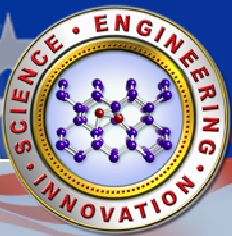


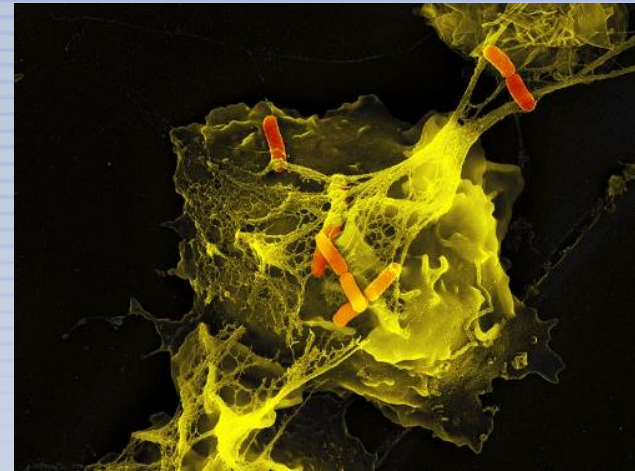
# Microscale Immune Studies Laboratory: Studying Cell Signaling with Single-Cell Resoluton

Anup K Singh



# Our Overarching Goal is Elucidation of Signaling Pathways in Innate Immunity

**Goal:** To elucidate molecular mechanisms of the innate immune response in host cells to pathogens such as bacteria and viruses.

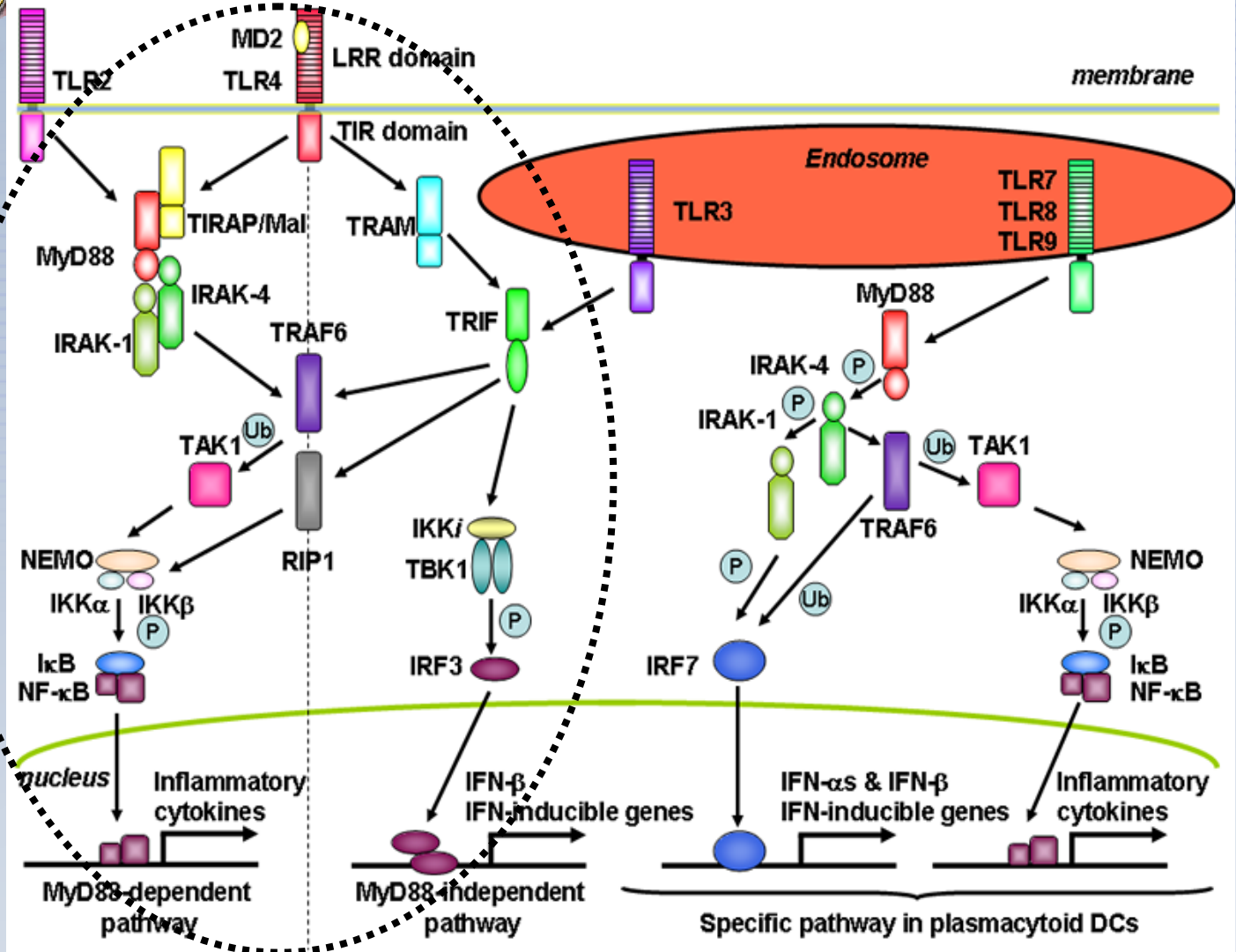


**Why:** Innate immunity is our first line of response to a bacterial or viral invasion. Subversion of innate immunity is the common denominator used by many pathogens, especially the emerging ones. Molecular-level understanding is key to improvements in:

**Diagnostics & Therapeutics**



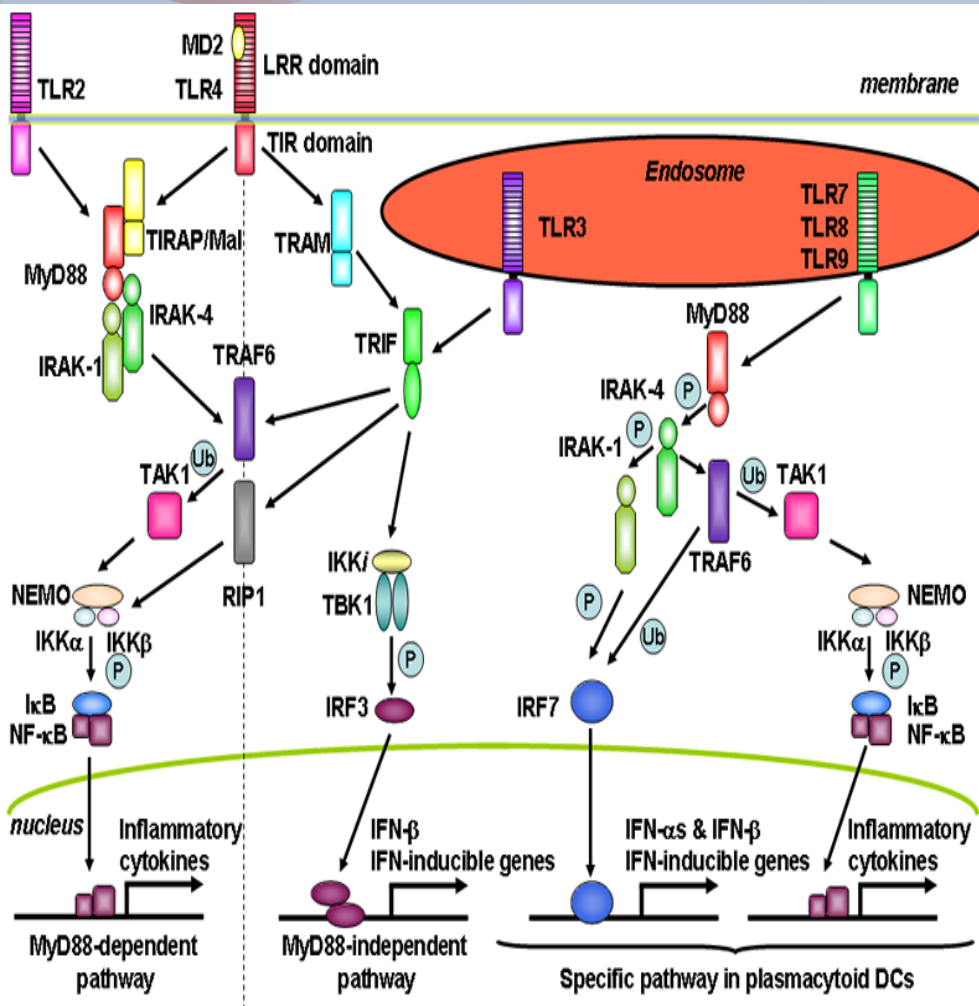
# Signaling Pathways in Innate Immunity



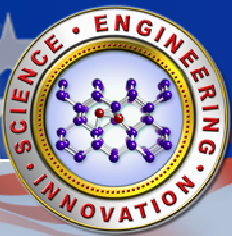
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# Critical gaps exist in our understanding of Signaling Pathways



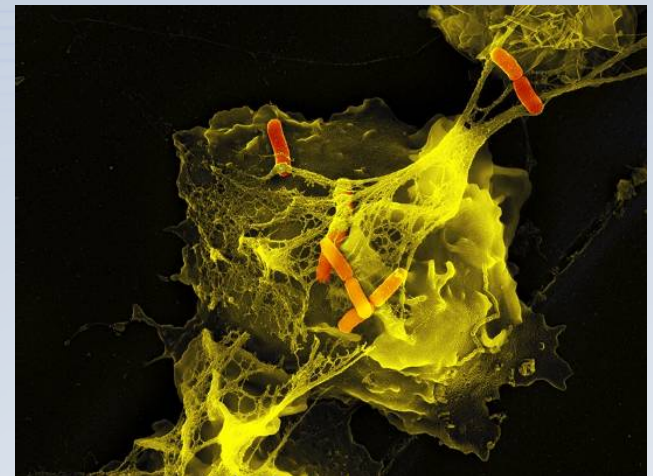
- While much is known, a lot remains unknown about signaling pathways-
- Network dynamics is poorly understood
  - Existing pathway models lack quantitative data
  - Current methods do not provide a systems-level view
  - Current methods lack single-cell resolution



# The MISL Grand Challenge

To create an integrated single-cell manipulation and interrogation platform and predictive models to provide molecular- and cellular-level understanding of innate immunity signaling pathways with *unprecedented speed, resolution, sensitivity, and multiplexing.*

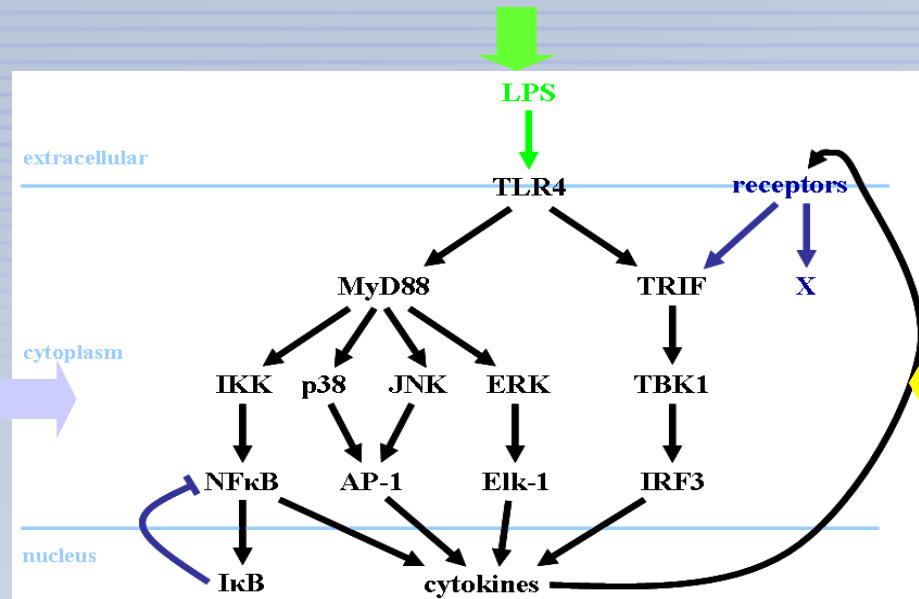
- The benefits will be:
  - ✓ Key discoveries in the understanding and application of innate immunity to anticipate, detect and counter biothreats
  - ✓ An enabling tool for high-throughput biological pathway studies – also applicable to cancer, asthma, cell differentiation, and microbial communities





# We are using a Systems Biology Approach to Interrogate Signaling Pathways

Hyperspectral Confocal Imaging

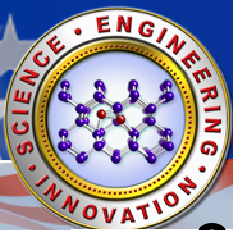


Microfluidic Platform for Proteomic Measurements

Biological Reagents & Assays

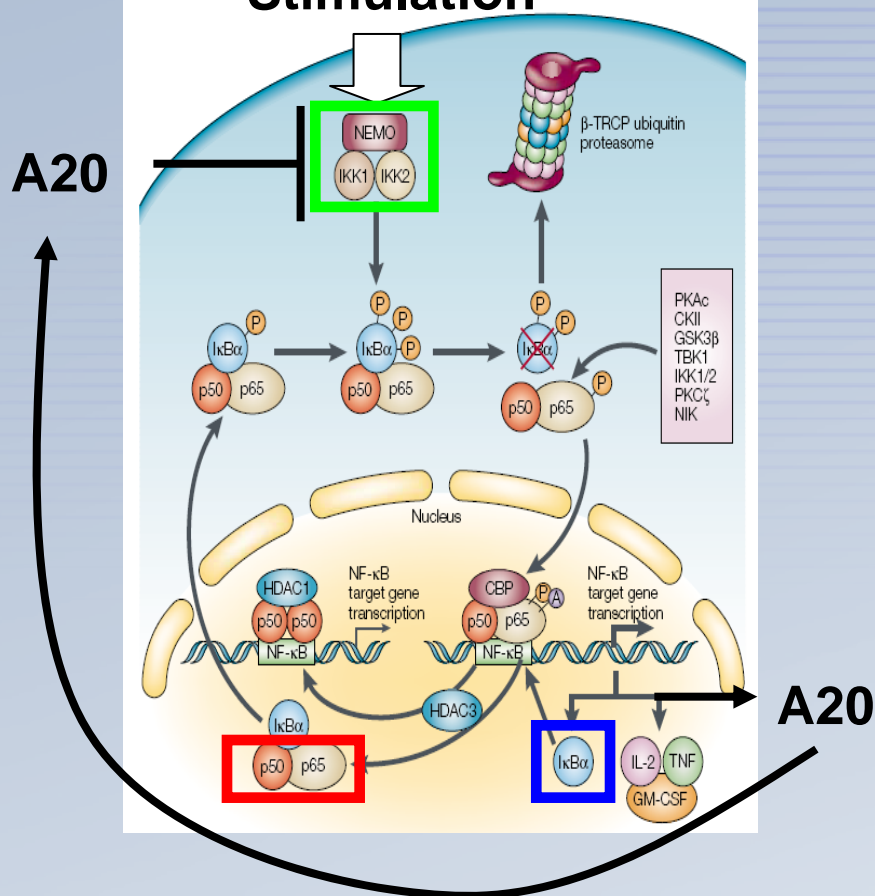
Bioinformatics & Computational Modeling

LDRD Day, 2008

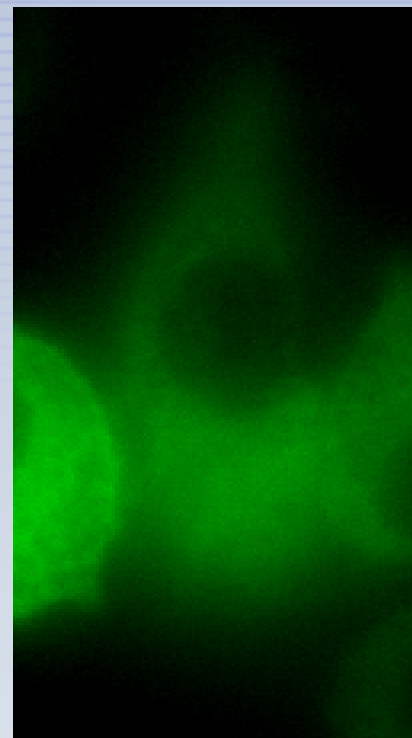


# Oscillations in NF- $\kappa$ B localization observed in macrophages for the first time

## Stimulation



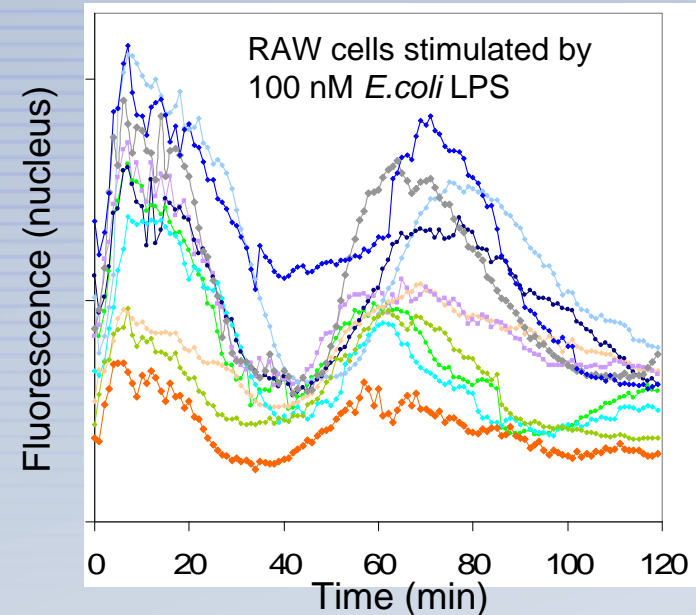
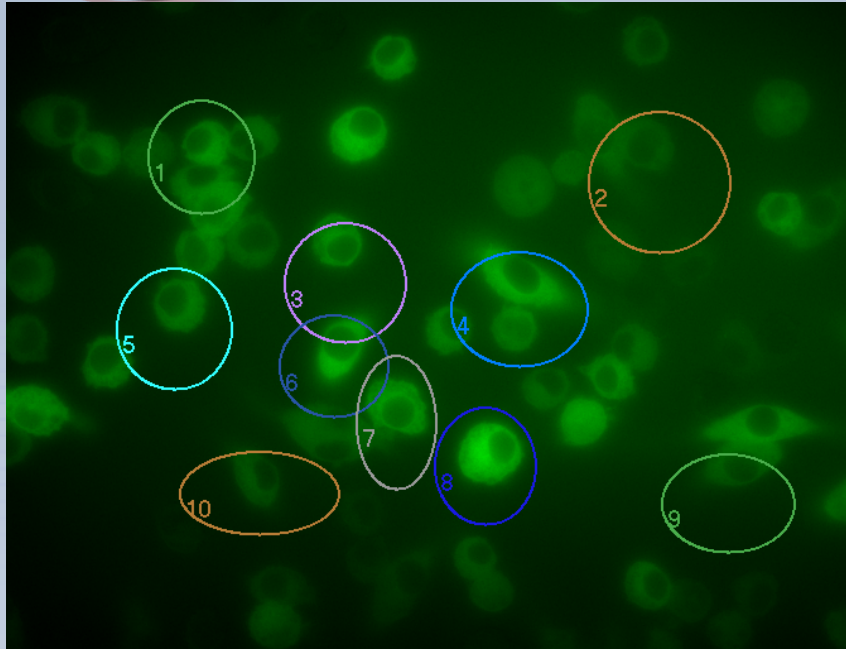
Macrophages challenged with 100 nM *E. coli* LPS



Nature Rev. Immunol. 2:725 (2002)



# NF- $\kappa$ B translocation behavior is heterogeneous

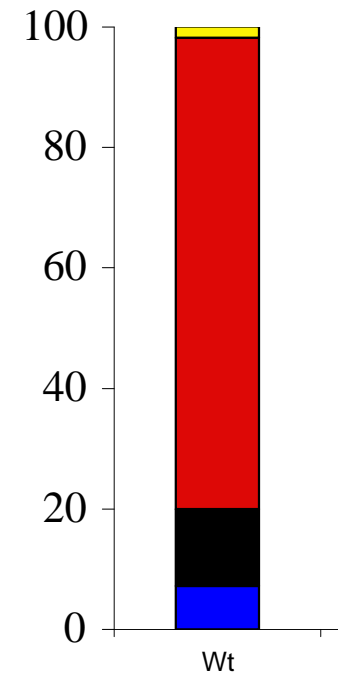
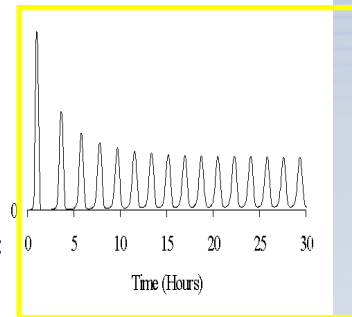
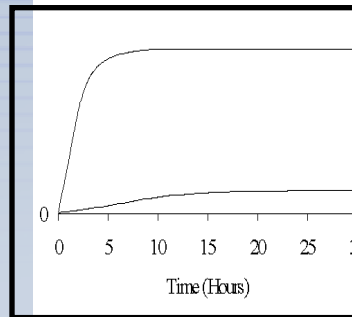
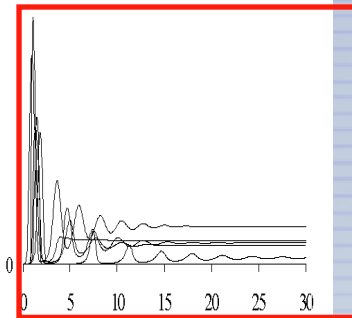
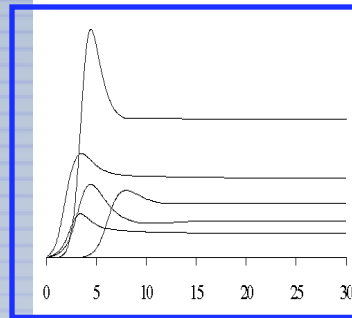
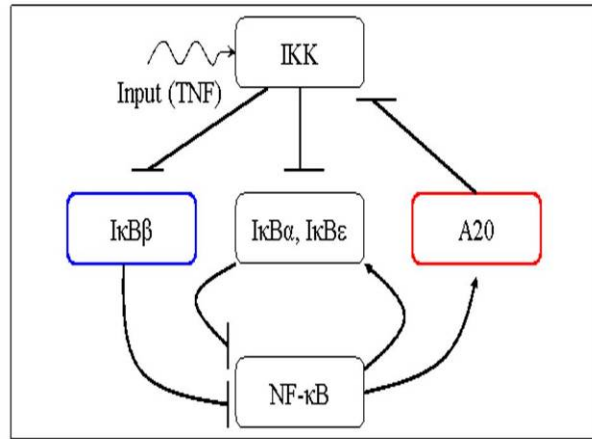


- Multiple oscillations of NF $\kappa$ B observed in macrophages challenged with LPS
- Oscillation behavior is heterogeneous across the population of cells
- Modeling predicted the oscillatory behavior, as well as the heterogeneity in this behavior



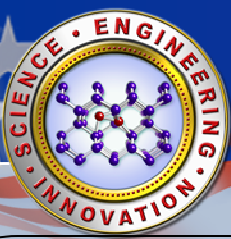


# Computational modeling predicts the heterogeneity in oscillatory behavior

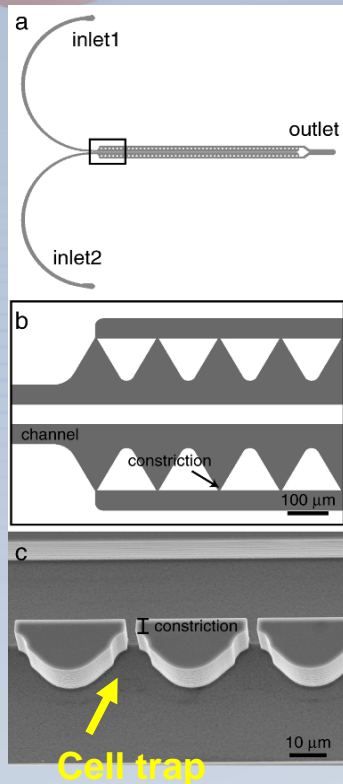


NF- $\kappa$ B model: 28 species, 70 reactions. Oscillatory pattern induced by negative regulators (A20, IKB)

- **Modeling predicts, and experiments confirm, four possible dynamics responses in translocation behavior of NF- $\kappa$ B in macrophages challenged with LPS**
- **Quantifying cell-to-cell variability requires experimental platform with single-cell resolution**

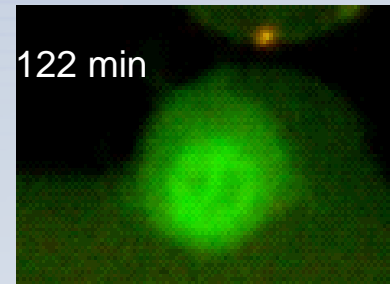
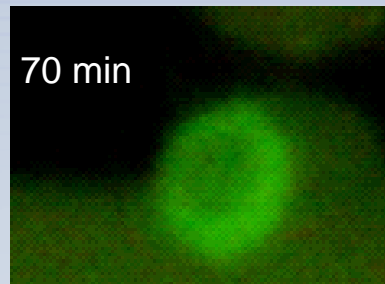
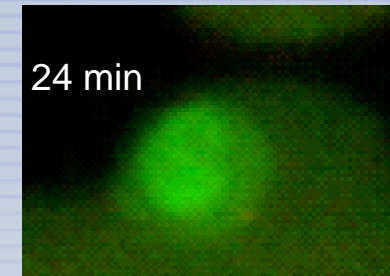
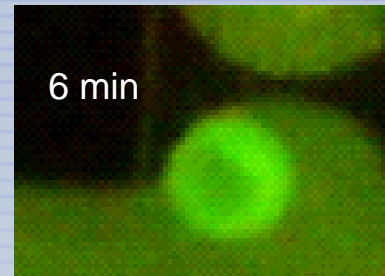


# Single-cell array chip greatly improves study of NF- $\kappa$ B oscillation in macrophages



- Cells trapped at constrictions using hydrodynamic forces
- 100 traps per device
- Cell viability maintained for ~18 hrs

RAW 264.7 cells display NF- $\kappa$ B oscillation upon challenge by 1 nM *E. coli* LPS

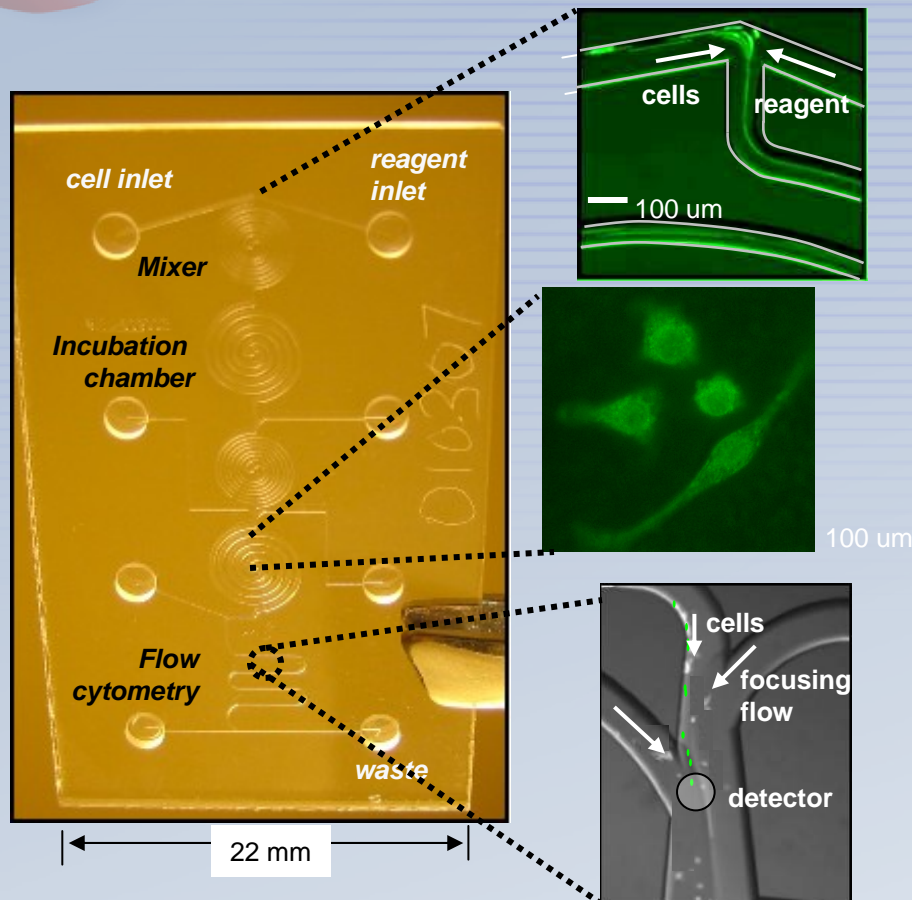


## Single-Cell Array provides:

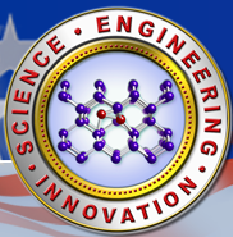
- precise localization of cells
- individual addressing of cells
- facile interfacing with commercial or custom microscopes



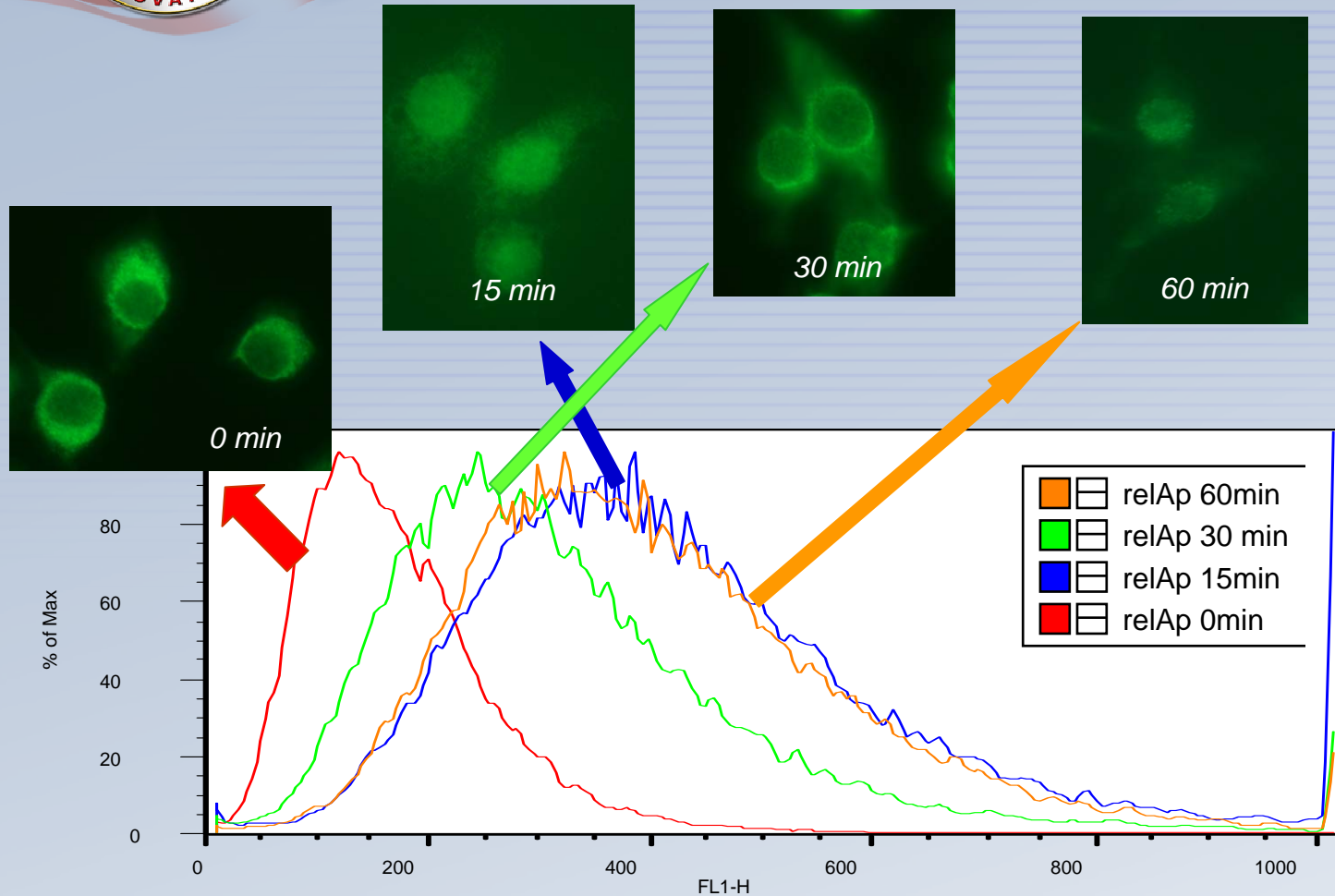
# Imaging and Phosphoassays Performed in the Same Population of Cells in a Single Chip



*Integrated flow cytometry and imaging has allowed, for the first time, measurement of kinase activity and their translocation in the same population of cells*

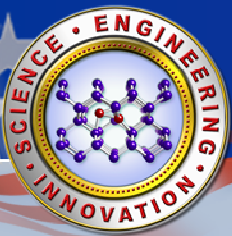


# Kinase Activity Correlated with NF $\kappa$ B Translocation in the Same Population of Cells

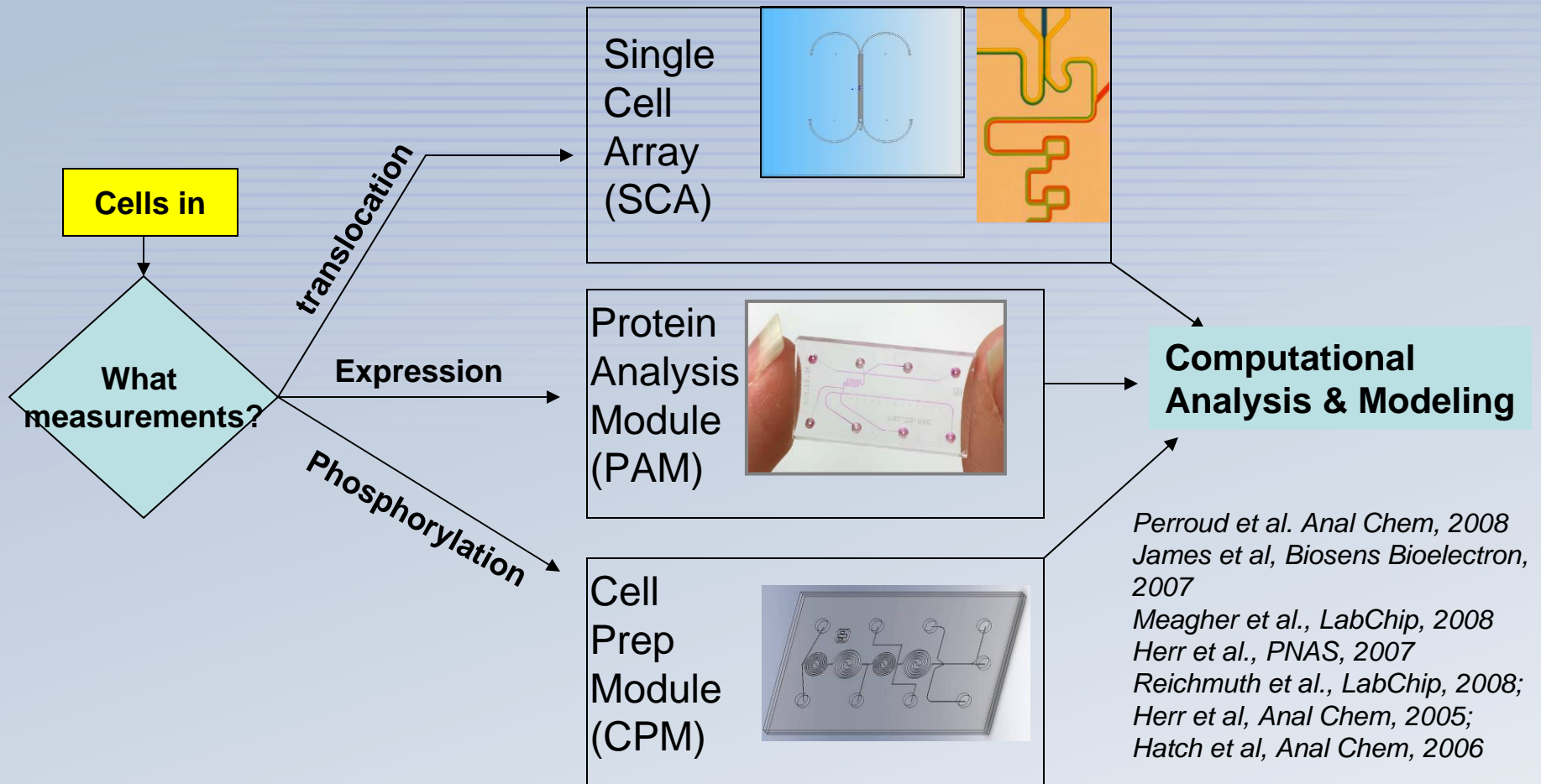


**Correlated imaging and phosphoassay can not be done with conventional instruments!**

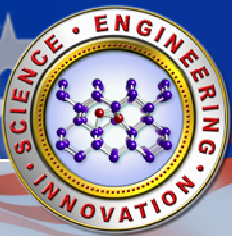




# MISL Integrated Platform

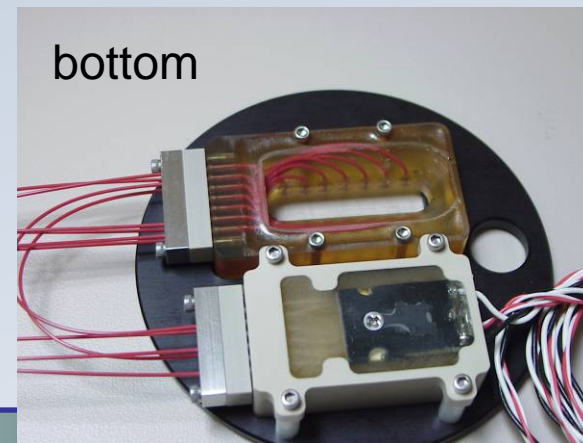
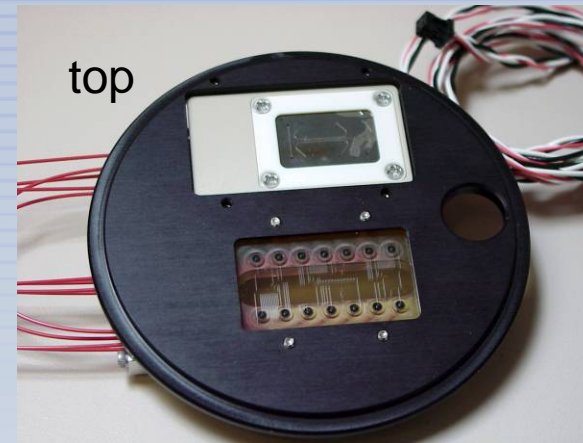
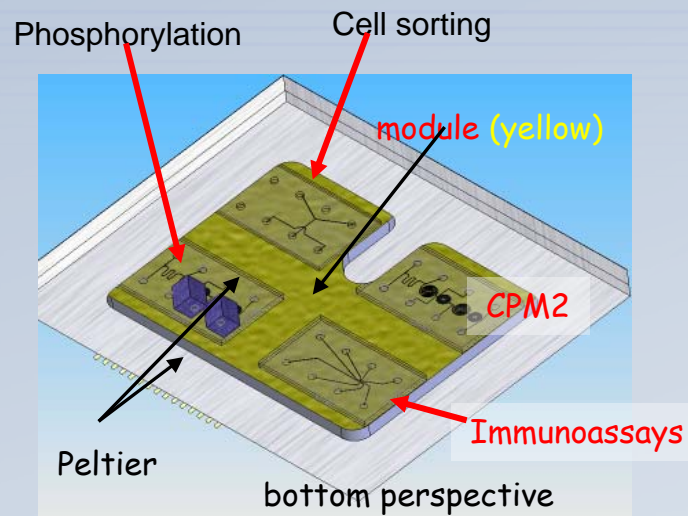
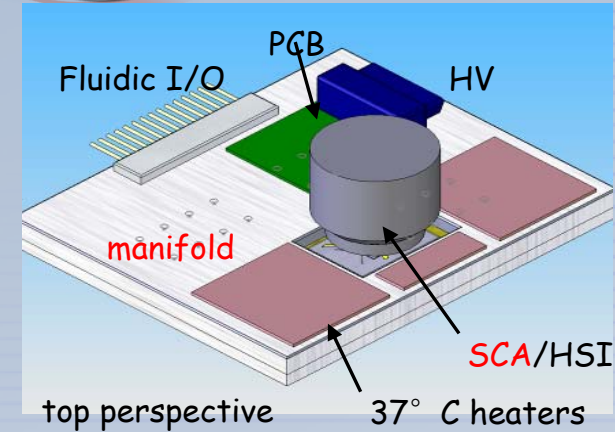


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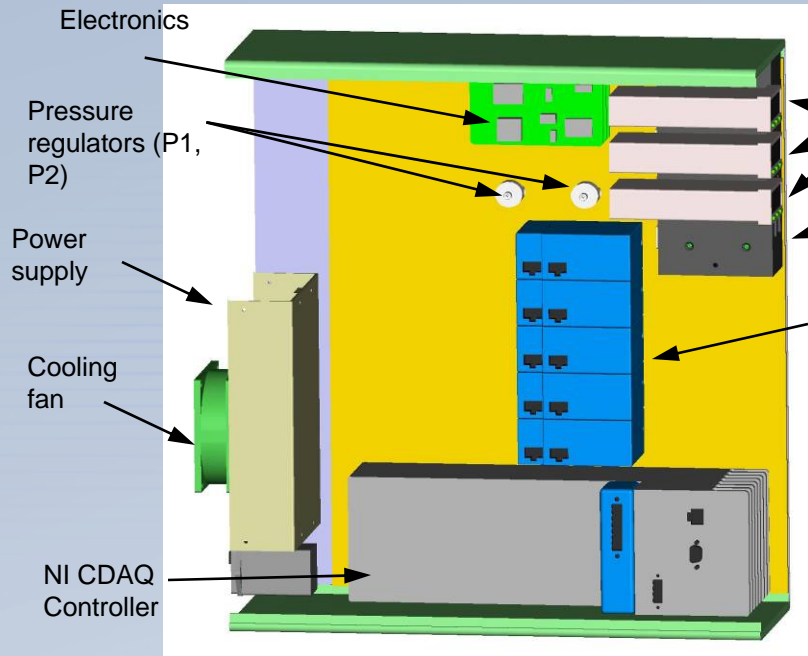
# MISL Integrated Platform

Single-cell array and cell sorter mounted in a microscope plate





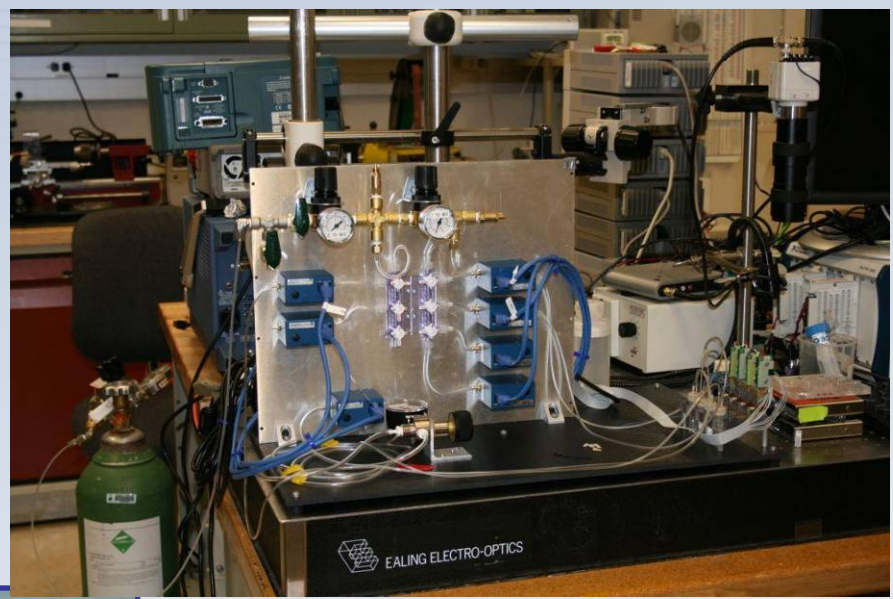
# MISL has created a self-contained, automated platform for studying cell signaling



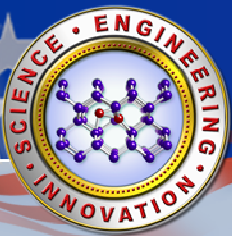
Approximate size: 14x15x5.5 inches

Schematic of the electronic and fluidic controller for MISL platform

- Automated operation
- Can be interfaced with hyperspectral confocal microscope or a commercial epifluorescence microscope
- Small foot-print will permit usage in BSL-3 & 4 environments







# How MISL has changed the landscape: an example

Goal: study crosstalk between TLR4 and TNFa pathways

Experimental design: monitor activation of 10 TLR4 pathway kinases and 3 TNFa pathway kinases over 10 time-points, in response to mixed challenges of 5 LPS concentrations and 5 TNFa concentrations

Represents ~150 Western blots

## Conventional Approach

Western: 6-8 hours  
1 FTE, 5 gels a day, 1 month  
Additional 2-4 weeks for data analysis

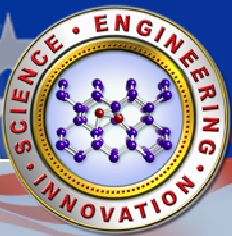
## MISL Approach

With automated controller and 5 CPM chips running simultaneously, and with a 4-color detector, will take ~3 days

**Slow, labor-intensive** → **Fast, automated**

**MISL approach will reduce time by a factor of ~20 and automate measurements**

LDRD Day, 2008



# How MISL has changed the landscape: an example

MISL approach allows measurements *not possible* with conventional assays (e.g., Western analysis)

## Conventional Approach

Semi-quantitative

Sensitivity: nM;

No single-cell resolution

Poor time-resolution (~2 min; miss early events)

Need large number of cells ( $10^6$  cells per assay)

Hence, impractical for primary cell assays

Reagent cost high

## MISL Approach

Quantitative

As low as ~50 fM

Single-cell resolution

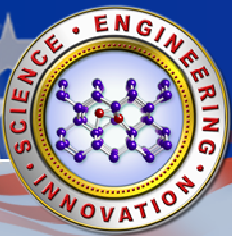
Time-resolution of ~sec

1000 cells per assay

HT expts with primary cells

1000-fold lower reagent consumption

Moreover, MISL platform allows correlated imaging and proteomic measurements



# A Multi-Disciplinary Team

PI: Anup Singh

PM: Glenn Kubiak

## Biology Core Team:

Tony Martino (coordinator)

Cathy Branda

Steve Branda

Elizabeth Carles

Amanda Carroll-Portill

Bryan Carson

Julie Kaiser

Todd Lane

Jaclyn Murton

Jens Poschet

Bryce Ricken

Meiye Wu

Zhaoduo Zhang\*



Allan Brasier



William Seaman

Elsa Ndiaye-Dulac

## Computational Biology Core Team:

Jean-Loup Faulon – Coordinator

Jaewook Joo

Shawn Martin

Milind Misra

Steve Plimpton

Susan Rempe

Ken Sale

## Platform and Detection Systems Core Team:

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Mark van Benthem

Jim Brennan

Susan Brozik

Ryan Davis

David Haaland

Amy Herr\*

Conrad James

Howland Jones

Ron Manginell

Matt Moorman

Kamlesh Patel

Thomas Perroud

Ron Renzi

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East Carolina University

Paul Gemperline

Diane Lidke, UNM

Funding: Sandia

LDRD Program



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