## Localising proteins to and within membranes

Part II

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Membranes

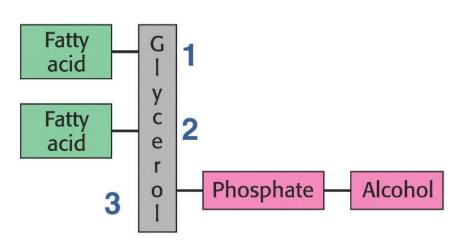
- Lipidation
  - GPI anchors
  - Prenylation
  - Myristoylation
  - Palmitoylation
- Modulation of signalling

ງ 1

## Membrane lipids: Major classes

#### Phospho-glycerides

#### Sterols, e.g. cholesterol (Chol)



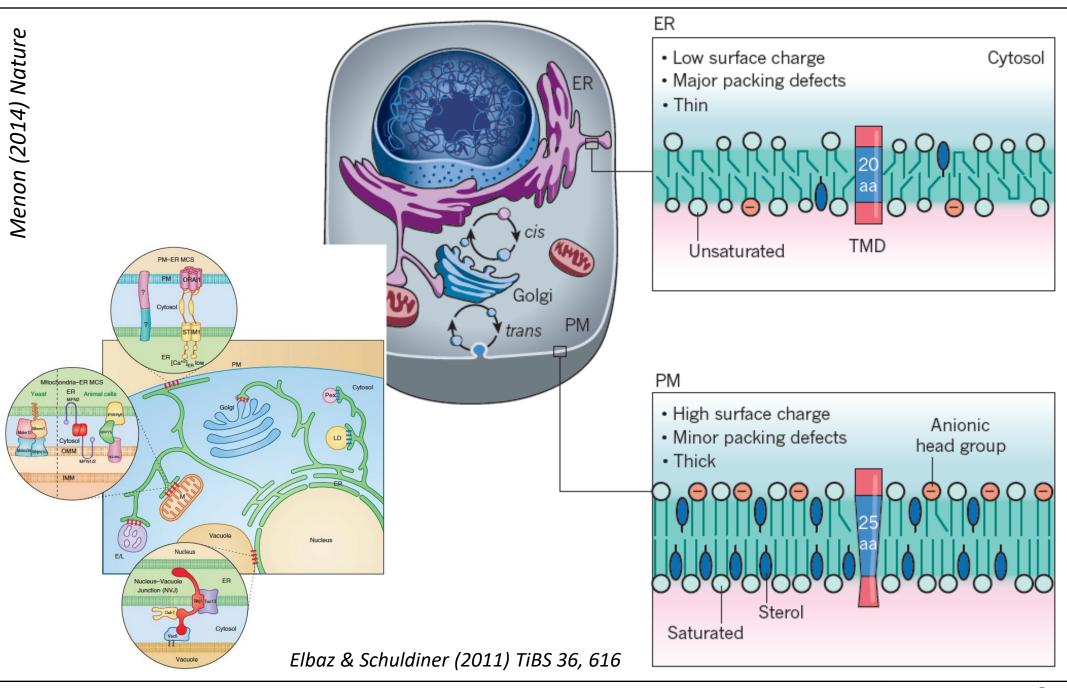
Phospho -sphingolipids, e.g. sphingomyelin (SM)

$$H_3C(H_2C)_{12}$$
 $H_0$ 
 $H_1$ 
 $H_2$ 
 $H_2$ 
 $H_3$ 
 $CH_3$ 
 $CH_3$ 
 $CH_3$ 

5 - Lipidation

Membranes

## Transfersal lipid asymmetry in Eukaryotic membranes

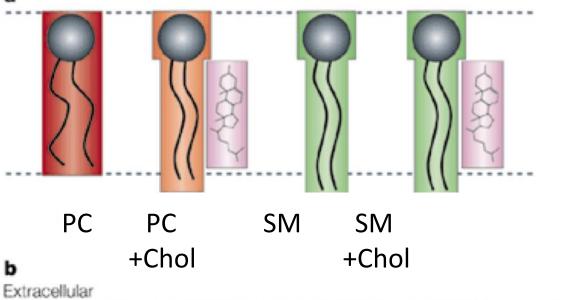


5 - Lipidation

Membranes

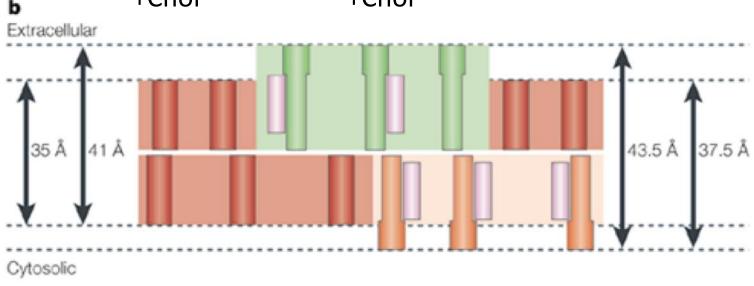
#### Lateral lipid asymmetry and phase-coexistence: Plasma membrane

• Cholesterol: Preference for sphingomyelin and not so "fluid" lipids



"Cholesterol domains":

- membrane thickening
- fluidity decrease



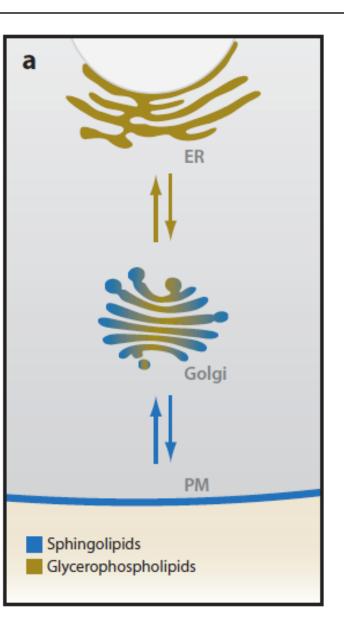
Nature Reviews | Molecular Cell Biology

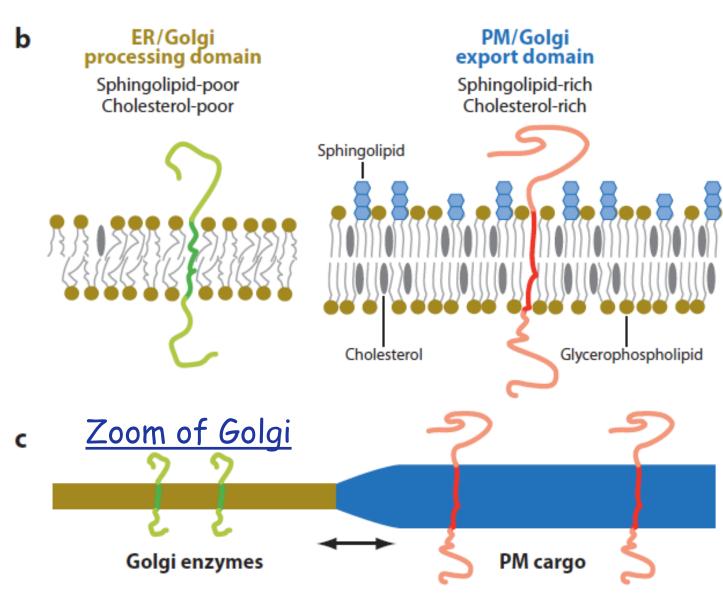
5 - Lipidation

Membranes

p 4

## Phase separations facilitate sorting and transport



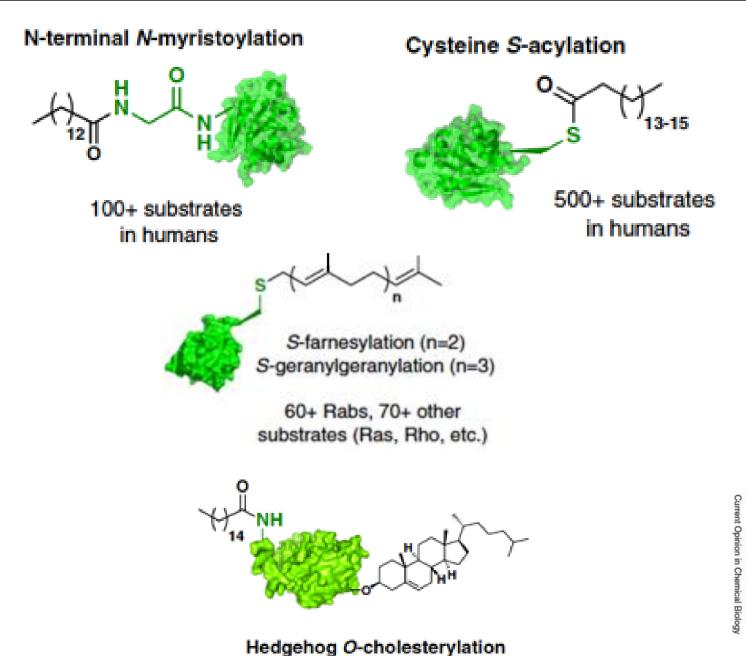


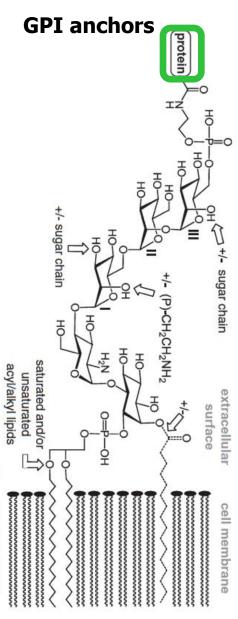
Lippincott-Schwartz, Ann Rev Biophys 2010

5 - Lipidation

Membranes

# Lipidation of proteins





5 - Lipidation p 6

## S-Prenylation close to the C-terminus

Post-translational addition to Cys residues at the C-terminus:

NB: upon farnesylation a-a-X are proteolytically removed

→ Motif 2: 2 Cys in a short amino acid motifs, e.g.

=> Geranylgeranylation of one or both Cys-residues

## S-Palmitoylation

Addition of a palmitate (C16:0) via of a labile thioester bond

<u>Post-translational</u> attachment of a C16:0 to thiol group of a Cys within the endoplasmic reticulum or Golgi system.

$$\begin{array}{c} \text{CH}_3(\text{CH}_2)_{14} \\ \text{SCoA} \\ \text{S}^- \\ \text{Nw} \\ \text{H} \end{array} \qquad \begin{array}{c} \text{S-palmitoyl-} \\ \text{transferase} \\ \text{O} \\ \text{H} \end{array} \qquad + \quad \text{CoASH} \\ \end{array}$$

- Targets: Intrinsic membrane proteins

  Cys a few (3-6) residues next to a TM domain on cytosolic side
  - Soluble proteins
- => No clear consensus sequence, but often close to myristoylation or prenylation site

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## S-Palmitoylation: To be or not anymore to be

Palmitoylation is dynamic and reversible due to labile thioester

=> regulation of location, sorting and activity

- Acylation:
  - => protein-S-acyltransferease (PAT) in ER and Golgi

- De-acylation:
  - => S-acylprotein thioesterase (APT) in cytosol
  - => Palmitoyl protein thioesterase (PPT) in lysosomes, plasma membrane

Modification close to C-terminus

# **Lipidation of proteins**

S	u	m	ır	na	ar	y
						_

GPI anchor C-term co-trans "perm" raft & Cell surface

S-prenylation C-term "post-trans perm non-raft

N-myristoylation N-term co-trans perm raft

S-palmitoylation post-trans reversible raft

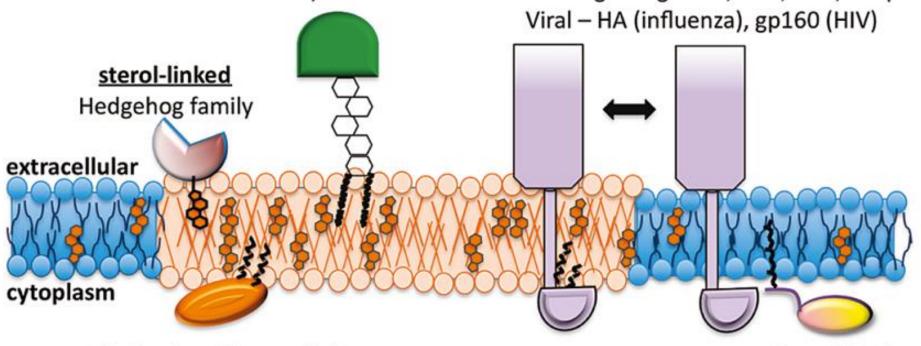
## Lipidation rules location of proteins in membrane

#### **GPI-anchored**

enzymes - PLAP, 5' nucleotidase receptors – FR, GDNFR, FcRyIII, CD14 adhesion – NCAM, CD58

#### Palmitoyl-dependent raft partitioning TM

Immune signaling – LAT, CD4, CD8, FcRylla



#### Palmitoylated intracellular

Src-family kinases H-ras G protein α subunits

#### **Prenylated**

G protein βγ K-ras4B Rab family

**NON-RAFT** RAFT Levental 2010

5 - Lipidation

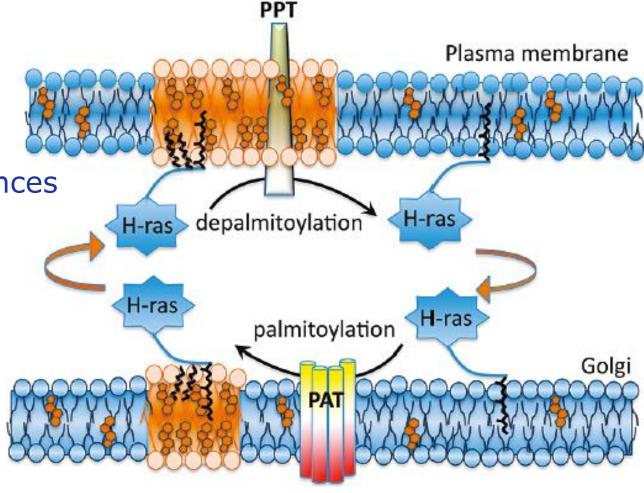
Localisation

#### An example : H-ras

#### H-ras:

- farnesylated
- 2 palmitoylation sites

=> H-*ras* activation enhances de-palmitoylation



- T-lymphocytes reaction upon antigen presence:
  - i strong antigens => negative selection => DEATH :: ras in PM
  - ii weak antigens => positive selection => proliferation :: ras in ER

#### **Protein lipidation**

- Attachment of one or several acyl chain or lipids
  - reversible or irreversible modifications
- => translocation from cytosol to membrane
  - => location to a specific membrane or membrane domain
- => change in protein structure/function
- => change in accessibility

- ♦ Manipulation of location in space & time
  - In general, location rimes with activity.

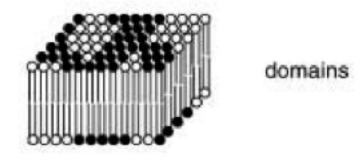
5 - Lipidation p

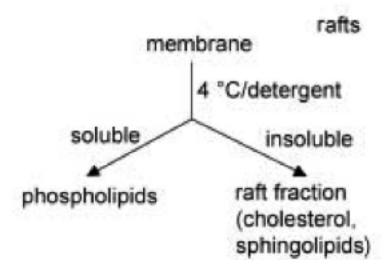
# Modulation of signalling by lipids and membrane domains

#### Biological lateral phase separations: Rafts

#### Historically, lipid rafts have been defined as:

- insoluble in cold 1%-solution of Triton X-100, a detergent.
  - => thus named: **D**etergent-**R**esistant **M**embrane (DRM)
- low buoyant density





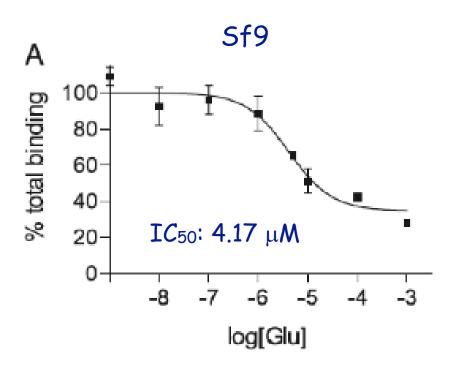
Binder, Angew Chem Intl Ed 2003.

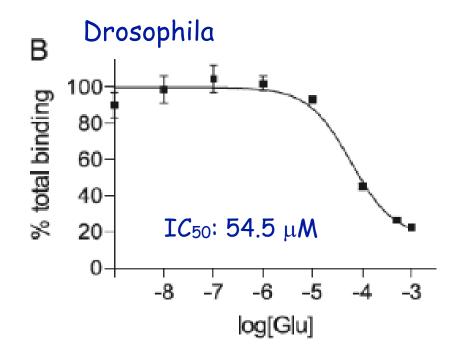
p

#### Case 1: Modulation of GPCR signalling by lipids domains

E.g., a metabotropic glutamate receptor (mGlu-R) expressed in Sf9 insect cells or Drosophila eyes

Radioligand competition binding assays :





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## Modulation of mGlu-R signalling by lipid domains

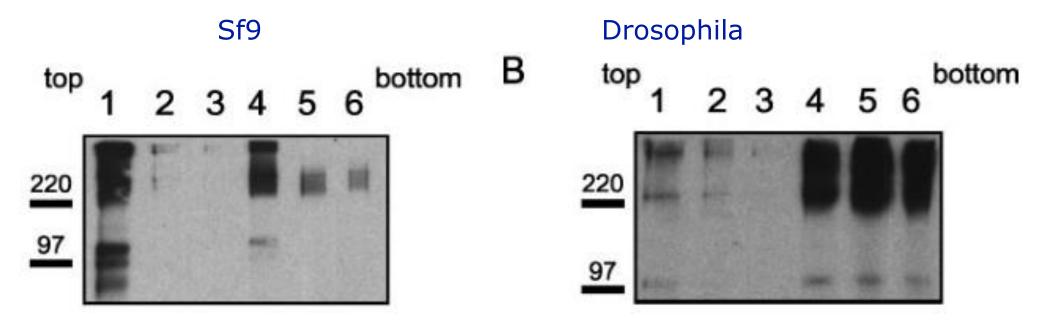
Are rafts involved?

Sf9 insect cells

or

Drosophila eyes

Membrane density fractionation followed by SDS-PAGE analysis:



- -

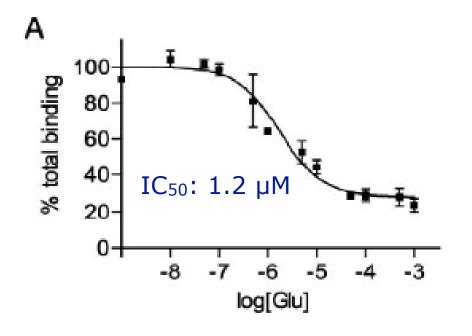
## Modulation of mGlu-R "fitness" by lipid domains

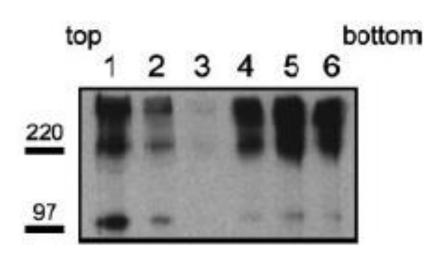
Observation: Drosophila membranes contain very little cholesterol
 Q: Is cholesterol needed for high affinity?

#### Experiment 1:

- ♦ Cholesterol addition to Drosophila membranes
  - => receptor gains affinity  $IC_{50}$  54.5 => 1.2  $\mu$ M

=> receptor goes to rafts
"light" fractions gradient



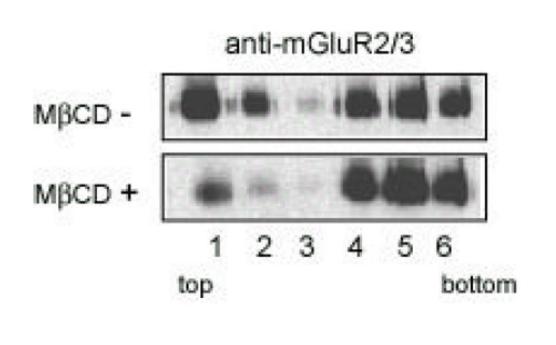


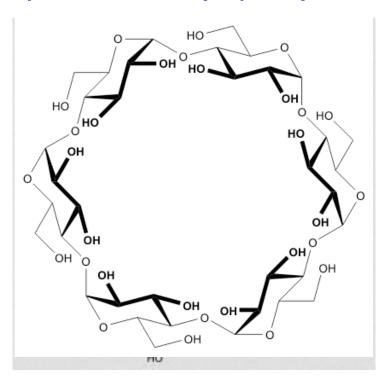
Eroglu PNAS 2003

## Modulation of mGlu-R "fitness" by lipid domains

#### Experiment 2:

Cholesterol depletion in Sf9 by methyl-β-cyclodextrin (mβCD)





=> receptor goes to heavy membranes upon mβCD treatment

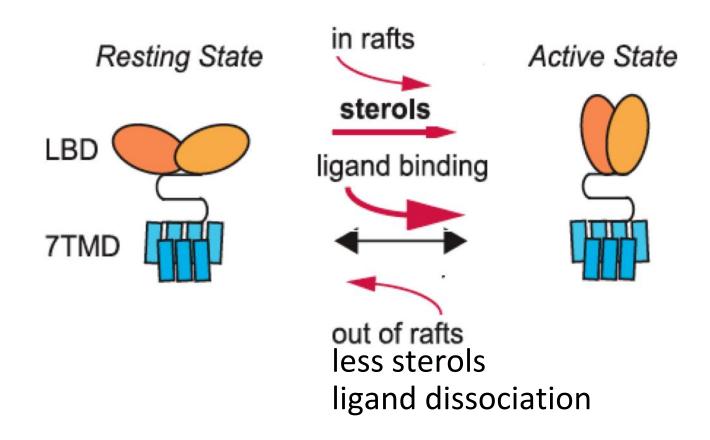
=> Yes, cholesterol is needed for both high affinity & raft localisation!

Eroglu PNAS 2003

## Modulation of mGlu-R "fitness" by lipid domains

Model to explain effect cholesterol:

Cholesterol rich domains act as positive allosteric modulator, favouring active state that has a higher affinity.



Eroglu PNAS 2003

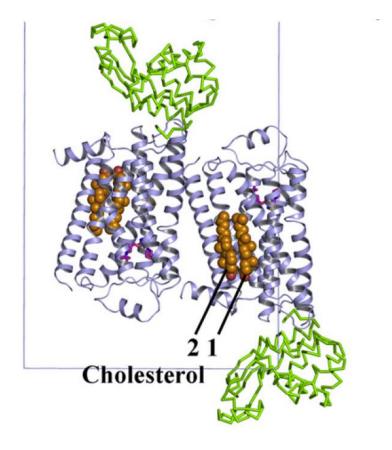
## Cholesterol binding site on GPCRs

Crystal structure of the 2β-adrenergic receptor

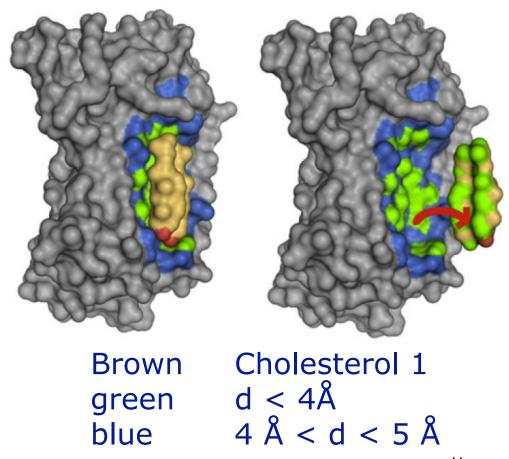
=> 2 cholesterol molecules / receptor within the protein structure

Unit cell

Cholesterol 1 docks on receptor



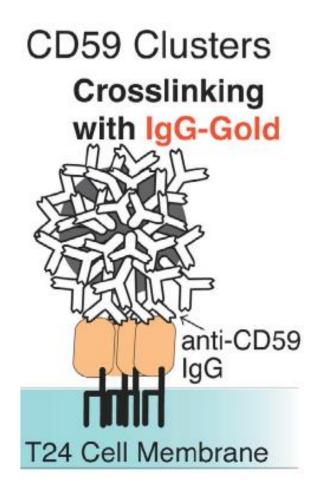
Green: T4 lysozyme



Hanson Nature 2008

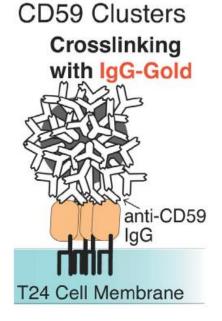
## Case 2 : Signaling cascade of CD59

- CD59 is a GPI anchored receptor



## Single molecule observation of CD59 and Lyn

#### Observations of signalling pathway:



Supplemental video 1

G40-crosslinked CD59 on T24 Cells

Real time replay Scale = 1 µm CD59 and Lyn

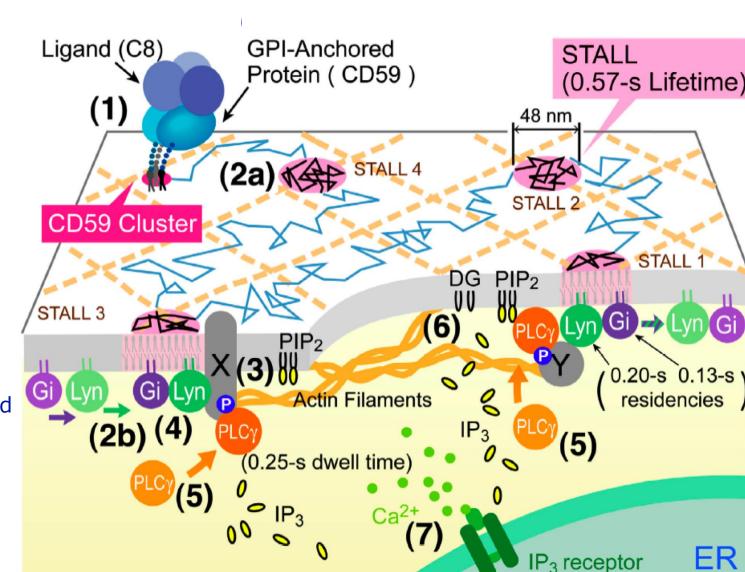
Supplemental video 2

Simultaneous observation of a CD59 cluster and a single Lyn-GFP molecule

Real time replay, 10 sec Scale = 500 nm

## Single-molecule imaging reveals transient interactions

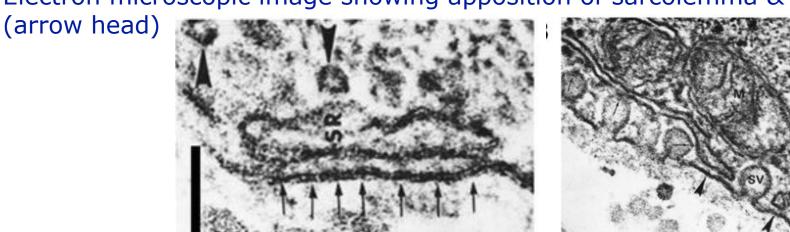
1) Clustering of the GPI-anchored receptor CD59



STALL = Stimulation-activated transient arrest of lateral diffusion

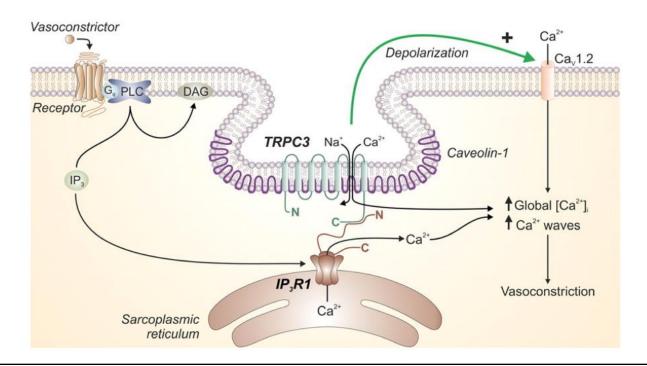
## Close proximity between plasma membrane and ER

Electron microscopic image showing apposition of sarcolemma & plasma membrane



Scale bar : 100 nm

#### Schematic representation



#### Further reading:

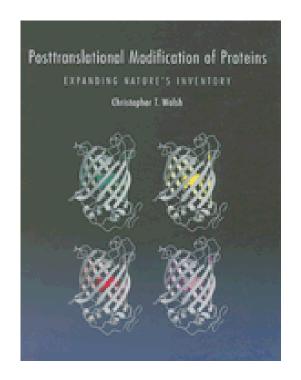
Walsh Post-translational modifications of proteins Chpt. 7

Van Meer Membranes & lipids (2008)

Yu GPI (2013)

Levental Membrane association (2010)

Tate Lipidation profiling (2014)

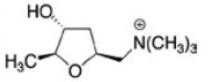


#### Next week



Amanita muscaria

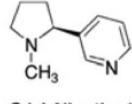
#### **Muscarinic**



(+)-Muscarine\*

Isolation 1954 Structure 1957 Pharmacology 1911

#### **Nicotinic**



S-(-)-Nicotine\*

Isolation 1828 Structure 1893 Pharmacology 1889



Nicotiana tabacum

Does membrane localisation enhance diffusion-limited (inter/re)actions?

A cell with a radius of 10 uM contains 10'000 molecules of each A and B.

How long will it take for a molecule A to meet for the first time a molecule B?

Make an educated guess using the following diffusion constants D:

2D diffusion in the membrane :  $D = 10^{-9}$  to  $10^{-10}$  cm<sup>2</sup>/s

3D diffusion in the cytosol :  $D = 10^{-8} \text{ cm}^2/\text{s}$ 

A hint: what is the average distance between the molecules of the same species either in the membrane or in the cytosol?

Do submit your answer or questions to the Moodle site.

#### N-Myristoylation at the N-terminus

<u>Co-translational</u> addition of a myristate (C14:0) through formation of a <u>stable **amide bond**</u> to amino group of **N-terminal glycine** 

if N-terminus is :  $H_2N-Met-Gly-x-x-x-[Ser/Thr]-y-y$  x: small & uncharged

y: basic

Enzyme: myristoyl-CoA:protein N-myristoyl transferase

Substrate: myristoyl-CoA

Step 1: removal of Met

$$H_3N$$
 $H_3N$ 
 $H_3N$ 

Step 2: addition C14:0

$$CH_{3}(CH_{2})_{11}CH_{2}$$

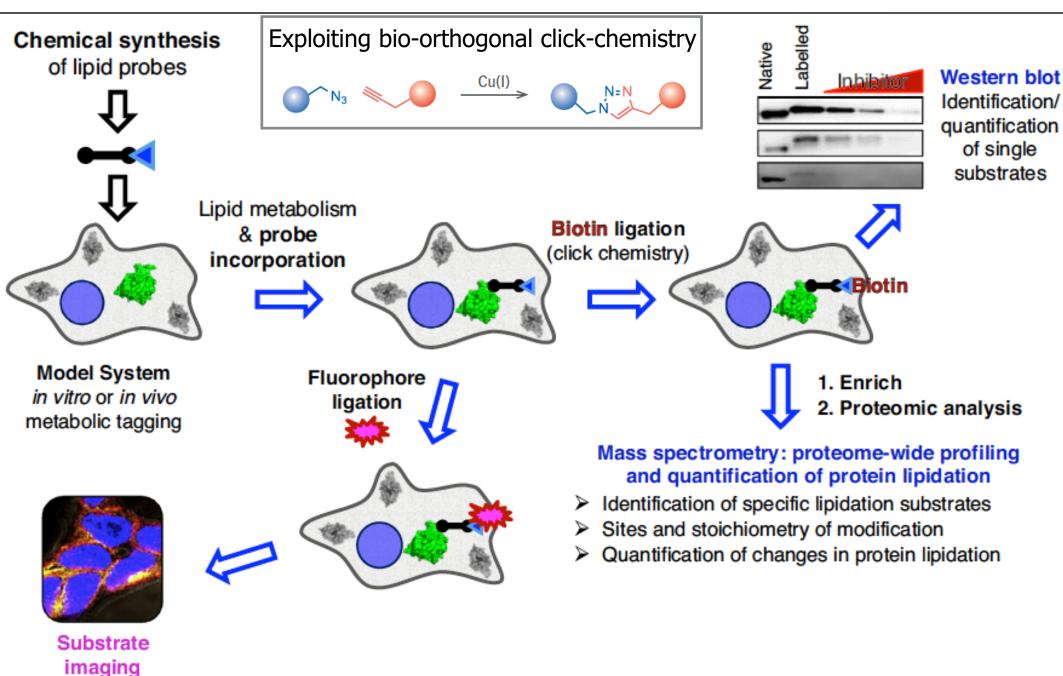
$$COASH$$

$$CH_{3}(CH_{2})_{11}CH_{2}$$

$$CH_{3}(CH_{2})_{11}C$$

6 - Lipidation

# Identifying & localising lipidated proteins



## 

O<sub>H</sub>

O<sub>H</sub>

O<sub>H</sub>

O<sub>H</sub>

Acylation: myristate and palmitate probes

Transferases: DHHC class
Hydrolases: APT1, APT2...?

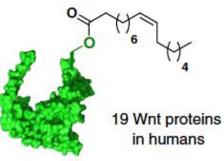
O

13-15

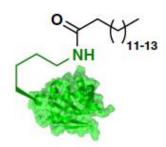
500+ substrates
in humans

Cysteine S-acylation

NH 14 NH 0 HHH Wnt O-acylation Transferase: Porcupine

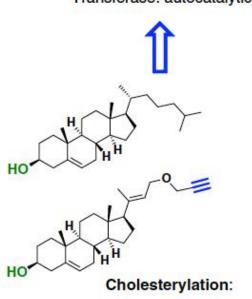


Lysine N-acylation Modulated by: sirtuins (Sirt6; Sirt2?; Sirt3?)



TNF-α; other substrates?

#### Hedgehog *O*-cholesterylation Transferase: autocatalytic

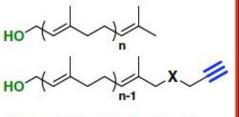


Cysteine S-farnesylation and Sgeranylgeranylation

Transferases: FTase & GGTase at CAAX box, and by RabGGTase on Rab proteins

S-farnesylation (n=2)
S-geranylgeranylation (n=3)

60+ Rabs, 70+ other substrates (Ras, Rho, etc.)



Prenylation: farnesyl and geranylgeranyl alcohol probes