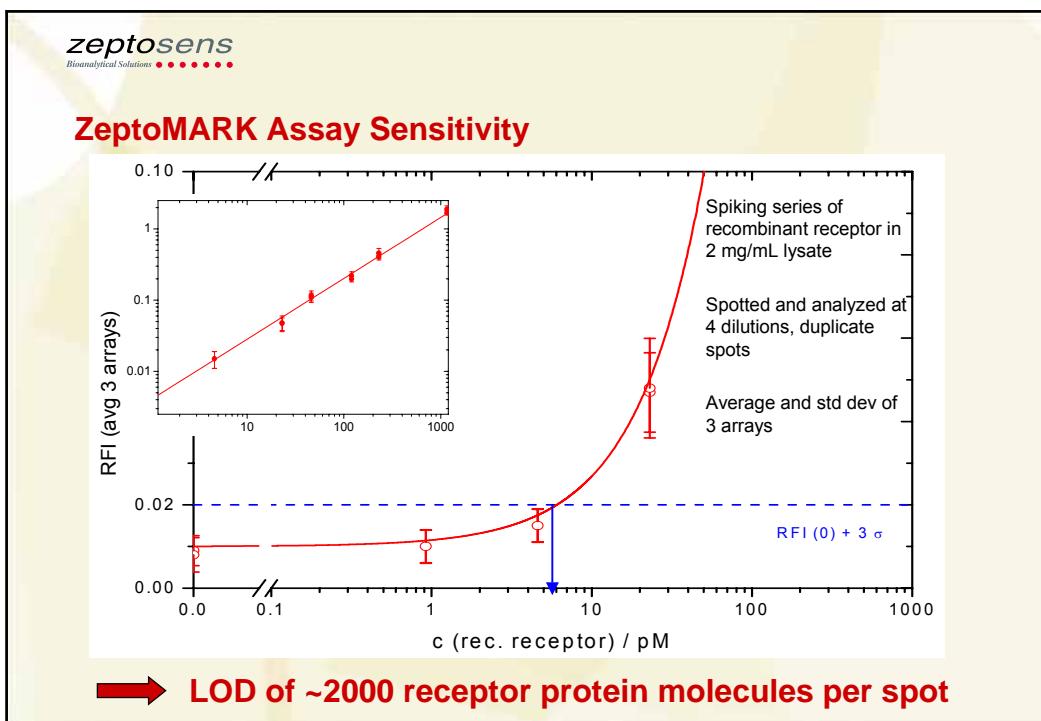


1. Laser
2. Shutter
3. Gray filter wheel
4. Coupling unit
5. ZeptoCHIP™
6. Front lens unit
7. Emission filter wheel
8. Camera lens unit and CCD

## High Sensitivity of PWG Signal Detection



→ **LOD = 1 zeptomol (600 proteins) per spot**



## High detection sensitivity

### What is the value in the real world?

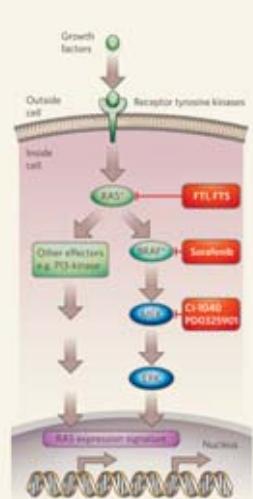
### The Systems Approach

- “...the **rate of mortality** from cancer has changed very little over the past 50 years“
- “Cancer therapies are still essentially “**one size fits all**”,.....”
- “**Targeting systems**, rather than single molecules, will likely result in **more durable responses** in cancers considered non-responsive to treatment.”
- “Thus the ”**omic**“ technology is promising an approach both
  - to evaluate the **heterogeneity** of cancer patients
  - and as a means of **identifying biosystems** as target for new drug development”



Science, Vol 312, May 26, pp 1157, 1165, 1166, (2006)

## Signatures Guide Drug Choice Julian Downward

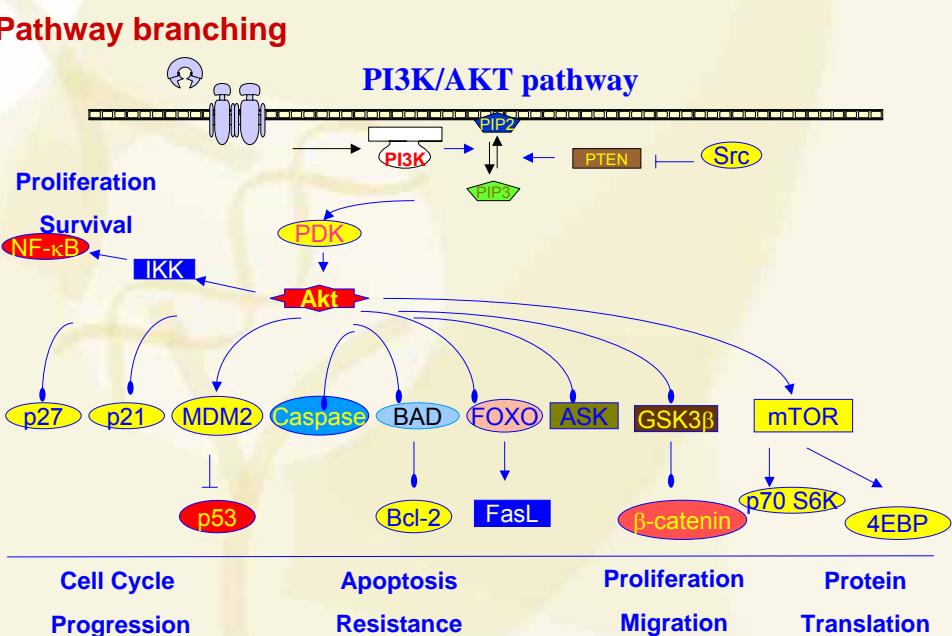


....“Cancer drugs are increasingly designed to target specific cell-signalling pathways...”

....“Pathways can be activated at different points [ ]. If a factor at the top of a signalling cascade is unaffected, for instance, one cannot assume that the pathway is not involved, as a factor further downstream might have been activated”...

*Nature* 439, 274-275 (19 January 2006)

## Pathway branching



## Requirements for Pathway Proteomics Approaches

- Signaling is highly dynamic
  - protein phosphorylations in seconds/minutes
  - protein synthesis/degradation in hours/days
  - extensive sampling required to obtain time resolution
- Many signals are post-translational modifications
  - issue for classical MS-based methods
- Highly parallel measurements of analytes is important
  - a thorough pathway profile can easily comprise 100 or more elements
- Conclusion:  
an array-based solution will provide the required scalability and throughput

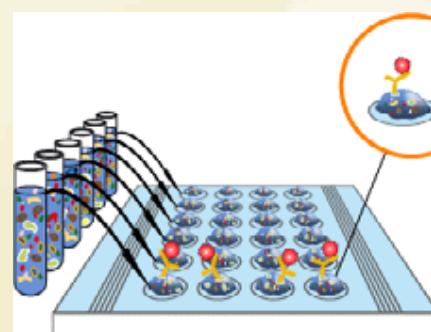
## Protein Microarrays – Two Formats

### Forward Protein Arrays



- Array of target-specific capture molecules (e.g. antibodies)
- One sample measured per array

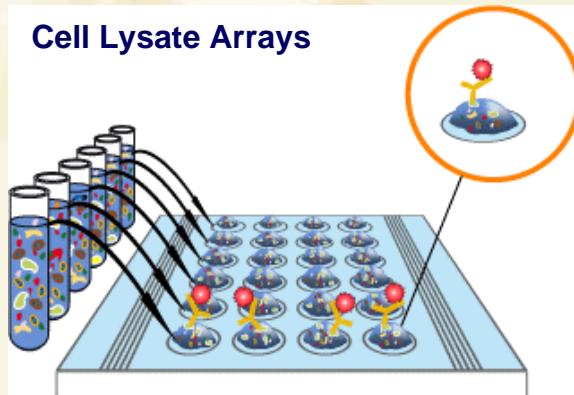
### Reverse Protein Arrays



- Array of samples on chip
- One analyte measured per array

## Reverse Protein Microarrays

### Cell Lysate Arrays



- Array of samples
- Sample volume 400 pL
- Specific detection with target-specific antibodies
- One Ab per target /array
- High flexibility in study design – minimum assay development effort
- Sample volume is never a bottle neck to measure multiple analytes

## ZeptoMARK Reverse Arrays – From Cells to Protein Profiles



Cellular systems



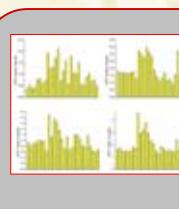
Cell lysis



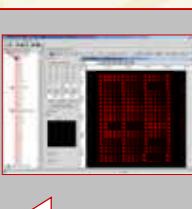
Spotting



Blocking



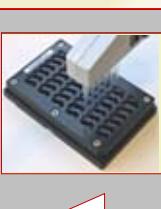
Pathway Profiles



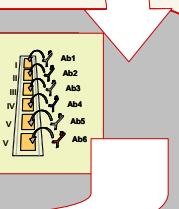
Data evaluation



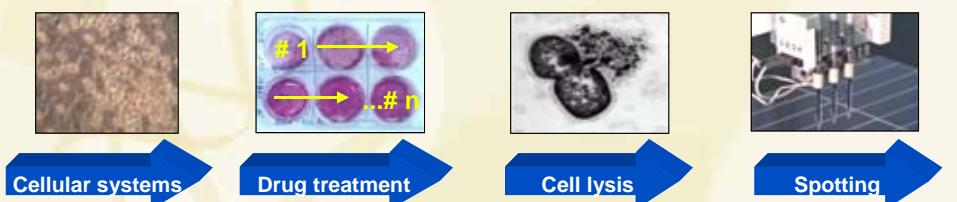
Readout



Assay

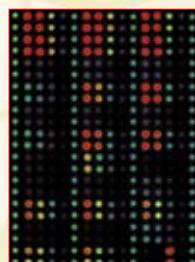


## Zeptosens Reverse Arrays – From Cells to Protein Profiles

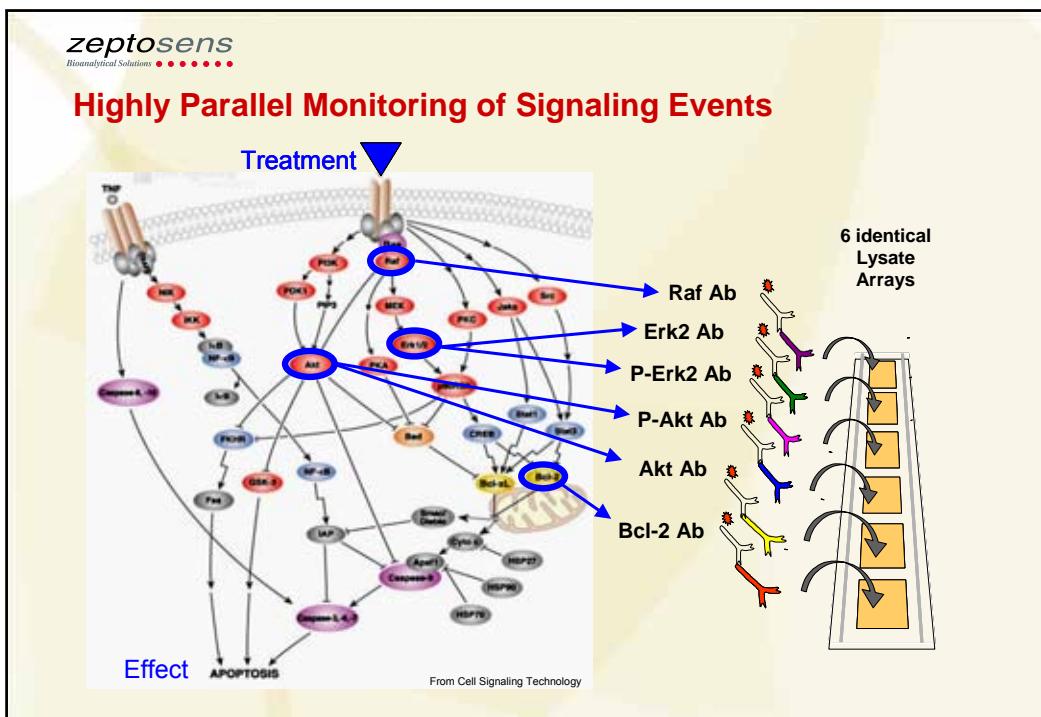
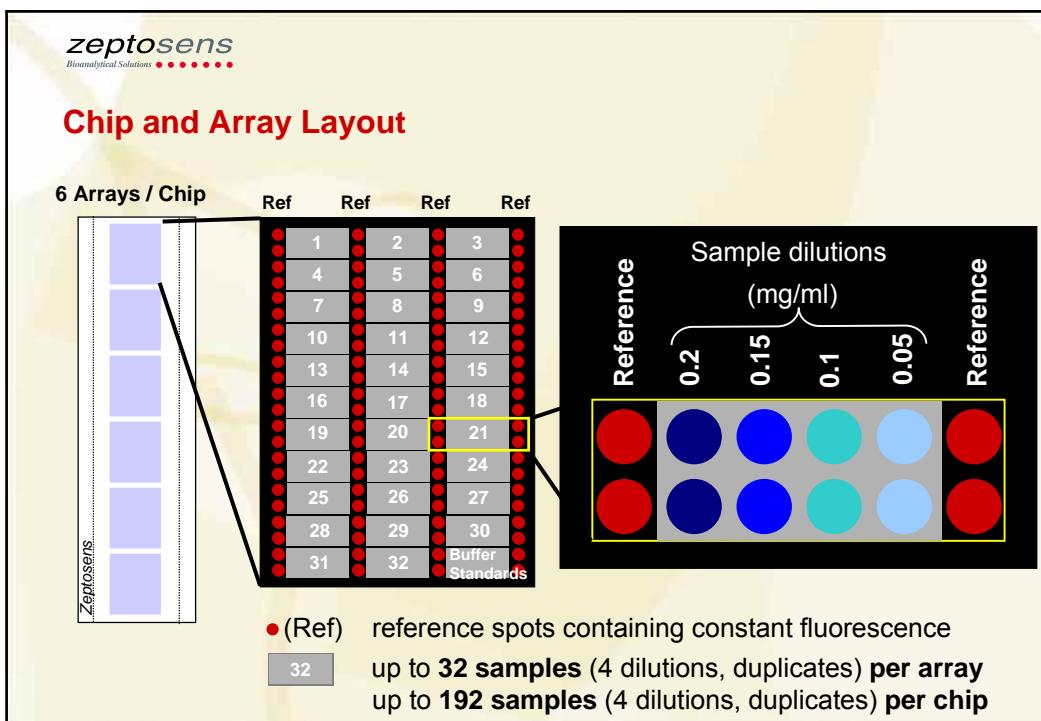


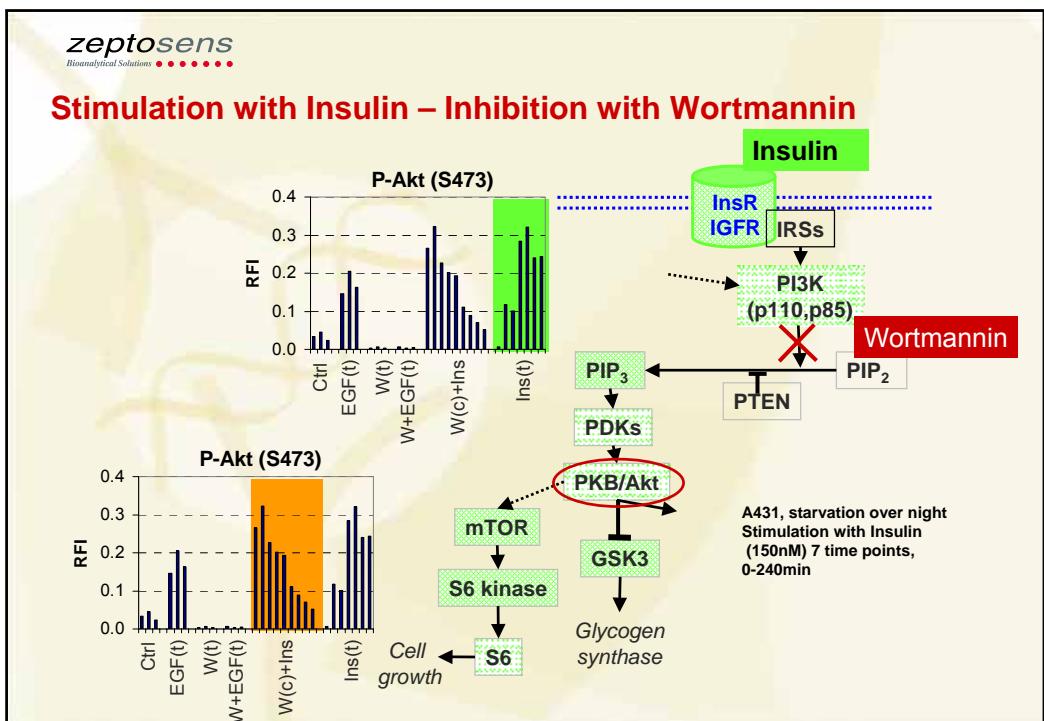
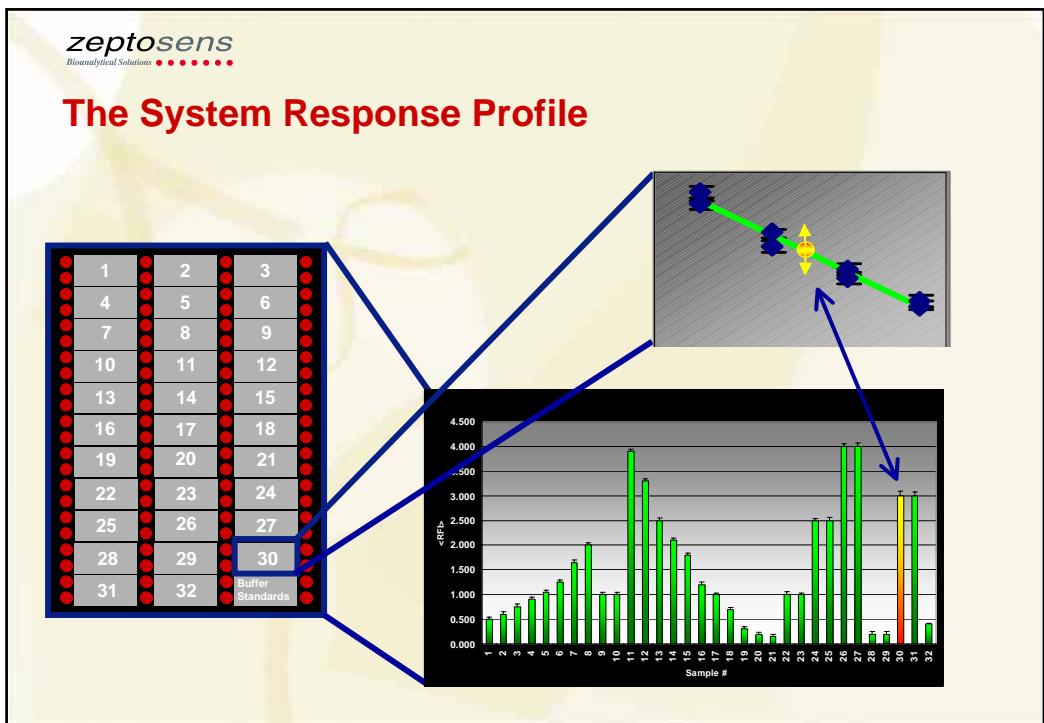
- |  |   |   |
|--|---|---|
| <ul style="list-style-type: none"><li>• <b>Sample</b><br/>~<math>10^5</math> cells<br/>~ 1 mg tissue</li></ul> | <ul style="list-style-type: none"><li>• <b>Lysis</b><br/>50 <math>\mu</math>L lysis<br/>2 mg total protein/mL</li></ul> | <ul style="list-style-type: none"><li>• <b>Spotting</b><br/>400 pL spotting</li></ul> |
|--|---|---|

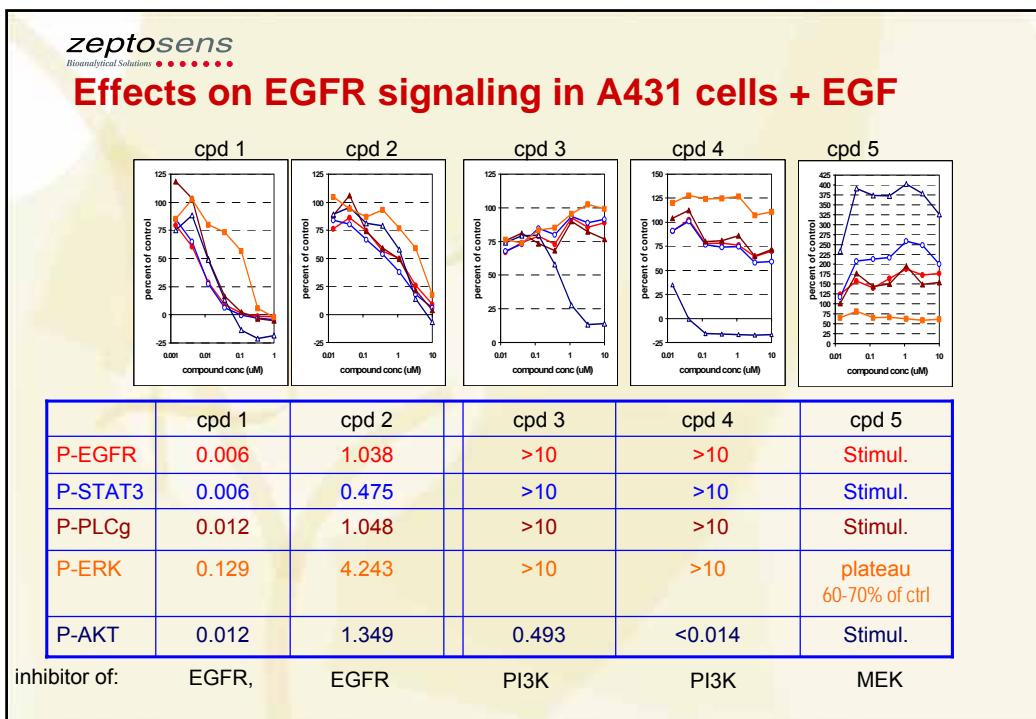
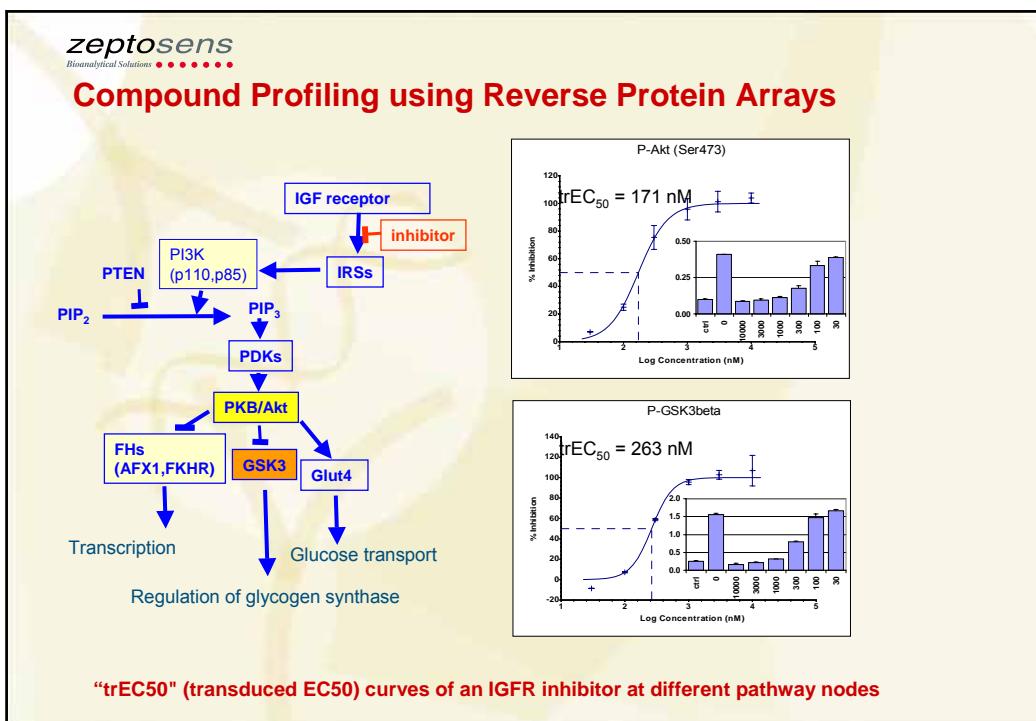
## Spotting: Reproducibility & Quality

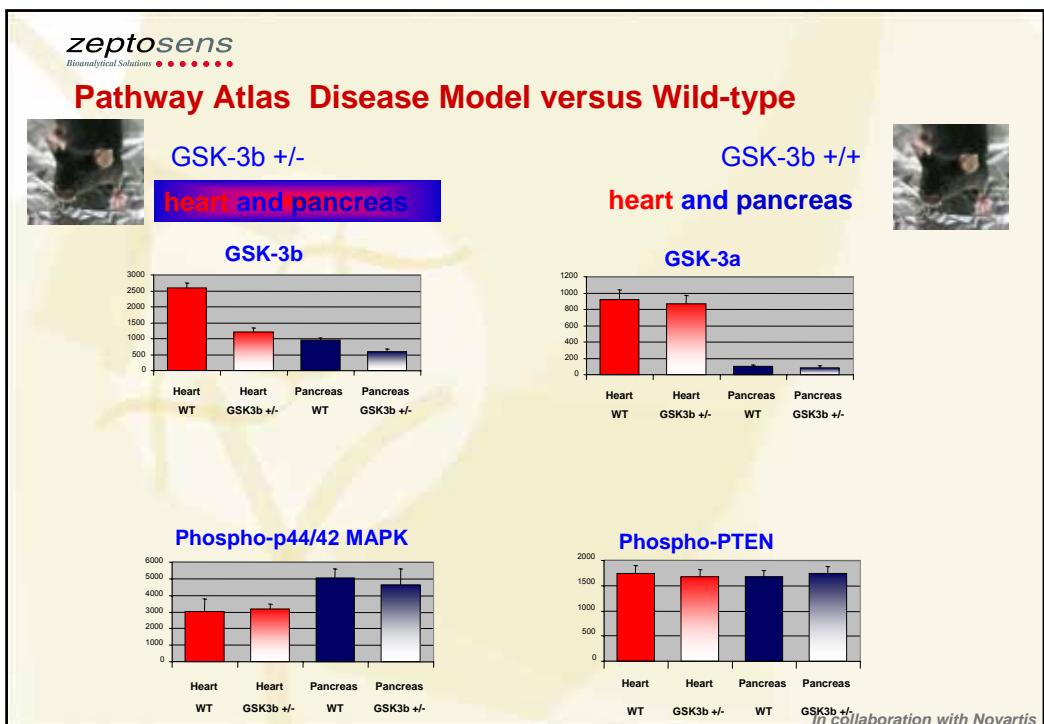
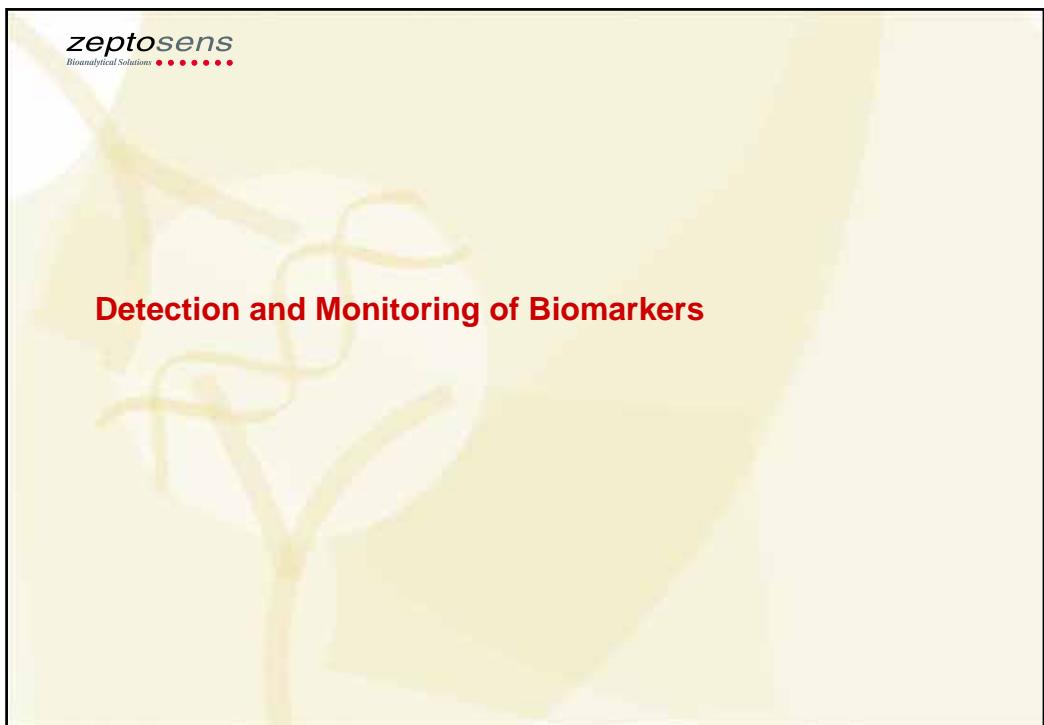


- 400pL sample volume
- Non-contact ink-jet spotting technology
- Up to 256 lysates/array or 1536 lysates/chip
- Reproducibilities of mean spot signals: CV's ≤ 2%

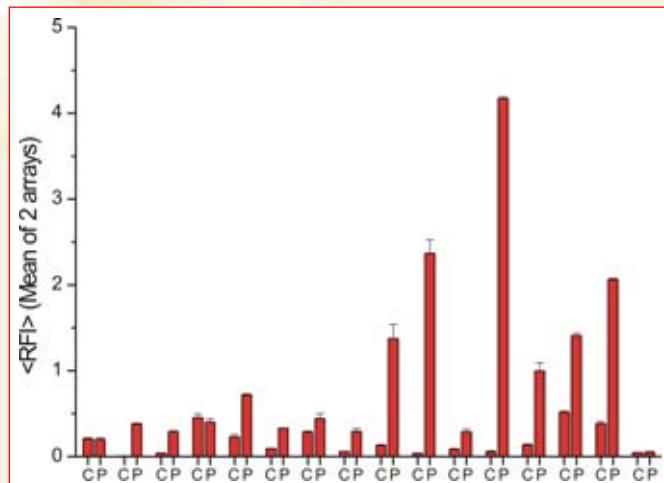








## Liver Cirrhosis Biomarker Evaluation in Urine



Comparison of 16 pairs of sex and age matched Controls (C) / Patients (P)

10 liver cirrhosis candidate markers were measured whereas results for one are illustrated here

Protein concentrations between 2.5 to 10 µg/ml  
No concentration step required

In collaboration with Fernando Corrales, CIMA

## Microarrays for Highly Efficient Reconnaissance of Complex Signaling Network Systems

