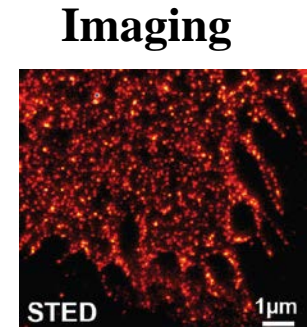
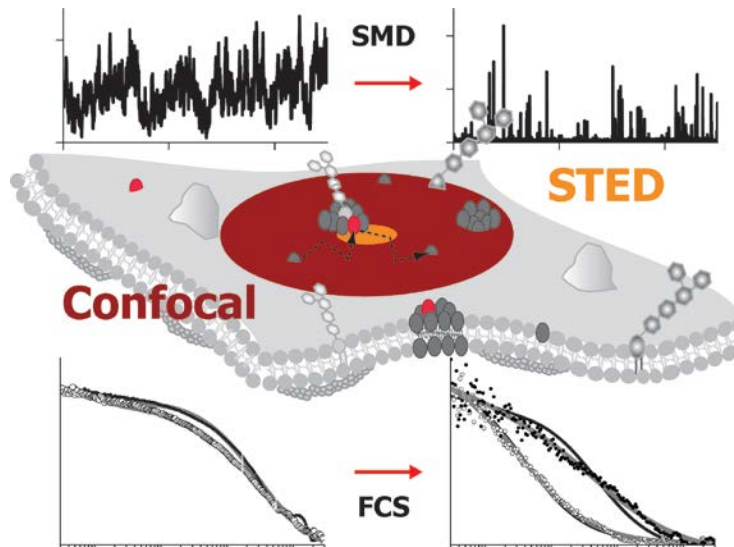
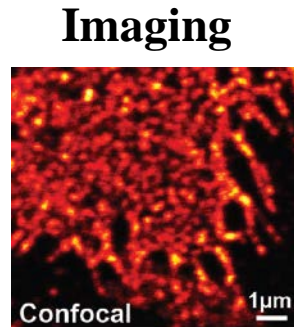


Christian Eggeling

Previously:  
Max Planck Institute for biophysical Chemistry  
Dep. NanoBiophotonic (Prof. Hell)  
Göttingen, Germany



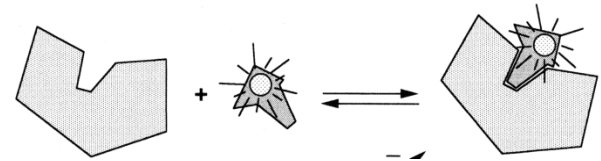
# Molecular Diffusion/Mobility

## *Bioactivity*

### Example 1

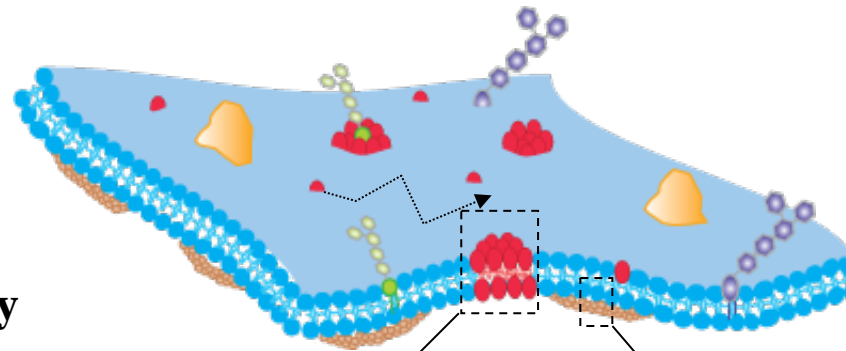
Binding of small peptide to large protein  $\Rightarrow$  increase of mass  $\Rightarrow$  increase of diffusion time  $\tau_D$

$\Rightarrow$  Determination of binding affinity via mobility

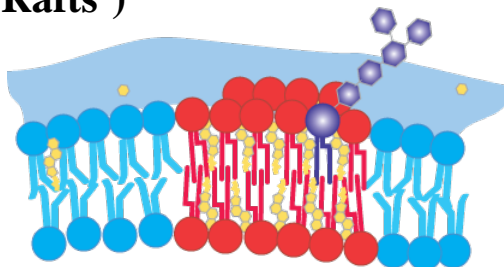


### Example 2

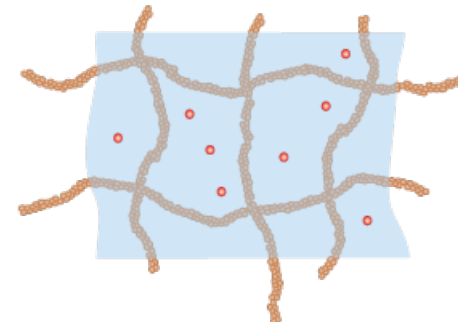
Plasma Membrane:  
Constrained diffusion  
on the nanoscale  
 $\Rightarrow$  determines bioactivity



Lipid-dependent Nano-/Microdomains  
(‘Rafts’)



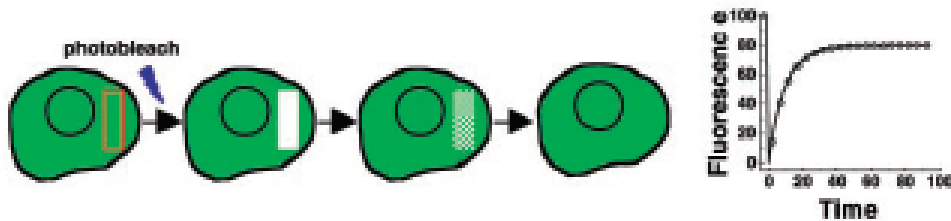
Cytoskeleton- based Meshwork



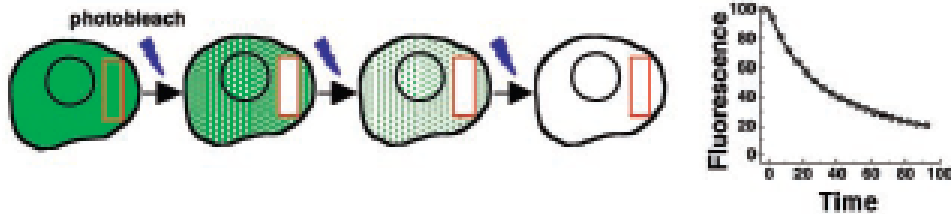
# Molecular Diffusion/Mobility

## Bioactivity

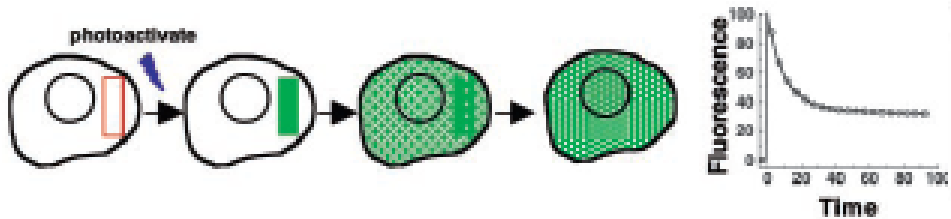
**A** Fluorescence Recovery After Photobleaching (FRAP)



**B** Fluorescence Loss in Photobleaching (FLIP)



**C** Photoactivation

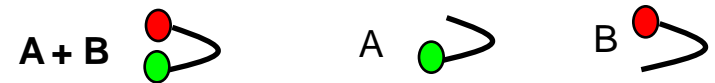


### Measuring Mobility in Cells

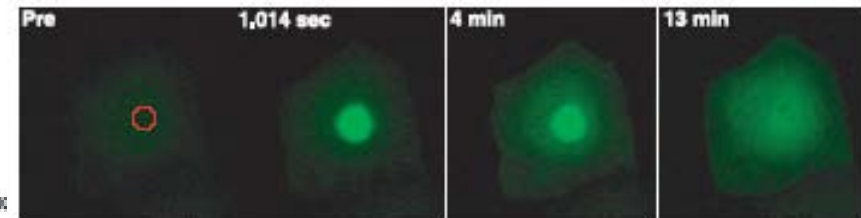
- FRAP (Fluorescence Recovery After Photobleaching)
- Photoactivation

### Problem

- Trigger – disturb system?
- Correlated diffusion



Photoactivatable fluorescent proteins  
(PA-GFP, Kaede, Dronpa, asFP595, ...)



Lippincott-Schwartz, Science 2003

# Molecular Diffusion/Mobility

## *Single-Molecule Detection*

---

**Aim** observe biochemical reaction in equilibrium

### Why Single-Molecule based experiments?

Monitor thermodynamical fluctuation around equilibrium due to kinetics/diffusion  
⇒ no trigger of experiment

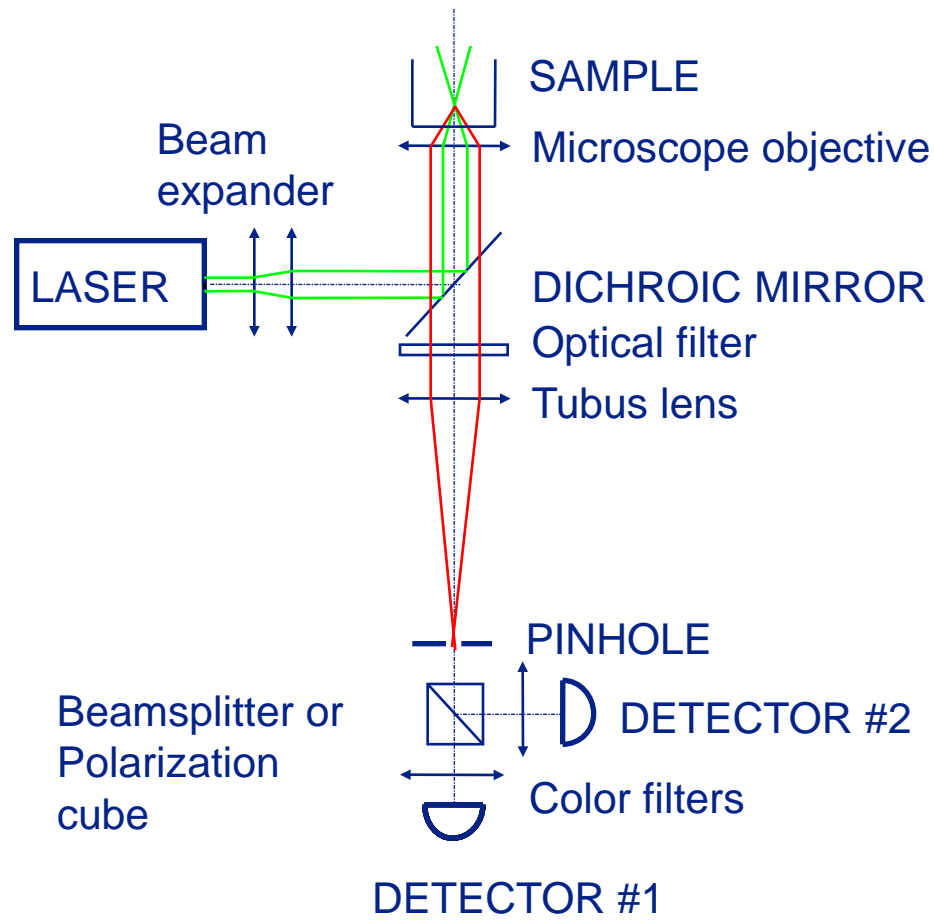
Analysis on single-molecule level

⇒ distinguish / quantify components with different molecular characteristics  
(e.g. weight, brightness)

⇒ detect (small) heterogeneities

# Far-Field Fluorescence Spectroscopy

## *Single-Molecule Detection*



### Background Reduction

- ⇒ **small detection volume (femto-liter)**
- ⇒ **confocal detection**

**Not a problem to detect signal from single molecule**

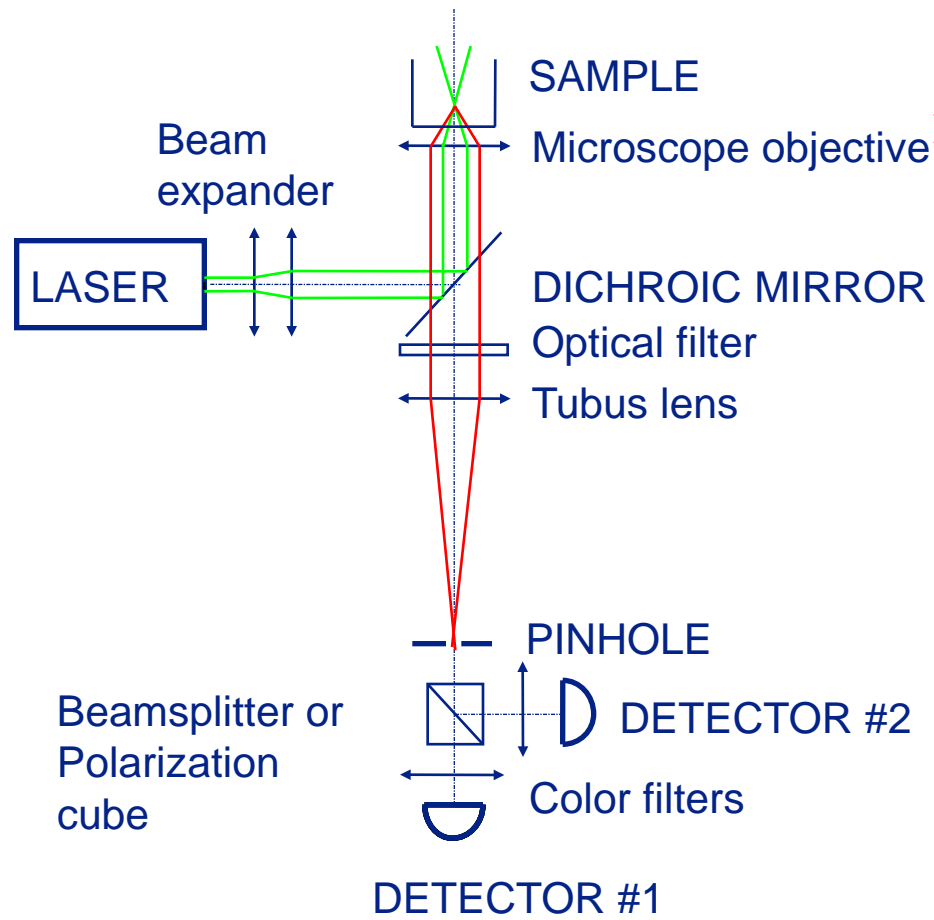
**But: problem to see it in front of background!**

### Enhanced fluorescence detection

- Multi-color (excitation + detection)
- Polarized excitation + detection
- Fluorescence lifetime (pulsed exc. + TCSPC)
- Raw data detection (photon-by-photon)
- Online analysis (correlation, distribution)

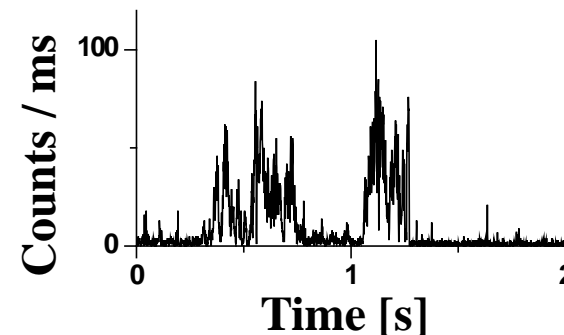
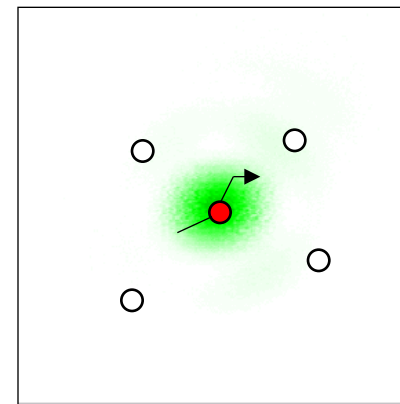
# Far-Field Fluorescence Spectroscopy

## *Single-Molecule Detection*



**Fluorescence intensity over time**

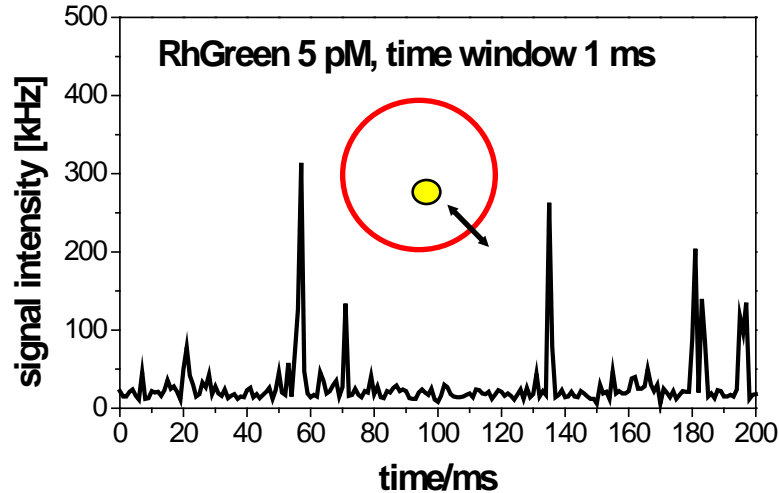
**Low fluorescent concentration**  
⇒ **diffusion of single-molecules**  
= **fluorescence bursts**



# Single-Molecule Detection

## *Signal Fluctuations*

---



### Single molecule

- diffusion in/out detection volume
- fluorescence changes due to reaction kinetics

### ⇒ Fluctuations

Only detectable if mean number of observed molecules small (near one)

⇒ **small detection volume** ( $< \mu\text{m}$ )

⇒ **low concentration** (nM)

### Information

**Length** – diffusion time (or reaction kinetic)

**Height** – brightness

**Density** – concentration

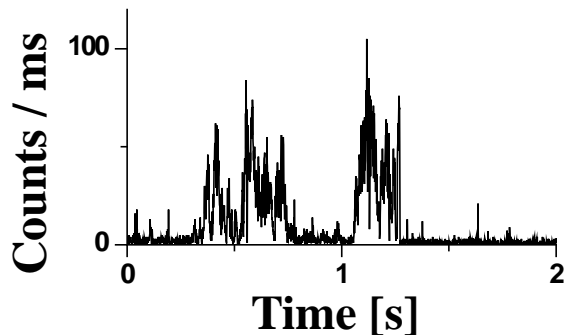
### Analysis

Statistics in **time** – correlation

Statistics in **amplitude** – distribution analysis

# Fluorescence Fluctuation Spectroscopy

## Fluorescence Correlation Spectroscopy (FCS)



### data analysis

$$G(\tau_c) = 1 + (1/N)[1 - T + T \exp(-\tau_c/t_T)] \times (1 - \tau_c/\tau_{diff})^{-1} \times (1 + (\omega/z)^2 \tau_c/\tau_{diff})^{-1/2}$$

⇒ **mean transit time**  $\tau_d$  (~ mass) of each fluorescent species – diffusion coefficient

⇒ **concentration N** (mean number of particles)  $N = \text{conc} * V_{\text{Det}}$

⇒ **kinetic rate constants**



**Small = fast**



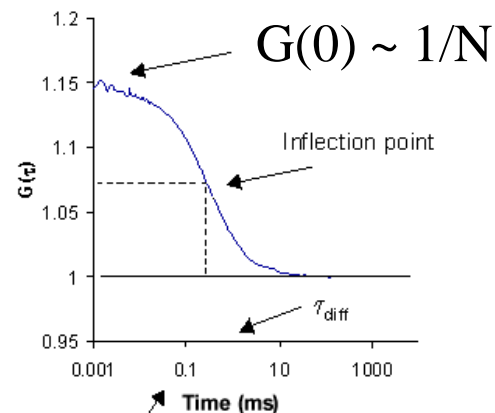
**Big = slow**

### data acquisition

calculation of correlation function

$$G(\tau_c) = \frac{\sum_t A(t) \cdot A(t + \tau_c)}{\text{normalize}}$$

### Statistics on Time Axis



logarithmic x-axis

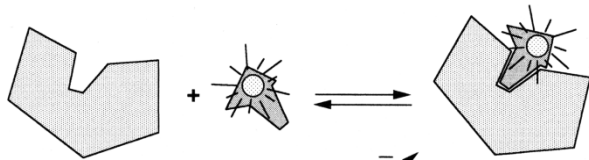


# FCS

## *Application: Mobility Measurement*

### FCS-Example

Binding of small peptide to large protein  $\Rightarrow$  increase of mass  $\Rightarrow$  increase of diffusion time  $\tau_D$



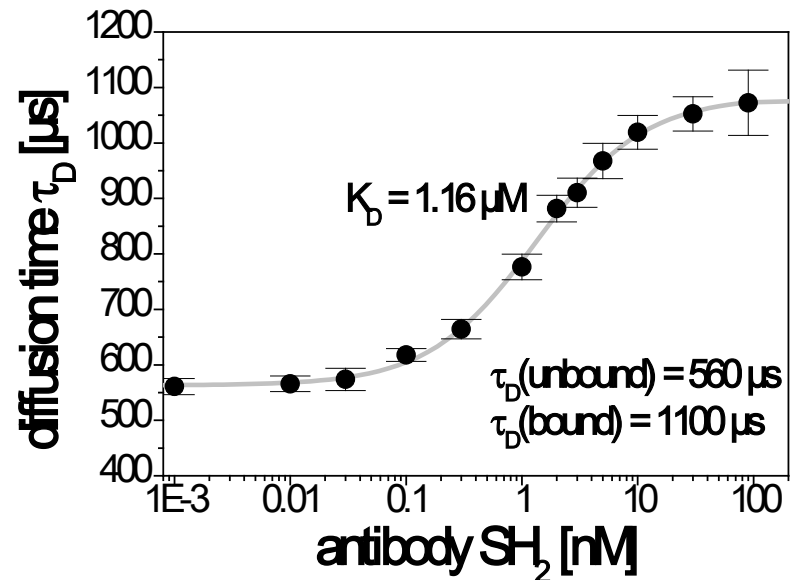
### *Measurement*

Tyrosine Kinase Growth Factor Receptor Bound  
**Protein** [Grb2 SH2]

+ **labelled ligand**

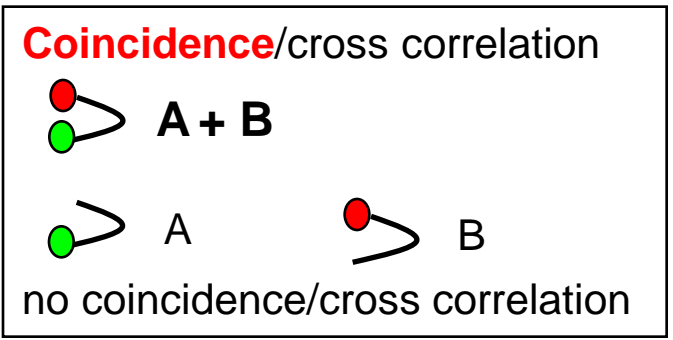
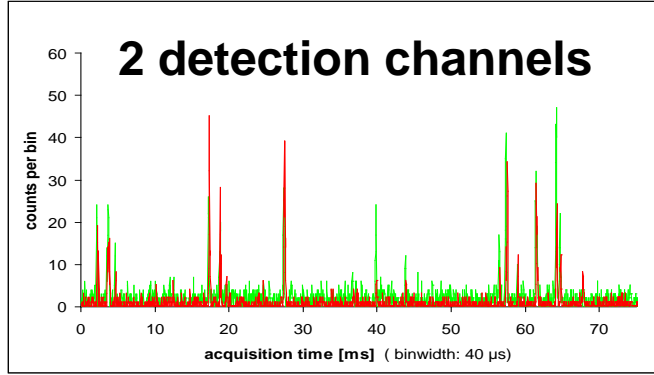
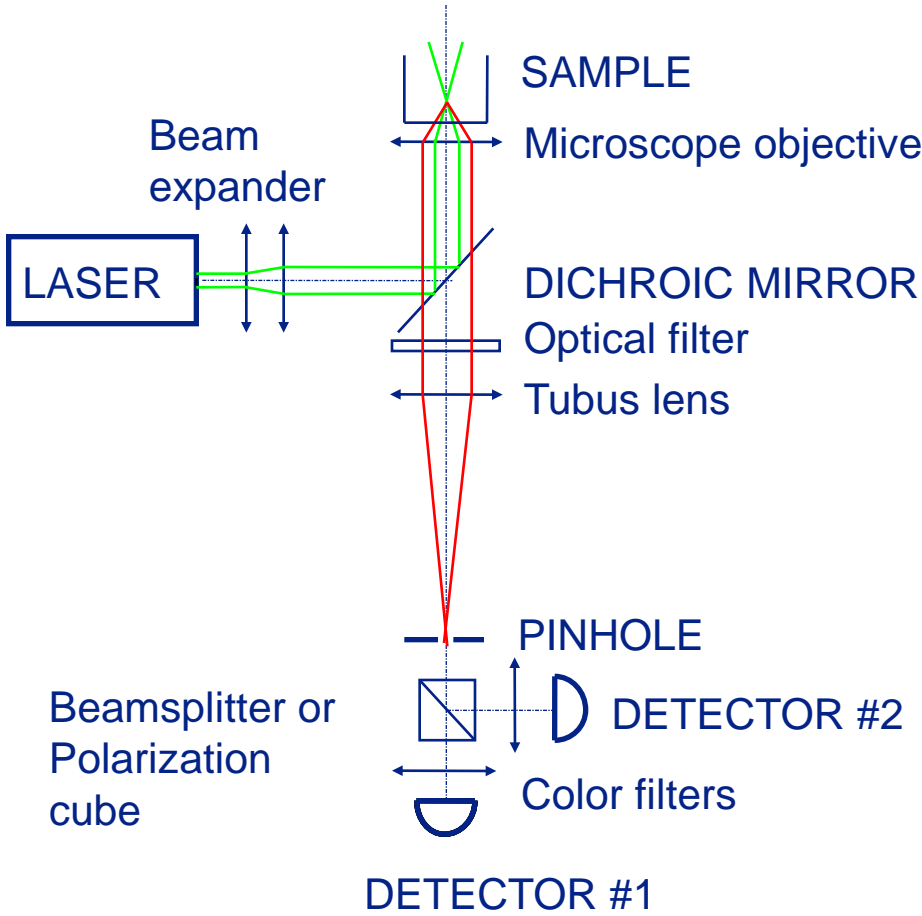
(phosphotyrosine Ac-Y\*VNVK(Cy5)-CO-NH2)

Titration of Grb2 SH2 (10 s measurement time)



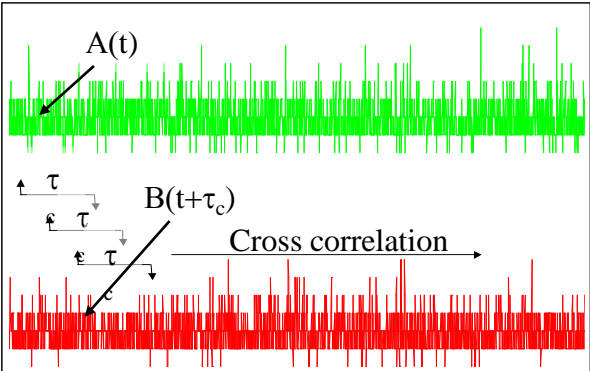
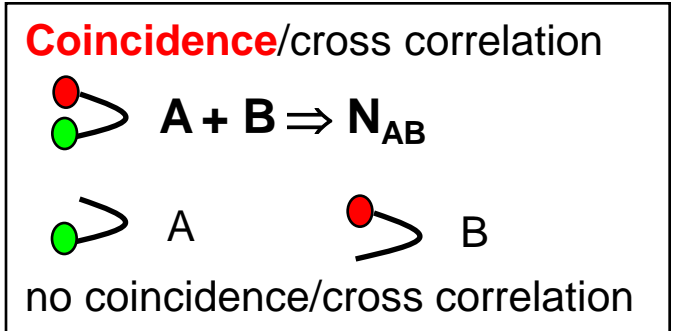
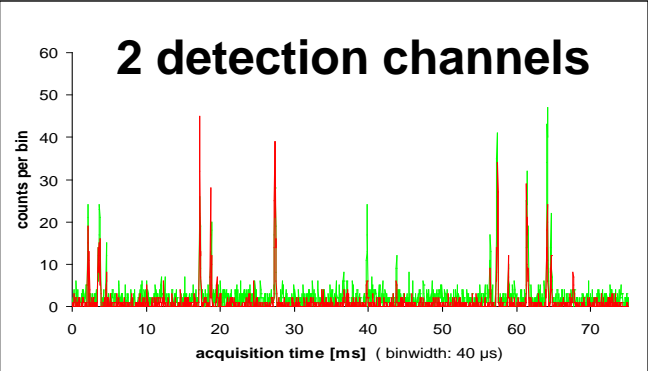
# Fluorescence Fluctuation Spectroscopy

## Two-Color FFS – FCCS



# Fluorescence Fluctuation Spectroscopy

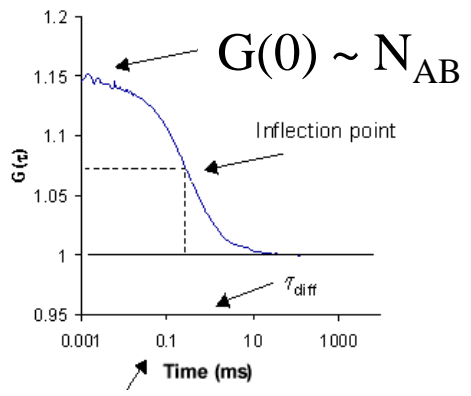
## Two-Color FFS – 2D-FIDA and FCCS



$$G(\tau_c) = \frac{\sum A(t) \cdot B(t + \tau_c)}{\text{normalize}}$$

—————→

### FCCS (cross correlation)

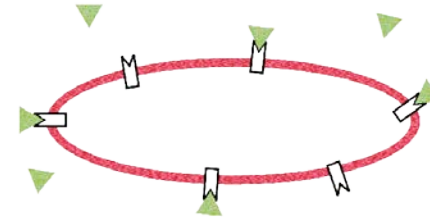


# Fluorescence Fluctuation Spectroscopy

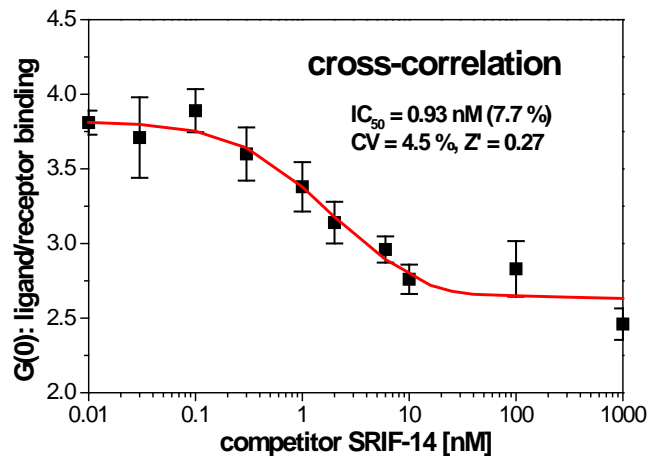
## *Two-Color FFS – 2D-FIDA and FCCS*

### SOMATOSTATIN Receptor (SST2)

- Human Type-2 High Affinity SOMATOSTATIN **Receptor** (SSTR2) + small fluorescently TAMRA-**labelled peptide ligand** (Somatostatin-14, SMS)
- Small Membrane **Vesicles** from overexpressing CCL39 cells (stained with red dye DiD) carrying SSTR-2
- Somatostatin-14 (SRIF-14) as **competitor** (unlabelled)
- **controls:**  $q(\text{unbound}) = 12 / 0 \text{ kHz} + 0 / 300 \text{ kHz}$   
 $q(\text{bound}) \approx 800 / 300 \text{ kHz}$
- **analysis:** 3-components (coincidence)  $\Rightarrow$  fraction bound/coincidence



Competition with SRIF-14

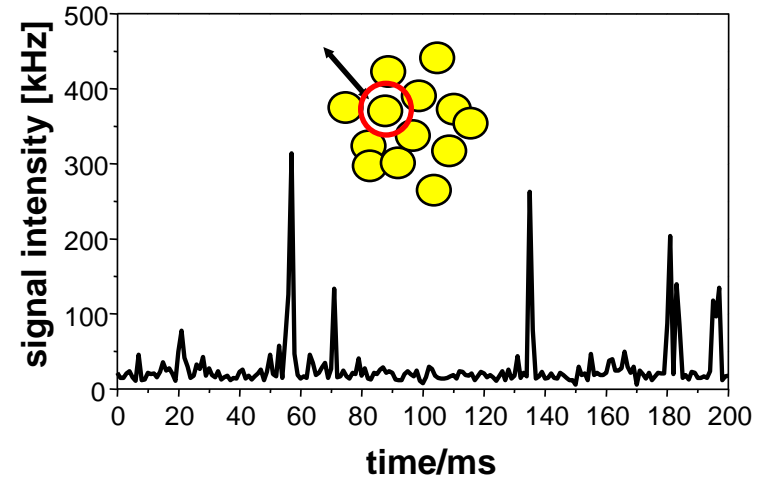
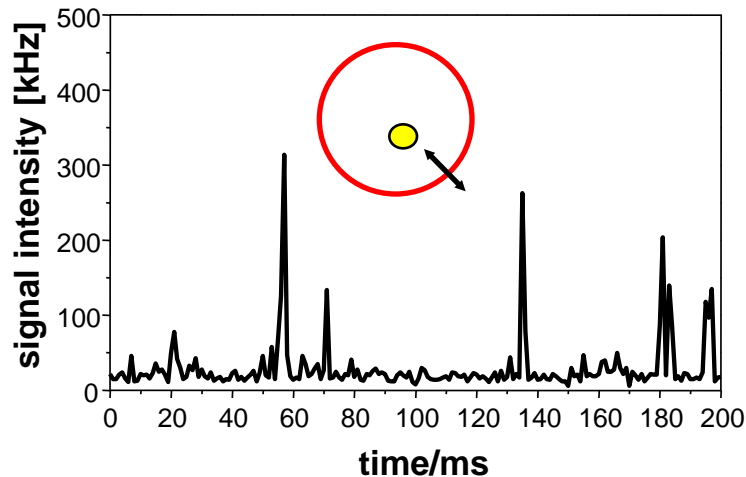


# Fluorescence Correlation Spectroscopy

## *Use of STED Nanoscopy?*

---

**FCS – need for low concentration (< 20 nM)**



### **Concentration Problem**

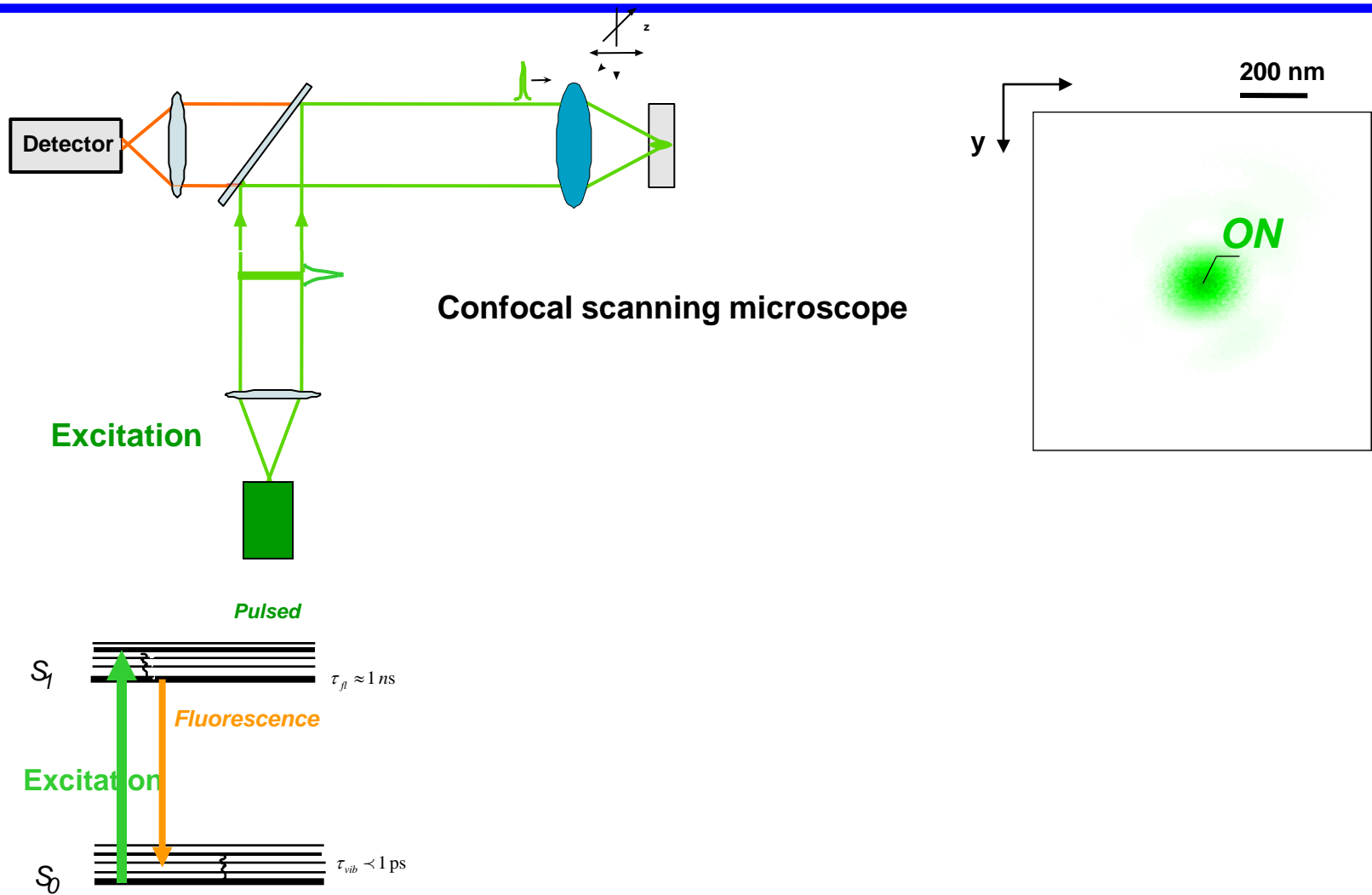
endogenous protein / molecule concentration higher

low affinity binding or enzymatic activity reactions - high concentration ( $\sim 1\mu\text{M}$ )

**$\Rightarrow$  smaller/more confined detection volumes:  
measure at higher concentration!**

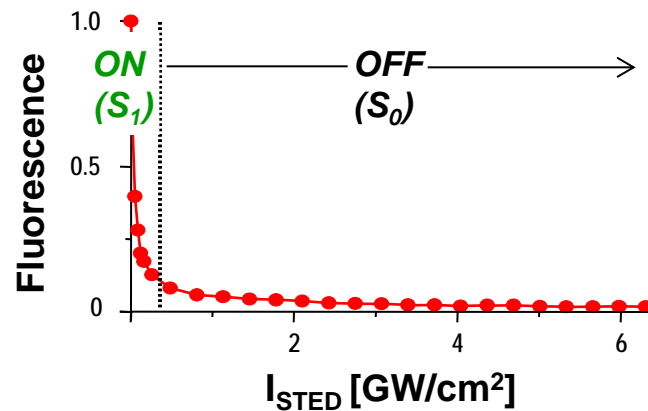
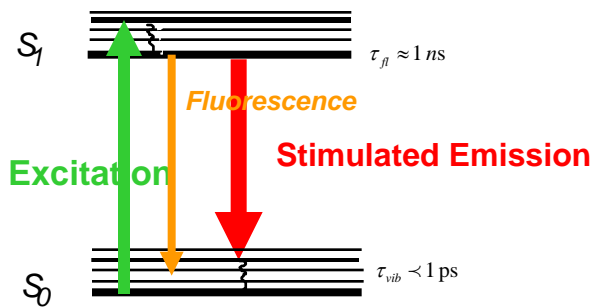
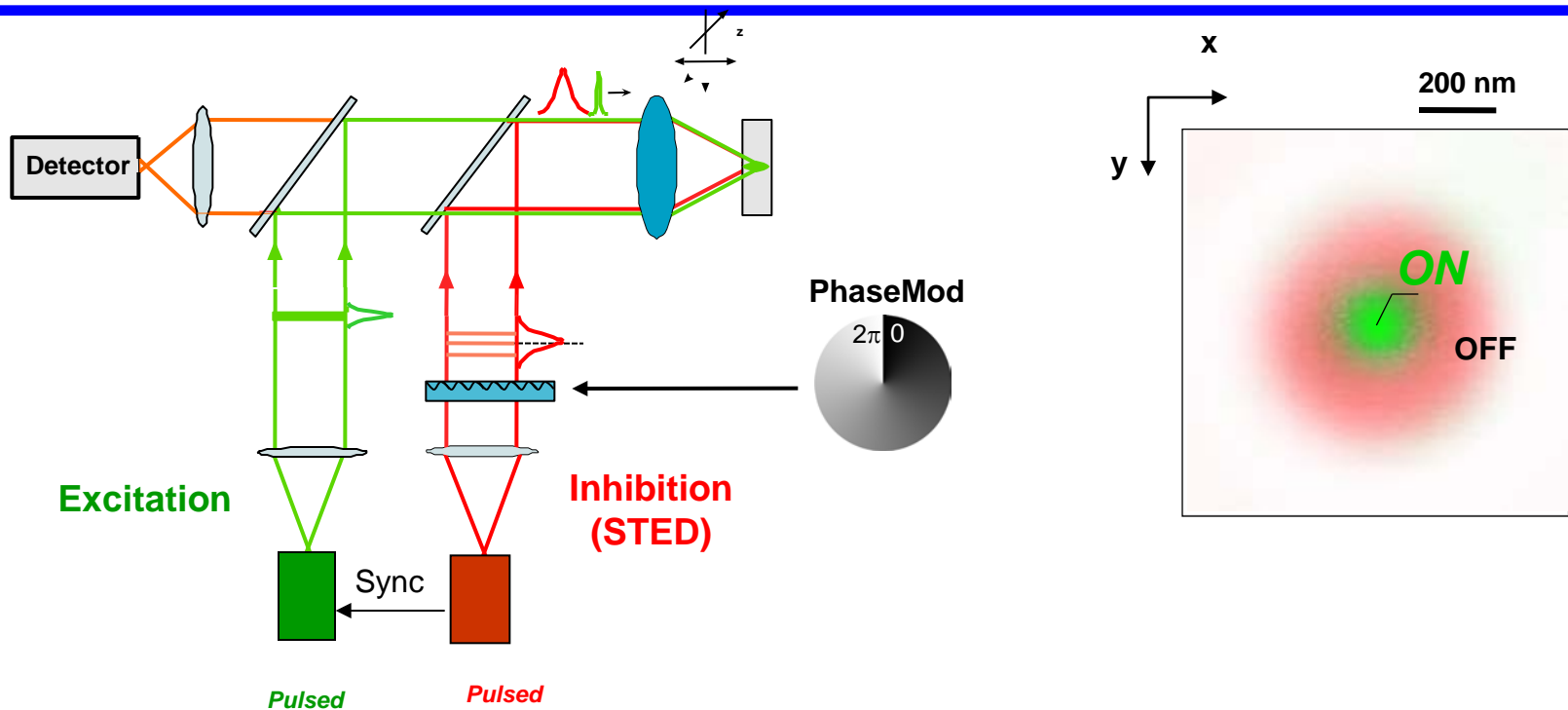
# Fluorescence Microscopy

## *STED Microscopy*



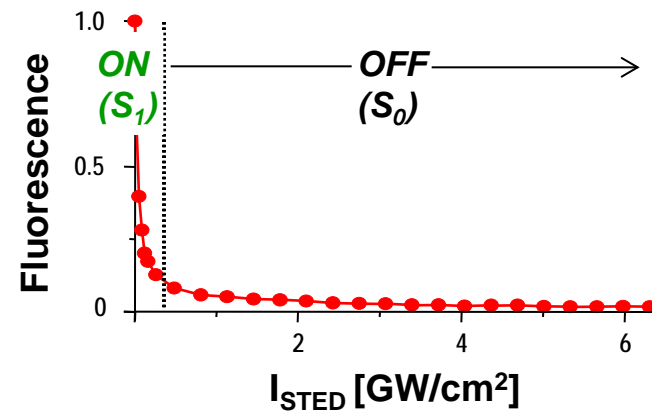
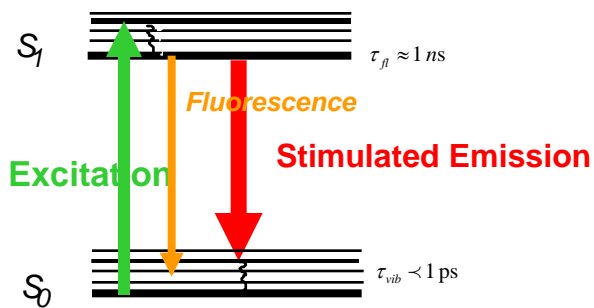
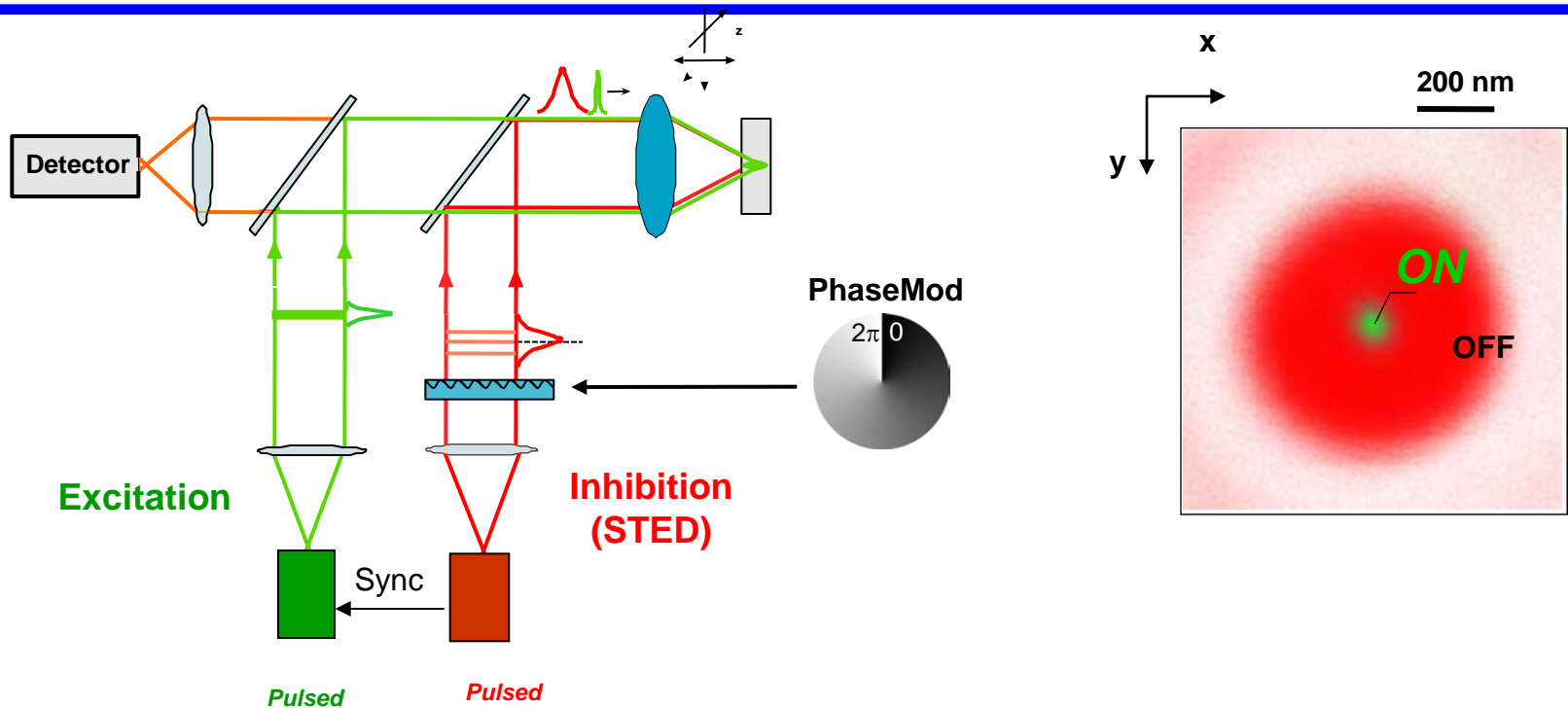
# Fluorescence Microscopy

## *STED Microscopy*



# Fluorescence Microscopy

## *STED Microscopy*

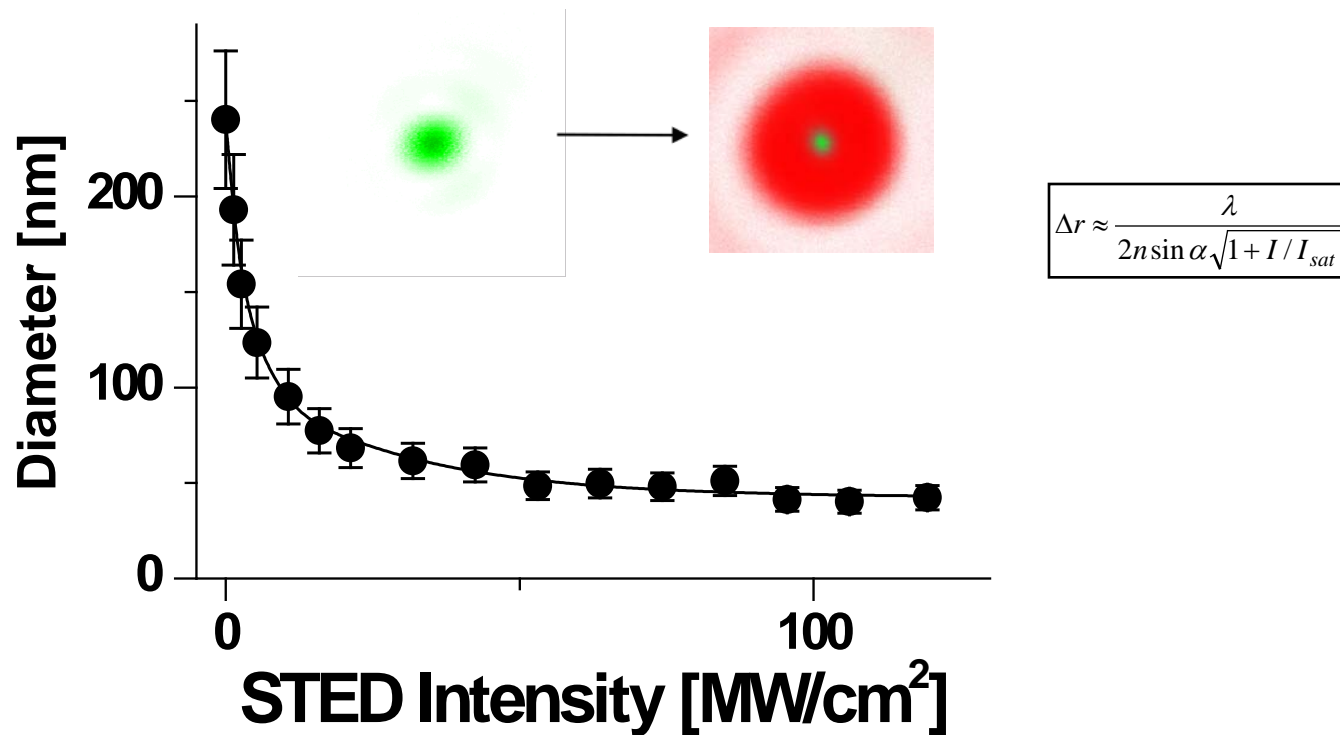




# STED Microscopy

## *Dynamical confinement of resolution*

**Nanoscale observation areas: CONTINUOUS TUNING of spatial resolution!**

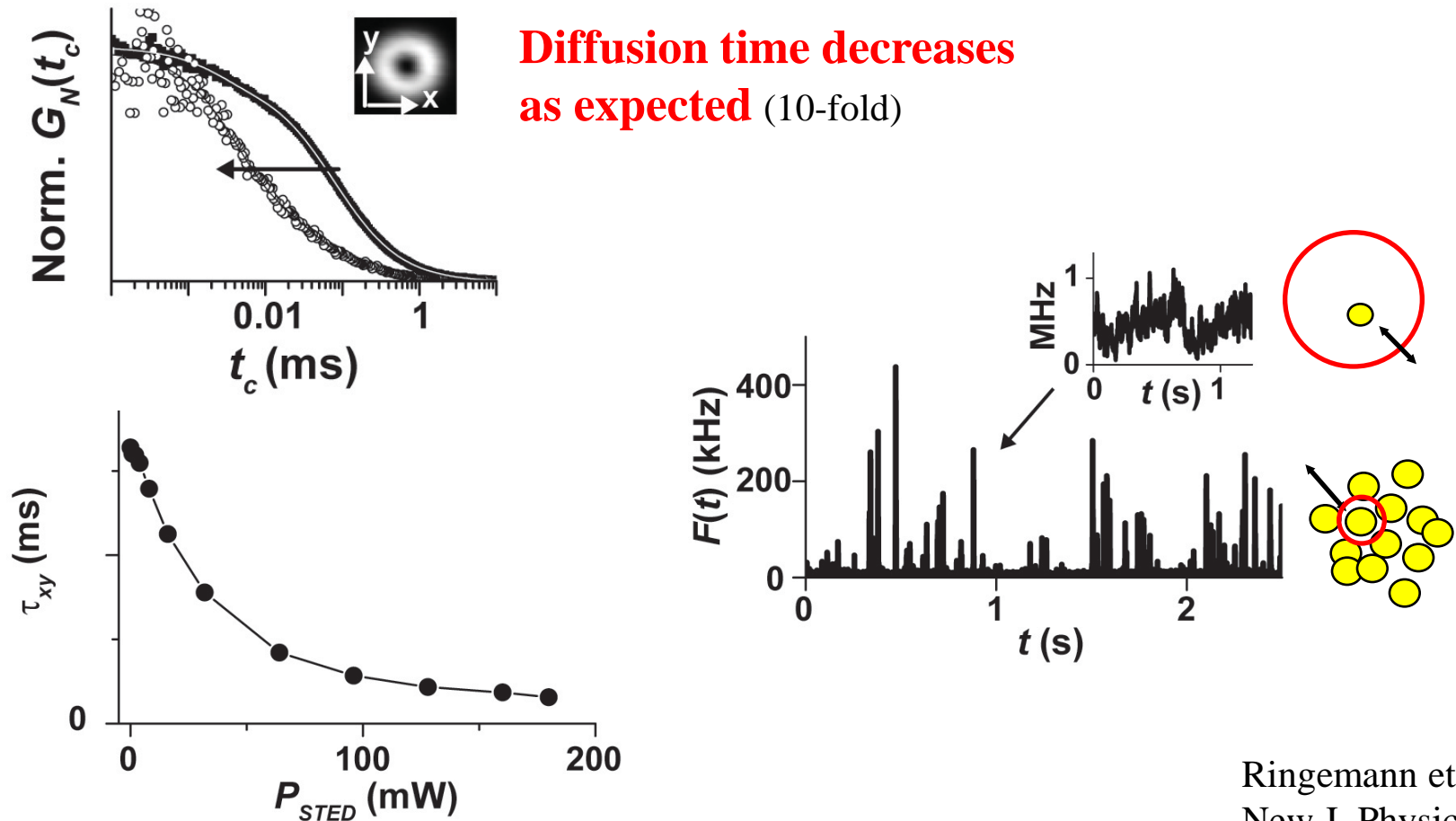


# Fluorescence Correlation Spectroscopy

## *STED Nanoscopy: Concentration Issue*

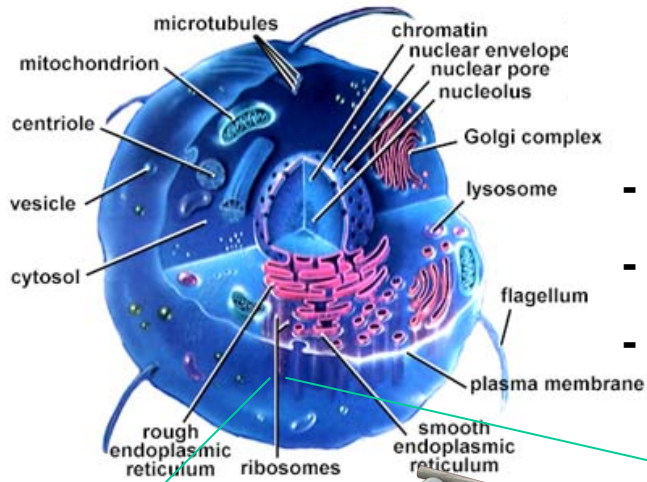
**STED-FCS in open volumes:** Atto647N in aqueous solution

FCS data with increasing STED power, i.e., increasing focal confinement



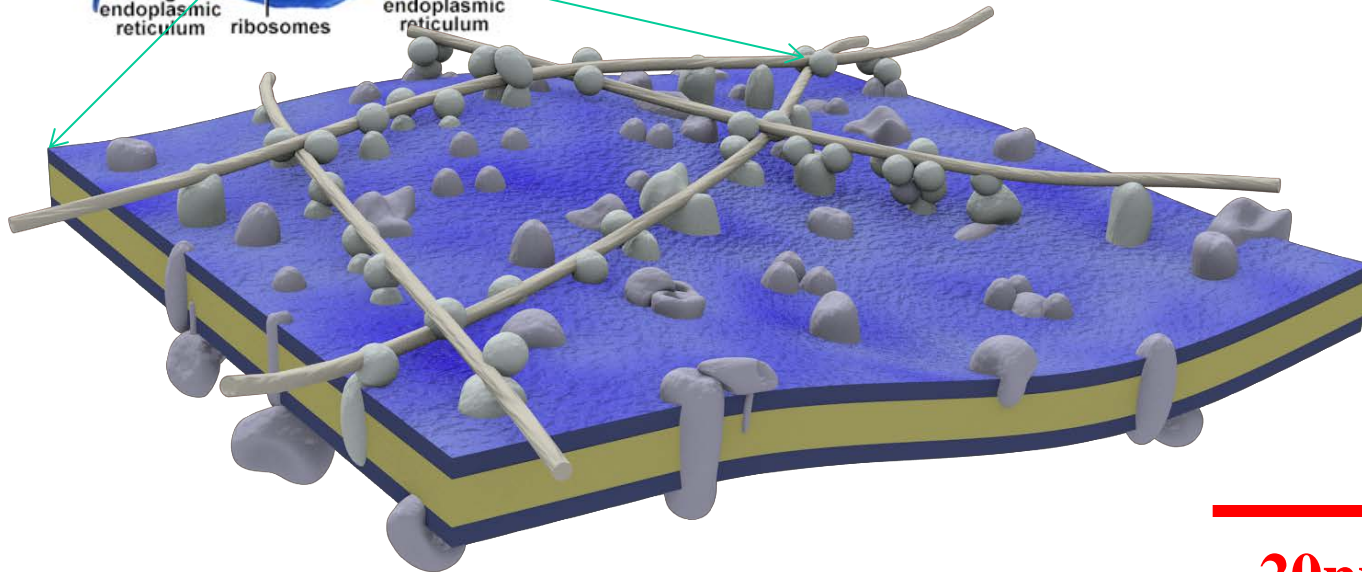
# Lipid Plasma Membrane Organization

## *Nanoscale*



## Lipid Plasma Membrane Organization:

- Heterogeneous distribution (viscosity, curvature, ...)
- Interaction with proteins
- Interaction with cortical cytoskeleton



20nm

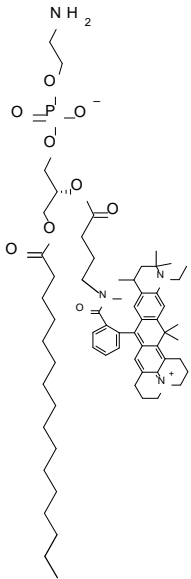
Small spatial  
scales!!!!

# Lipid Plasma Membrane Organization

## *Fluorescence Recordings: Lipids*

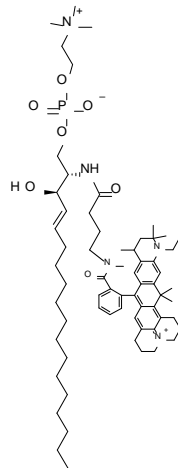
**Phosphoglycerolipid:**

**Atto647N-phosphoethanolamine (PE)**



**Sphingolipid:**

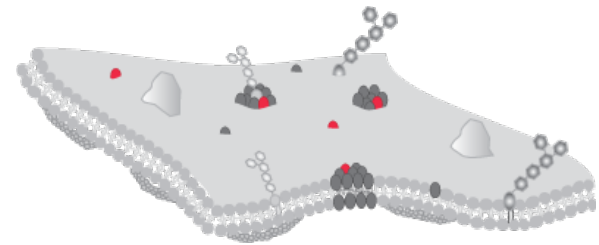
**Atto647N-sphingomyelin (SM)**



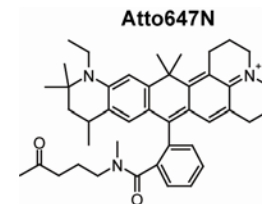
**Live PtK2 cells:**

physiological conditions

incorporation in plasma membrane

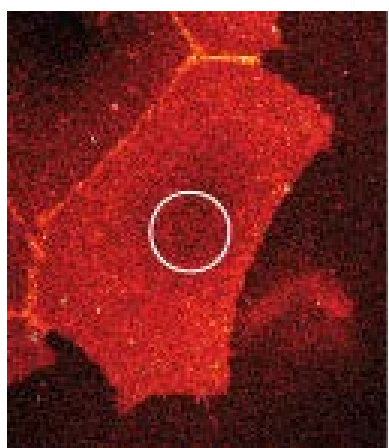
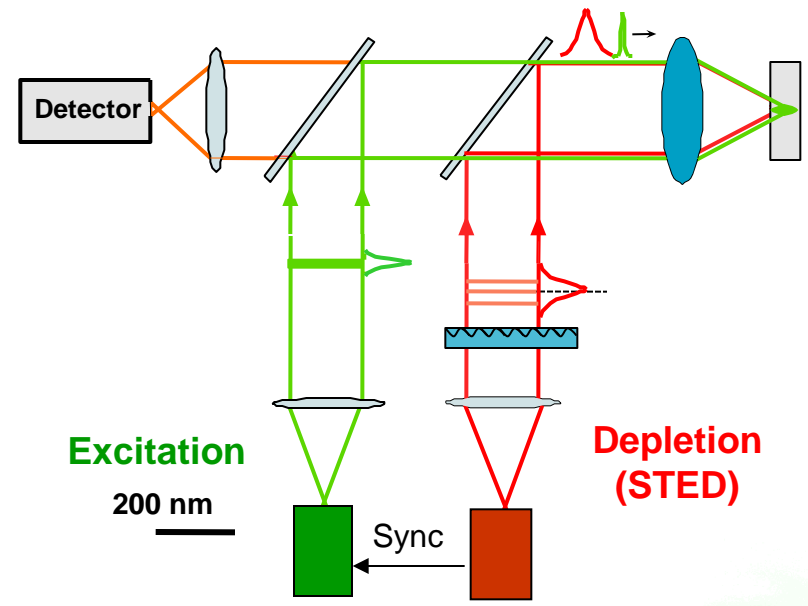
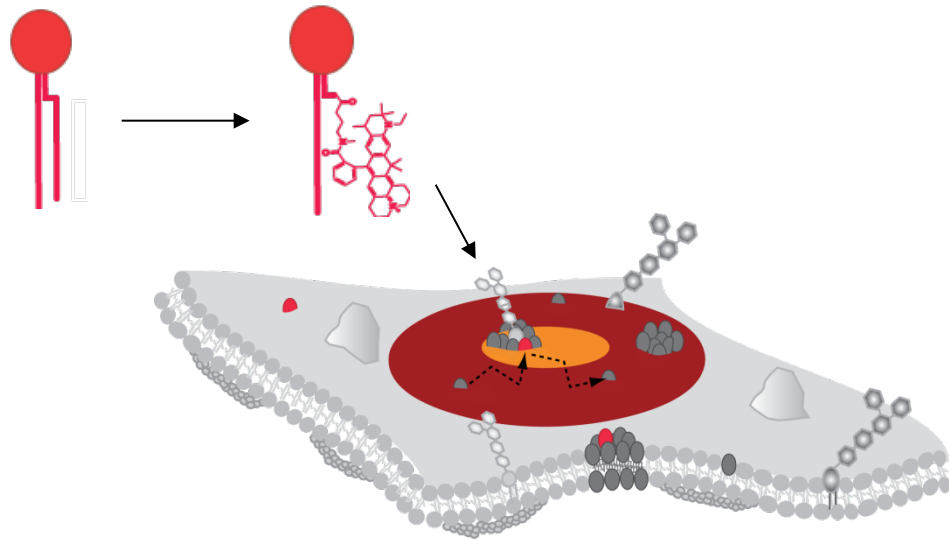


**BSA  
complex**

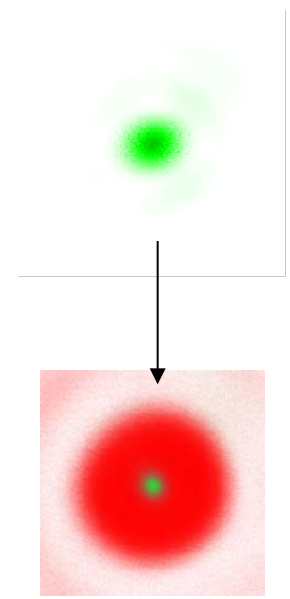


# Lipid Plasma Membrane Organization

## *STED Nanoscopy Measurement*

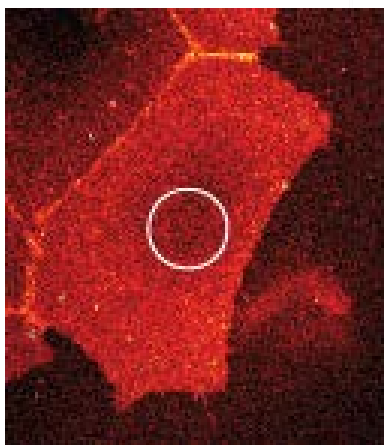
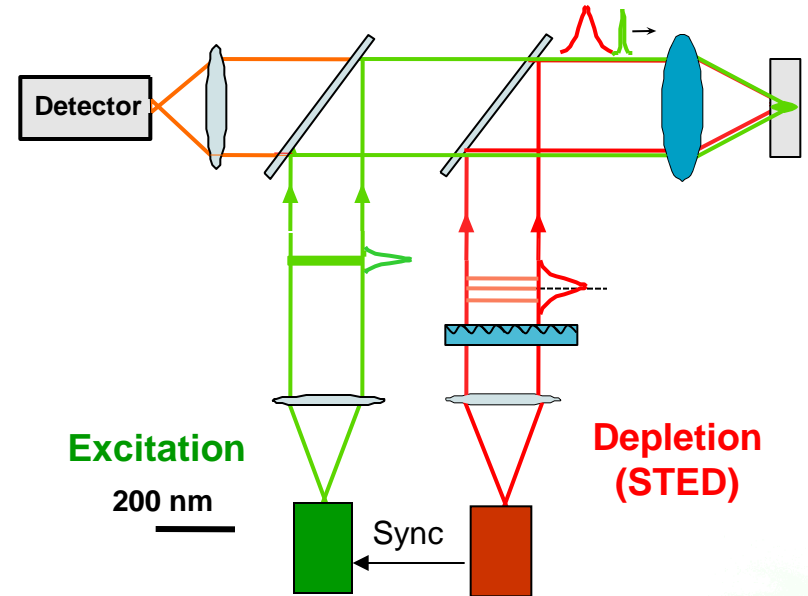
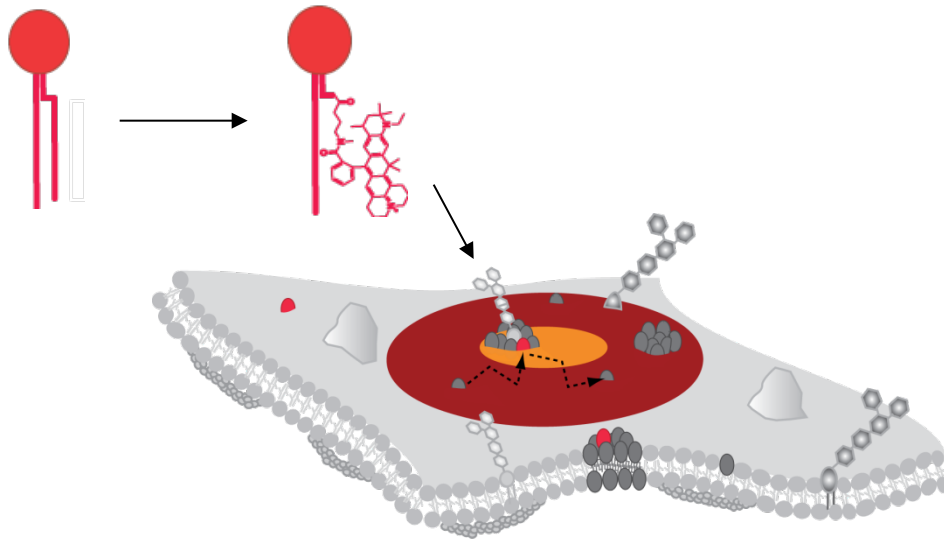


**Homogeneous distribution**



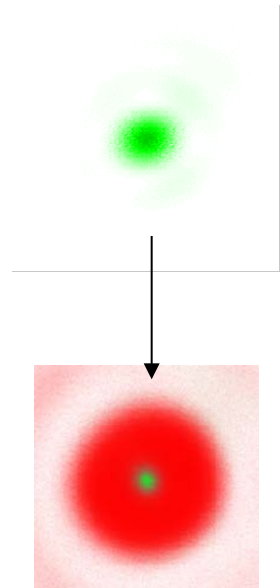
# Lipid Plasma Membrane Organization

## *STED Nanoscopy Measurement*



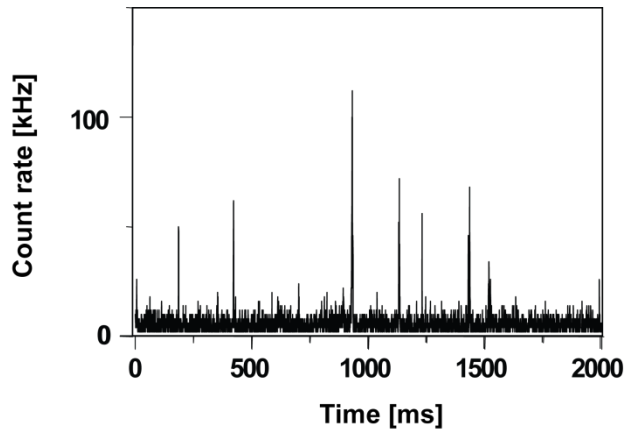
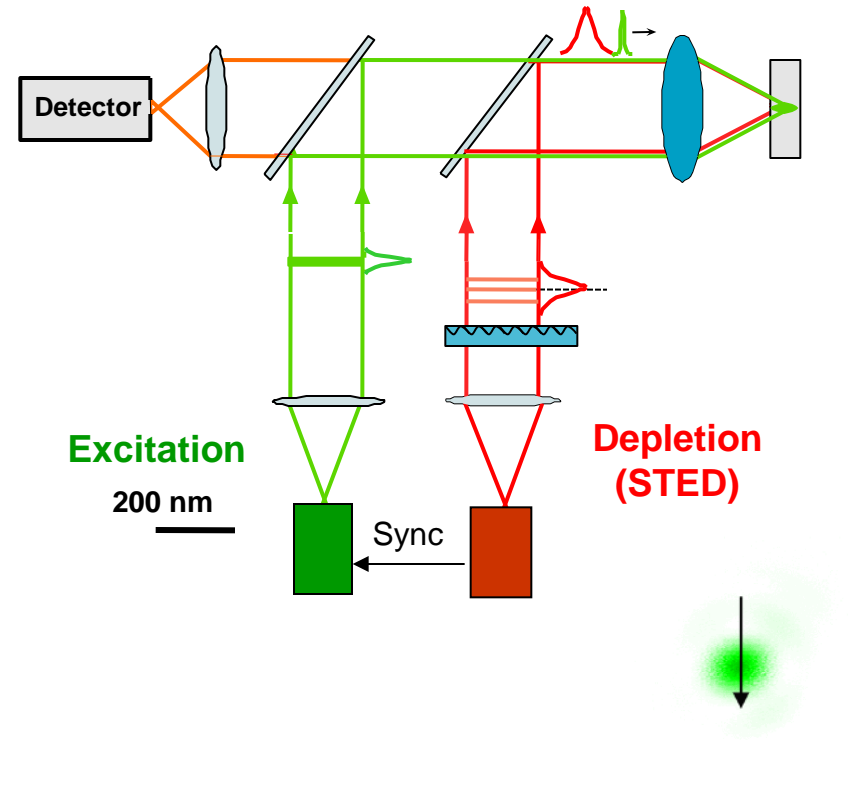
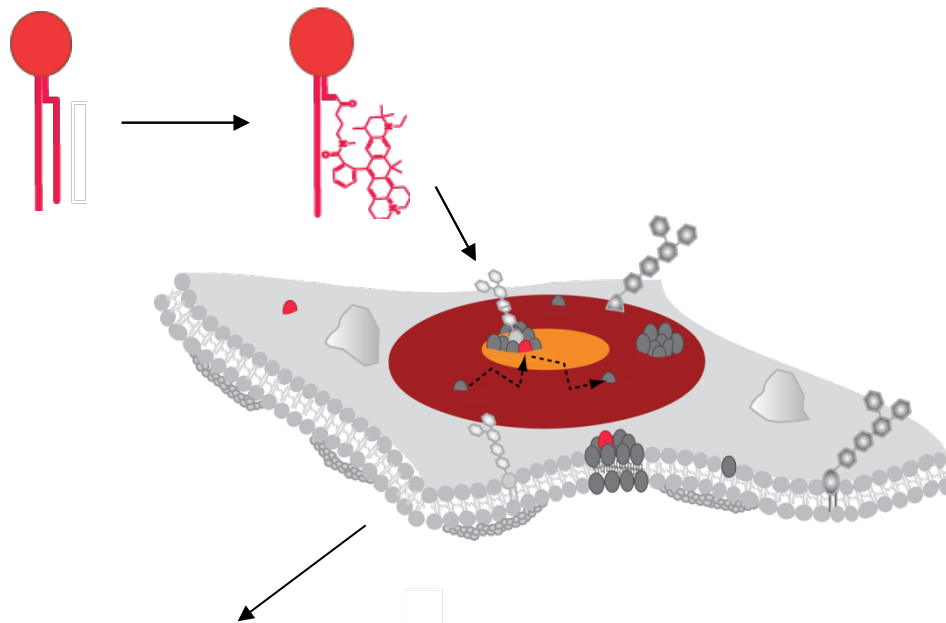
**Homogeneous distribution**

**Fast diffusion → Limited temporal resolution!**



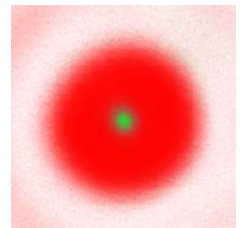
# Lipid Plasma Membrane Dynamics

## *STED Nanoscopy Measurement*



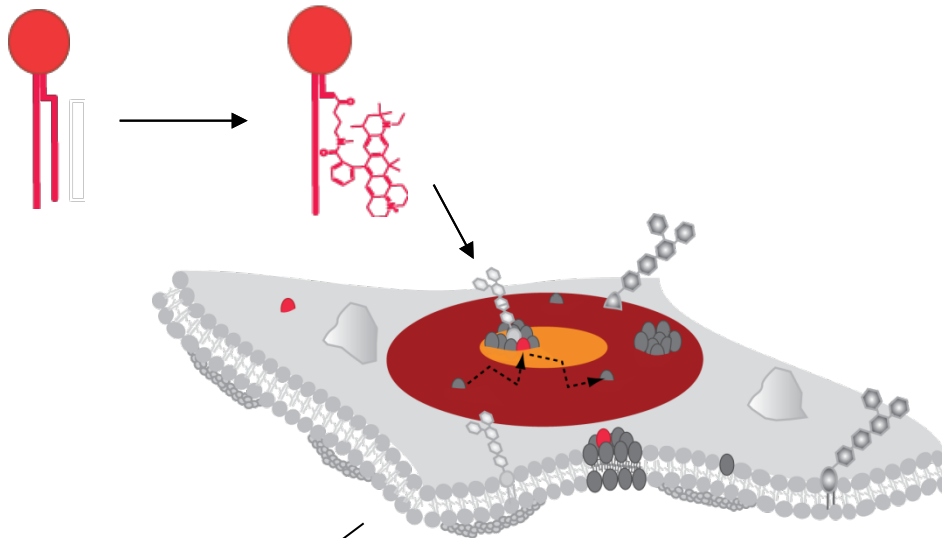
**Discover diffusion dynamics!!!**

Eggeling et al Nature 2009

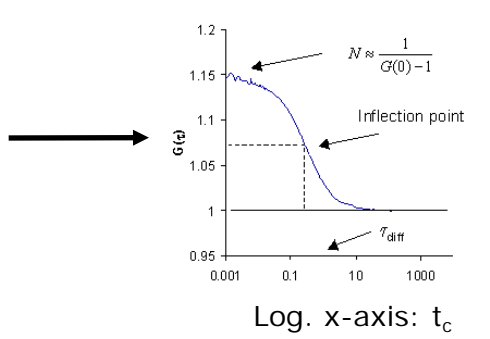
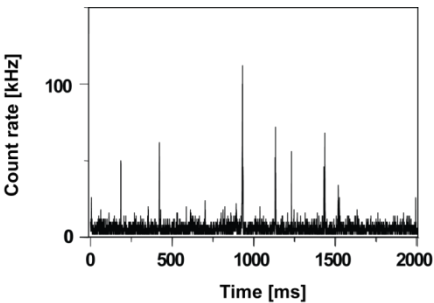
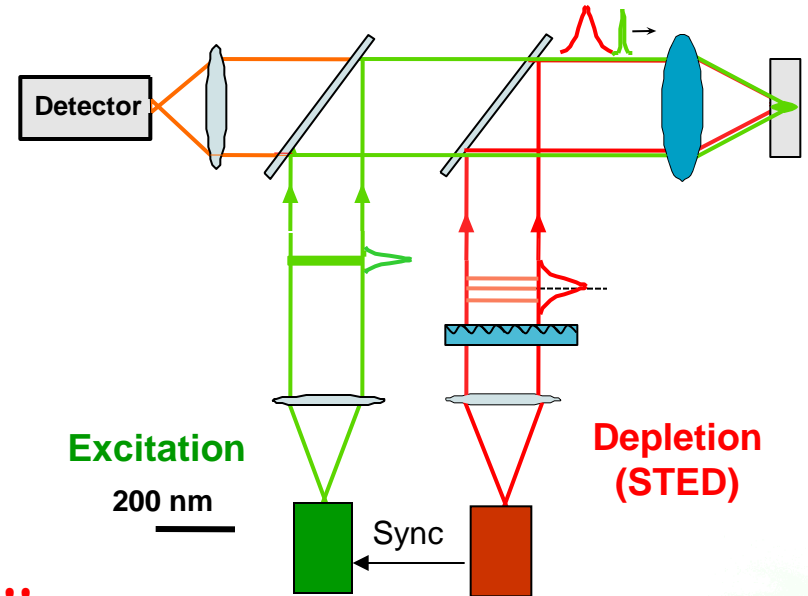


# Lipid Plasma Membrane Dynamics

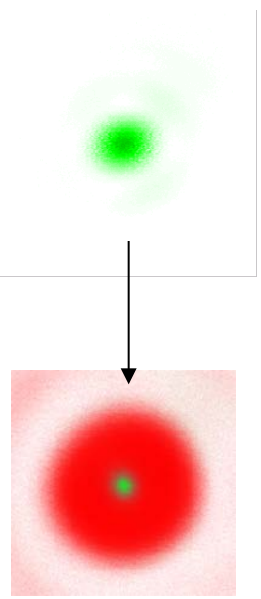
## *STED Nanoscopy Measurement*



**Discover diffusion dynamics!!!**  
**Fluorescence Correlation Spectroscopy (FCS)**



**molecular  
diffusion coefficient  
=  
molecular  
mobility**

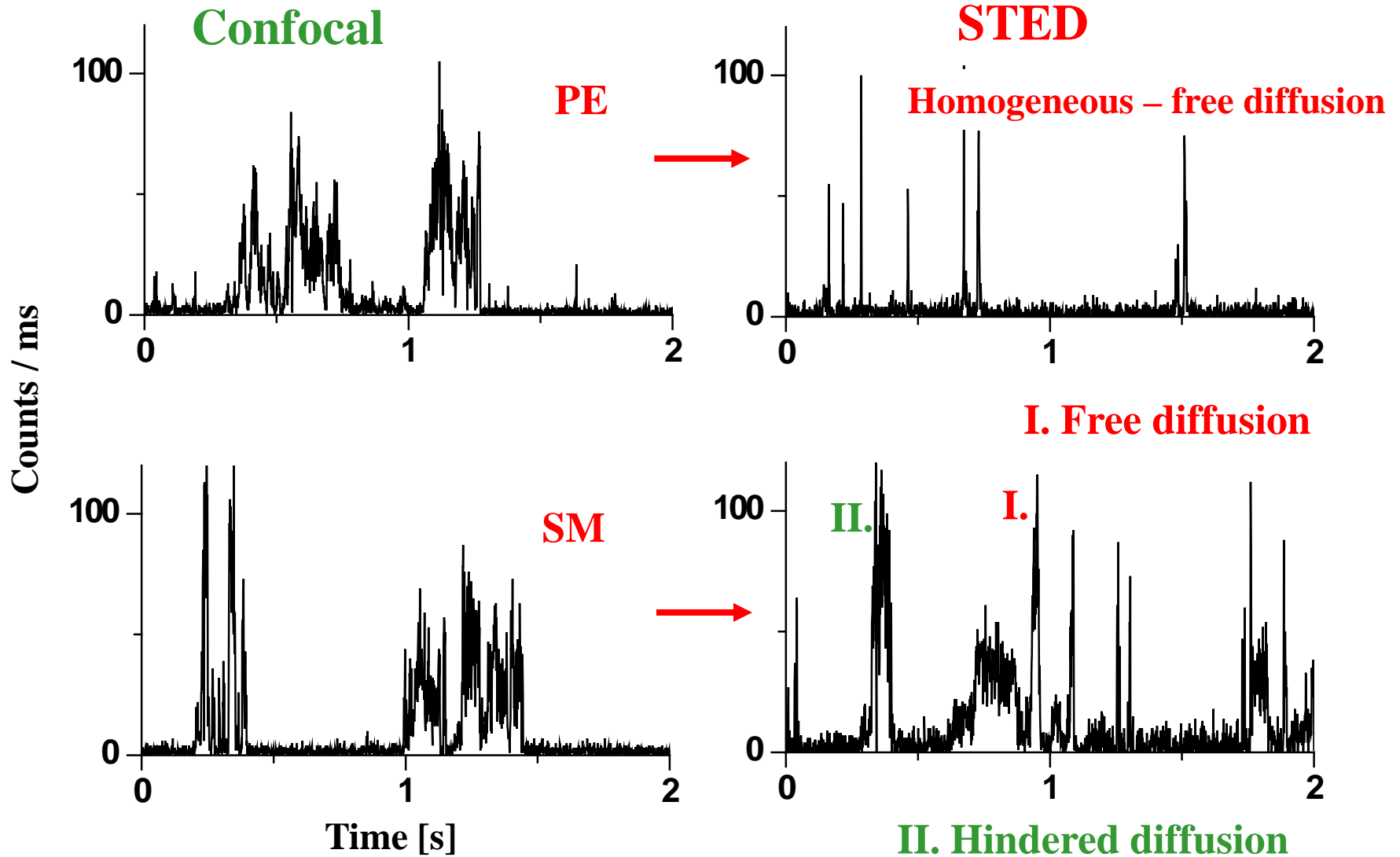




# STED Live Cell Spectroscopy

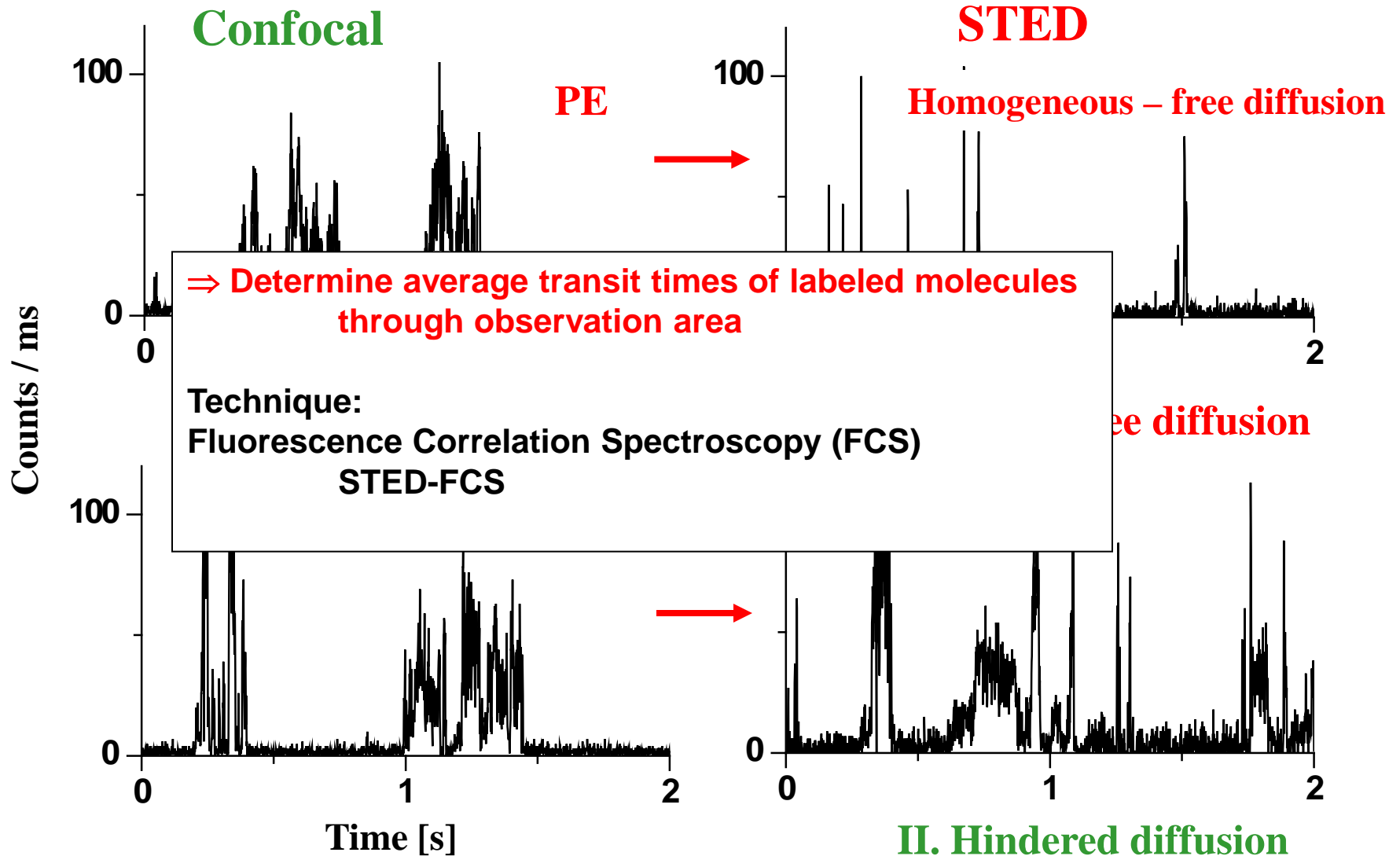
## *Single Lipid Dynamics*

---



# STED Live Cell Spectroscopy

## *Single Lipid Dynamics*

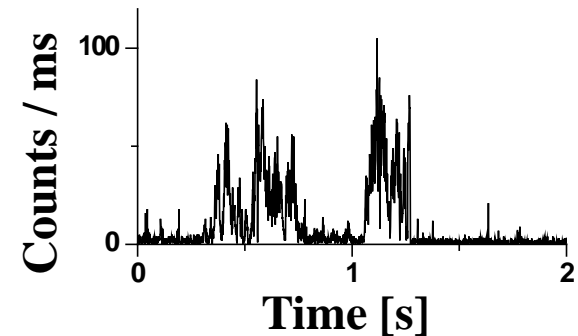
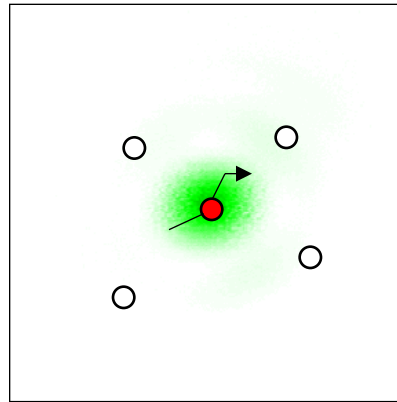


# Fluorescence Correlation Spectroscopy

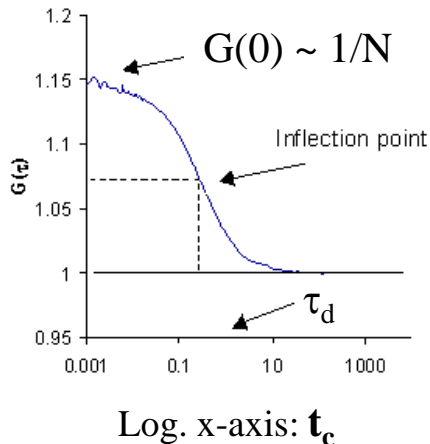
## FCS

**Fluorescence intensity over time**

**Low fluorescent concentration**  
 $\Rightarrow$  diffusion of single-molecules  
 = fluorescence bursts



### Statistics in Time



### Fluorescence Correlation Spectroscopy (FCS)

**data acquisition** - calculation of correlation function

**data analysis** – length and density of fluctuations

**Fitting: anomalous sub-diffusion:  $G(t_c) \sim 1/(1 + (t_c/\tau_d)^\alpha)$**

$\Rightarrow$  transit time  $\tau_d$  ( $\sim$  mass, obs. area) = decay time  
 $\sim d^2 / D$

$\Rightarrow$  anomaly  $1/\alpha$ :

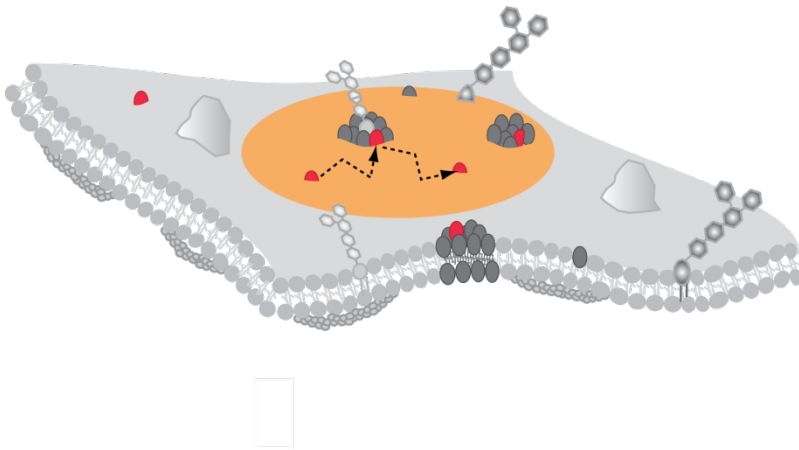
$(1/\alpha) = 1$ : normal free diffusion

$(1/\alpha) > 1$ : anomalous diffusion (e.g. trapping)

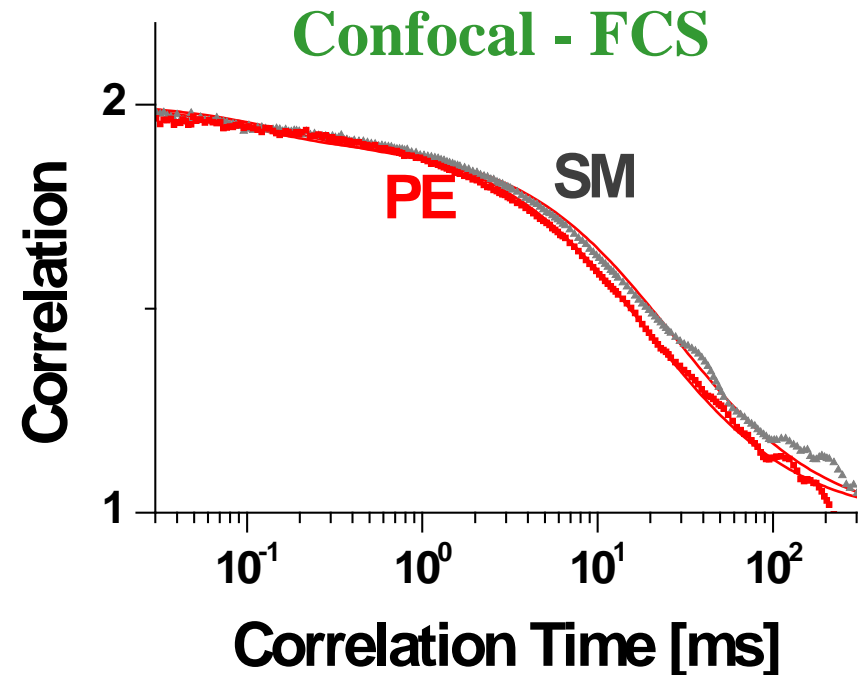
# Lipid Plasma Membrane Dynamics

## Confocal Recordings

**Confocal: Limited spatial resolution !!!**



**Relative large confocal observation area:  
averages over details on nanoscale  
cannot distinguish normal diffusion  
from nanoscale hindered diffusion**



**SM diffusion slightly prolonged but still normal**

$\tau_d \approx 20$  ms (PE) / 30ms (SM)

$(1/\alpha) \approx 1$  (PE / SM)

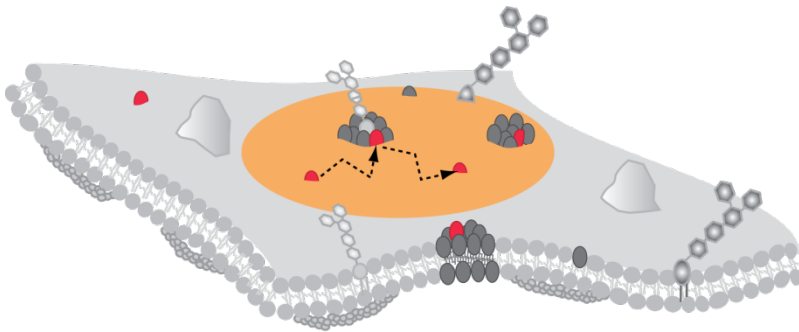
**Slower normal diffusion  
but no anomalous diffusion???**

# Lipid Plasma Membrane Dynamics

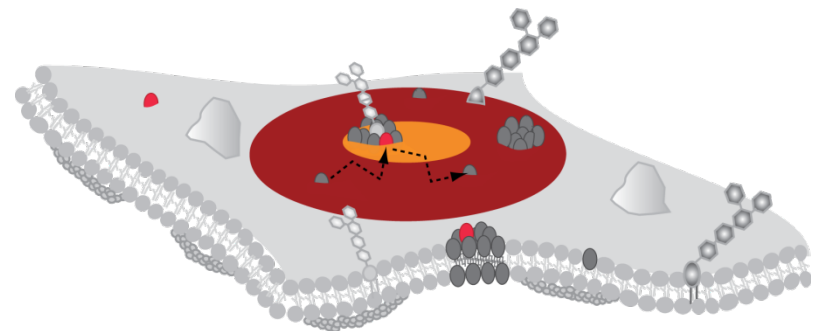
## *Move to STED*

---

**Confocal: Limited spatial resolution !!!**



**STED!!!!**

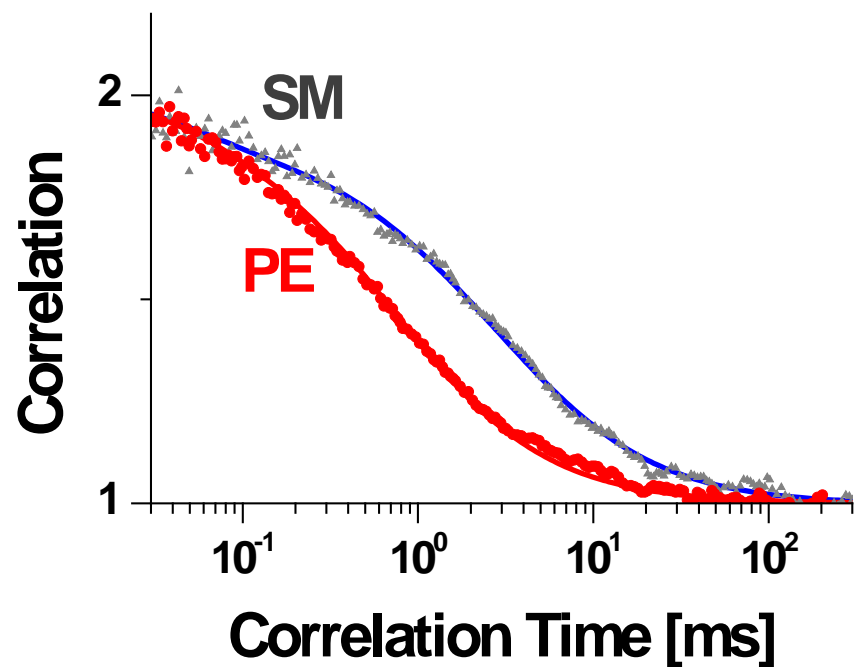
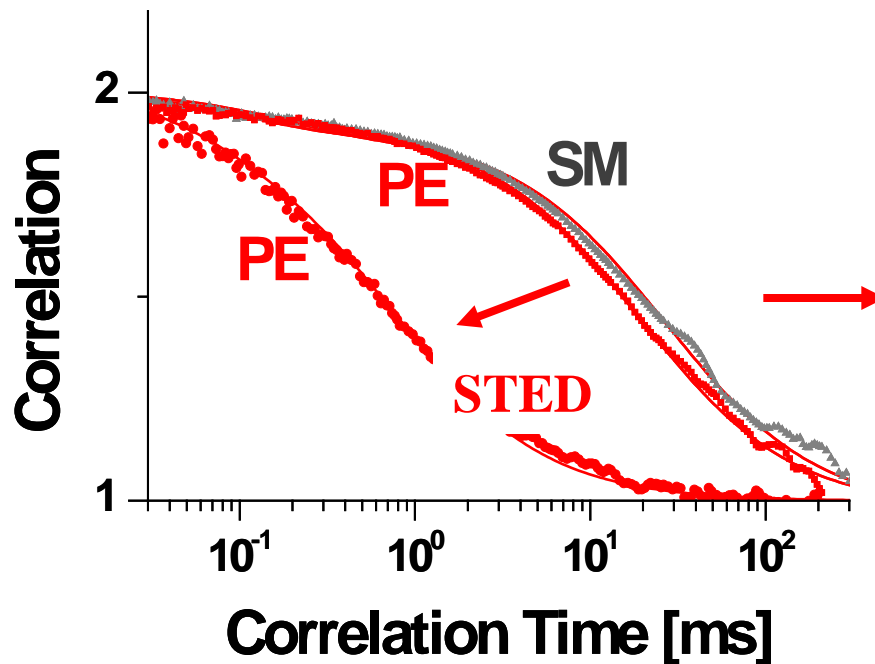


# STED Live Cell Spectroscopy

## Single Lipid Dynamics - FCS

Confocal

STED – 40nm



**STED (240 -> 40nm):**

PE diffusion scales with area reduction

$\tau_d$ : 20 -> 0.6ms (35-fold)

and still normal

$(1/\alpha) \approx 1$

**STED:**

SM diffusion much longer than PE

$\tau_d$ : 30 -> 3ms (10-fold)

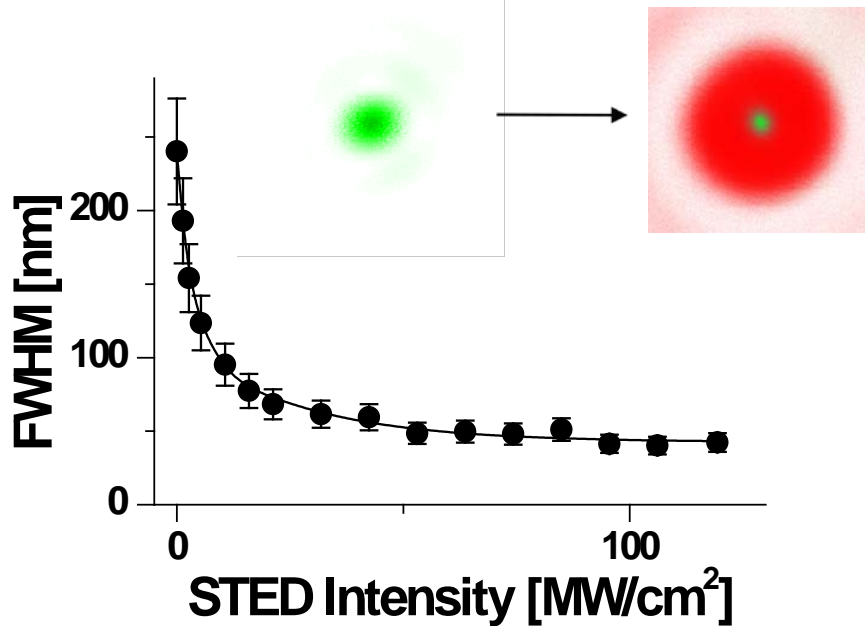
and anomalous

$(1/\alpha) \approx 1.5$

# Live Cell Nanoscopy

## STED-FCS

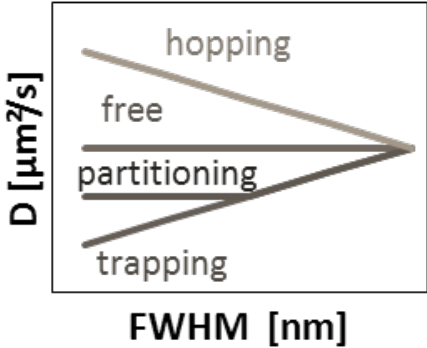
### STED-Microscopy: Tuning of observation area



**STED-FCS**  
Determine transit time  
for different sizes of observation areas  
(different STED intensities)

Calculate  
apparent diffusion coefficient:  
 $D \sim \text{area} / \text{transit time}$

Dependencies:  $D(\text{diameter})$   
 $240\text{nm} \rightarrow 30/40\text{nm}$   
Varies for different diffusion modes



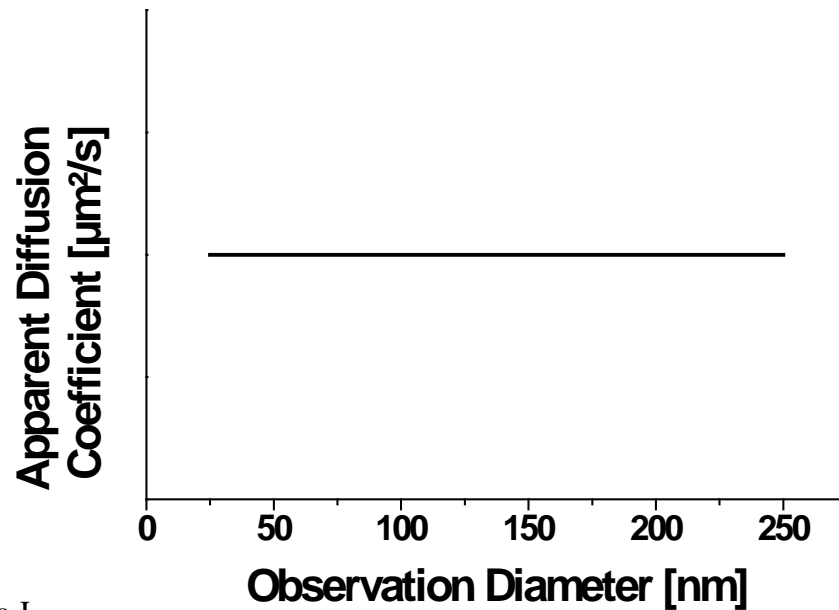
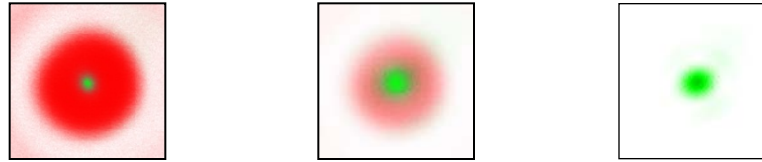
# Live Cell Nanoscopy

## *STED-FCS - Diffusion Models*

### Free diffusion



← **STED Intensity**



Wawrezynieck et al. *Biophys J.*  
2005 December; 89(6)  
Eggeling et al. *Nature* 457,  
1159-1162 ,2009  
Mueller et al. *Biophys J* 2011

**Apparent diffusion coefficient:**

**$D \sim \text{area} / \text{transit time}$**



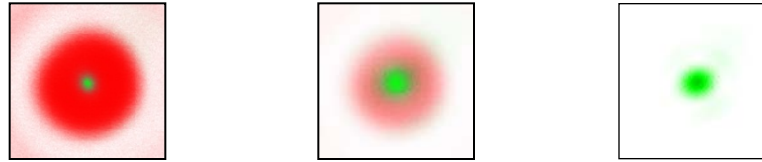
# Live Cell Nanoscopy

## STED-FCS - Diffusion Models

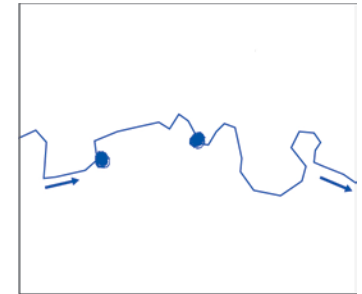
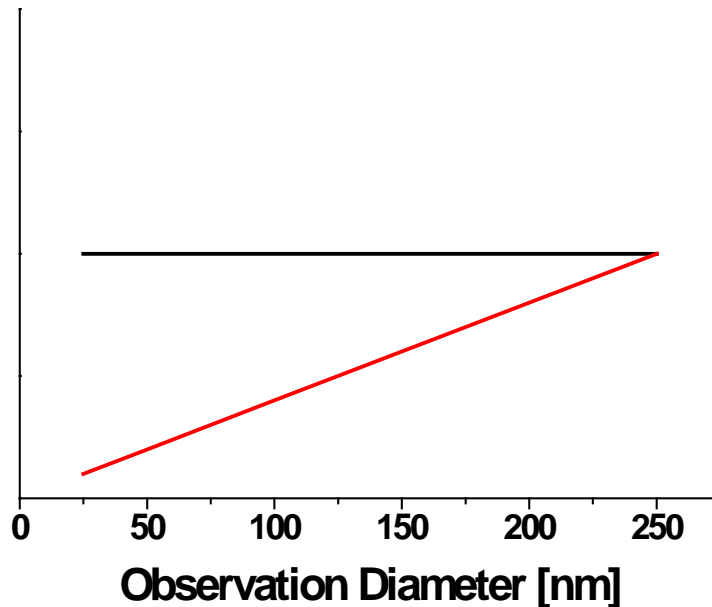
### Free diffusion



← **STED Intensity**



Apparent Diffusion Coefficient [ $\mu\text{m}^2/\text{s}$ ]

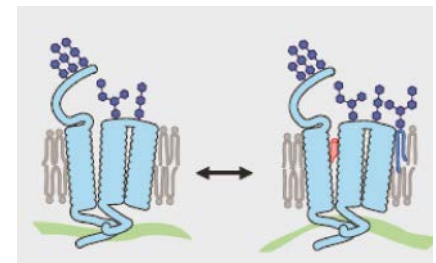


**Trapping**

Wawrezynieck et al. *Biophys J.*  
2005 December; 89(6)  
Eggeling et al. *Nature* 457,  
1159-1162, 2009  
Mueller et al. *Biophys J* 2011

**Apparent diffusion coefficient:**

**$D \sim \text{area} / \text{transit time}$**



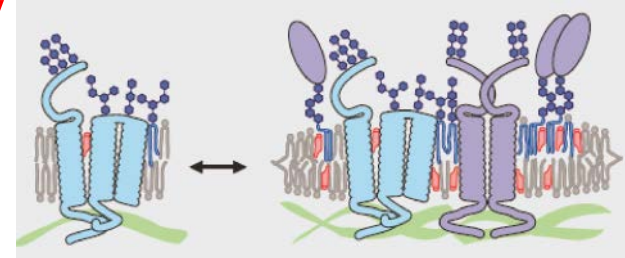
# Live Cell Nanoscopy

## STED-FCS - Diffusion Models

### Free diffusion

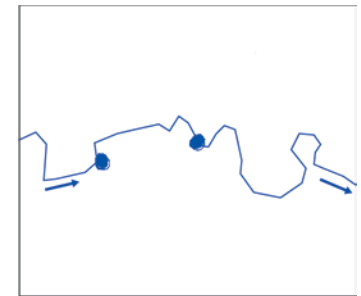
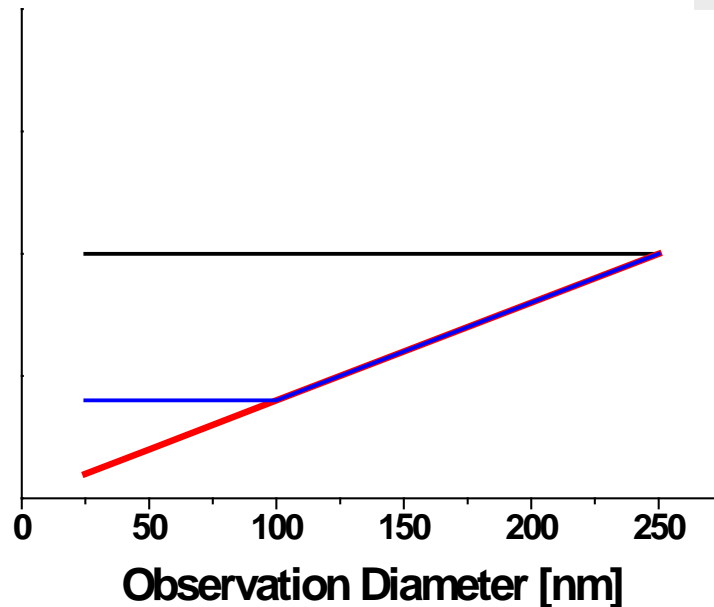


← **STED Intensity**

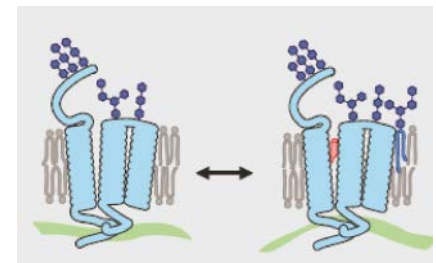


**Domain incorporation**

Apparent Diffusion Coefficient [ $\mu\text{m}^2/\text{s}$ ]



**Trapping**



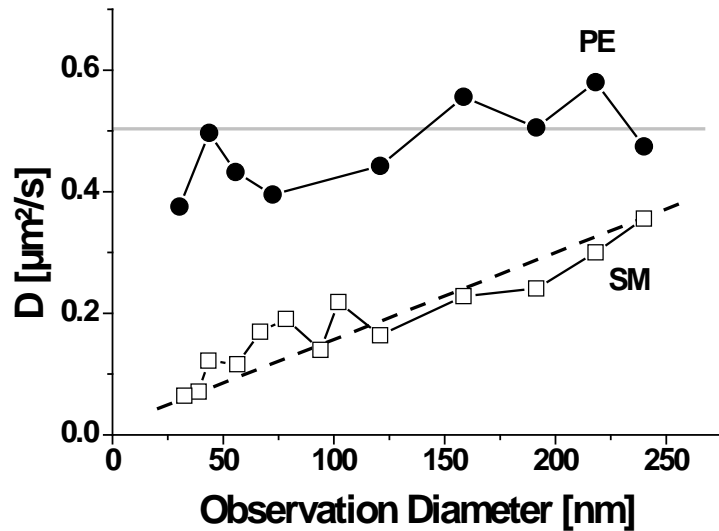
Wawrezynieck et al. *Biophys J.*  
2005 December; 89(6)  
Eggeling et al. *Nature* 457,  
1159-1162, 2009  
Mueller et al. *Biophys J* 2011

**Apparent diffusion coefficient:**

**$D \sim \text{area} / \text{transit time}$**

# STED-FCS

## Lipid Membrane Diffusion + Interactions: PE + SM



→ **Complex on molecular scale**

(proteins, lipid-shells, ...)

~10 ms, no movement during trapping

**Cholesterol-assisted**

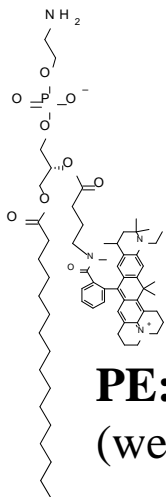
(COase/ $\beta$ -Cyclo-Dextrin/Zaragozic acid...)

**Binding partner bound to cytoskeleton**

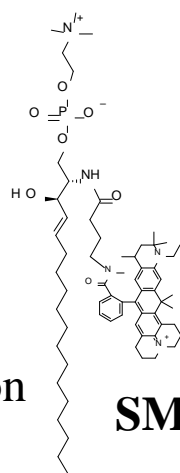
(Latrunculin/Jasplakinolide/Nocodazole...)

**Dependence on lipid structure – proteins as well**

(not label)

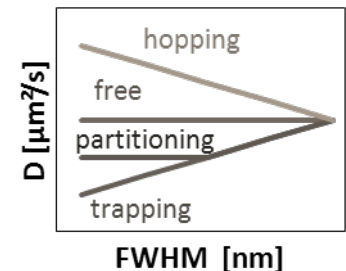
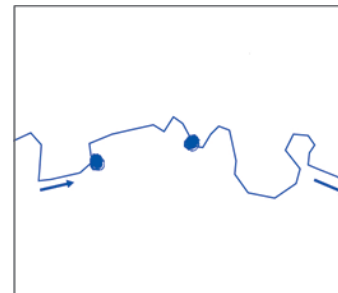


**PE: free diffusion**  
(weak trapping)



**SM: trapping**

Eggeling et al. *Nature* 2009  
Mueller et al. *Biophys J* 2011

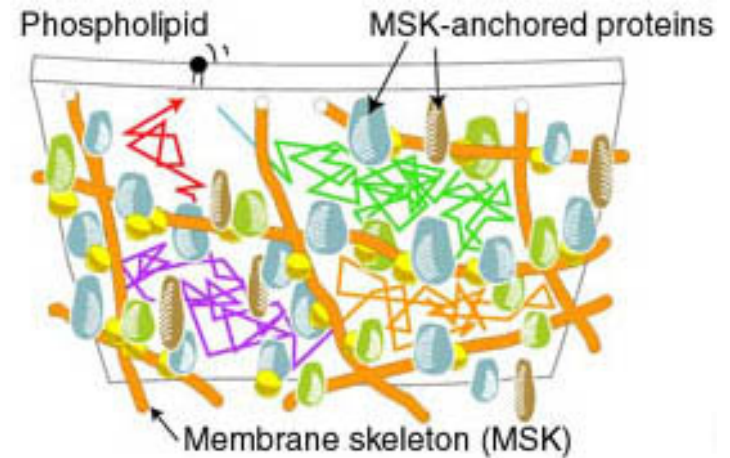
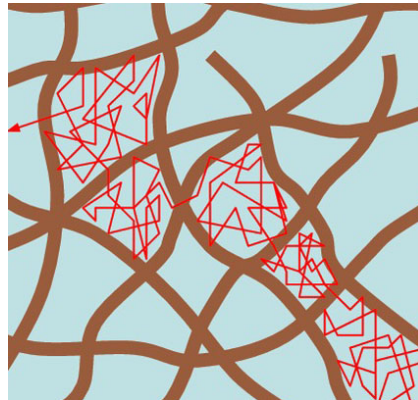
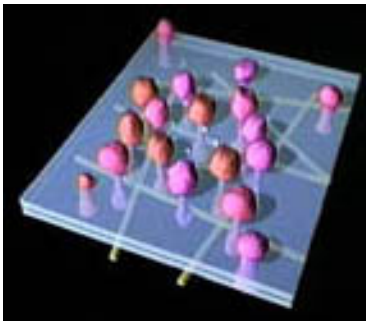


# Lipid Plasma Membrane Organization

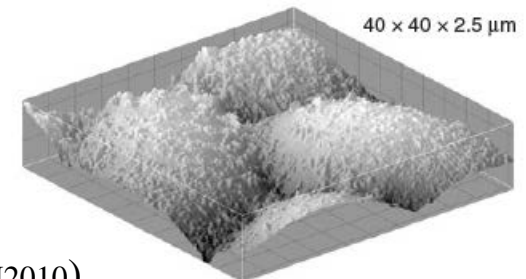
## *Interactions on the Nanoscale: Cytoskeleton*

### Cytoskeleton

- Membrane divided in compartments
- Proteins: fence/hindrance in diffusion path
- Hopping diffusion



**Kusumi**

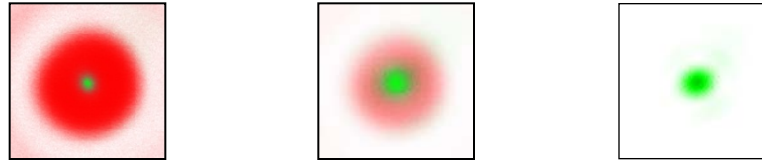


**Curvature** (Parmryd, NM2010)

# Live Cell Nanoscopy

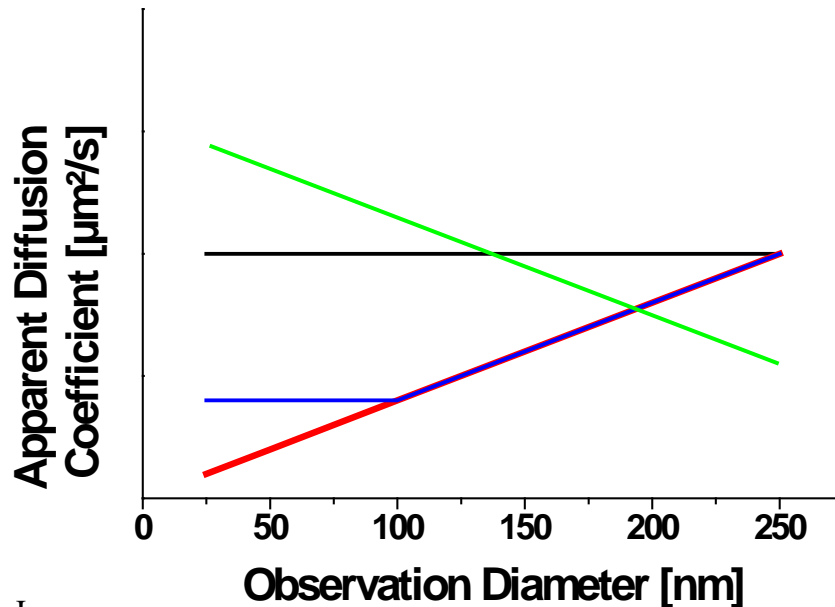
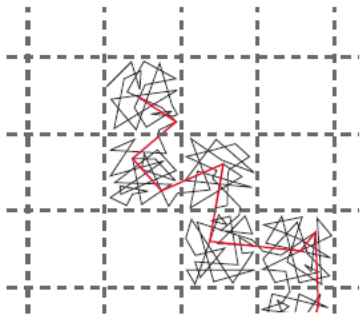
## *STED-FCS - Diffusion Models*

← **STED Intensity**



**Hopping** (Kusumi)  
meshwork, curvature,...

25- $\mu$ s resolution (62-ms observation; 2,500 points)



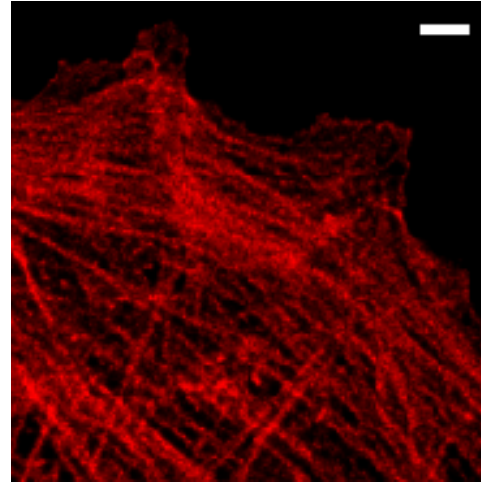
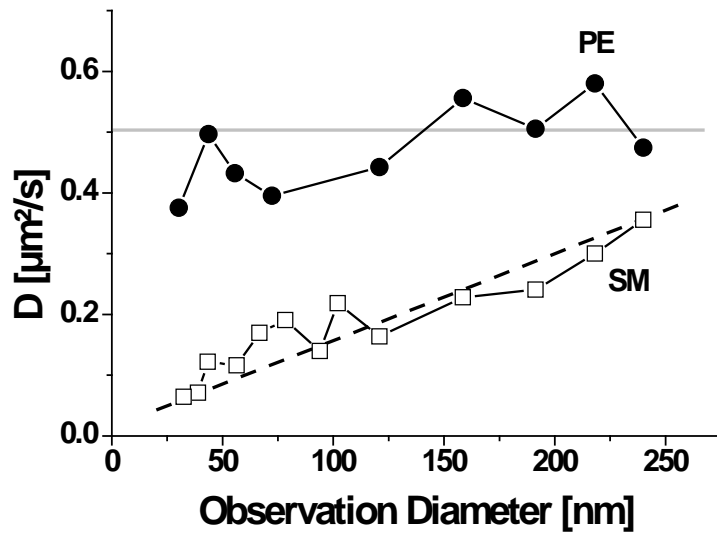
Wawrezynieck et al. *Biophys J*.  
2005 December; 89(6)  
Eggeling et al. *Nature* 457,  
1159-1162, 2009  
Mueller et al. *Biophys J* 2011

**Apparent diffusion coefficient:**

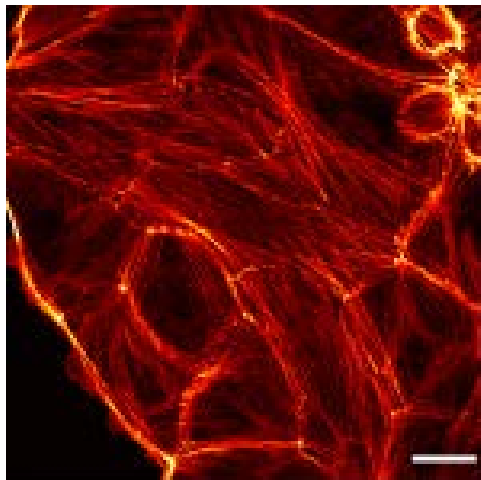
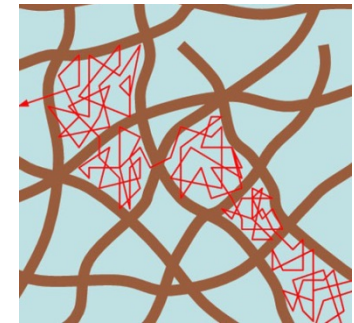
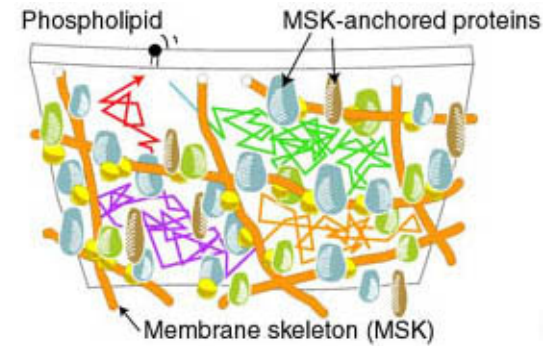
**$D \sim \text{area} / \text{transit time}$**

# Lipid Plasma Membrane Dynamics

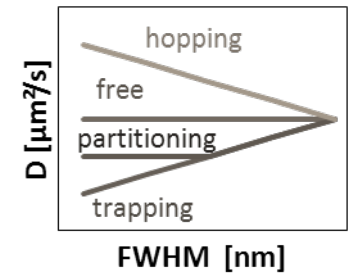
## *Hopping of Lipids?*



NRK cells

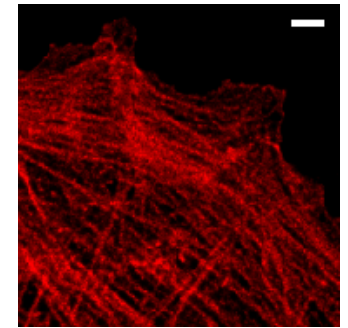
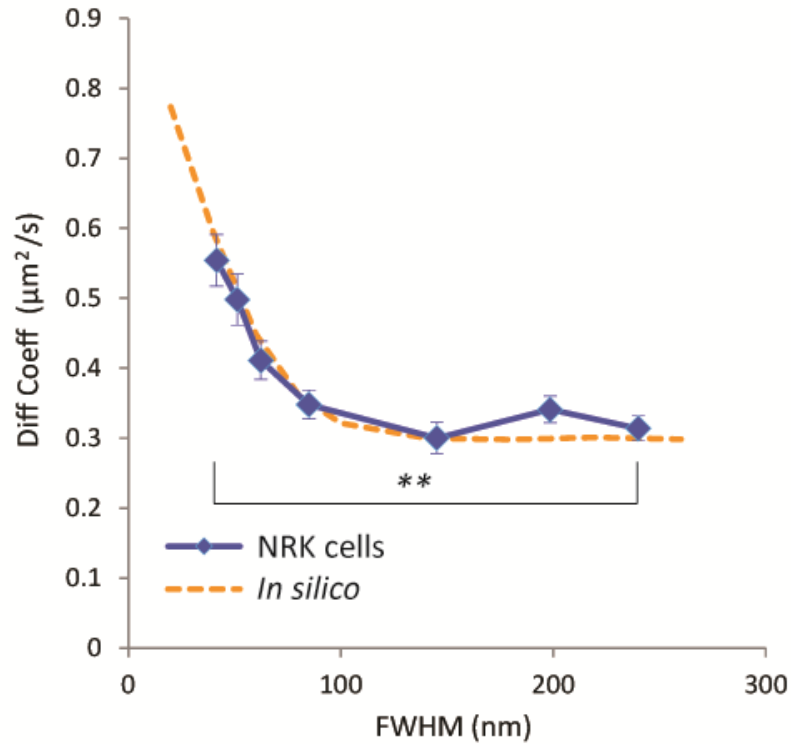


PtK2

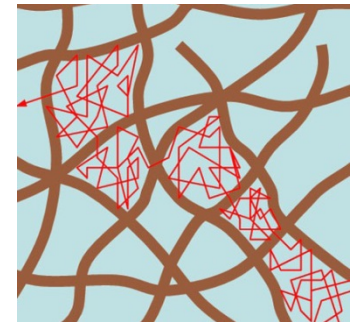


# Lipid Plasma Membrane Dynamics

## *Hopping of Lipids?*



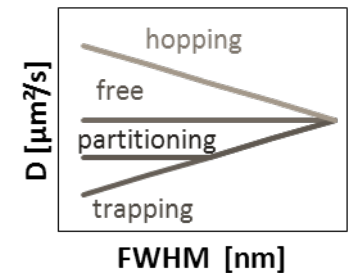
NRK cells



$$D = 0.8 \mu\text{m}^2/\text{s}$$

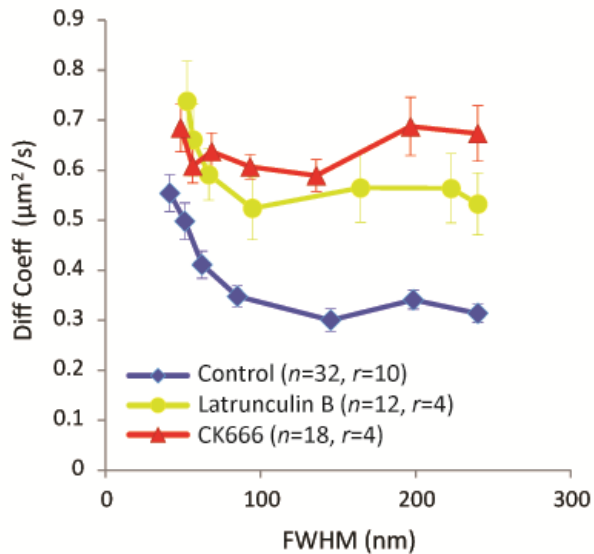
$$P_{\text{hop}} = 0.1$$

$$L = 80\text{nm}$$



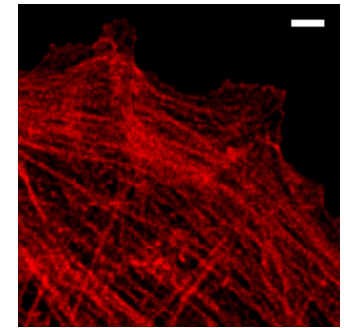
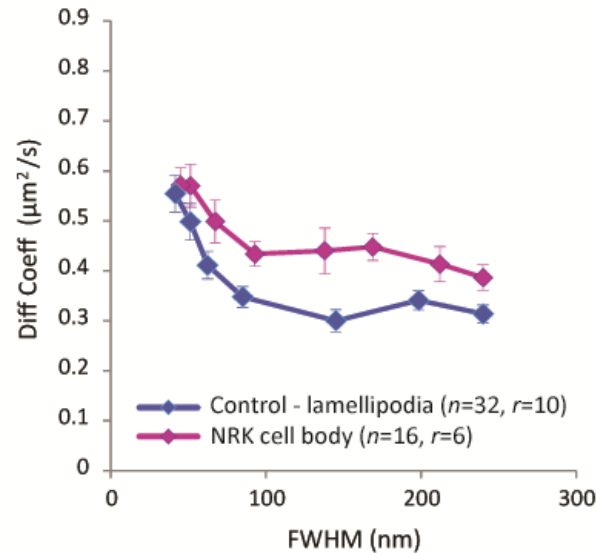
# Lipid Plasma Membrane Dynamics

## *Hopping of Lipids?*

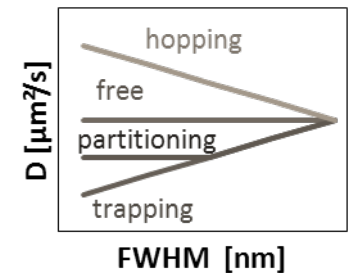
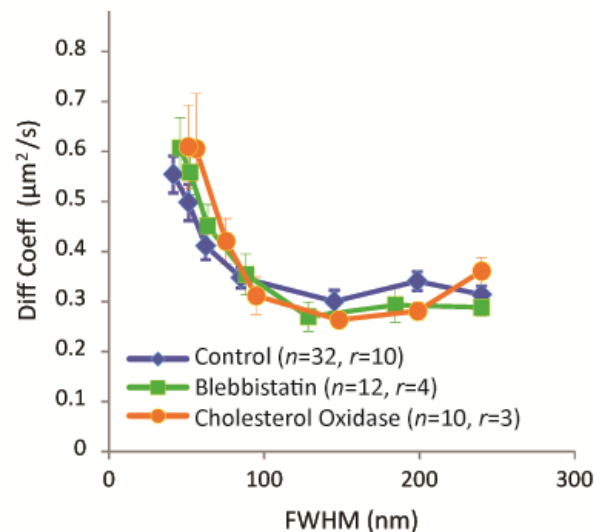
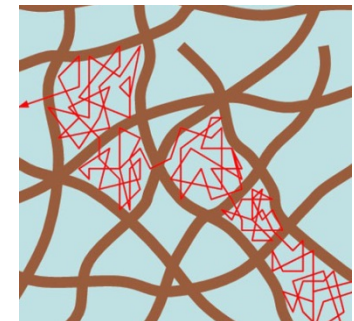


Latrunculin B: actin depolymerization  
 CK666: Arp2/3 inhibitor  
 (nucleation core/new branching)

COase: cholesterol oxidation  
 Blebbistatin: Inhibitor myosin II



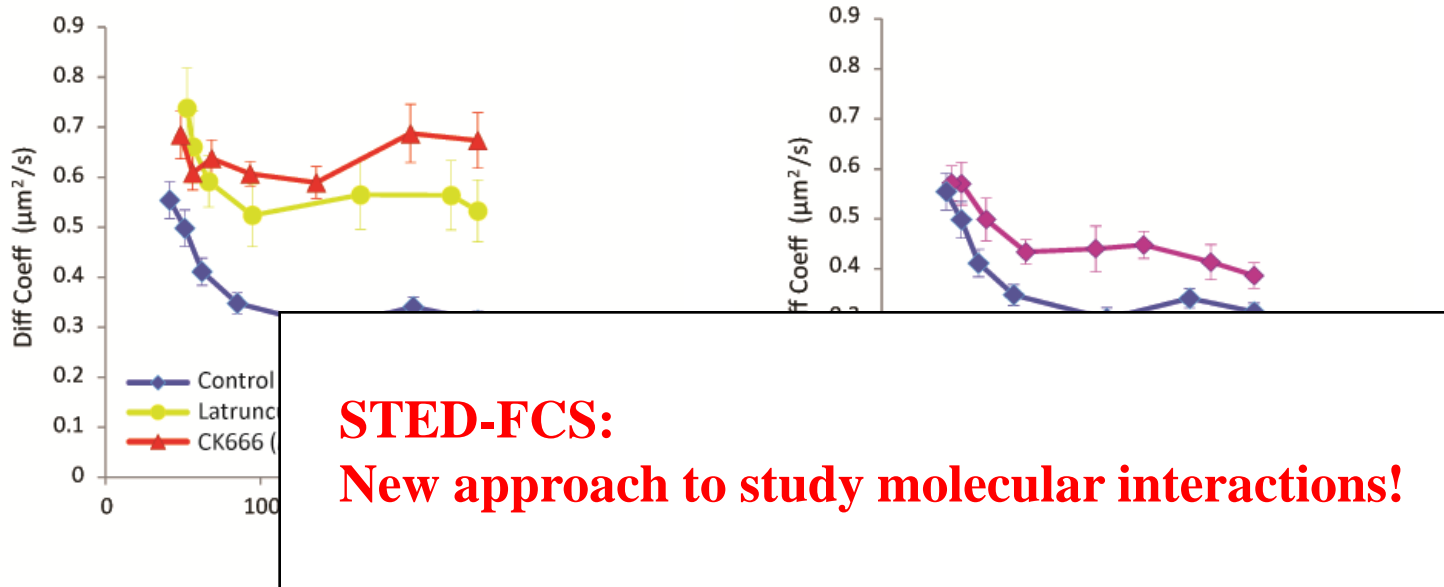
NRK cells





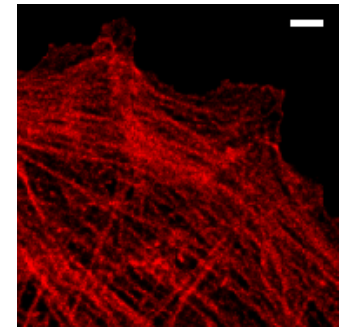
# Lipid Plasma Membrane Dynamics

## *Hopping of Lipids?*

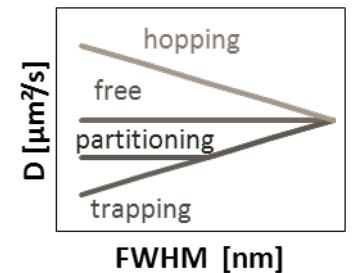
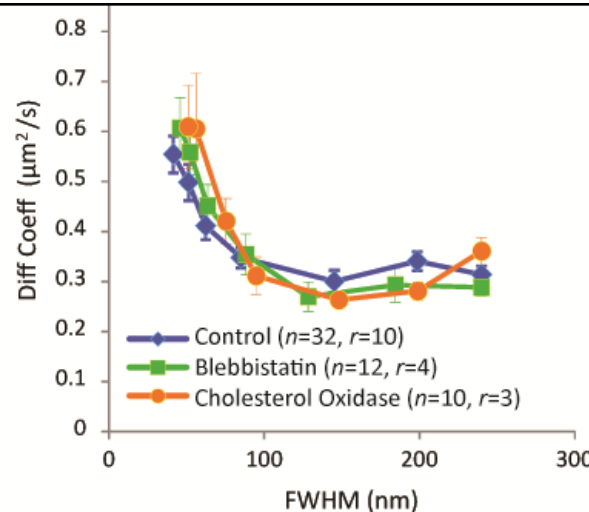
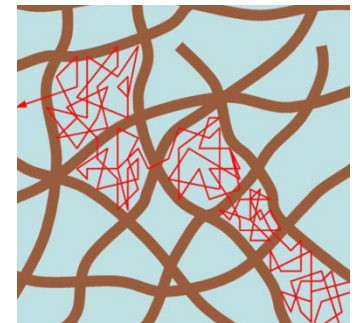


Latrunculin B: actin depolymerization  
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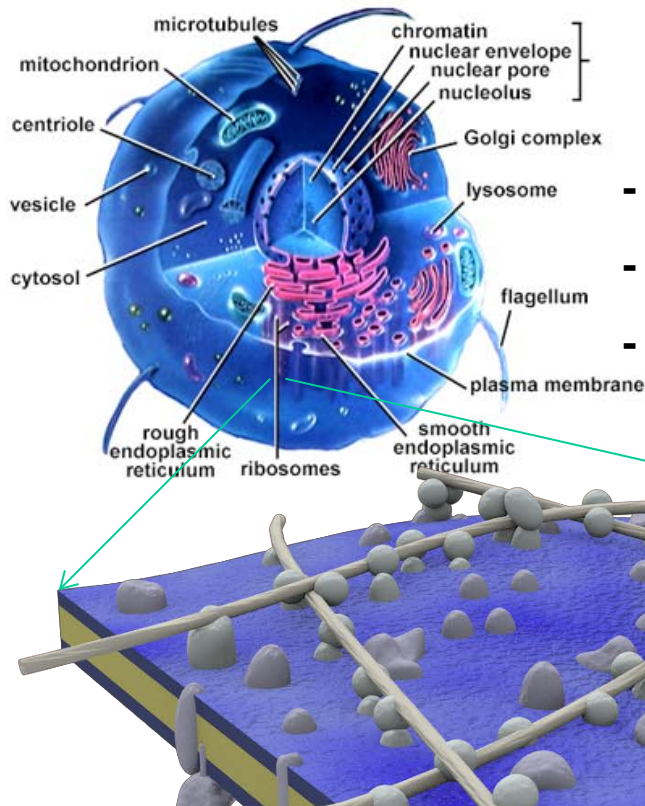


NRK cells



# Lipid Plasma Membrane Dynamics

## *Nanoscale Diffusion*



### **Molecular Membrane Dynamics:**

- Heterogeneous diffusion (viscosity, curvature...)
- Interaction with proteins / lipids
- Interaction with cortical cytoskeleton

**Highly dynamic!**

**Very molecule-specific!!!!  
(lipids specific function)**

**Link to functionality!?**

### **Purpose**

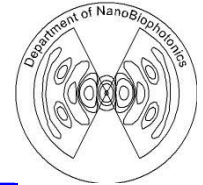
- increase probability of interactions of less abundant molecules
- trigger cellular signaling

**20nm**

**Small spatial  
scales!!!!**



# Acknowledgement



**MPI, Göttingen**

**Lipid Experiments**

**Veronika Mueller**

**Alf Honigmann**

Debora Machado Andrade

Christian Ringemann

Rebecca Medda

Birka Lalkens

Giuseppe Viccidomini

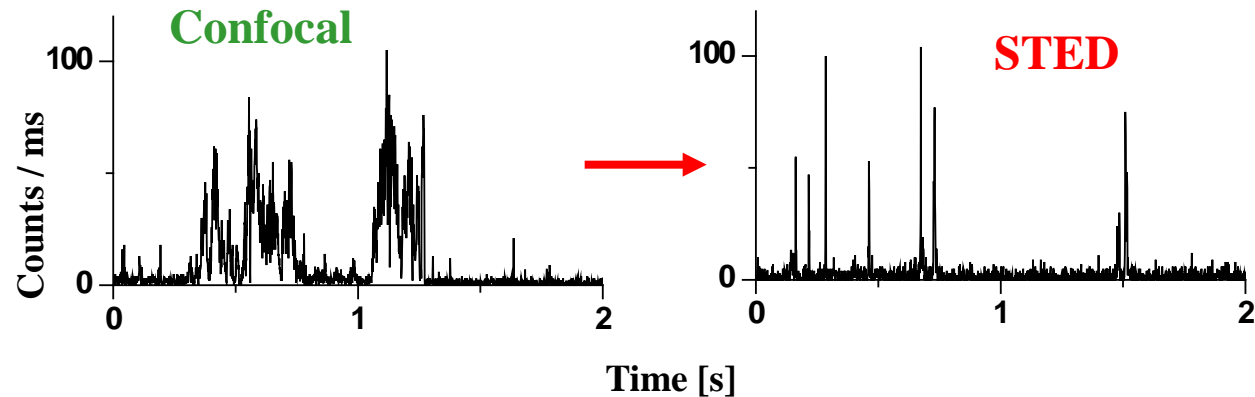
Haisen Ta

Andreas Schönle

**Lipid labeling**

Dr. V. Belov

S. Polyakova



**Stefan Hell**

**+ whole group**



## **Team – HIU/WIMM:**

**Jorge Bernardino de la Serna (Biophysics – membrane)**

**Mathias Clausen (Biophysics - membrane)**

**Silvia Galiani (Physics – nanoscope setup/organelles)**

**Marco Fritzsche (Physics - cytoskeleton)**

**Erdinc Sezgin (Biophysics – membrane)**

**Jakub Chojnacki (Biochemistry - virus)**

**Huw Colin York (Physics – microscopy/force)**

**Tess Sanley (Biology – receptor)**

**Antonio Gregorio Dias (Biology – virus)**

**Sumita Ganglui (Biology)**

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**Veronica Buckle**

## **WIMM**

**Vincenzo Cerundolo**

**Doug Higgs**

**Simon Davis**

**David Jackson , Graham Ogg ...**

## **Micron/Oxford**

**Ilan Davis, Lothar Schermelleh, ...**

**Martin Booth, Achillefs Kapanidis,**

**Philipp Kukura...**

**Mike Dustin...**

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**Del Besra (Birmingham)**