

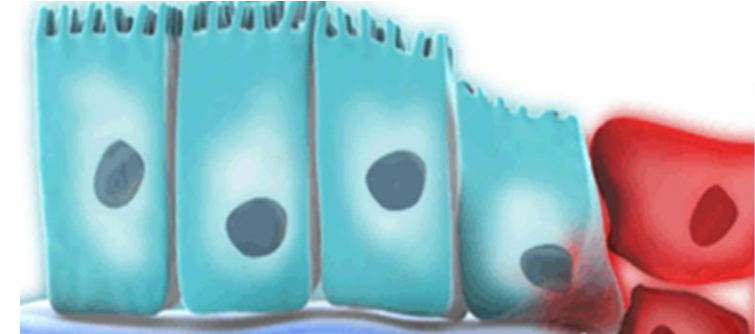


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Instituto Nacional de Saúde
Doutor Ricardo Jorge

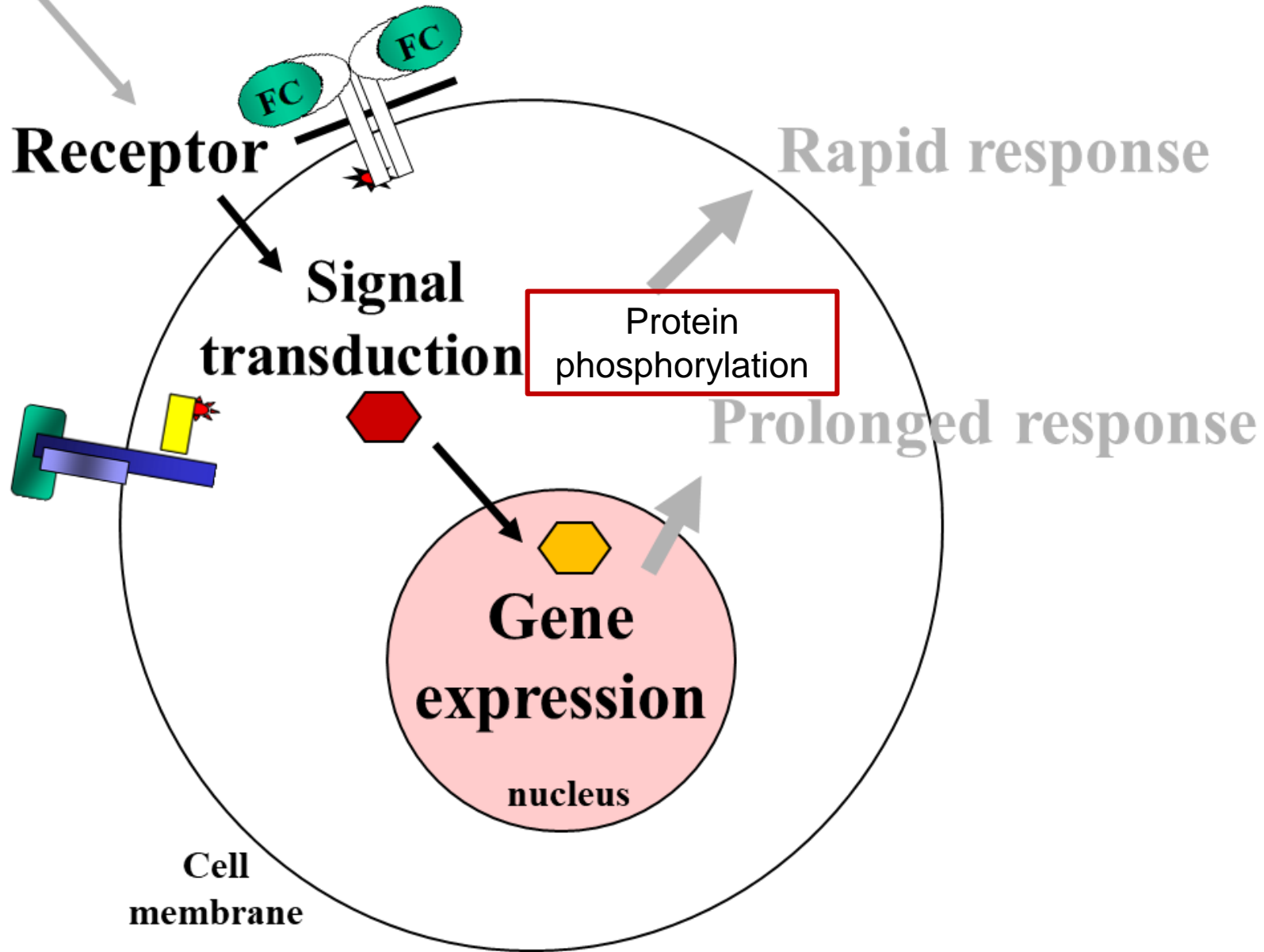


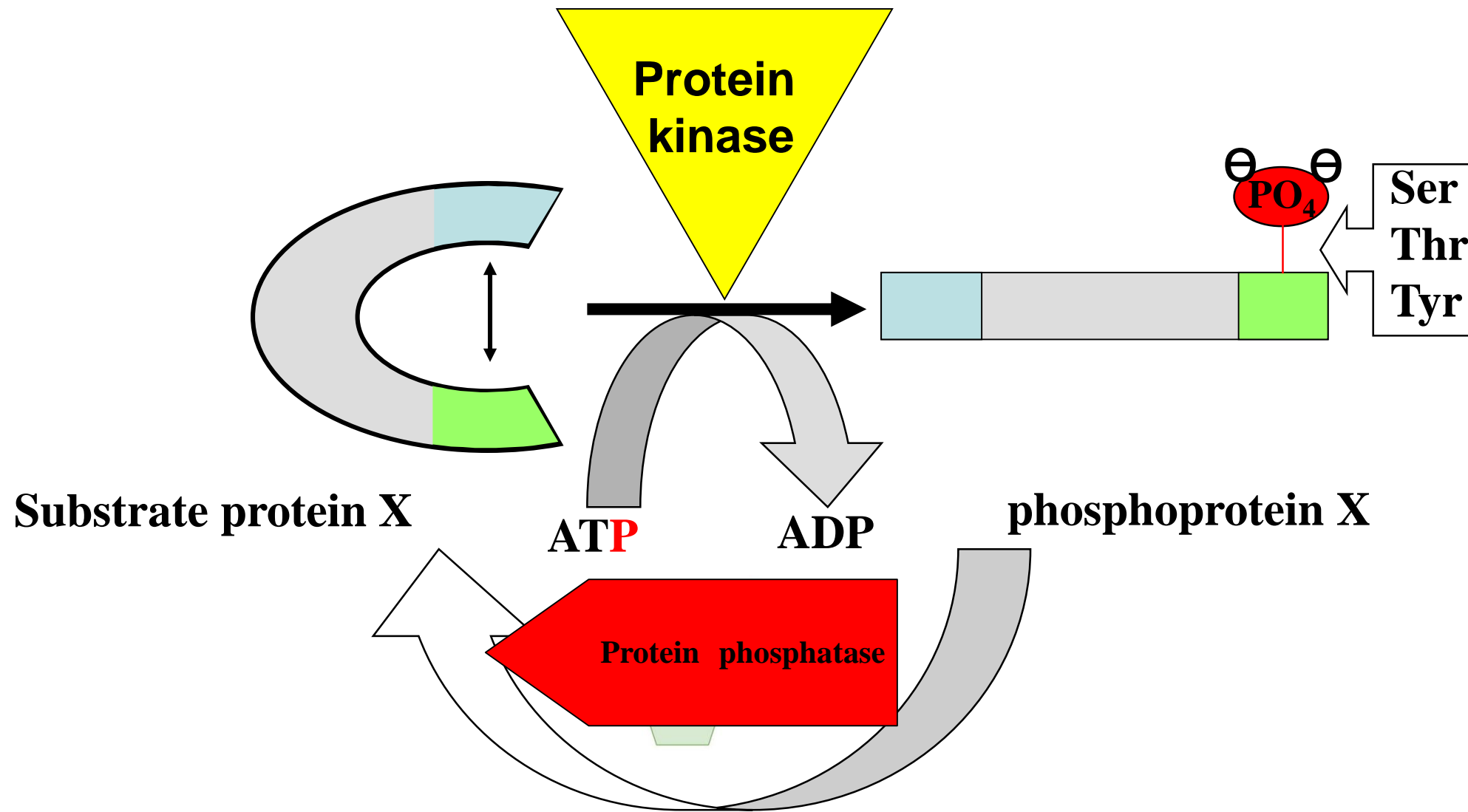
Oncobiology

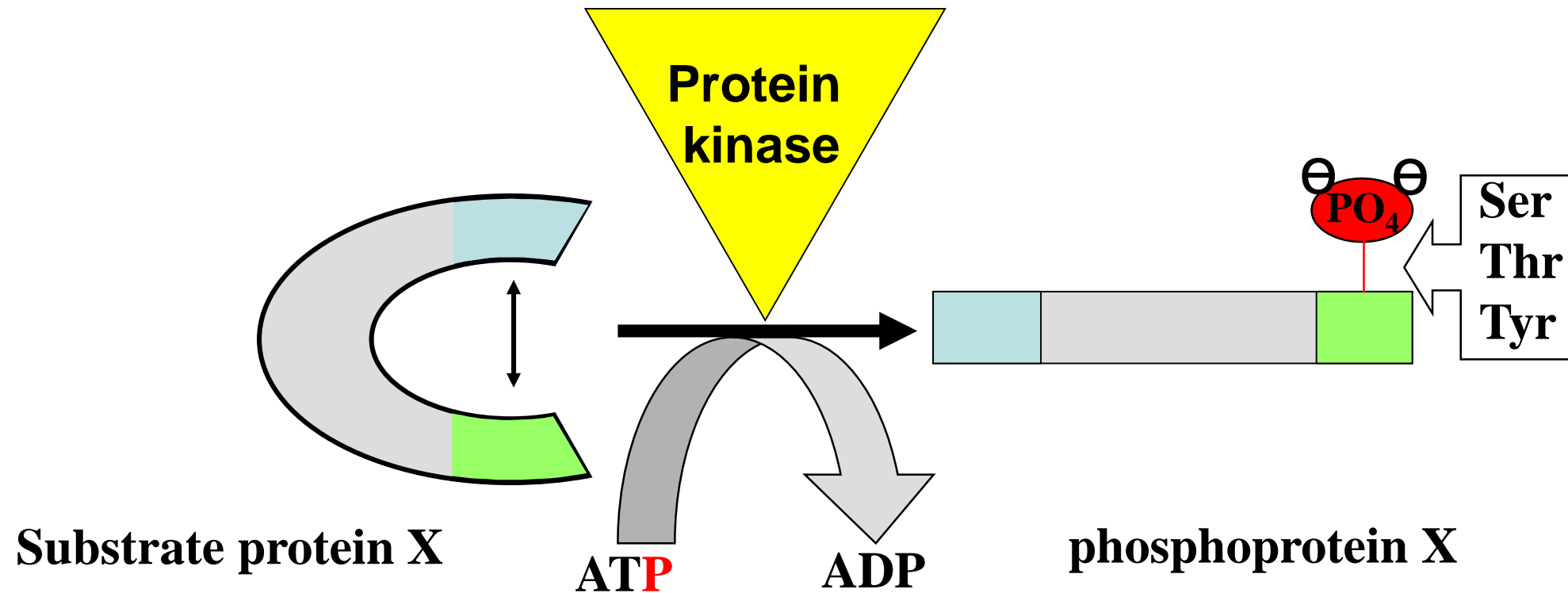
Margarida Gama-Carvalho (DQB/FCUL) and Peter Jordan (INSA)

The protein kinase superfamily

Stimulus







phosphorylation:

- can alter 3D conformation and activity of substrate protein;
- can create or mask protein interaction motifs in the substrate

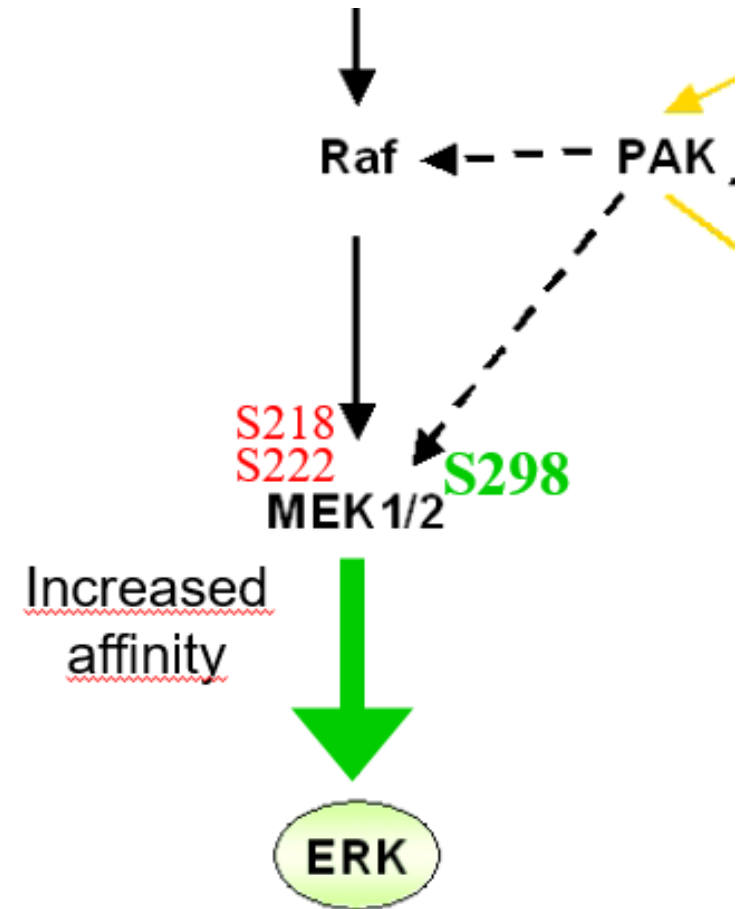
inactive

← 'Molecular switch' →

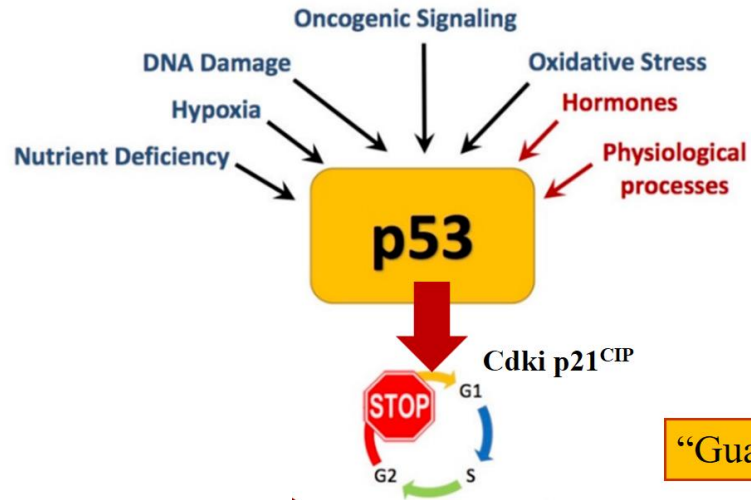
active

Some examples

- Can alter 3D conformation and activity
- Can create or mask protein interaction

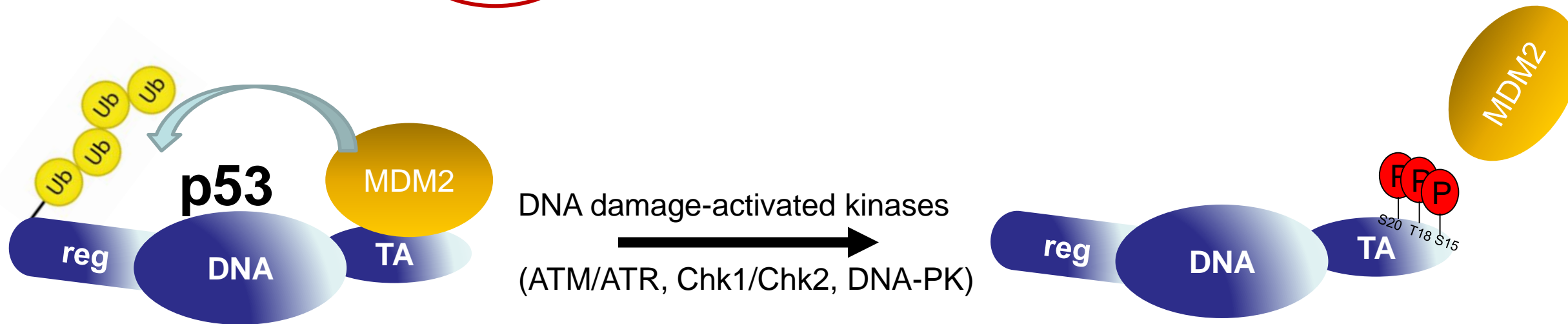


The activity of protein kinases themselves is regulated by their phosphorylation



and activity of substrate protein;

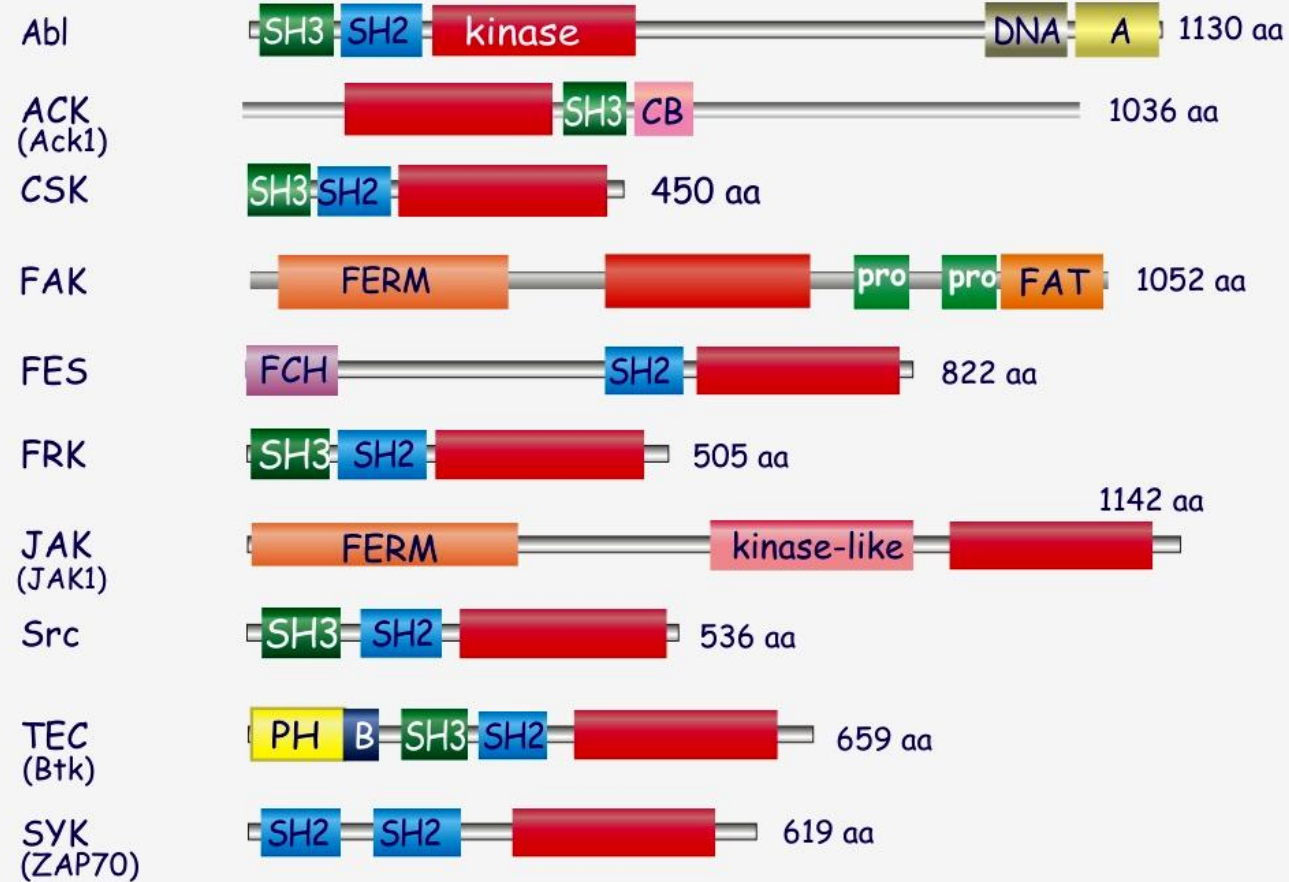
- Can create or **mask** protein interaction motifs in the substrate



MDM2 binds p53 to promote degradation and inhibit binding to target gene promoters

p53 stabilization and activation of target genes

Protein kinase= catalytic domain + remaining protein



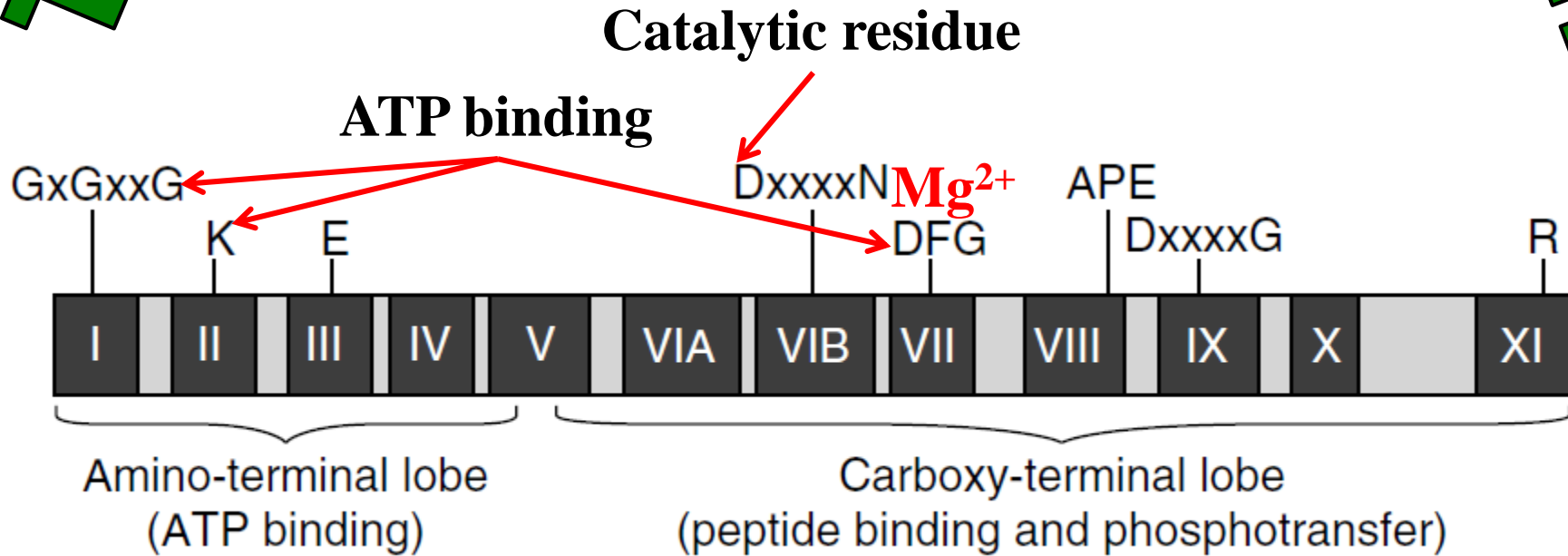
A	actin binding domain	FAT	focal adhesion targeting	PH	pleckstrin homology
B	Btk motif, Zn ²⁺ finger	FCH	Fes/CIB4 homology domain	pro	proline rich region
CB	Cdc42 binding domain	FERM	4.1-protein, ezrin, radixin, moesin	SH2	Src homology 2
DNA	DNA binding motif	kinase	protein tyrosine kinase	SH3	Src homology 3

Regulation
Recruitment
Localization

kinase

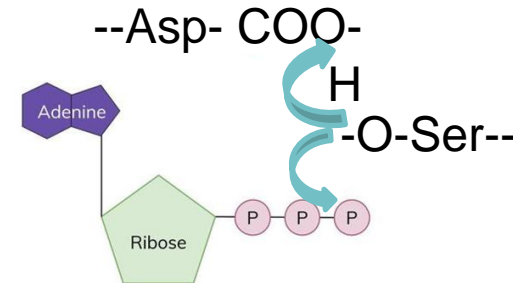
The catalytic domain

~250 aa



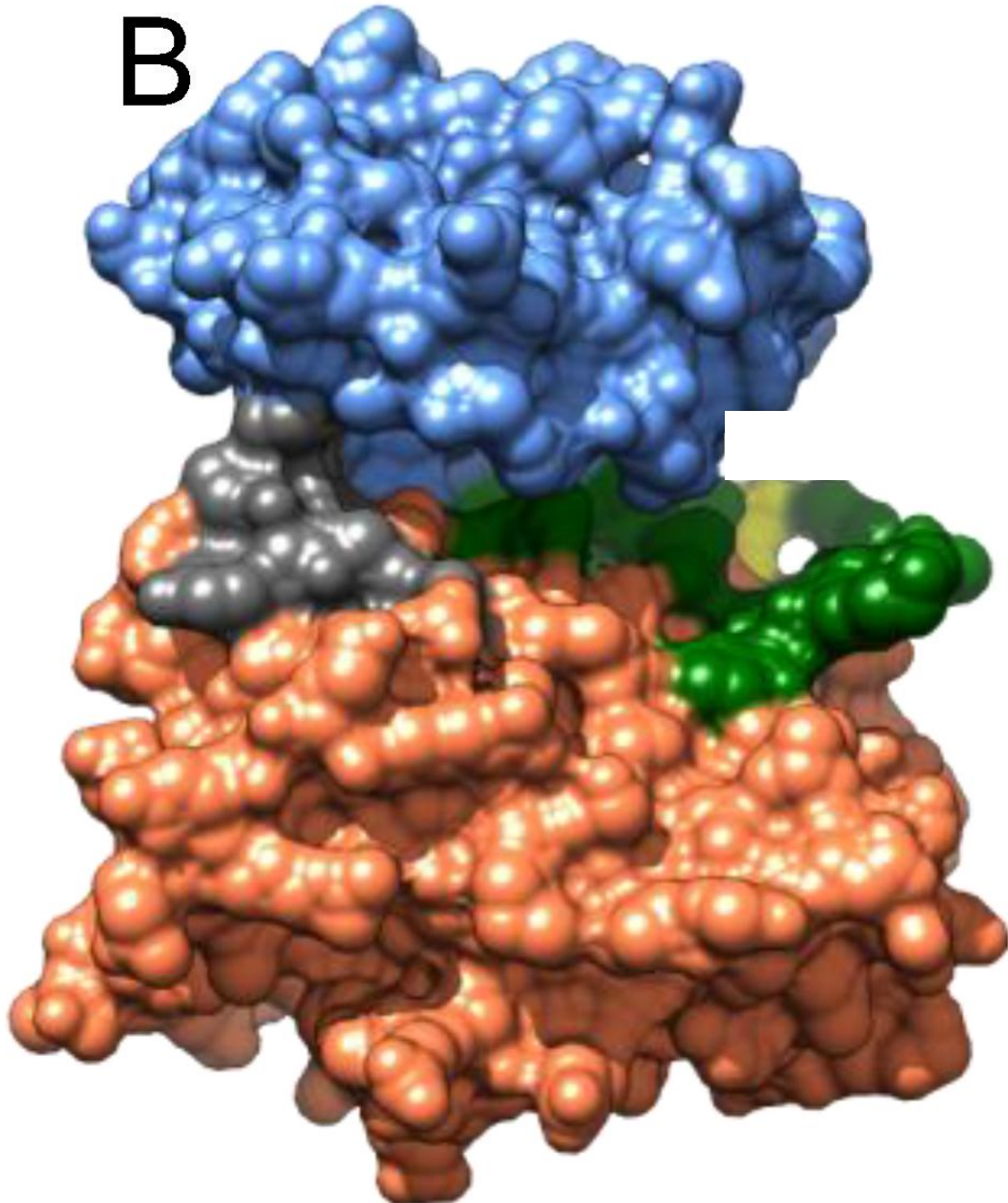
The catalytic Asp=D polarizes with its negative charge the hydroxyl oxygen of a Ser, Thr or Tyr of the protein substrate.

Then, the deprotonated oxygen residue performs a nucleophilic attack on the terminal (γ) phosphoryl group (PO_3^{2-}) of ATP.

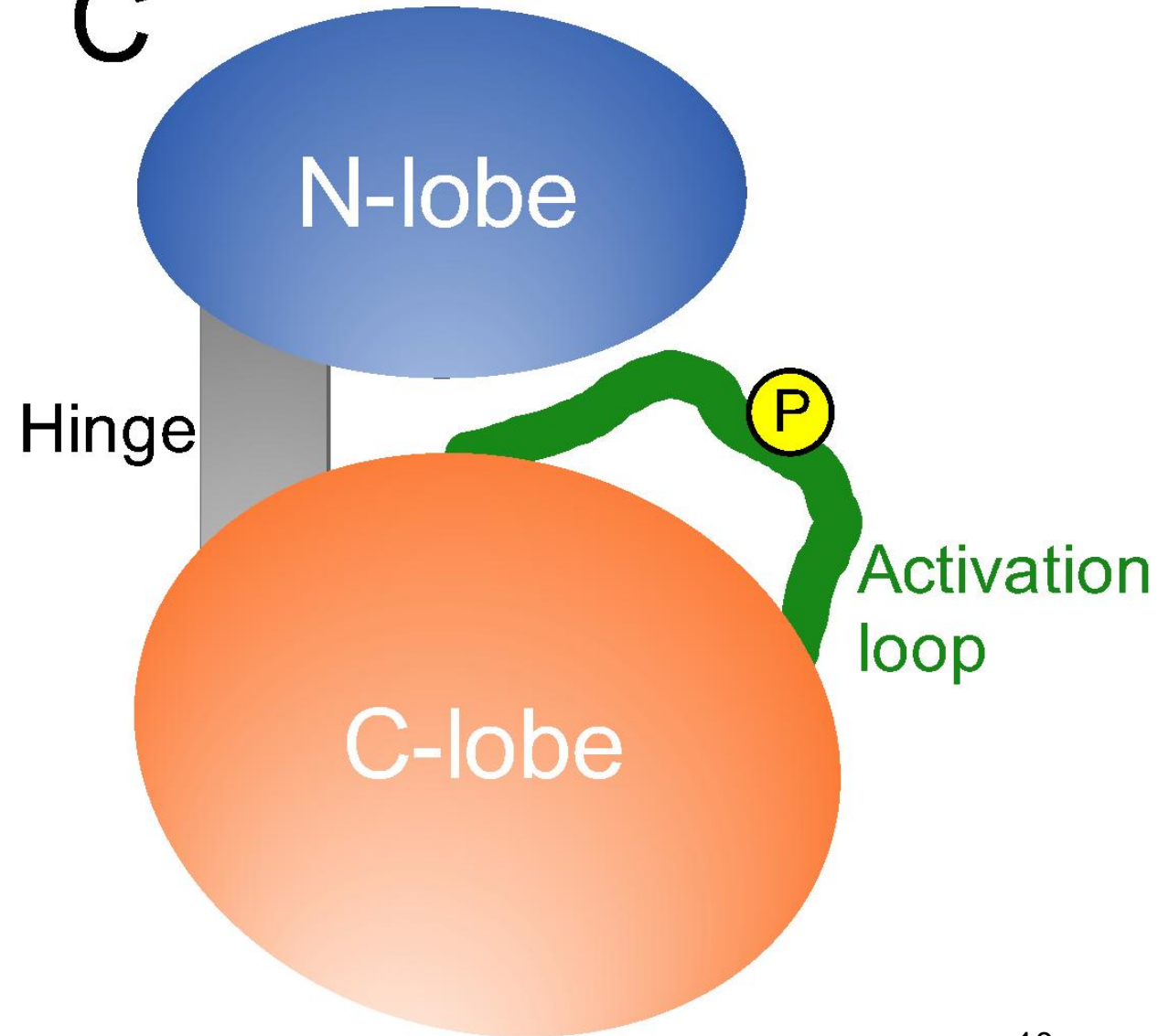


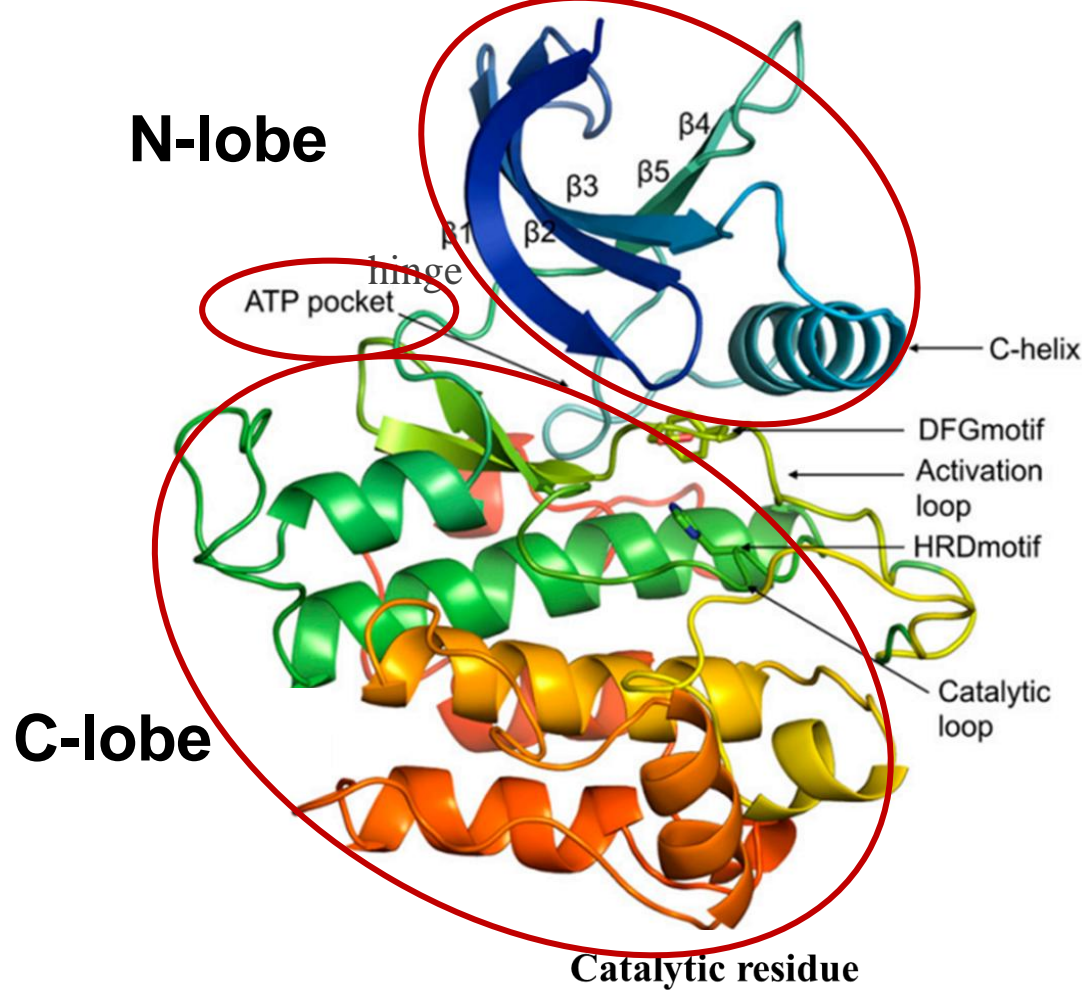
Protein kinase catalytic domain

B



C

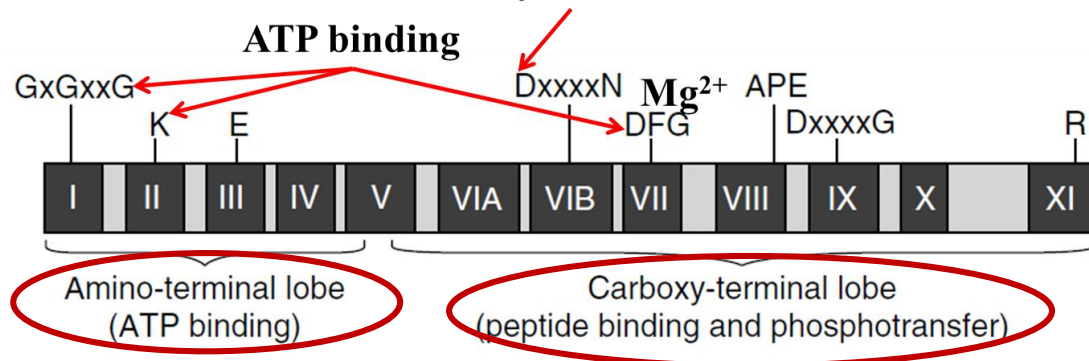


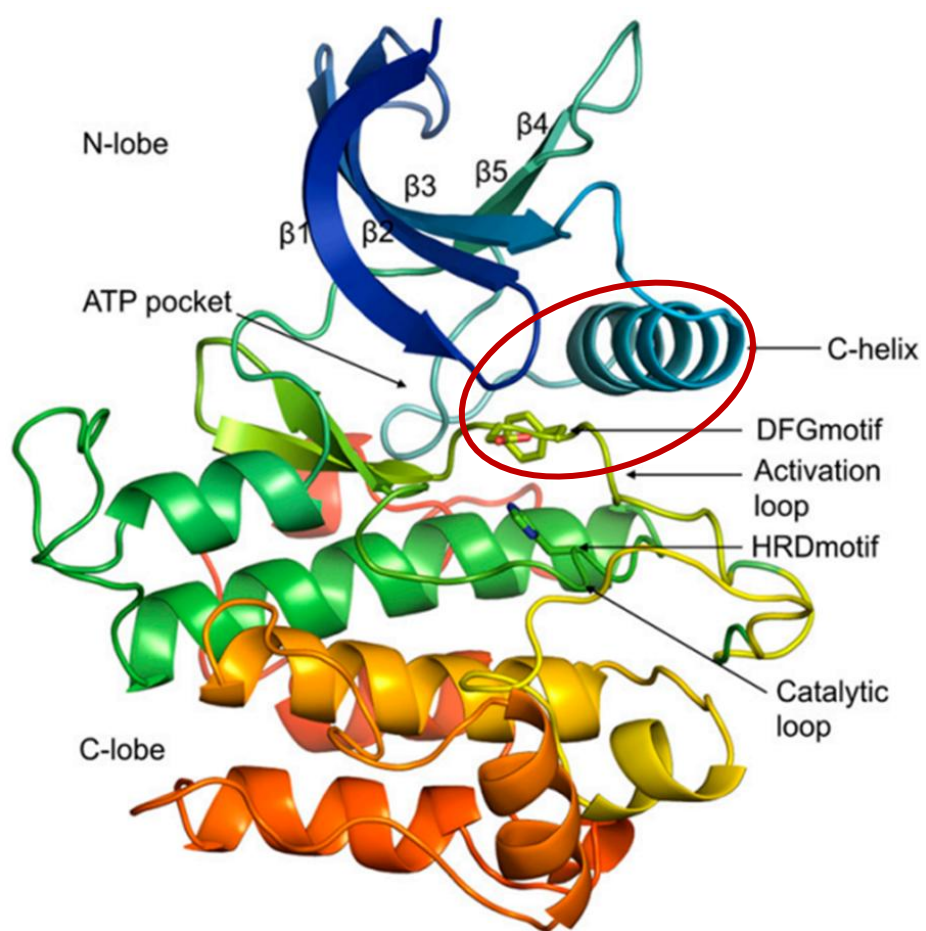


Catalytic PK domain:
a common folding consisting of an amino-terminal and carboxy-terminal lobe

Binding of Mg-ATP:
in a cleft between the two lobes, determined by the amino-terminal lobe and hinge region

Substrate binding:
peptide-substrate binding is mediated by the carboxy-terminal lobe.



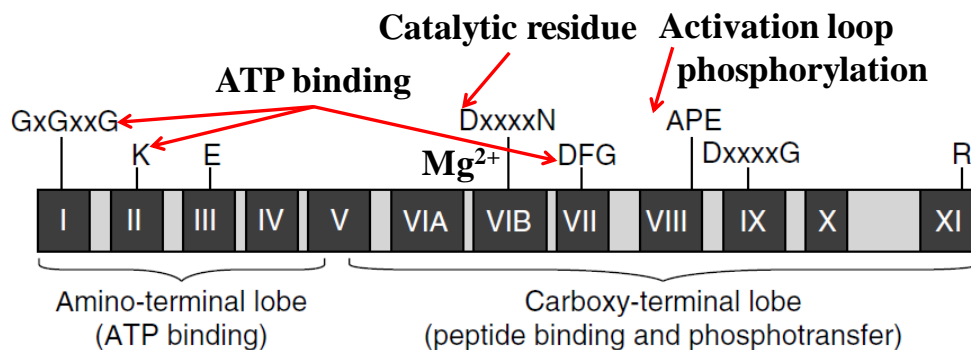


Activation of catalytic activity:

the C-helix and the activation loop with the DFG motif need to approach;

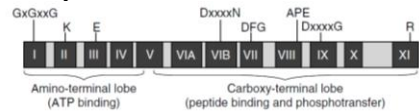
Both peptide regions are flexible between 2 conformational positions:
C-helix out/in; DFG out/in;

(Auto)phosphorylation in the activation loop further stabilizes the catalytically active 'in' conformational positions and leads to full kinase activation



➡ phosphorylation:
- can alter 3D conformation and activity of substrate protein

The human kinome



518
protein kinase genes

478 ePKs
conserved eucaryotic domain

40 aPKs
atypical catalytic domain

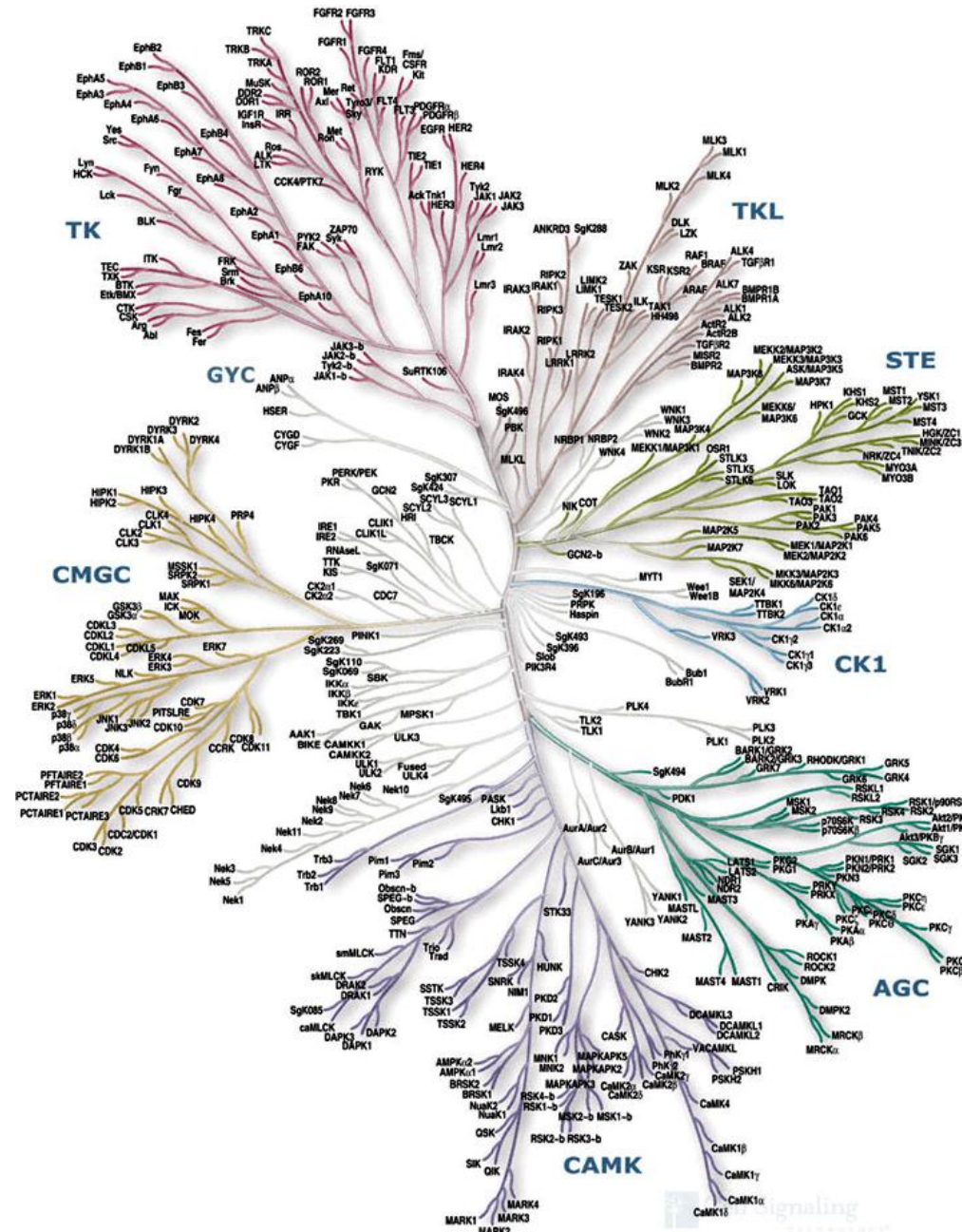
50 Pseudo-ePK kinases lacking conserved residues

428 ePKs with known or likely kinase activity

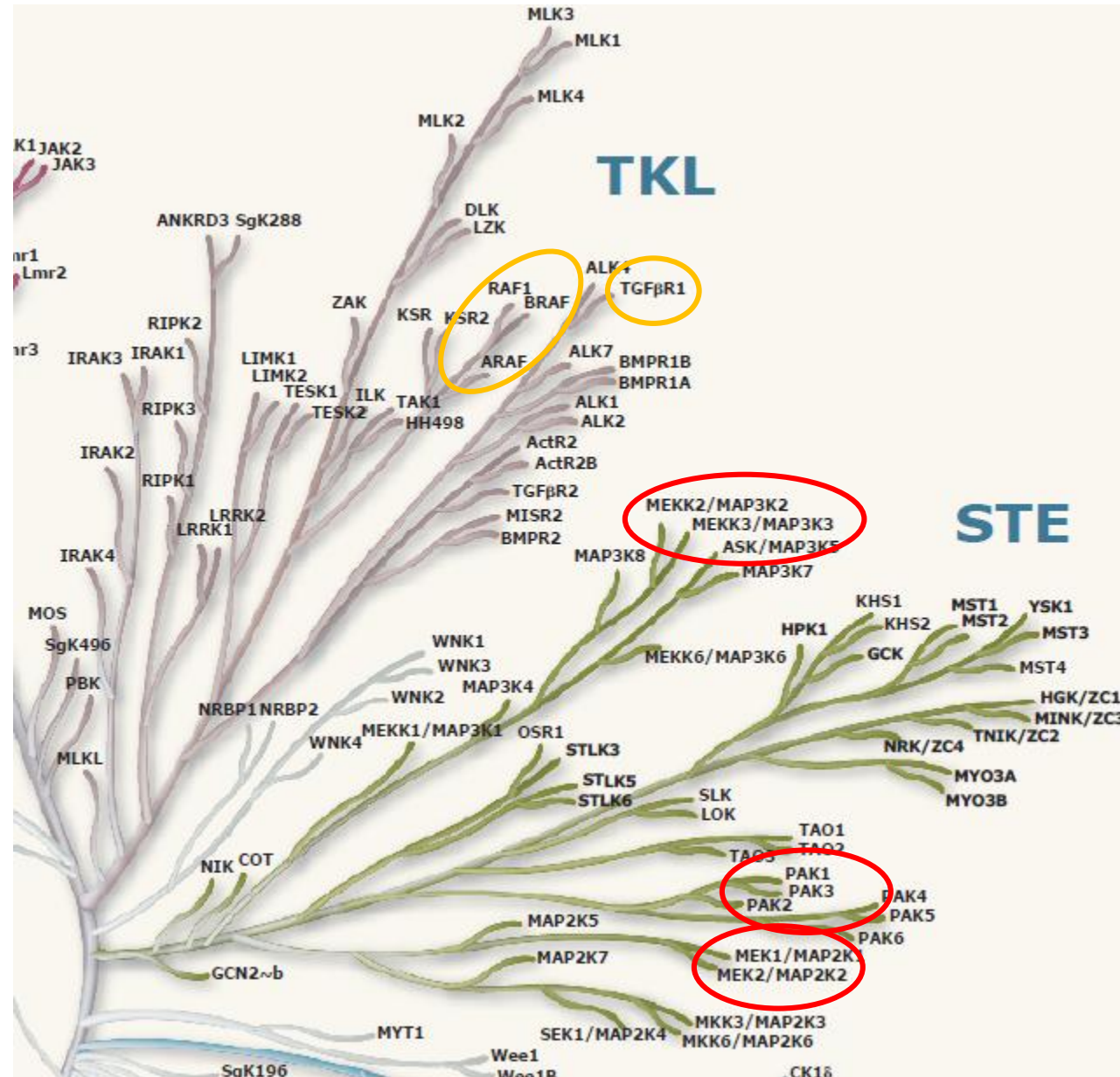
8 subgroups:

TK- 84; CAMK- 66; AGC- 61; CMGC- 61;
STE- 45; TKL- 37; CK1- 11; Other- 63

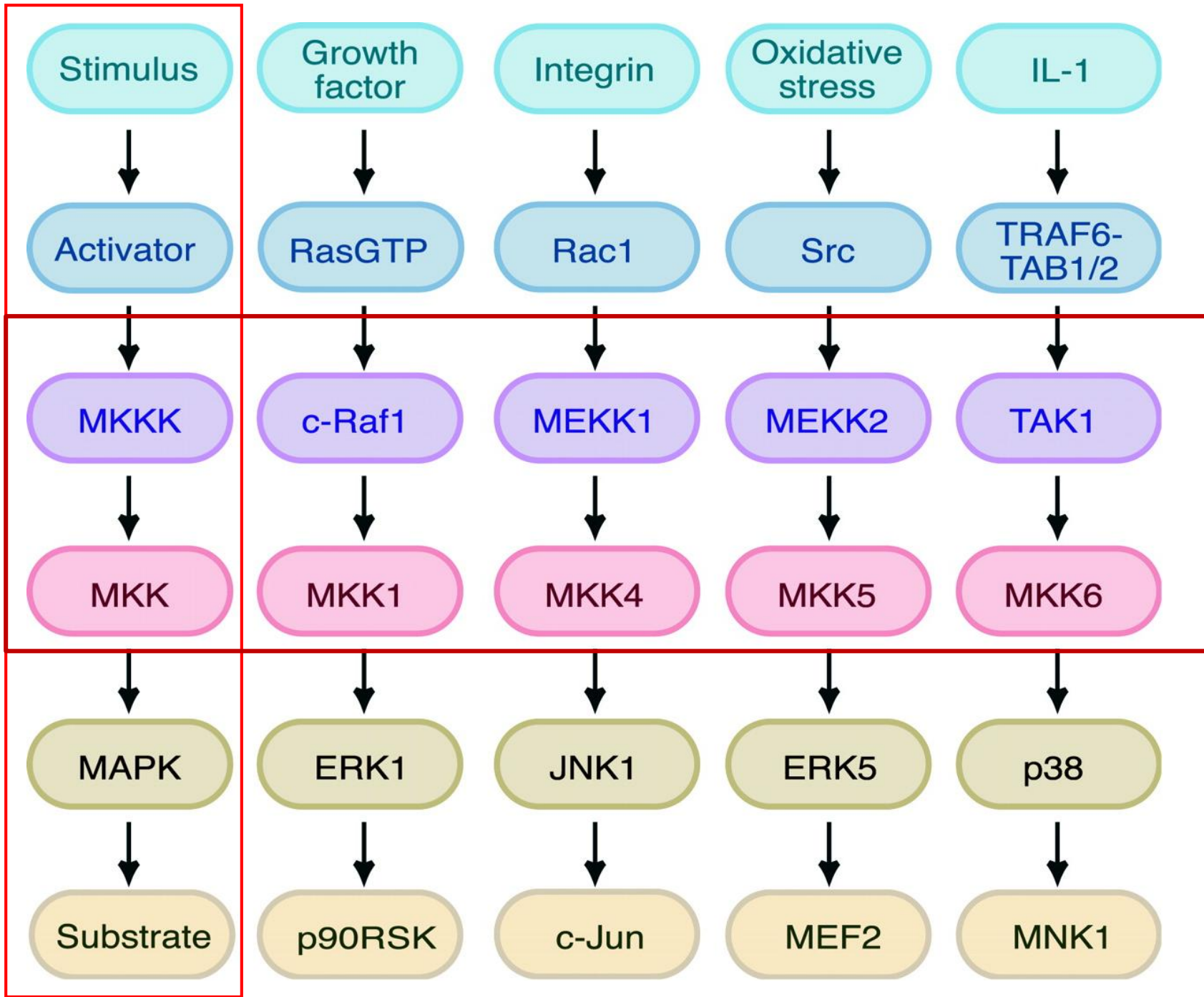
The human kinome tree:
 clustering by sequence
 similarity in the kinase
 domain led to identification
 of different subfamilies
 (incl. 60 receptor kinases)



STE group (yeast **ST**erile mutants-related kinases) and TKL (“tyrosine-kinase like”) group



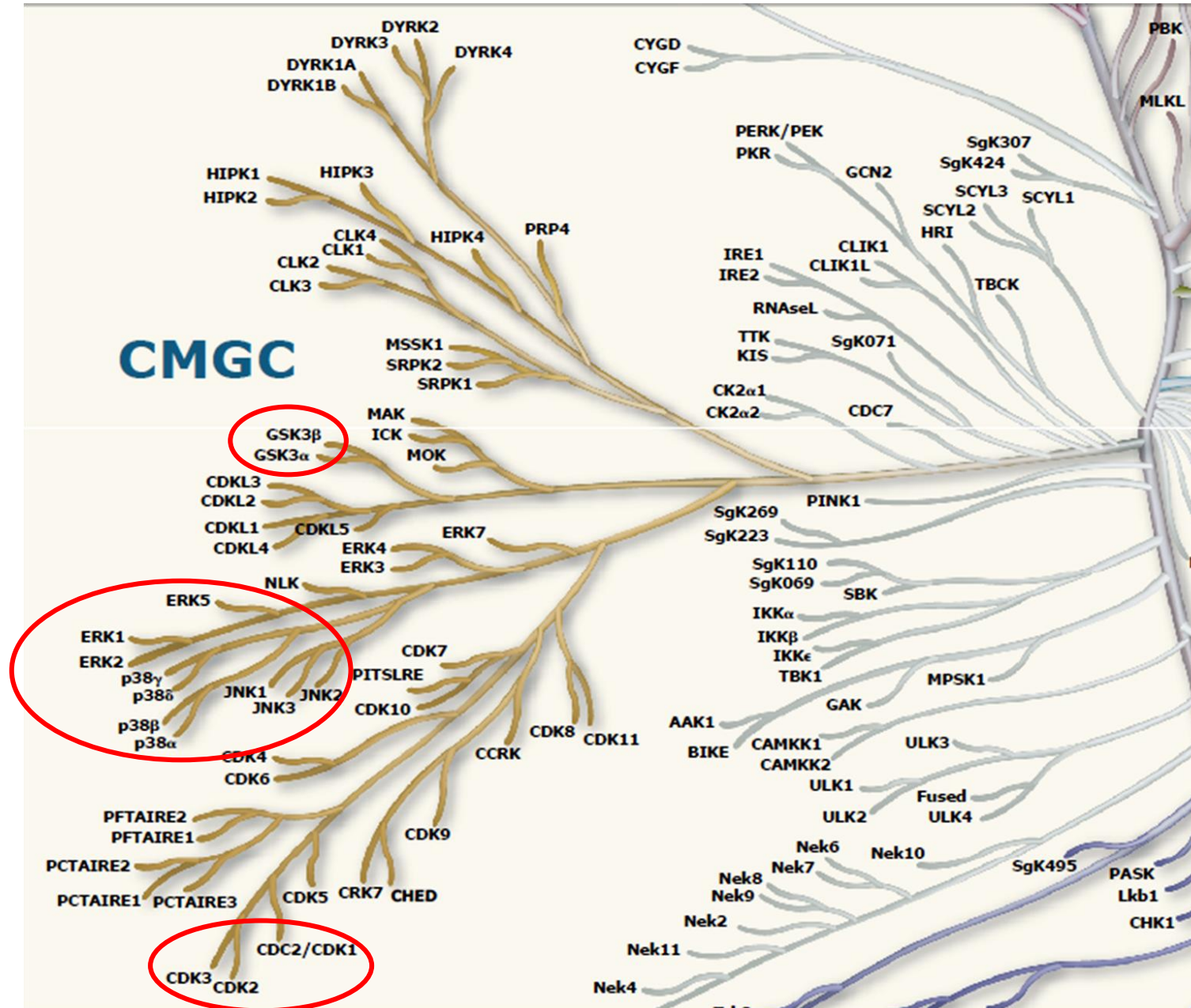
MAPK group members



Four
MAP
kinase
cascades
exist

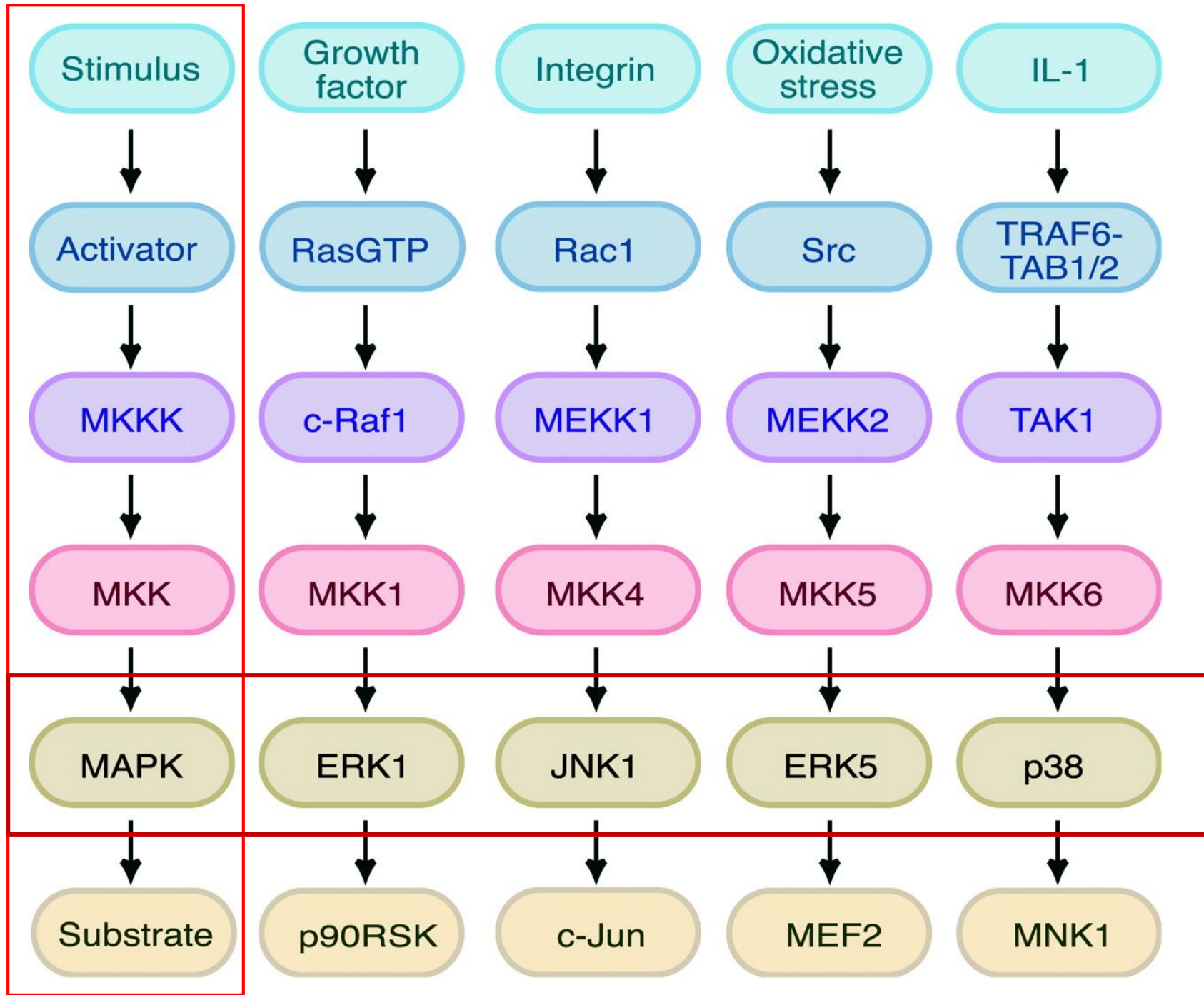
STE group

CMGC group, including the CDK, MAPK, GSK3



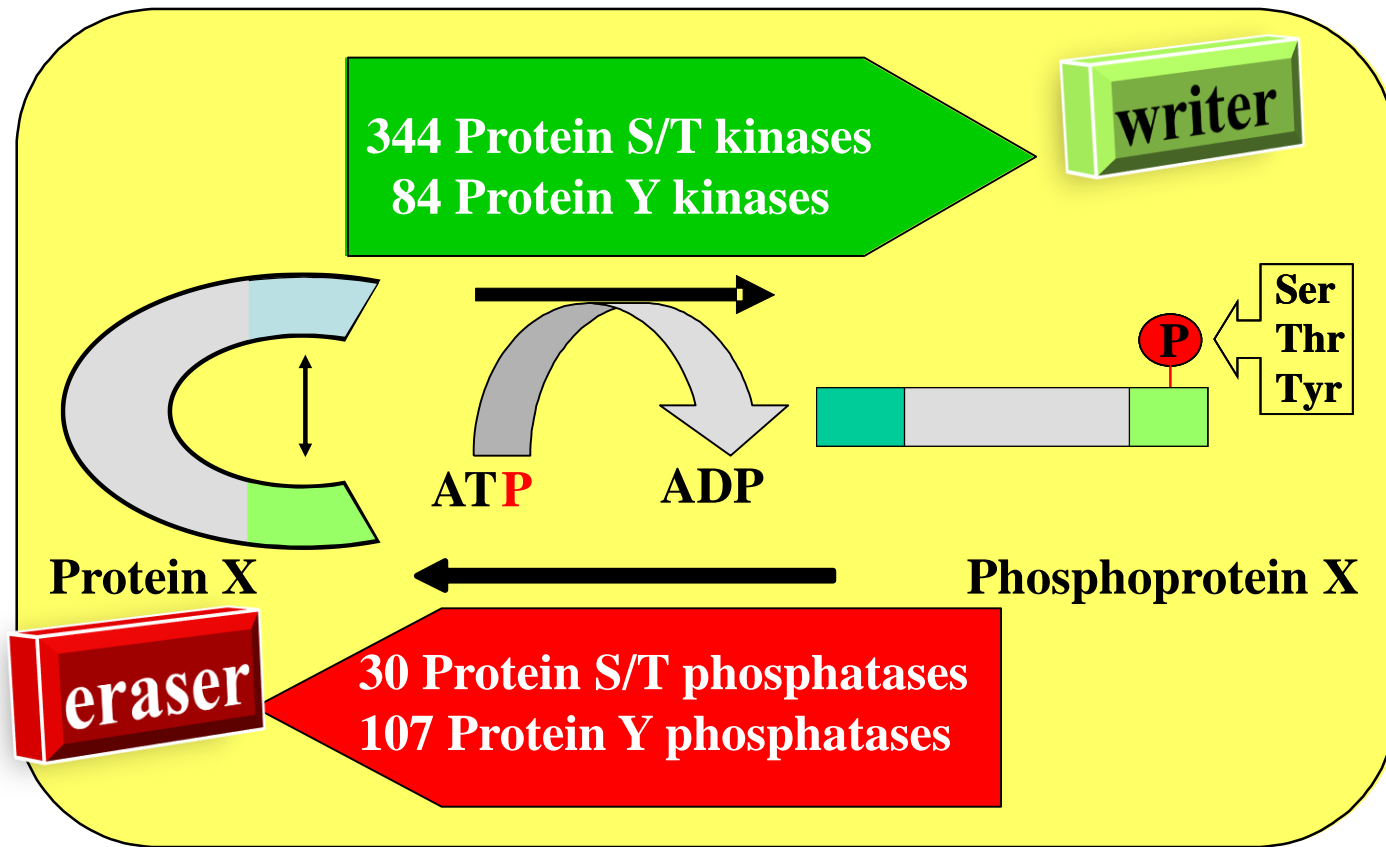
Cyclin-dependent kinases

ERK



Four
MAP
kinase
cascades
exist

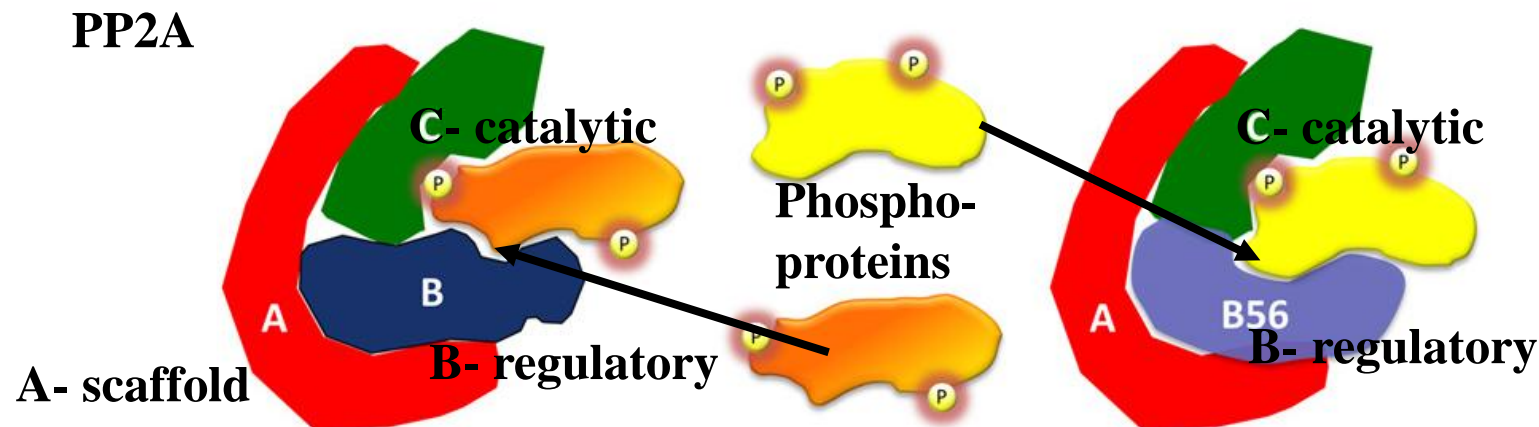
CMGC group



PTPs have high specificity for their phospho-protein.

PSTPs exhibit low intrinsic sequence specificity.

Specific substrate recognition mediated by regulatory subunits

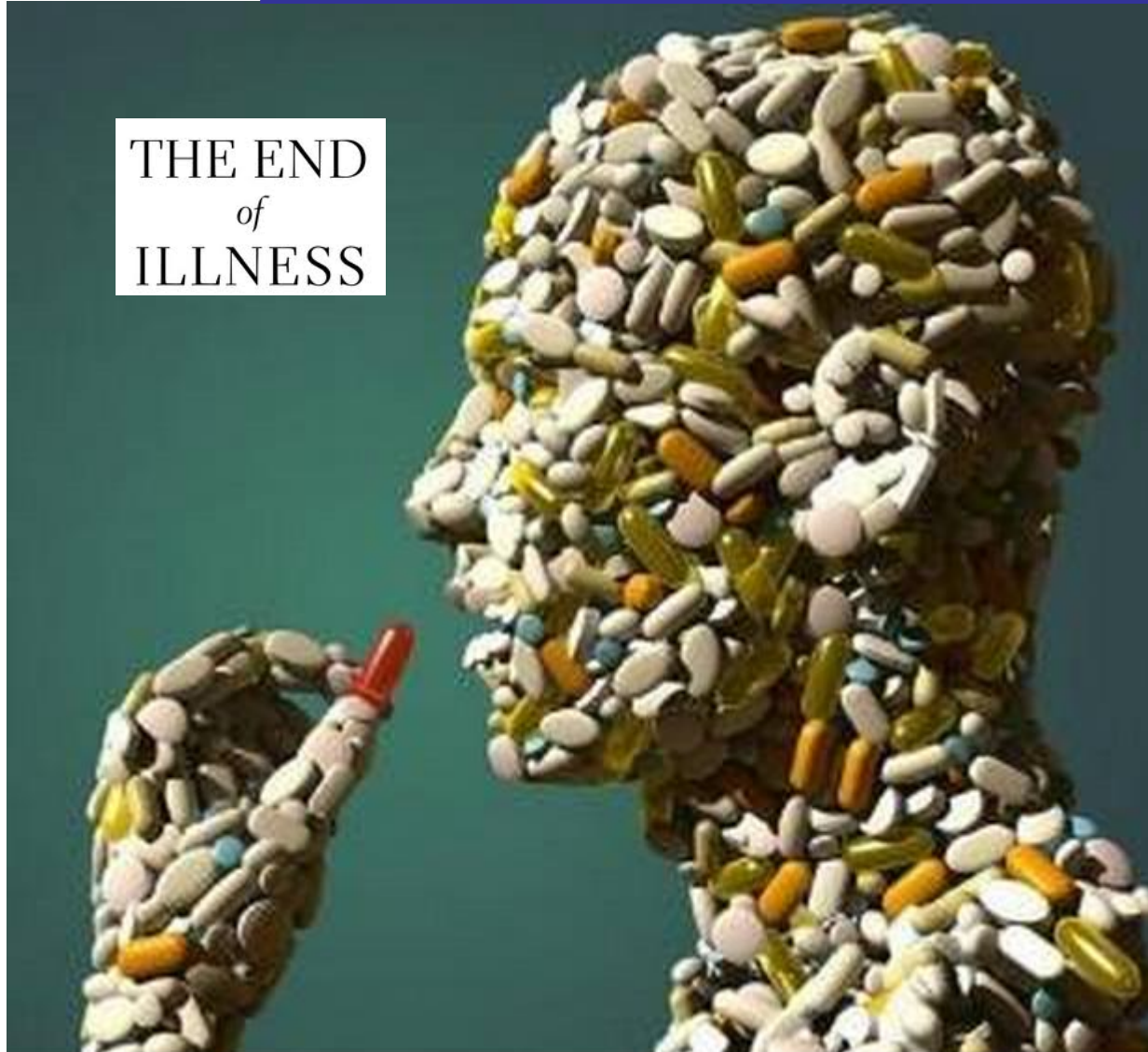


S/T phosphatases are hetero-oligomers of 2 subunits:

- one catalytic (few genes)
- one substrate-specific regulatory (many genes)

Signal Transduction Therapy

Protein kinase inhibition for disease therapy

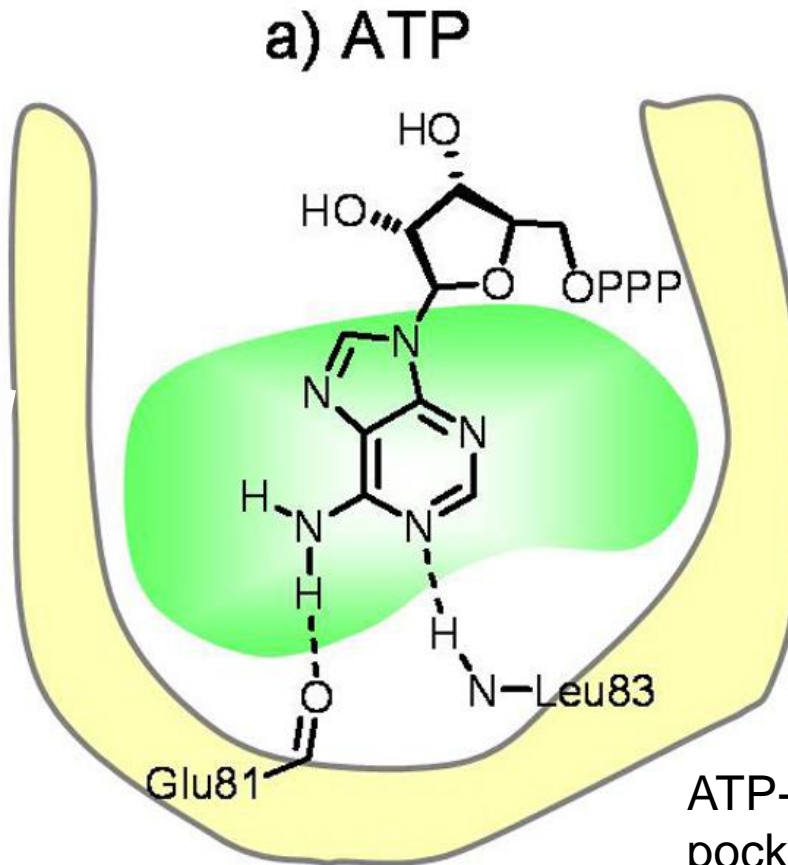
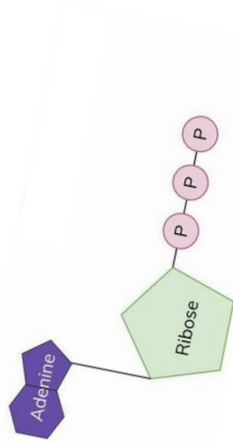
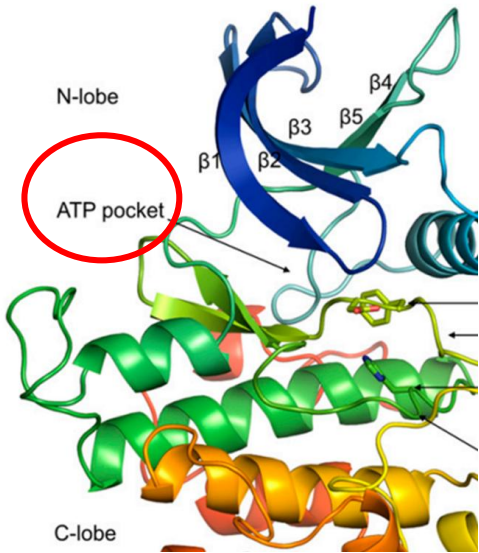


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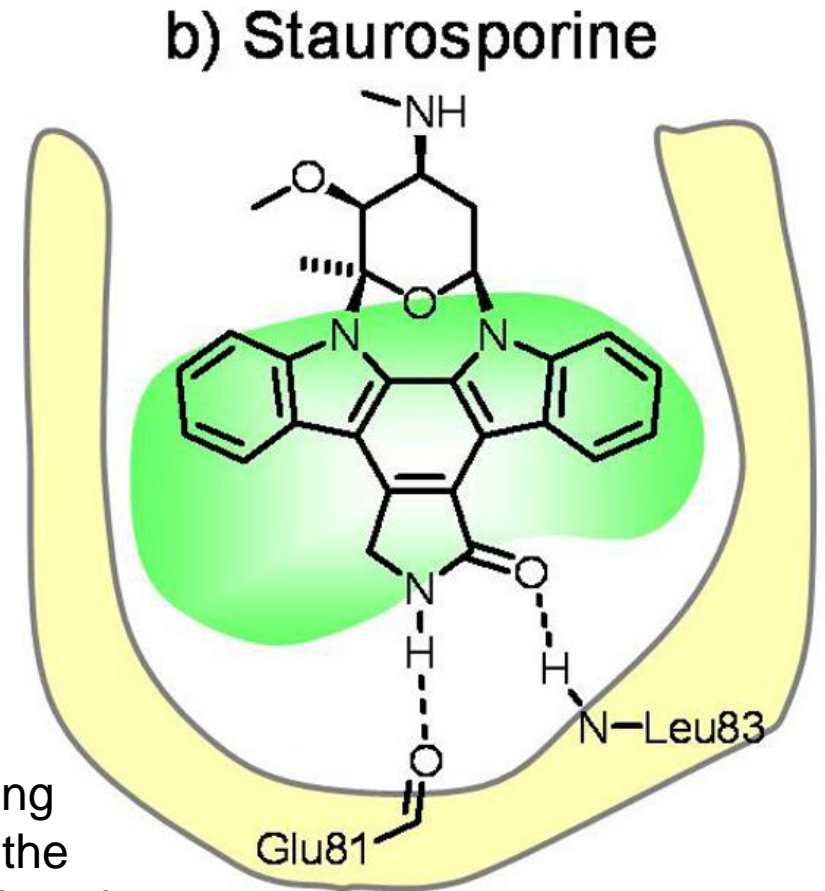
Fast growing list of inhibitors

- ~80 FDA-approved in 2024;
- ~180 in clinical trials;
- approximately 30% of current R&D budget spend in pharmaceutical companies;
- only about 10% of kinases have been studied in detail

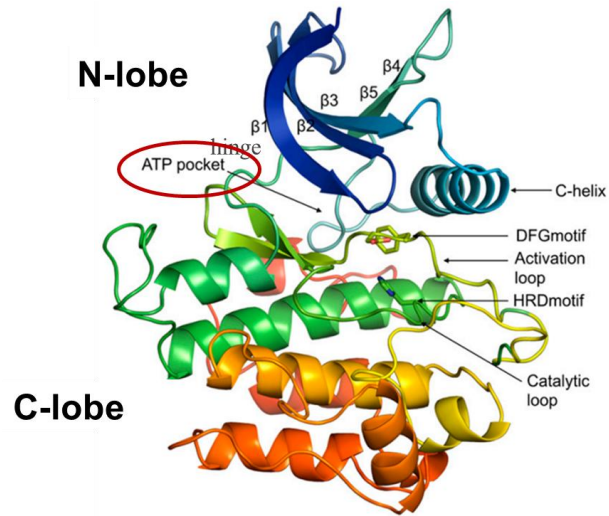
General protein kinase inhibition by ATP-competitive compounds



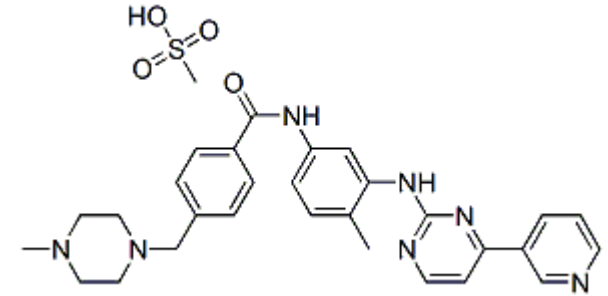
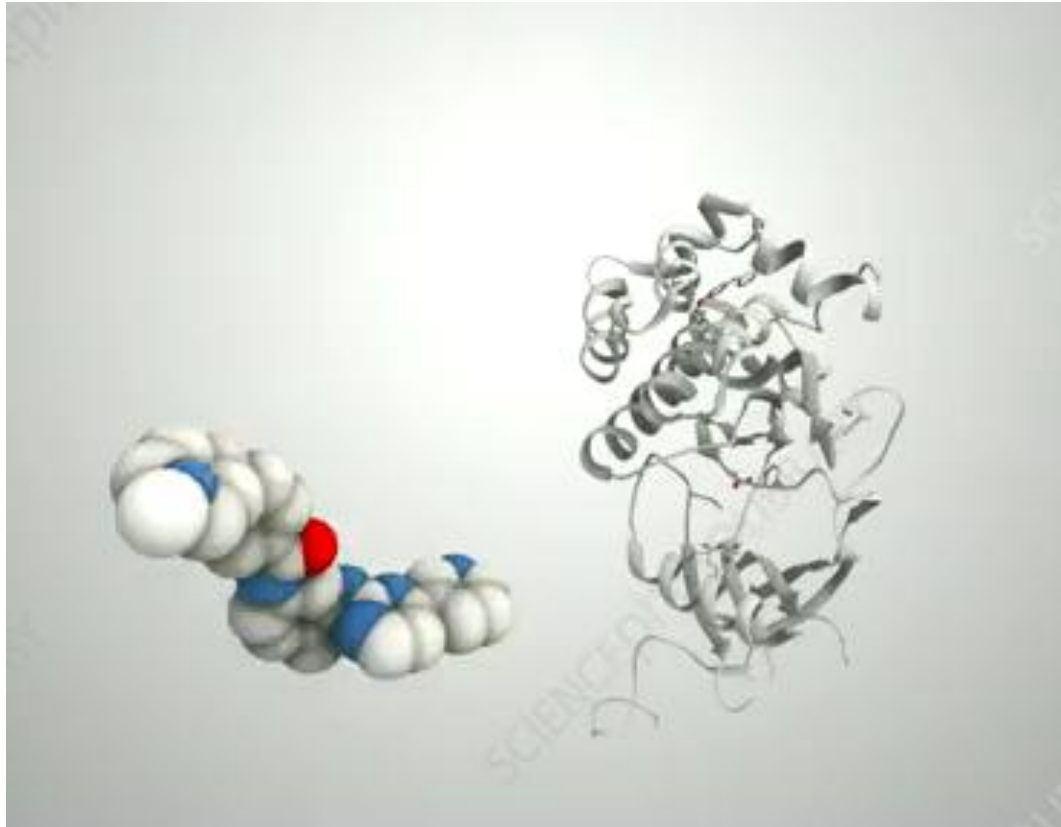
ATP-binding
pocket of the
catalytic domain



Therapies based on signaling inhibitors



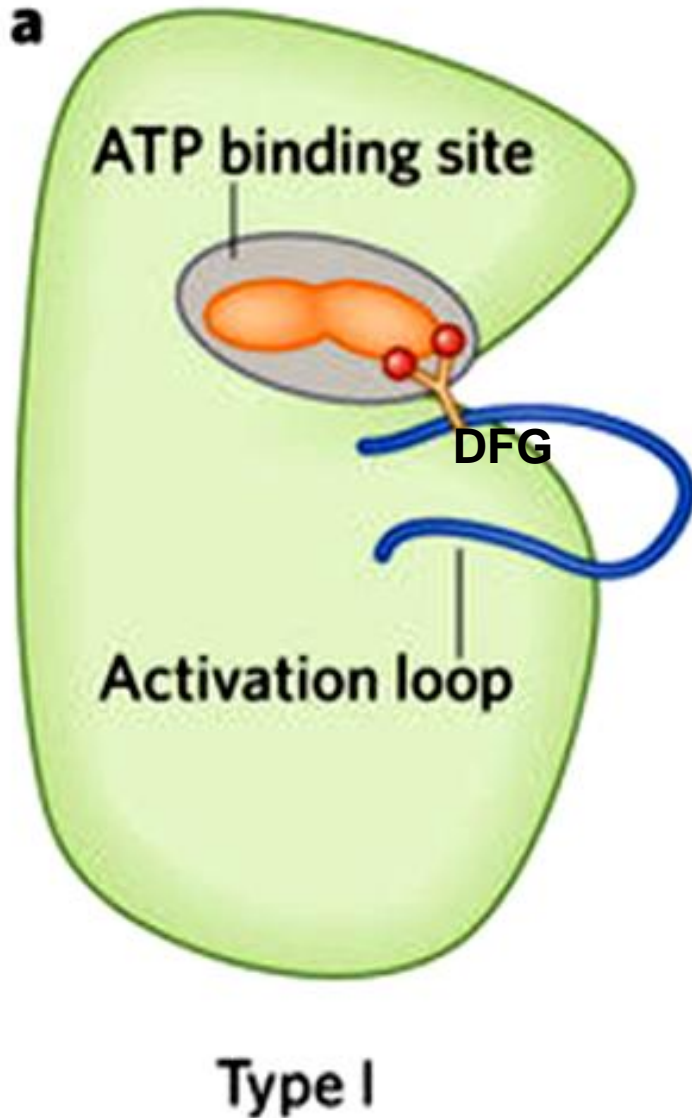
Inhibitor binds to the ATP binding site



Imatinib or STI-571 or Gleevec

Imatinib
Published in 1996
Clinical trials 1998
FDA approval in 2001.

for the treatment of Chronic myeloid leukemia with constitutively active ABL
(due to BCR-ABL fusion gene resulting from translocation t(9;22)(q34;q11))



(a) Type I inhibitors (orange)

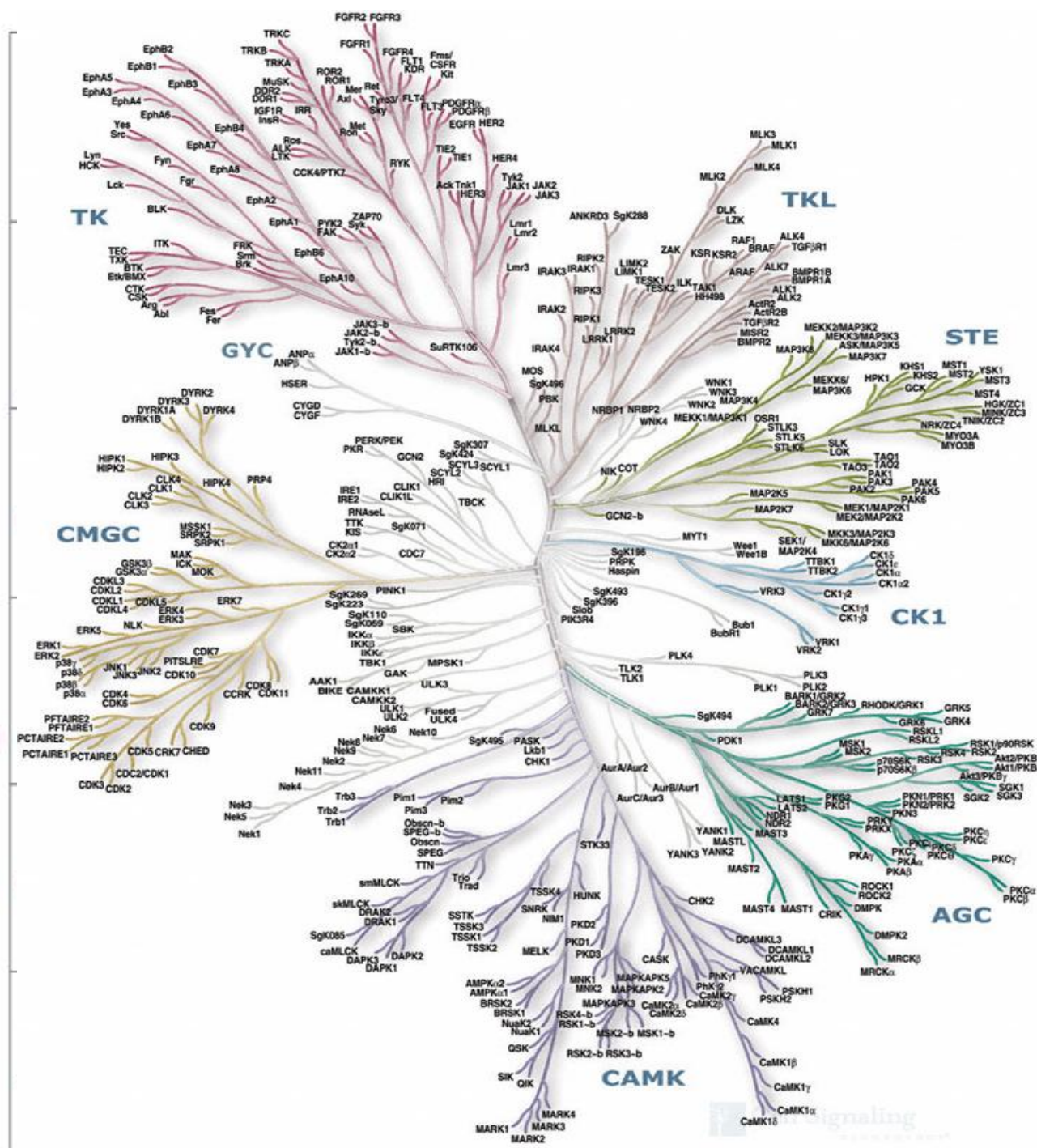
bind the ATP binding site (gray) of the protein kinase domain (green).

‘DFG in’ conformation:

(aspartate side chain in the conserved DFG motif at the beginning of the activation loop (blue) faces into the active site).

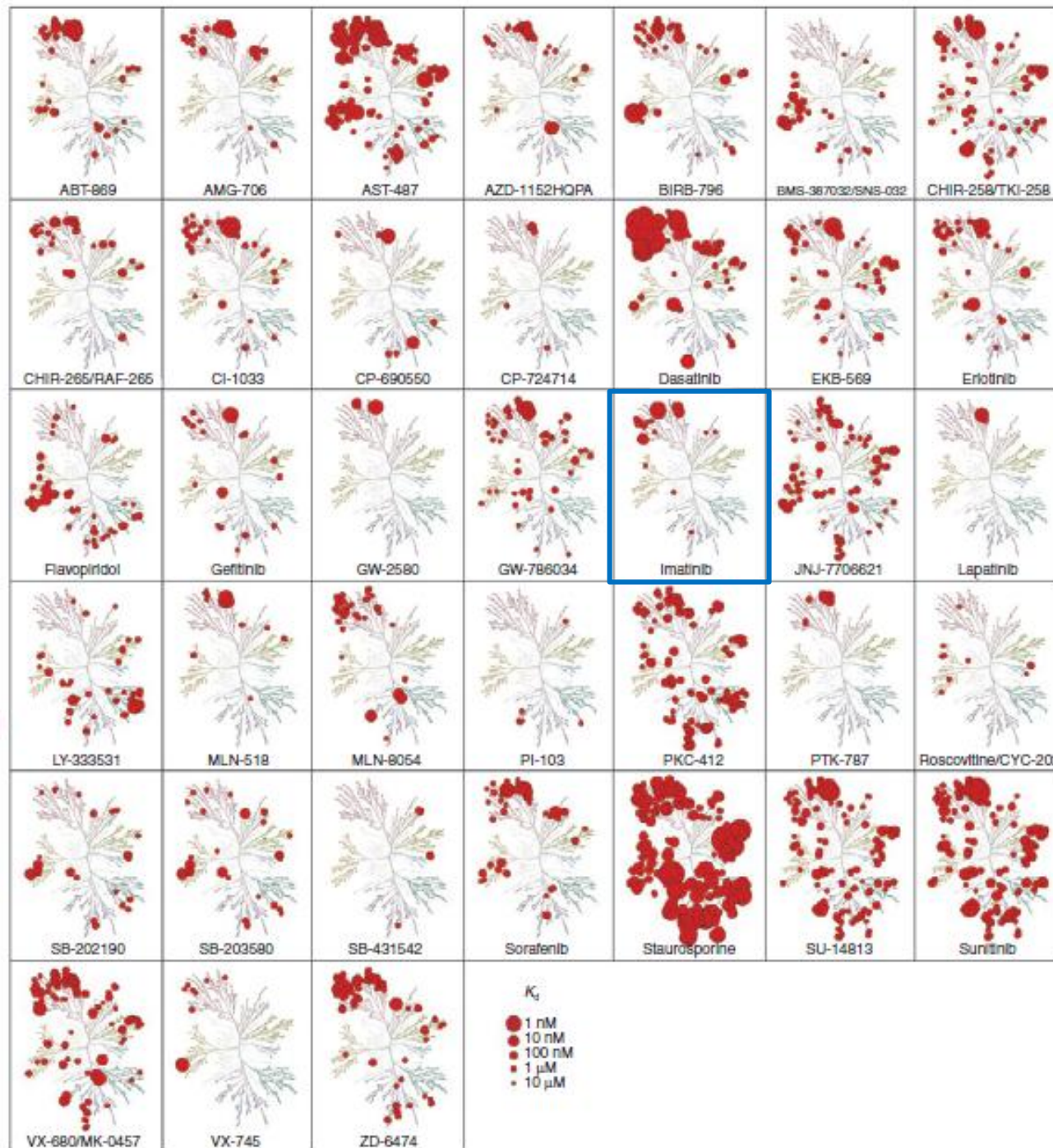
At present, the majority of clinical and preclinical kinase inhibitors are ATP-competitive

Most ATP binding-site inhibitors
have issues



Selectivity of protein kinase inhibitors

NATURE BIOTECH 26 (2008)
 Measured in *in vitro* protein kinase assays



Selectivity of protein kinase inhibitors

NATURE BIOTECH 26
(2008)

Measured in *in vitro* protein kinase assays

In rare cases, lack of selectivity may be of clinical advantage if

Example 1: the compound may be effective in more than one cancer type

In rare cases, lack of selectivity may be of clinical advantage if

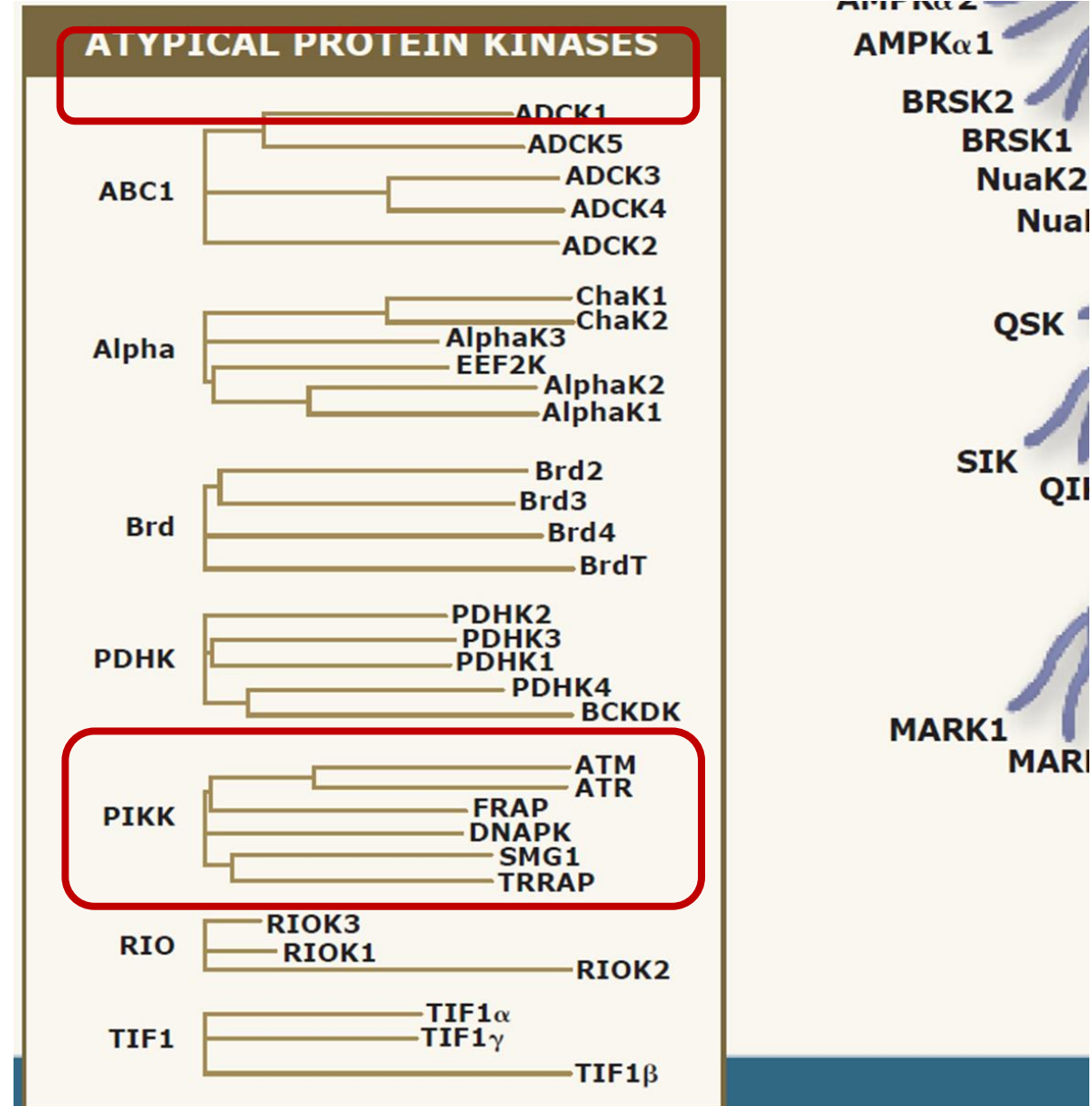
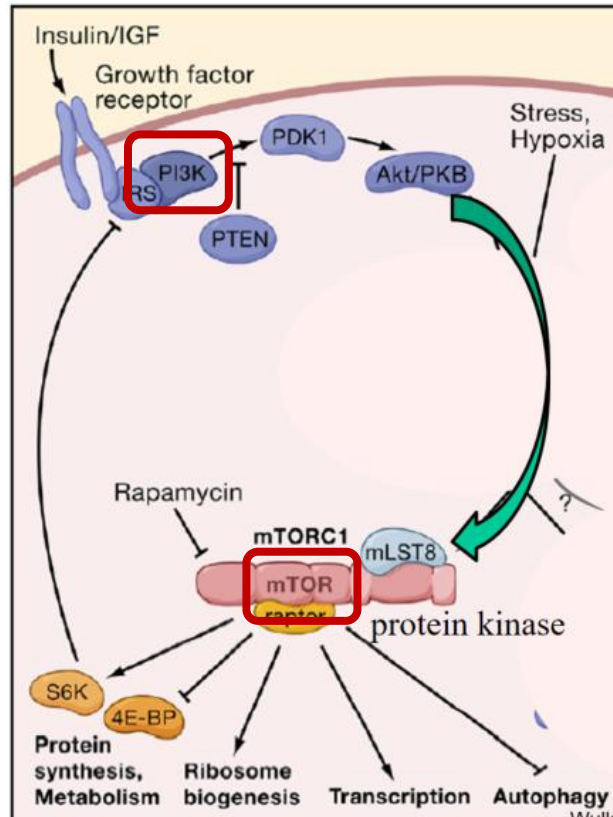
Example 1: the compound may be effective in more than one cancer type

Example 2: the compound inhibits several different kinases in the same signalling cascade (reduces likelihood to develop therapy resistance)

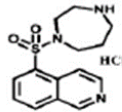
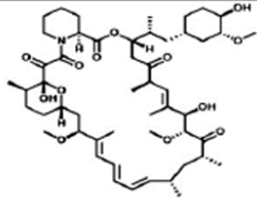
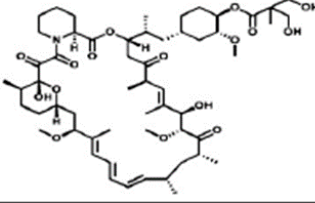
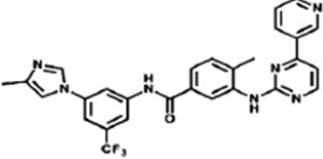
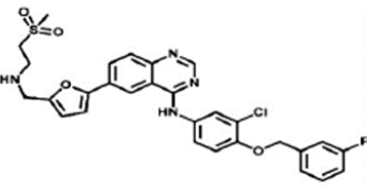
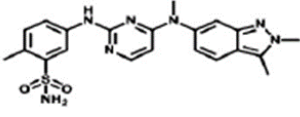
Example 2: dual PI3K/mTOR inhibitors

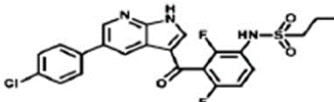
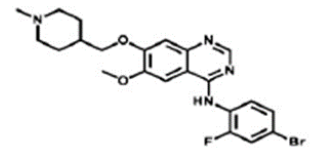
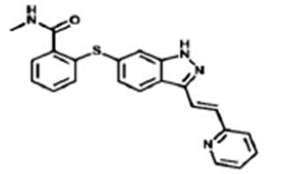
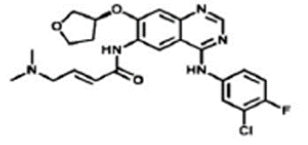
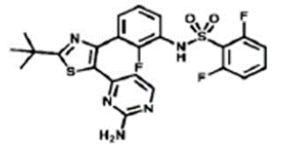
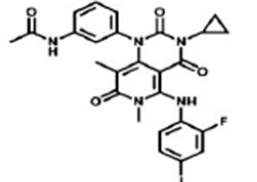
(bind to the ATP-binding cleft of PI3K and mTOR kinase)

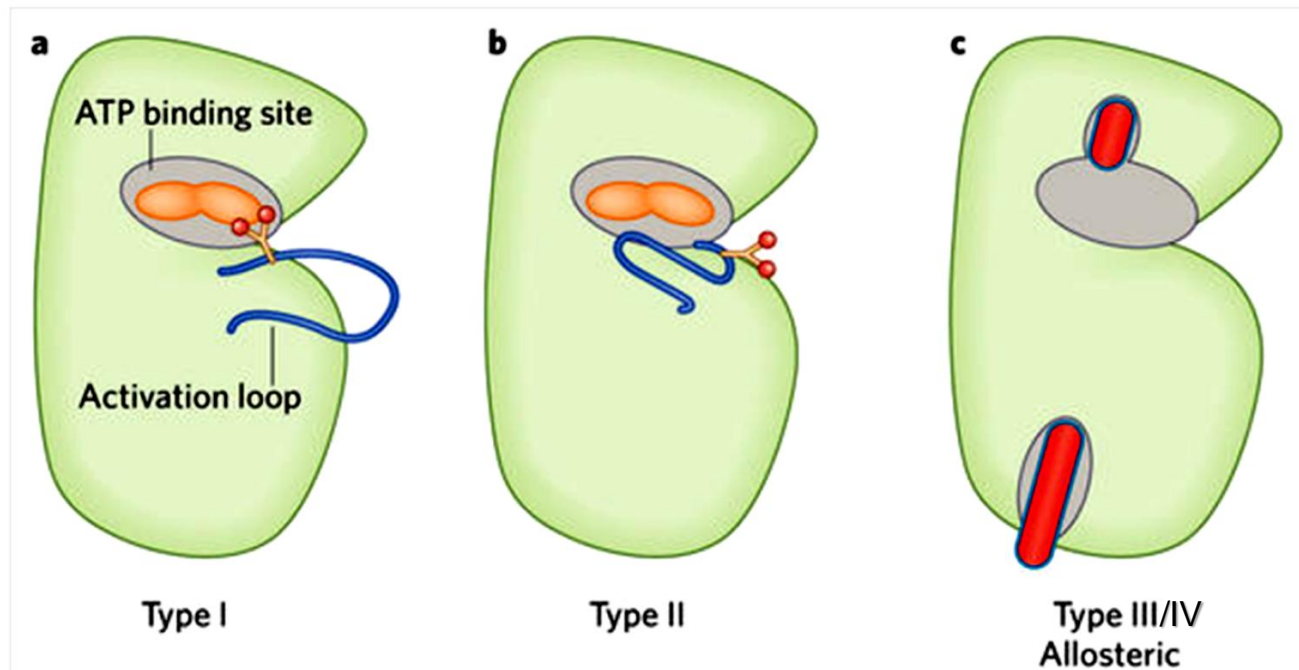
mTOR (FRAP) shares high sequence similarity in its catalytic domain with PI3K and belongs to a family of PI3K-like kinases (PIKK)



Some structural examples of approved PK inhibitors

Name	Structure	Reported target	Company	Approved for clinical use
Eril		ROCK	Eisai	1995 cerebral vasospasm (Japan)
Rapamune		mTOR	Wyeth Pfizer	2000 kidney transplantation
Temsirolimus		mTOR	Wyeth Pfizer	2007 advanced renal cell carcinoma
Nilotinib		Bcr-Abl	Novartis	2007 chronic myelogenous leukaemia
Lapatinib		Her2 EGFR	GlaxoSmith Kline	2009 renal cancer
Pazopanib		VEGFR2 PDGFR c-KIT	GlaxoSmith Kline	2009 renal cancer

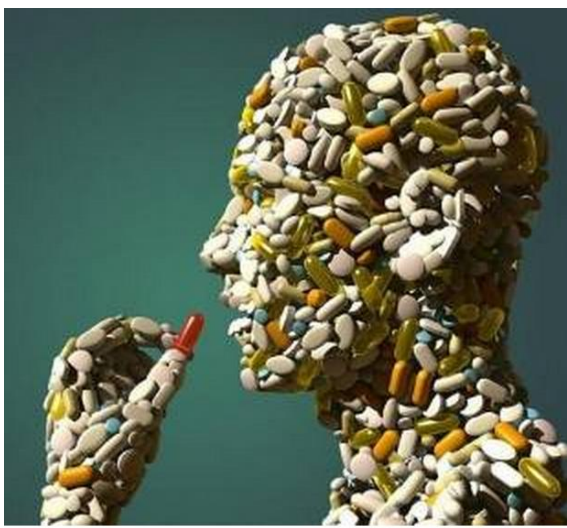
Name	Structure	Reported target	Company	Approved for clinical use
Vemurafenib		BRAF	Roche	2011 melanoma
Vadetinib		Multiple Tyrosine kinases targeted	Caprelsa IPR Pharms	2012 thyroid cancer
Axitinib		VEGFRs PDGFRB c-KIT	Pfizer	2012 renal cell carcinoma
Afatinib		Her2 EGFR	Boehringer Ingelheim	Not yet NSCLC
Dabrafenib		BRaf	GlaxoSmith Kline	Not yet metastatic melanoma
Trametinib		MEK1/2	GlaxoSmith Kline	Not yet metastatic melanoma



(a) Type I inhibitors (orange) bind the ATP binding site (gray) of the protein kinase domain (green). The aspartate side chain in the conserved DFG motif at the beginning of the activation loop (blue) faces into the active site ('DFG in').

(b) Type II inhibitors stabilize a flipped inactive conformation of the DFG motif in which the aspartate side chain faces outwards ('DFG out').

(c) Allosteric ligands (red) bind to binding pockets that do not overlap with the active site of the kinase. These binding pockets can be adjacent to or distant from the active site



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Therapeutic obstacles

- Thorough characterization of the molecular pathways is required
- **Side-effects due to** a requirement of the targeted kinase or signalling molecule in other physiologically important functions
- **Off-target effects of inhibitors** (on other PKs or ATP-binding proteins) due to lack of specificity
- **Emergence of resistance** (e.g. through mutations that allow the protein to escape the inhibitor action)

How to study and measure protein kinase activity?

***In vitro* protein kinase assays for inhibitor development**

**Screen chemical compounds in an *in vitro* assay
measuring the activity of a specific PK**

**Profiling of an identified compound against ~200 other
PKs in *in vitro* assays**



Selectivity of protein kinase inhibitors

NATURE BIOTECH 26
(2008)

Measured in *in vitro* protein kinase assays

1. In vitro protein kinase assays to measure activity

Assay component	comment
Buffer	HEPES or TRIS-based, pH 7.5 (why no phosphate buffer ??)
Co-factors	10 mM MgCl ₂ (or MnCl ₂)
ATP	0.1 -0.5 mM
Substrate	Recombinant protein or synthetic peptide
Kinase	Recombinant or immunoprecipitated
Radioactive ATP*	2.5-5 mCi

Incubation: 30-50 μ L volume, 30-37°C, 30 min

* Nowadays detection kits based on colorimetric enzyme assay for ATP consumption

Stop by adding 2x SDS sample buffer; analyze e.g. by SDS-PAGE \pm Western blot

Controls in the protein kinase assays

The problems:

1: Recombinant substrate proteins and protein kinases are usually purified from cell or bacterial lysates, thus, they may not be pure but contain residual amounts of other proteins (kinases or substrates)

2: Some cellular proteins contain ATP binding pockets that will retain radioactive ATP (eg BSA, Hsp90, ABC transporters)

The solutions:

-- Control tube containing a kinase-dead version of the kinase to be tested.

-- Control tube containing only: substrate protein, reaction buffer and radioactive ATP but not the kinase