

Contents lists available at ScienceDirect

Biochimica et Biophysica Acta

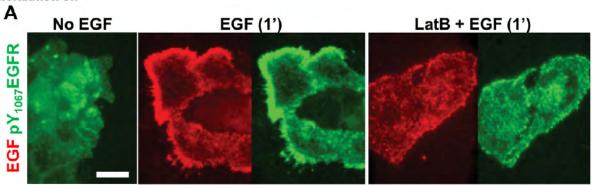
journal homepage: www.elsevier.com/locate/bbamem

Review

Optical measurement of receptor tyrosine kinase oligomerization on live cells*

Inhee Chung

Janelia Research Campus, Howard Hughes Medical Institute, 19700 Helix Drive, Ashburn, VA 20147, USA



ARTICLE

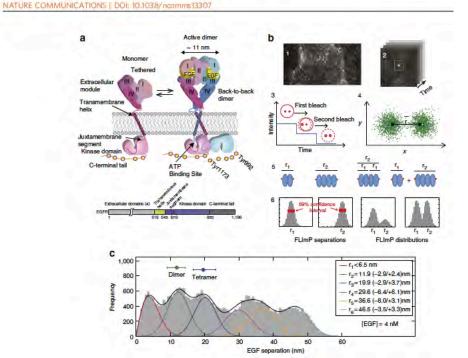
Received 18 Nov 2015 | Accepted 20 Sep 2016 | Published 31 Oct 2016

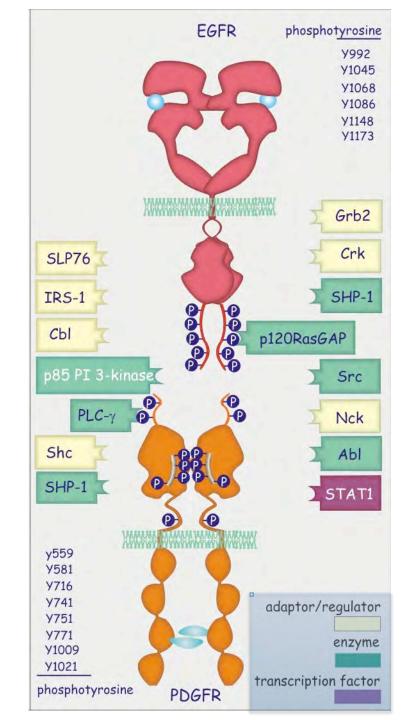
DOI: 10.1038/ncomms13307

OP

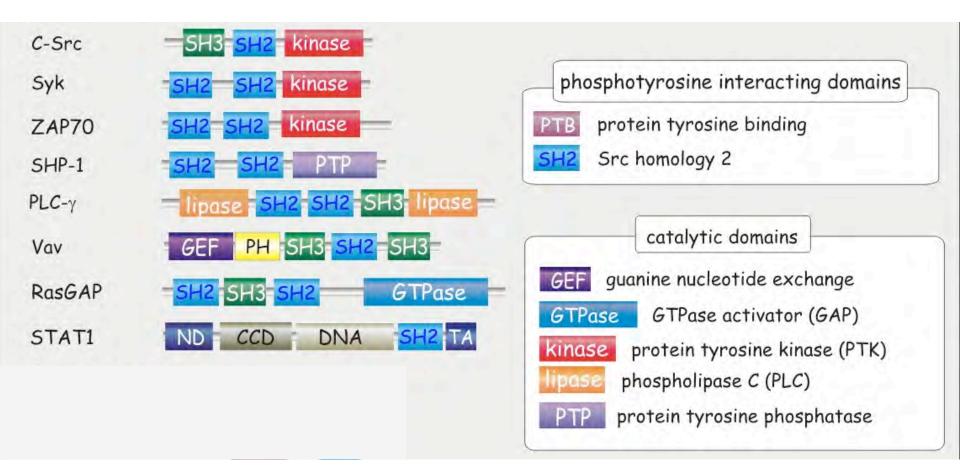
EGFR oligomerization organizes kinase-activ dimers into competent signalling platforms

Sarah R. Needham¹, Selene K. Roberts¹, Anton Arkhipov², Venkatesh P. Mysore², Christopher J. Laura C. Zanetti-Domingues¹, Eric T. Kim², Valeria Losasso³, Dimitrios Korovesis¹, Michael Hirs Daniel J. Rolfe¹, David T. Clarke¹, Martyn D. Winn³, Alireza Lajevardipour⁴, Andrew H.A. Clayton⁴ Michela Perani⁶, Peter J. Parker^{6,7}, Yibing Shan², David E. Shaw^{2,8} & Marisa L. Martin-Fernande

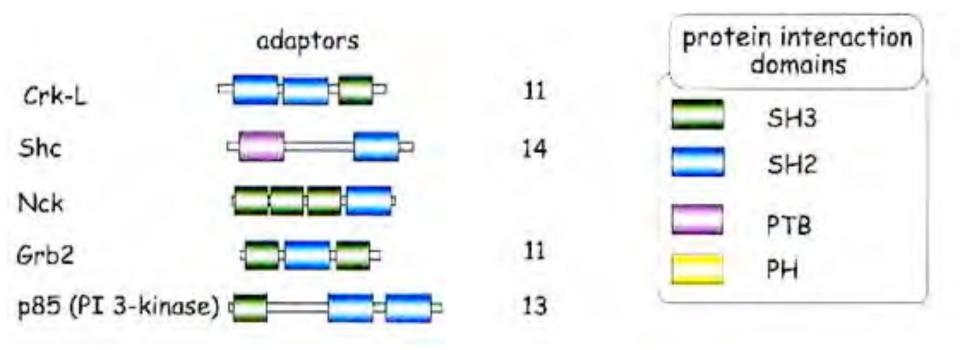


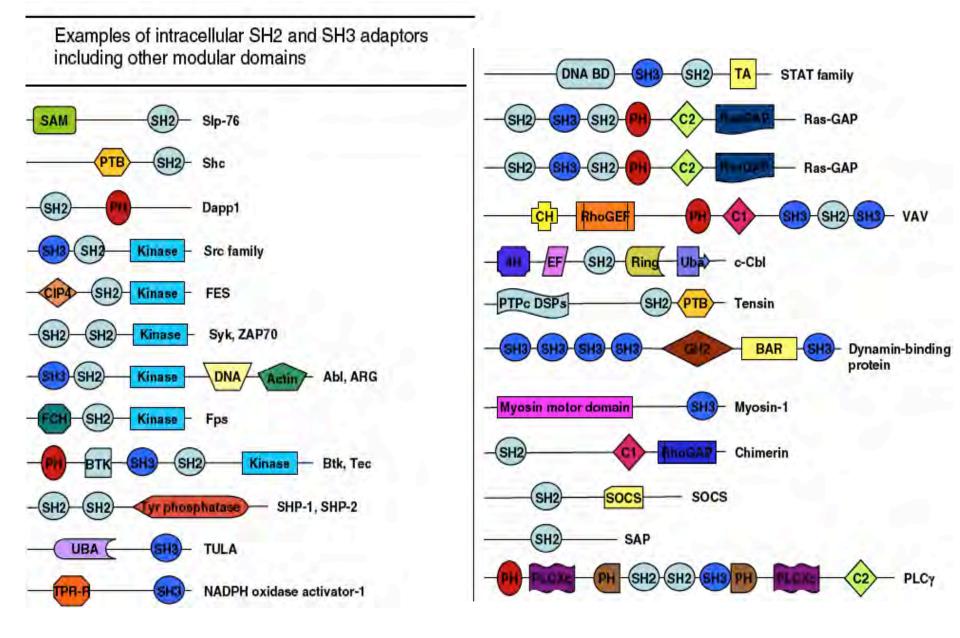


1) Enzymes/transcription factors



2) <u>Adaptors</u> lack intrinsic catalytic activity, but link phosphorylated receptors with other effector proteins.





Intracellular adaptor proteins containing SH2 and/or SH3 domains in addition to other modular domains. These domains are critical in cellular and biological functions.

Signaling Efficiency: Scaffolding Proteins and Signaling Complexes

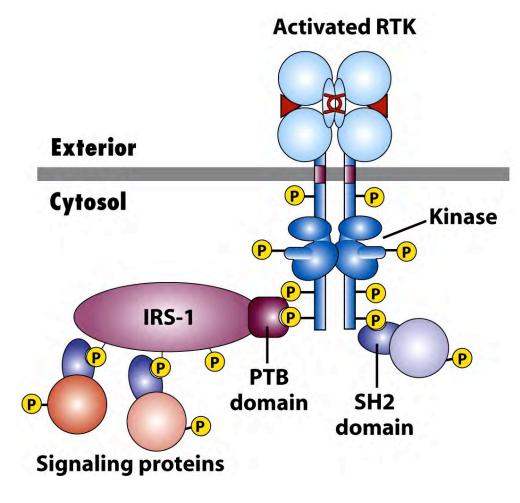
- Scaffolding proteins are large relay proteins to which other relay proteins are attached
- Scaffolding proteins can increase the signal transduction efficiency by grouping together different proteins involved in the same pathway
- In some cases, scaffolding proteins may also help activate some of the relay proteins

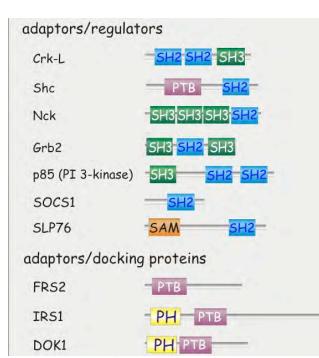
Recruitment of Signal Transduction Proteins to Activated Receptors

RTKs downstream effectors interact with phosphorylated RTKs via <u>phosphotyrosine binding</u> <u>domains</u>.

Two main binding domains <u>PTB</u> and <u>SH2</u> are involved in the recruitment of adaptors such as the <u>multi-</u> <u>docking protein</u> known as the <u>insulin receptor</u> <u>substrate-1 (IRS-1).</u>

The binding of signaling proteins allows them to be phosphorylated by the receptor.

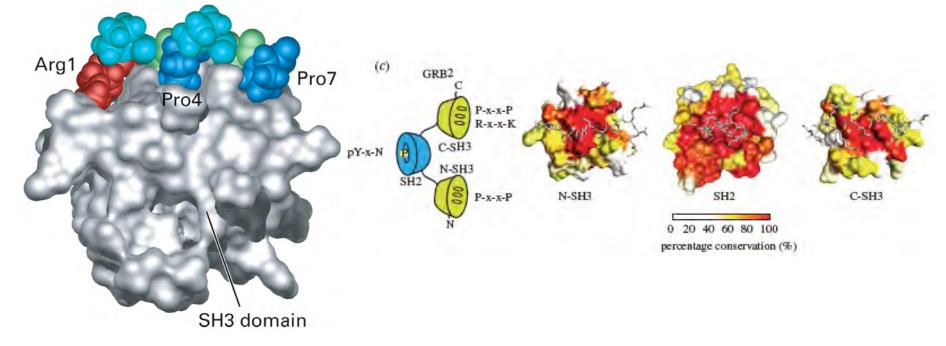


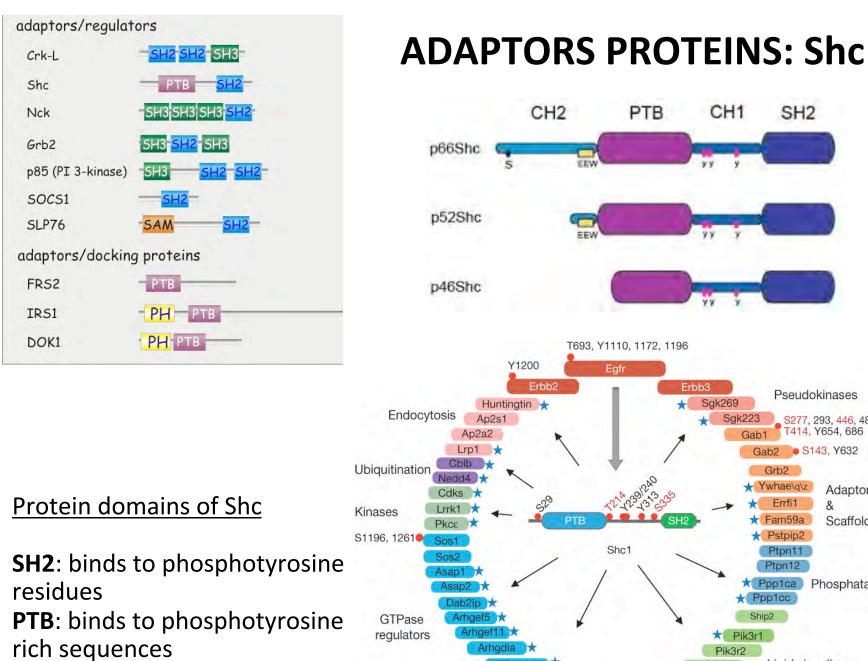


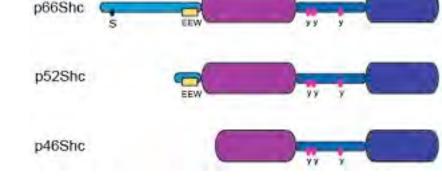
ADAPTORS PROTEINS: GRB-2

Protein domains of GRB2

SH2: binds to phosphotyrosine residuesSH3: binds to proline rich sequences

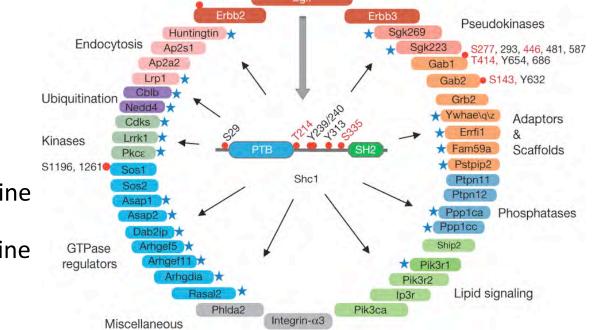


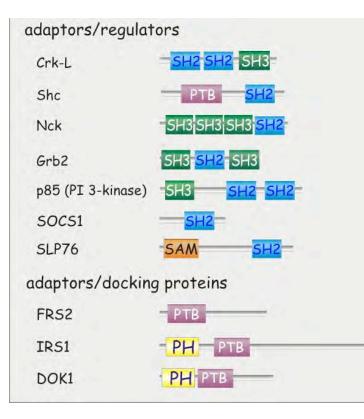




CH1

SH₂

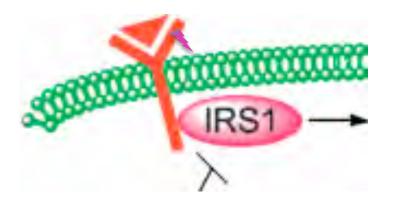


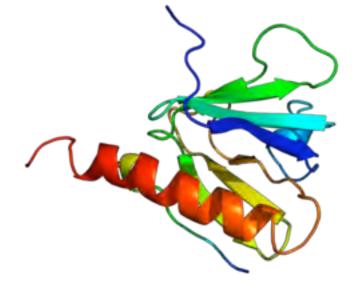


ADAPTORS PROTEINS: IRS-1

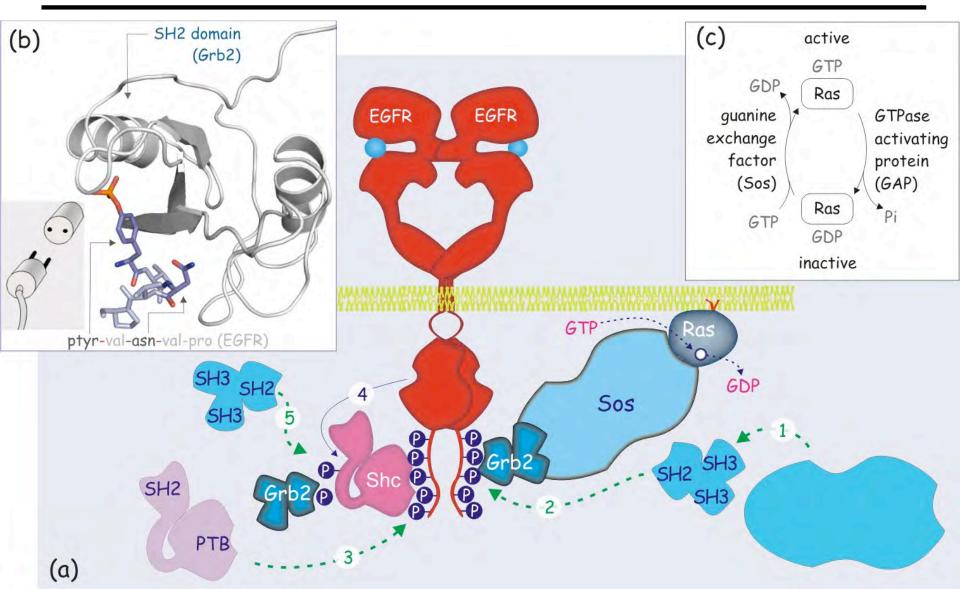
Protein domains of IRS-1:

PH: binds to bind PI lipids within biological membranes (PIP2-PIP3) and proteins such as the βγ-subunits of G proteins and PKc
PTB: bind to phosphotyrosine residues



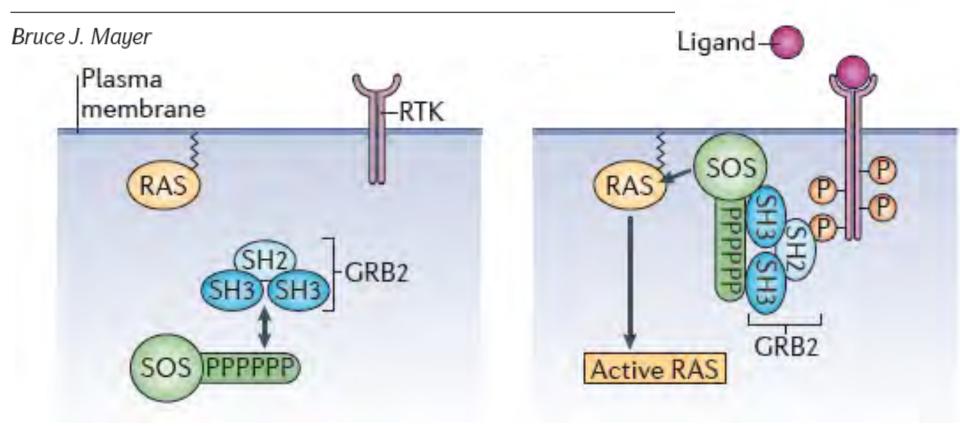


An example of a signaling complex – a protein relay system using phosphorylation as a signal



Nature Reviews Molecular Cell Biology | AOP, published online 30 September 2015; doi:10.1038/nrm4068

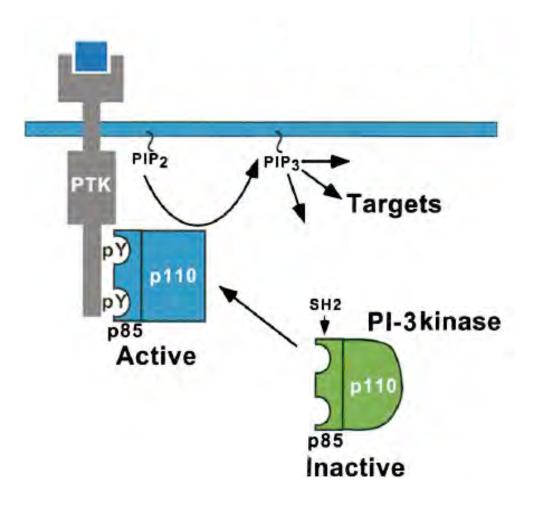
The discovery of modular binding domains: building blocks of cell signalling



Paradigms for activation of RTK signaling cascade:

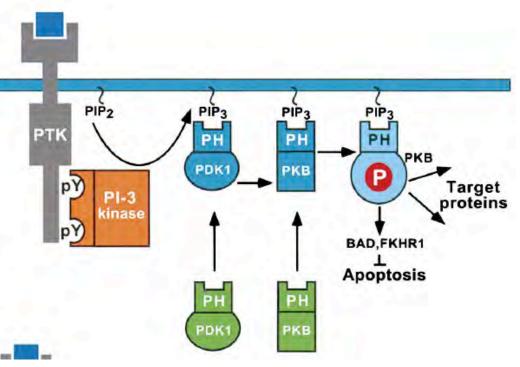
Translocation to the plasmalemma is essential for activation of most effector proteins

1- Activation by a conformational change



Binding of the SH2 domain of p85, the regulatory subunit of PI3-kinase to p-Tyr sites on activated receptors releases an autoinhibitory constraint that stimulates the catalytic domain (p110).

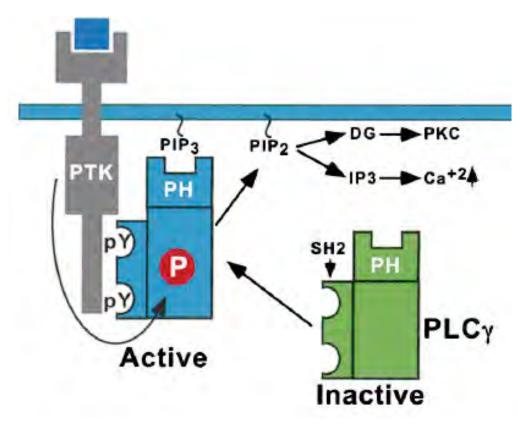
2- Activation by membrane translocation



PtdIns (3,4,5)P₃ generated in response to growth factor stimulation serves as a binding site for the PH domains of PDK1 and PKB.

Membrane translocation is accompanied by a release of an autoinhibition leading to activation of PDK1 and PKB kinase activities.

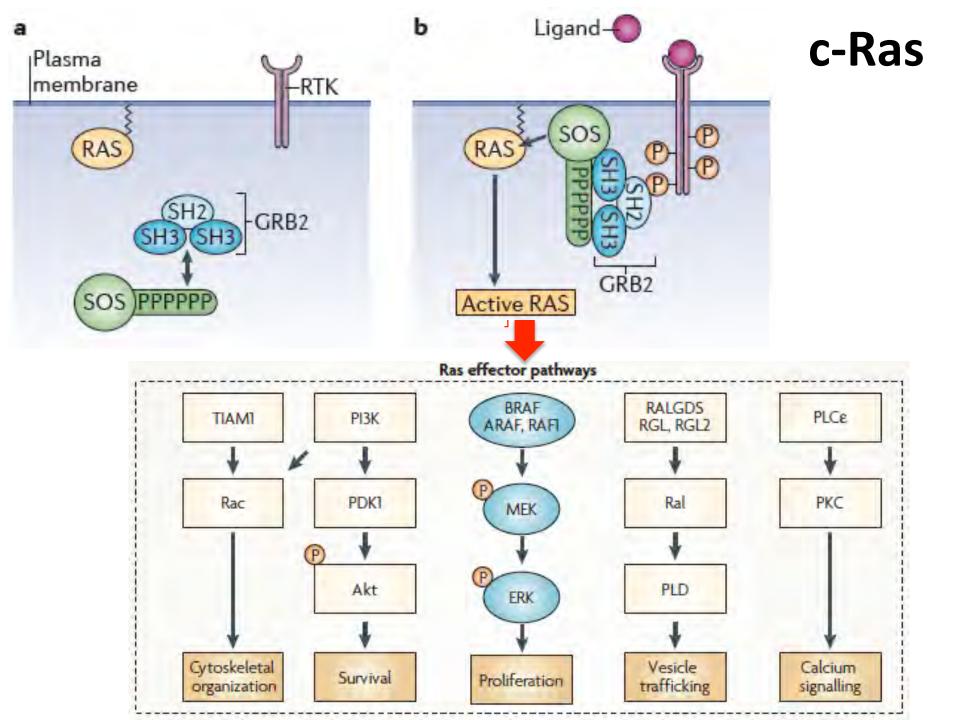
3- Activation by tyrosine phosphorylation



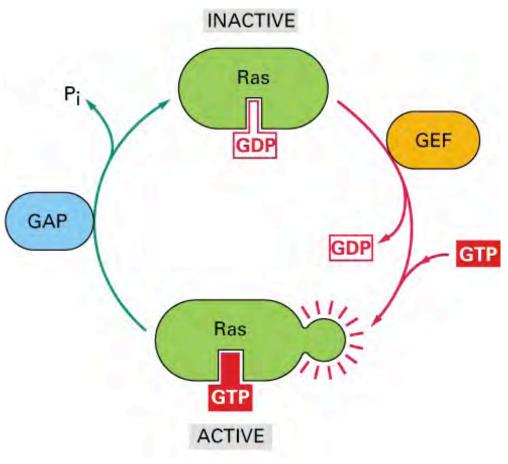
Binding of the SH2 domain of PLC-γ to P-Tyr sites in activated receptors facilitates tyrosine phosphorylation of PLC-γ, as well as membrane translocation. Tyrosine phosphorylation is essential for PLC-γ activation.

Ras (RAT-sarcoma) is a monomeric GTPase

- Ras is a G protein (guanosine-nucleotide-binding protein), a small GTPase
- The first two ras genes, HRAS and KRAS, were first identified from the Harvey sarcoma virus and Kirsten sarcoma virus, by Scolnick and colleagues at (NIH) in 1982. In 1982, activated and transforming human ras genes were discovered in human cancer cells. A third ras gene was subsequently discovered and named NRAS, for its initial identification in human neuroblastoma cells.
- Anchored at the plasma membrane owing to its prenylation and palmitoylation (HRAS and NRAS) or the combination of prenylation and a polybasic sequence adjacent to the prenylation site (KRAS).
- The C-terminal region of Ras first gets farnesylated at its Cys residue in the cytosol, allowing Ras to loosely insert into the membrane of the endoplasmatic reticulum and other cellular membranes.
- The three human ras genes encode extremely similar proteins made up of chains of 188 to 189 amino acids, designated H-Ras, N-Ras and K-Ras4A and K-Ras4B (from alternative splicing).

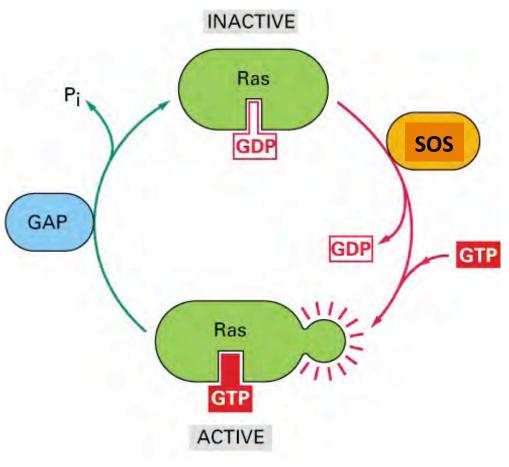


Ras is a monomeric[.] GTPase



Ras has an intrinsic GTPase activity: the protein on its own will hydrolyze a bound GTP molecule into GDP. However this process is too slow for efficient function, and hence the GAP for Ras, RasGAP, may bind to and stabilize the catalytic machinery of Ras. GEFs catalyze a "push and pull" reaction which releases GDP from Ras. Because intracellular GTP is abundant relative to GDP (approximately 10 fold more) GTP predominantly re-enters the nucleotide binding pocket of Ras and reloads the spring. Thus GEFs facilitate Ras activation. The balance between GEF and GAP activity determines the guanine nucleotide status of Ras, thereby regulating Ras activity.

Ras is a monomeric[.] GTPase



Ras has an intrinsic GTPase activity: the protein on its own will hydrolyze a bound GTP molecule into GDP. However this process is too slow for efficient function, and hence the GAP for Ras, RasGAP, may bind to and stabilize the catalytic machinery of Ras. GEFs catalyze a "push and pull" reaction which releases GDP from Ras. Because intracellular GTP is abundant relative to GDP (approximately 10 fold more) GTP predominantly re-enters the nucleotide binding pocket of Ras and reloads the spring. Thus GEFs facilitate Ras activation. The balance between GEF and GAP activity determines the guanine nucleotide status of Ras, thereby regulating Ras activity.

The activation of Ras by RTKs

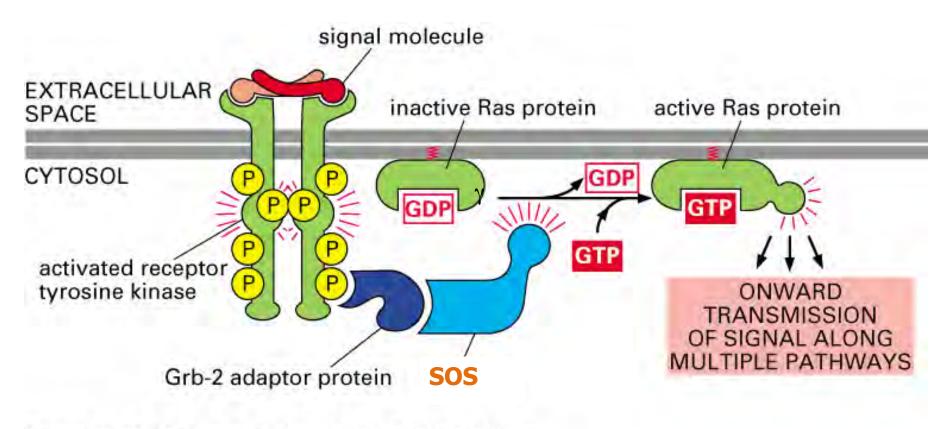


Figure 15–55. Molecular Biology of the Cell, 4th Edition.

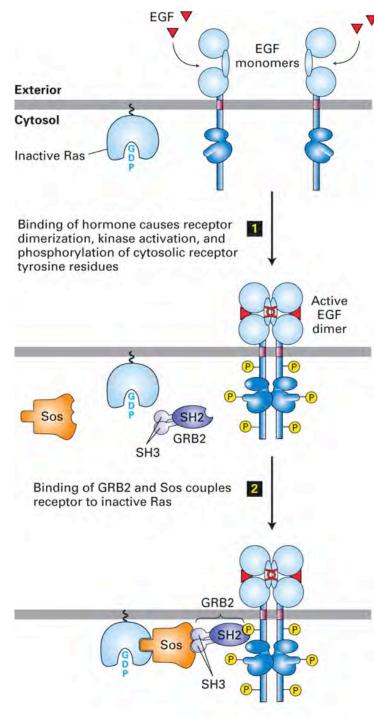
RTK Activation of Ras

EGF binding causes receptor clusterization and autophosphorylation on cytosolic tyrosines.

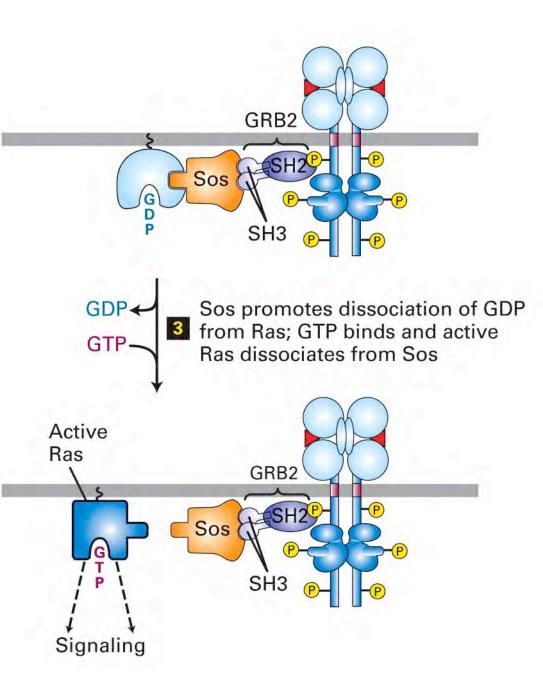
In <u>Step 2</u>, the <u>adaptor protein GRB2</u> binds receptor phosphotyrosine residues via its SH2 domain. GRB2 contains SH3 domains that allow the <u>GEF protein</u> known as <u>Sos</u> to bind to the membrane complex.

The C-terminus of Sos inhibits its nucleotide exchange activity; binding of GRB2 relieves this inhibition

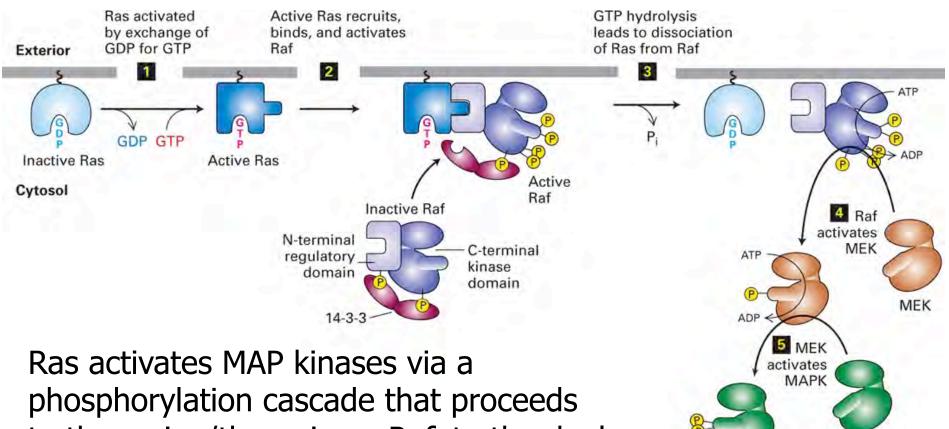
Sos converts inactive GDP-ras into active GTP-ras.



The activated Ras-GTP complex then dissociates from Sos, but remains tethered to the inner leaflet of the cytoplasmic membrane via a lipid anchor sequence. The active form of Ras then activates the MAP kinase portion of the signaling pathway.



Ras Activation of MAP Kinase



phosphorylation cascade that proceeds to the serine/threonine c-<u>Raf</u>, to the dual specificity kinase <u>MEK1</u> which in turn phosphorylates ERK2 on a threonine (T183) and on a tyrosine (Y185). MAP kinase then dimerizes and enters the nucleus.

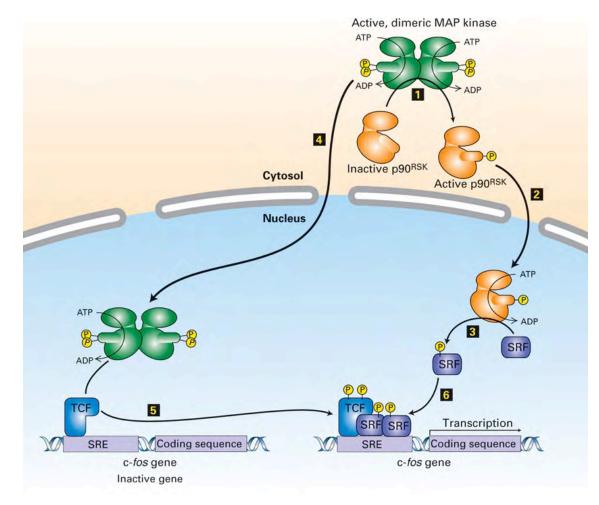
Active MAP kinase translocates to nucleus; activates many transcription factors

MAP kinase

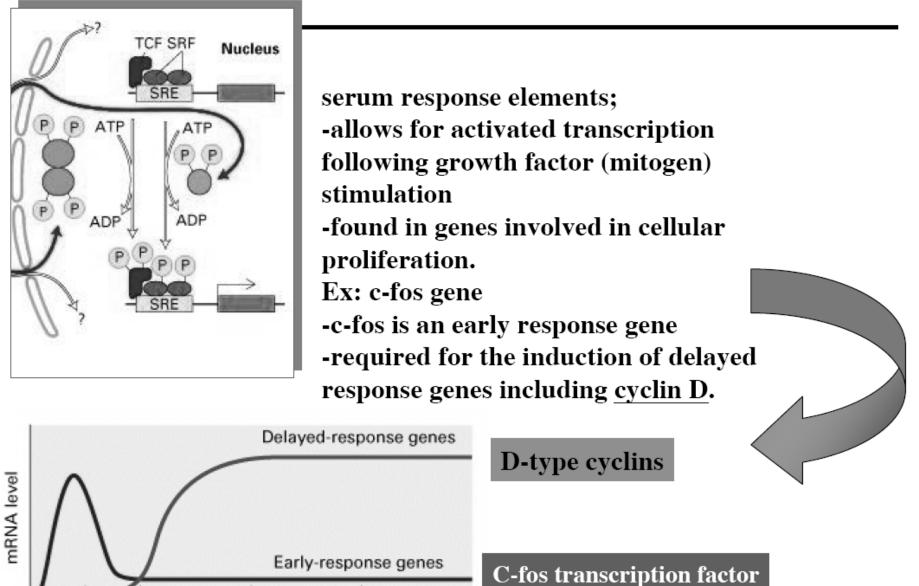
MAP Kinase Activation of Transcription

In the final steps of RTK-Ras/MAP kinase signaling, MAP kinase phosphorylates and activates the p90^{RSK} kinase in the cytoplasm. Both kinases <u>enter the nucleus</u> where they phosphorylate ternary complex factor (<u>TCF</u>) and serum response factor (<u>SRF</u>), respectively.

The phosphorylated forms of these TFs bind to serum response element (SRE) enhancer sequences that control genes regulated by growth factors present in serum (such as <u>c-fos</u>) and_propel cells through the cell cycle.



Genes regulated by RTK/Ras pathway include early response genes.



VM **Diainfa**



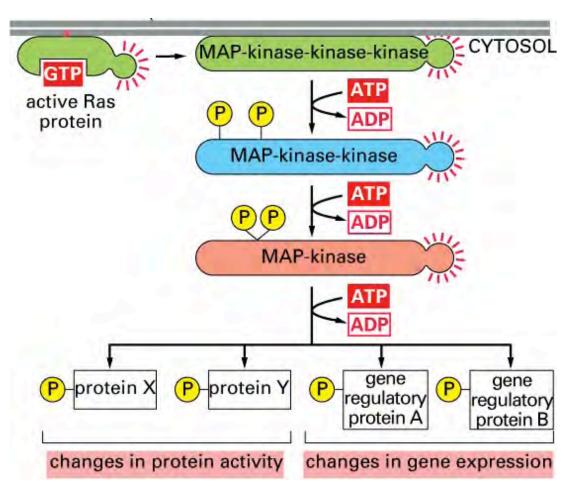
Mitogen-activated protein kinases are serine/threonine-protein kinases. They regulate proliferation, gene expression, differentiation, mitosis, cell survival, and apoptosis.

MAP kinases are found in eukaryotes only.

"Classical" MAPKs activation requires **two phosphorylation events**, both threonine and tyrosine residues, in order to lock the kinase domain in a catalytically competent conformation.

Inactivation of MAPKs is performed by a very conserved family of dedicated phosphatases is the so-called MAP kinase phosphatases (MKPs), dual-specificity phosphatases (DUSPs). They hydrolyze the phosphate from both phosphotyrosine and the phosphothreonine residues.

- Once activated, Ras propagates signaling further inside the cell via a kinase cascade that culminates in the activation of members of the <u>MAP kinase</u> family.
- MAP kinases phosphorylate TFs that regulate genes involved in the <u>cell</u> cycle, survival and in <u>differentiation</u>.
- As a result, mutations in *ras* genes can cause unintended and overactive signalling inside the cell and ultimately to cancer
- Ras is the most common oncogene in human cancer
 - mutations that
 permanently activate Ras
 are found in 20-25% of all
 human tumors and up to
 90% in certain types of
 cancer (pancreatic cancer).



Cancer type	HRAS	KRAS	NRAS	BRAF
Biliary tract	0%	33%	1%	14%
Bladder	11%	4%	3%	0%
Breast	0%	4%	0%	2%
Cervix	9%	9%	1%	0%
Colon	0%	32%	3%	14%
Endometrial	1%	15%	0%	1%
Kidney	0%	1%	0%	0%
Liver	0%	8%	10%	3%
Lung	1%	19%	1%	2%
Melanoma	6%	2%	18%	43%
Myeloid leukaemia	0%	5%	14%	1%
Ovarian	0%	17%	4%	15%
Pancreas	0%	60%	2%	3%
Thyroid	5%	4%	7%	27%

 Diversi tipi di cancro sembrano essere associati alla mutazione di una specifica isoforma RAS. Solitamente i carcinomi (in particolare quelli del colon e del <u>pancreas</u>) presentano mutazioni di KRAS, i tumori della vescica hanno mutazioni di HRAS e i tumori emopoietici presentano mutazioni di NRAS.

Oncogenes vs proto-oncogenes

- An **oncogene** is a gene that has the potential to cause cancer.
- In tumor cells, they are often mutated or expressed at high levels.
- The first confirmed oncogene was discovered in 1970 and was termed src. Src was in fact first discovered as an oncogene in a chicken retrovirus.
- In 1976 Dominique Stehelin, J. Michael Bishop and Harold E. Varmus demonstrated that oncogenes were activated proto-oncogenes, found in many organisms including humans (for this discovery Bishop and Varmus were awarded the Nobel Prize in Physiology or Medicine in 1989).
- A **proto-oncogene** is a normal gene that becomes an oncogene due to mutations or increased expression.
- Proto-oncogenes code for proteins that regulate cell growth and differentiation. Proto-oncogenes are often involved in signal transduction and execution of mitogenic signals.
- Upon *activation*, a proto-oncogene becomes a tumor-inducing agent, an oncogene.

CELLULAR ONCOGENES

- Present in cancer cells
- Contains introns characteristic of eukaryotic cells
- Encodes proteins triggering transformation of normal cells

VIRAL ONCOGENES

- Present in viruses
- Host cell origin
- Do not possess introns
- Also called 'cancer genes'
- Encodes proteins triggering transformation of normal cells into cancer cells

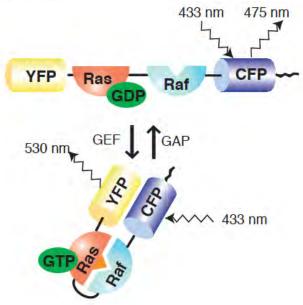
VIRAL ONCOGENE	HUMAN ONCOGENE	ORIGIN	NATURE
V-src	C-src	Chicken	Sarcoma
V-ras	C-ras	Rat	Sarcoma
V-myc	C-myc	Chicken	Leukemia
V-fes	C-fes	Feline	Sarcoma
V-sis	C-sis	Simian	Sarcoma
V-mos	C-mos	Mouse	Sarcoma

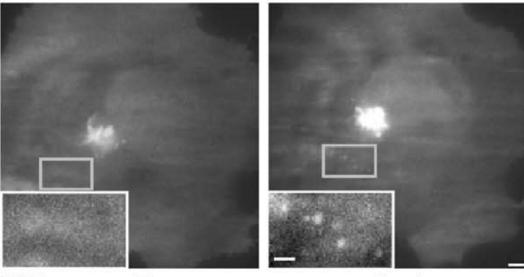
Visualizing Ras signalling in real-time

Simon A. Walker and Peter J. Lockyer*

Laboratory of Molecular Signalling, The Babraham Institute, Babraham Research Campus

Journal of Cell Science 117, 2879-2886 Published by The Company of Biologists 2004 doi:10.1242/jcs.01285

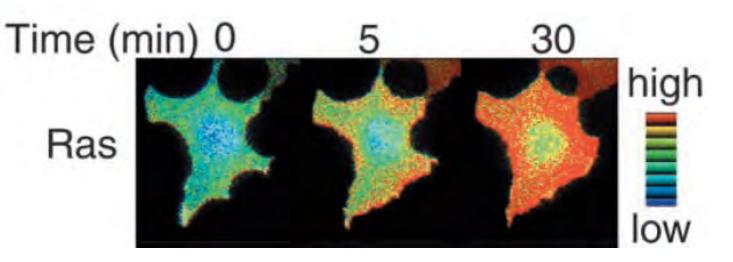




EGF

GFP-RBD+HRas

5 min



Biochimica et Biophysica Acta 1793 (2009) 1691-1702

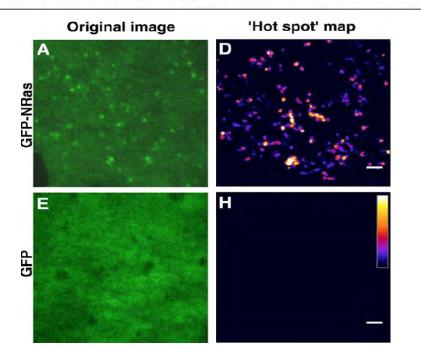


Contents lists available at ScienceDirect

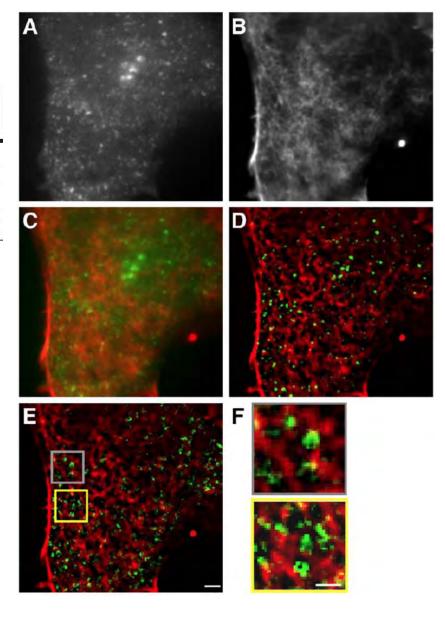
Biochimica et Biophysica Acta

journal homepage: www.elsevier.com/locate/bbamcr

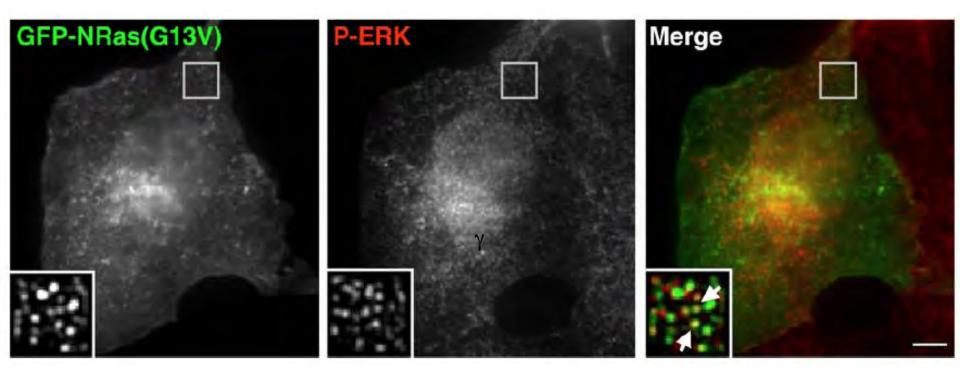
Rasosomes spread Ras signals from plasma membrane 'hotspots' Merav Kofer-Geles, Irit Gottfried, Roni Haklai, Galit Elad-Zefadia, Yoel Kloog *, Uri Ashery * Department of Neurobiology, The George S. Wise Faculty of Life Sciences, Tel Aviv University, 69978 Tel Aviv, Israel



Ras-osomes move within distinct areas, rasosomal 'hotspots', near the PM.



Rasosomes move within cortical actin cages.



GFP-NRas expressing cells were labeled with anti-phosphorylated-ERK Abs. Insets show filtered images of the boxed regions with arrows that indicate phospho-ERK positive GFP-NRas rasosomes