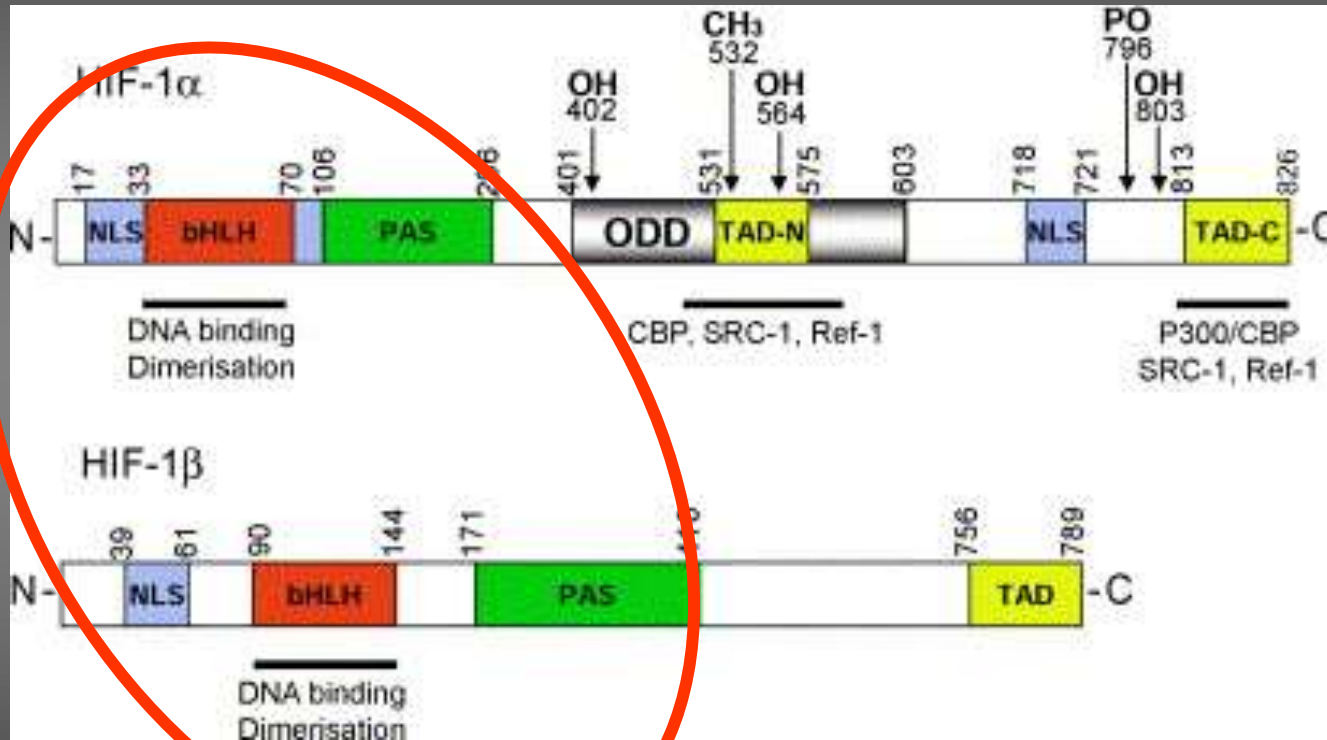


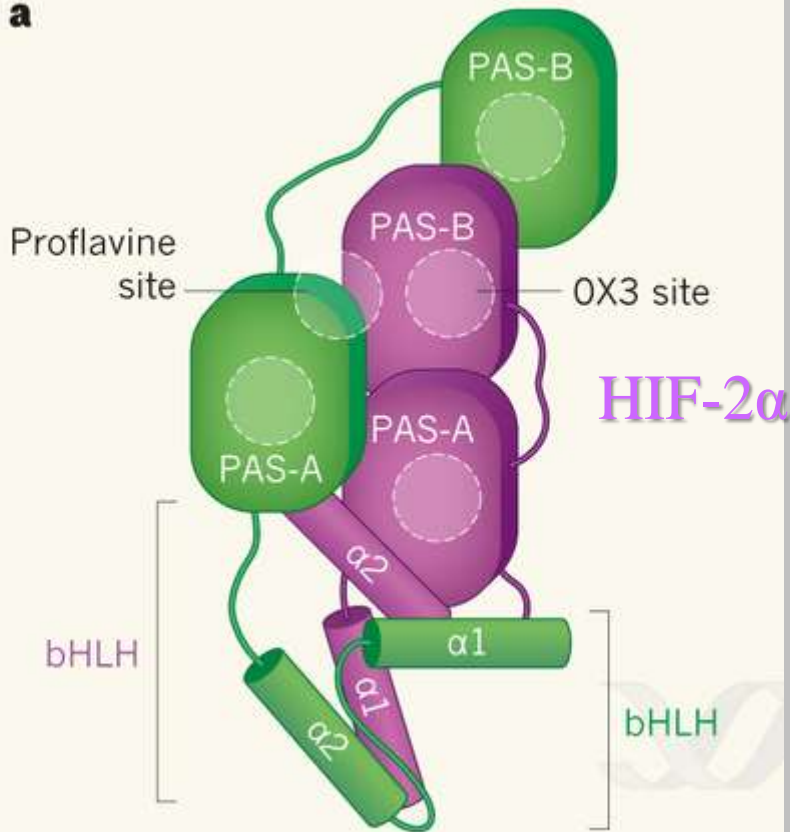
Struttura HIF

Struttura di HIF1 alpha/beta



HIF-2 β (ARNT)

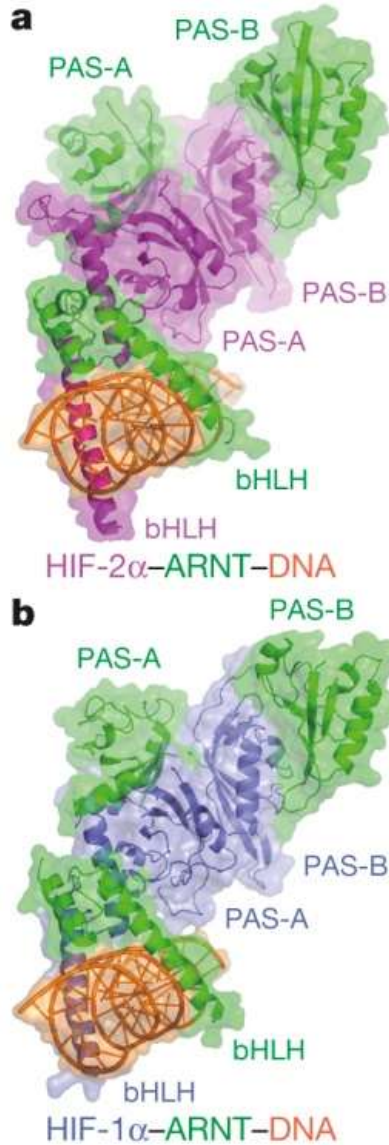
a



PAS, PAS-B (interaction domains)

bHLH (DNA Binding domain)

DNA-bound HIF- α -ARNT structures.

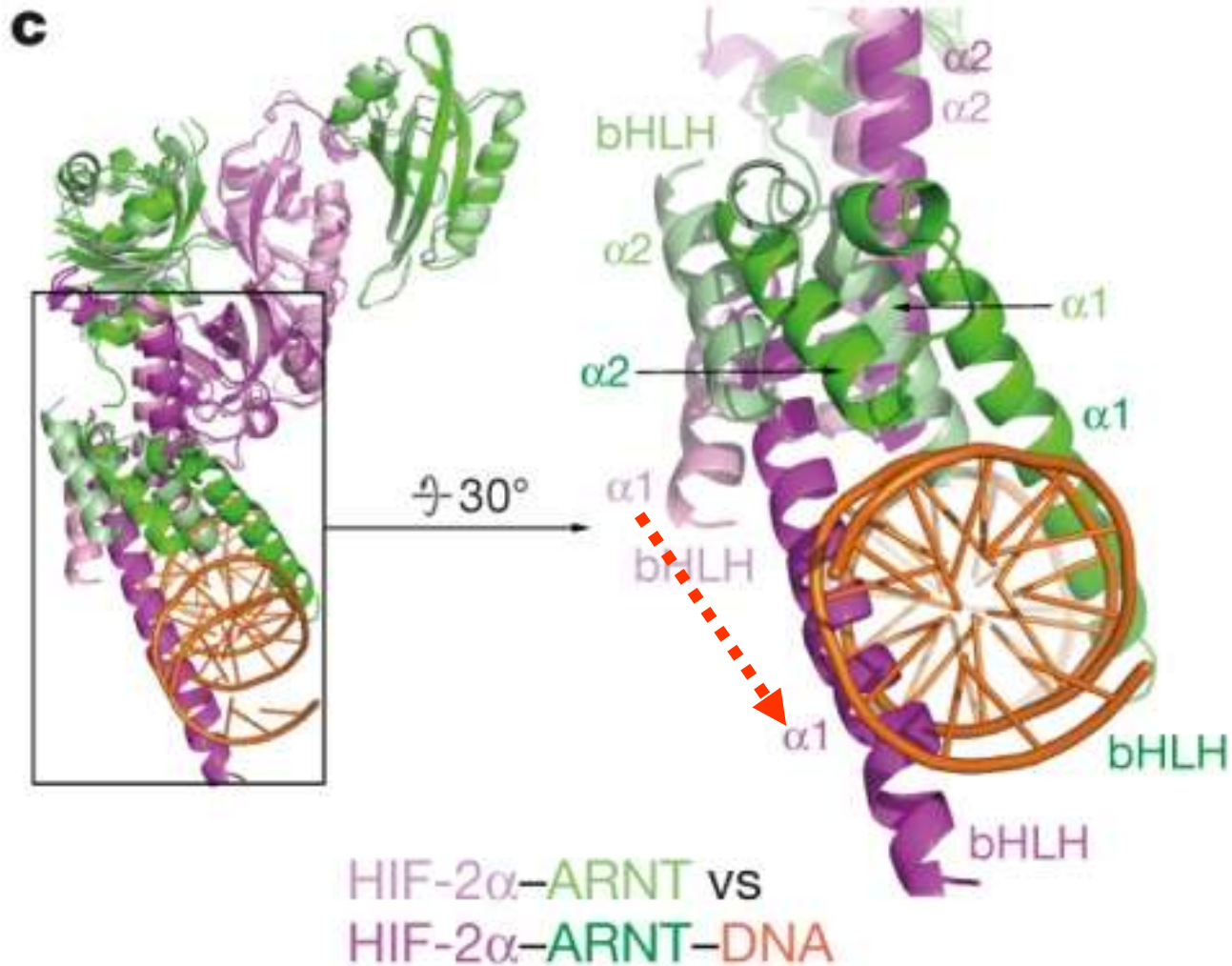


HIF-2 α -ARNT-DNA (a) and

HIF-1 α -ARNT-DNA (b)
complexes

nature

DNA-bound HIF- α -ARNT structures.

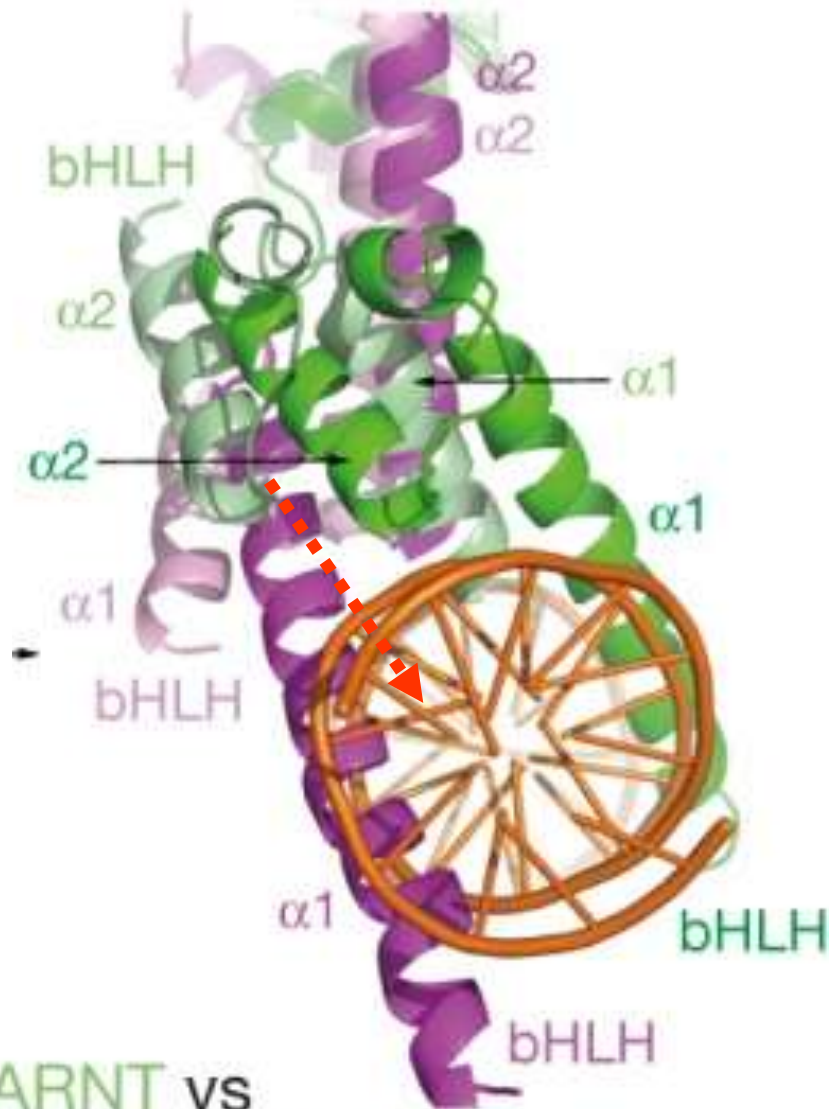


dramatic conformational changes at the bHLH domains

nature

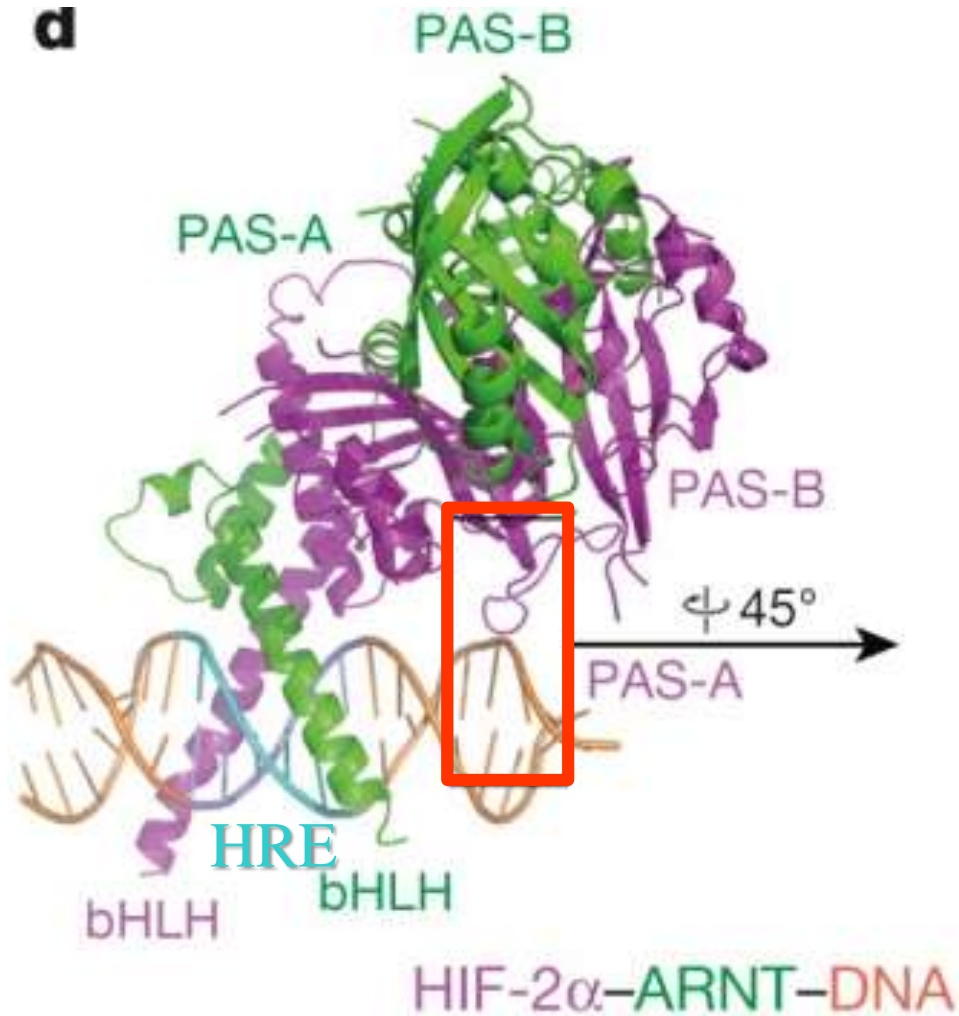
DNA-bound HIF- α -ARNT structures.

dramatic conformational changes at the bHLH domains



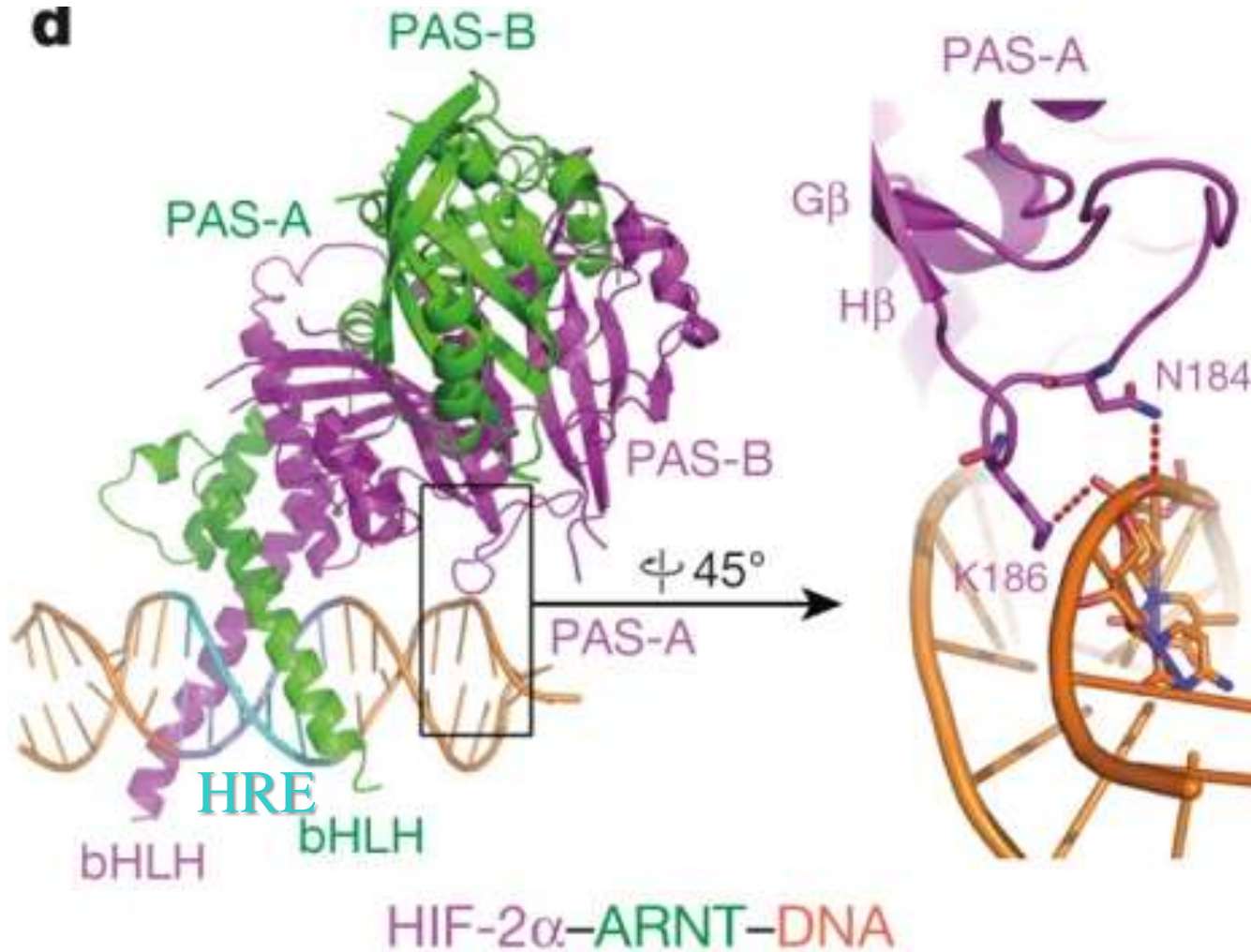
HIF-2 α -ARNT vs
HIF-2 α -ARNT-DNA

DNA (HRE)-bound HIF- α -ARNT structures.



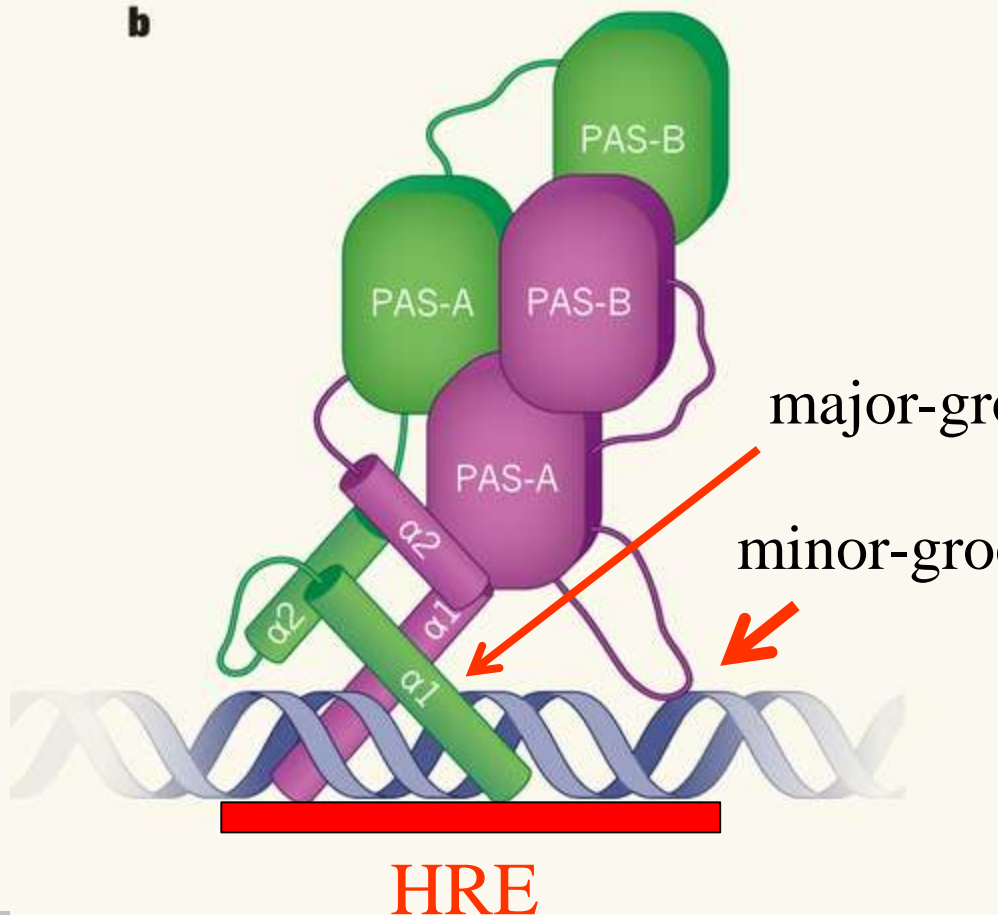
nature

DNA (HRE)-bound HIF- α -ARNT structures.



nature

bHLH (DNA Binding domain)
PAS,PAS-B (interaction domains)



The hypoxia-responsive element (HRE) is a regulatory element mediating transactivation by the hypoxia-inducible factor (HIF).

The data from over 70 genes suggest that endogenous HREs are composite regulatory elements comprising

- a) the conserved HIF-binding site with an **A/GCGTG** core sequence
- b) a **highly variable flanking sequence**.

the flanking sequence provides binding sites for additional transcription factors required to amplify the hypoxic response/
make the HRE tissue-specific

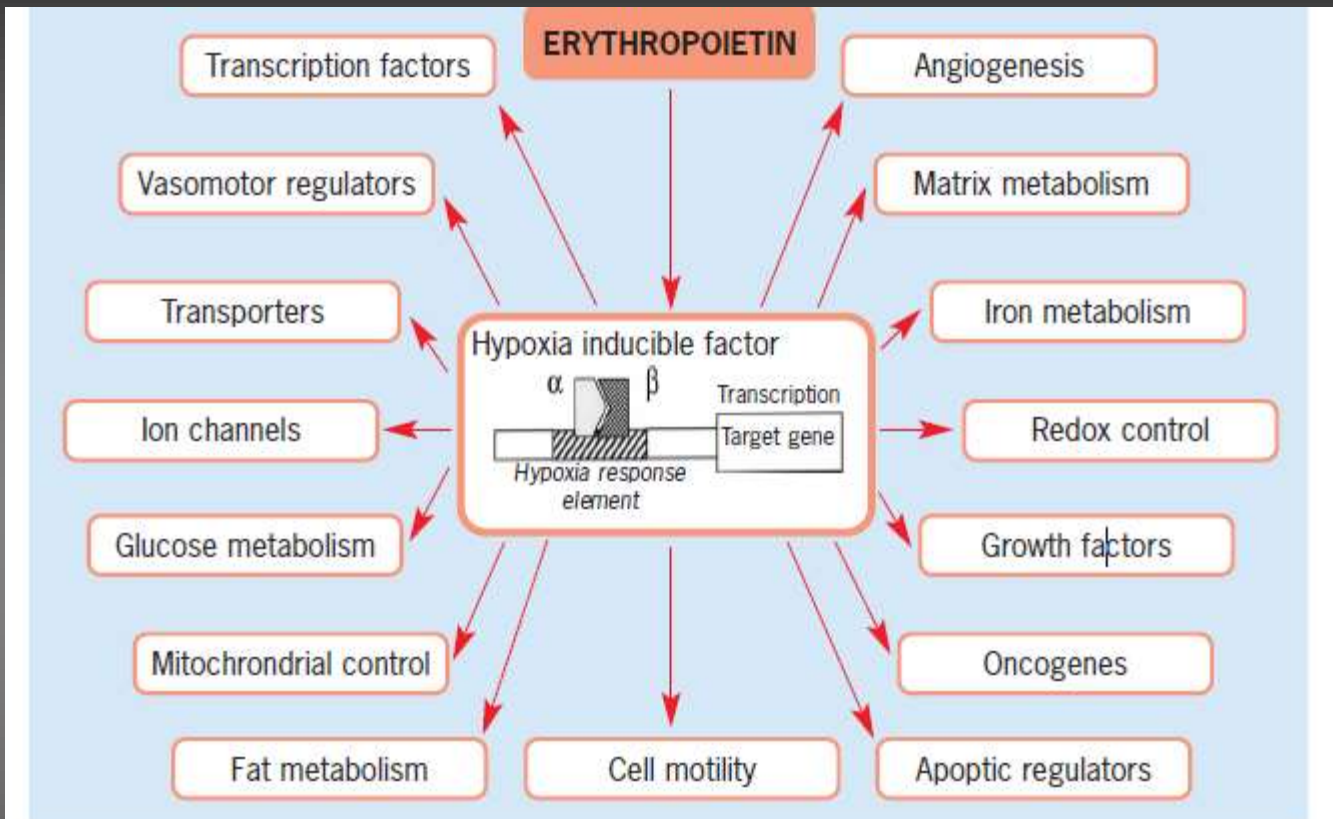
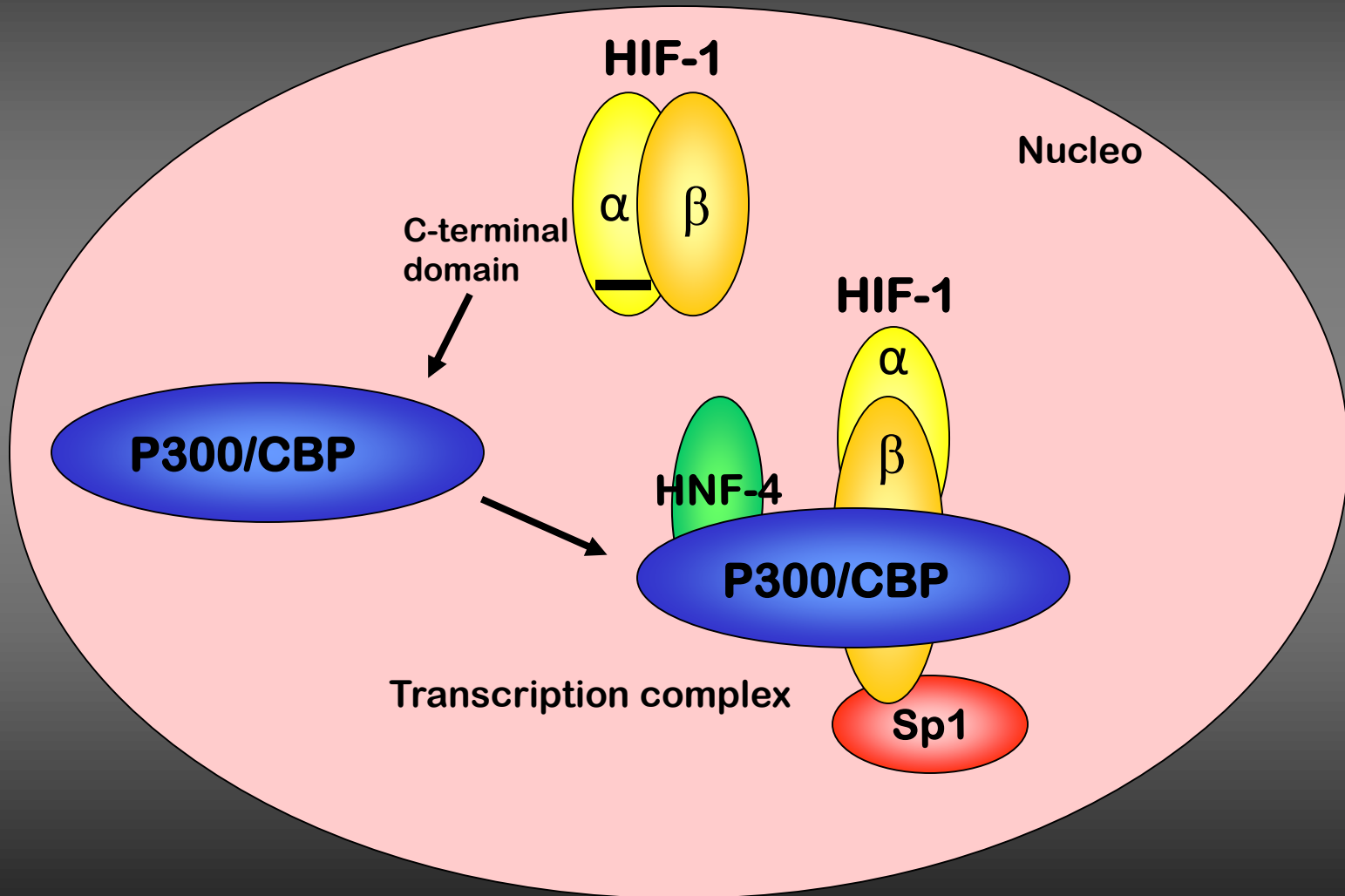


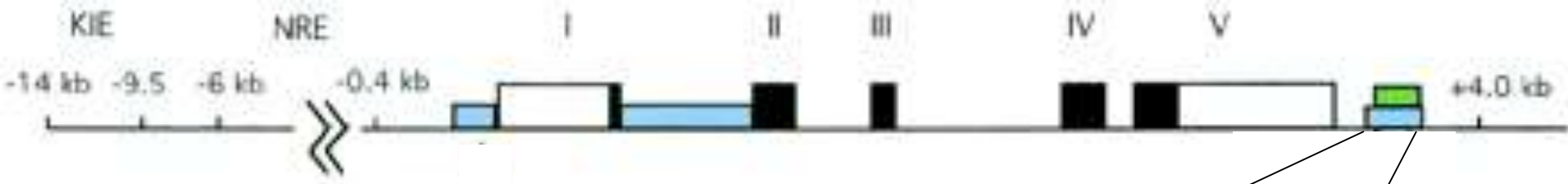
Fig 1. The hypoxia-inducible factor (HIF) transcriptional cascade directly regulates genes with key functions in a broad range of processes. The complex binds in a sequence-specific manner to control elements in DNA, termed hypoxia-response elements, at target gene loci.

**REGOLAZIONE
DELL'ESPRESSIONE
DELL'ERITROPOIETINA
DA PARTE
DELL'IPOSSIA**

Regolazione del gene Epo da parte dell'ipossia

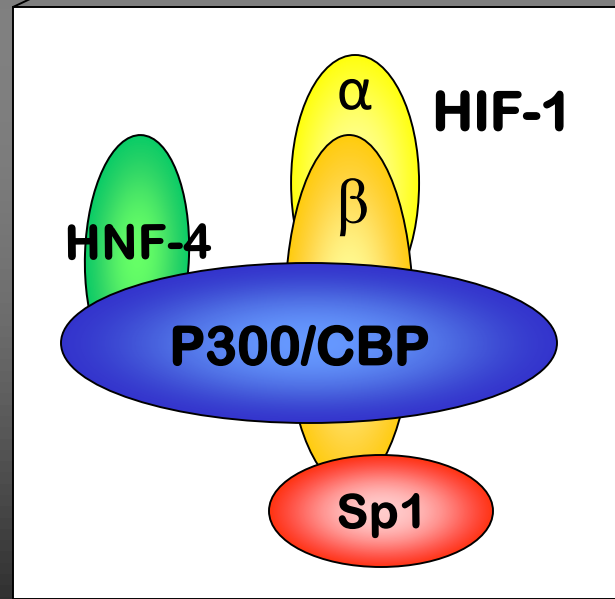


Regolazione del gene Epo da parte dell'ipossia

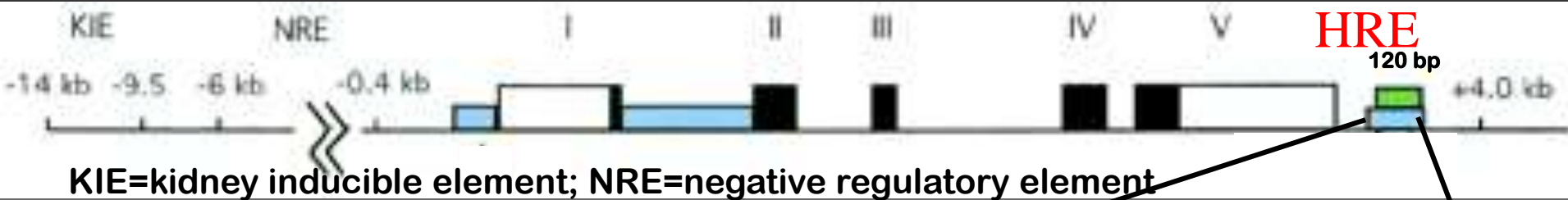


Promotore

Transcription complex



Regolazione del gene Epo da parte dell'ipossia



HNF-4 (Hepatocyte nuclear factor 4) fattore di trascrizione espresso nel cortex renale e nel fegato come Epo → contribuisce alla regolazione tessuto-specifica

50 pb nella Regione 3'

HRE

GGCCCTACGTGCTGTCACACAGCCTGTCCTGACCTCTCGACCTACCG

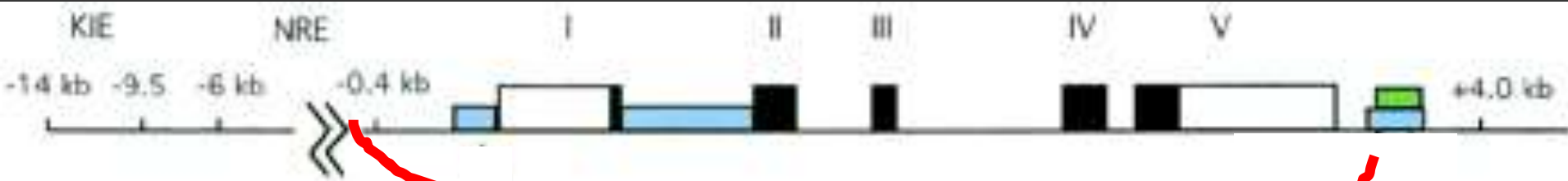
Diagramma delle sequenze di legame per HIF-1 e HNF-4. Tre rettangoli rossi sono sovrapposti alla sequenza di DNA sopra, indicando le regioni di legame per HIF-1 e HNF-4.

Sequenza di legame per *HIF-1*

Sequenza di legame per *HNF-4*

Mutazioni a carico di una di queste sequenze inibiscono l'induzione di Epo da parte dell'ipossia

Regolazione tessuto-specifica del gene Epo



Promotore

Sp1: fattore di trascrizione ubiquitario

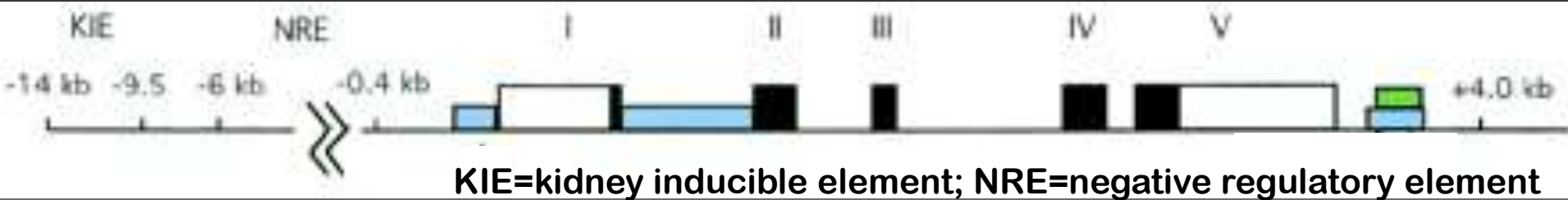
Regione -61 -45: contribuisce alla regolazione da parte dell'ipossia → sequenza di legame per

Sp1

Sito di legame per GATA: inibizione dell'espressione di Epo

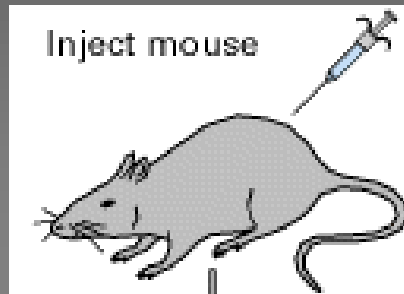
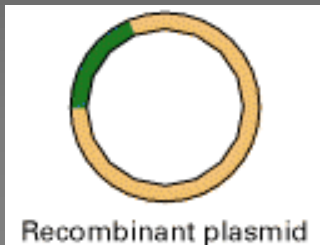
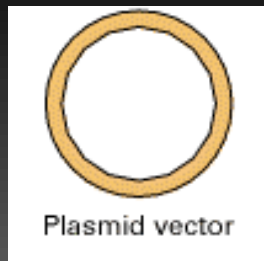
Sito CACCC: sequenza stimolatrice dell'espressione di Epo

Regolazione tessuto-specifica del gene Epo



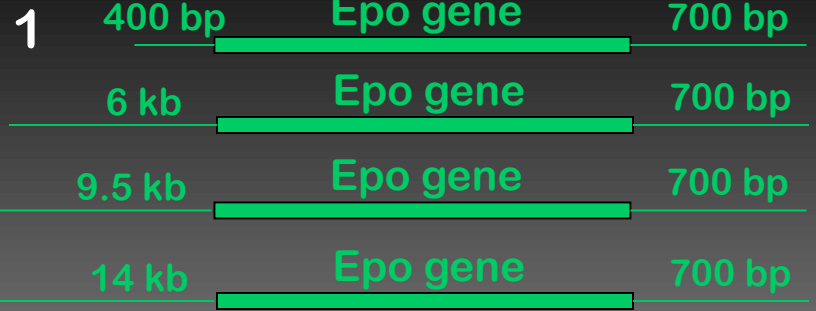
Regione 5'

- 9.5-14 kb → Sequenza richiesta per l'espressione nel rene KIE
- Entro le 9.5 kb → Sequenza richiesta per l'espressione nel fegato
- 0.4-6 kb → Sequenza regolatoria negativa NRE che inibisce l'espressione di Epo nei tessuti che non producono Epo



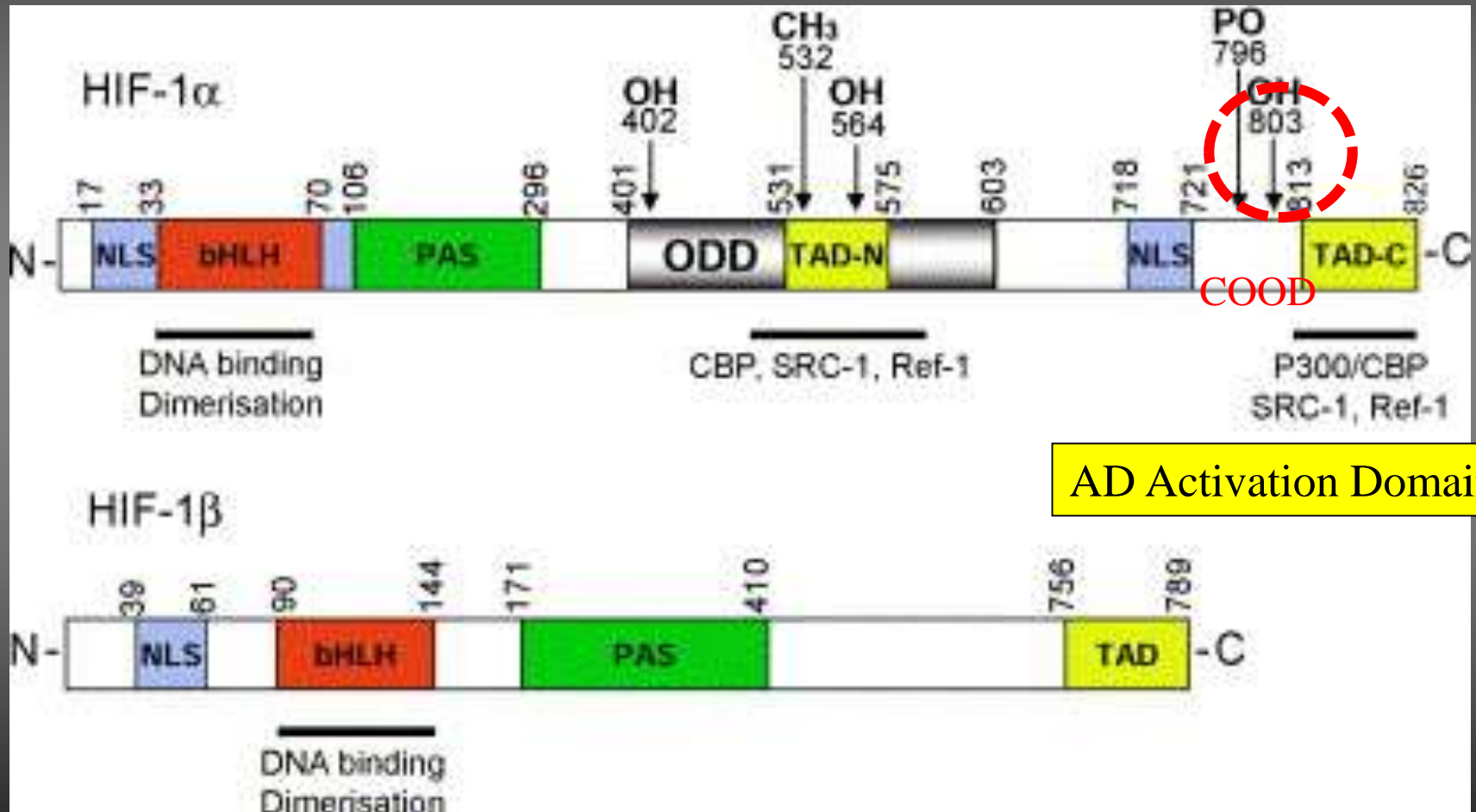
Regione 5'

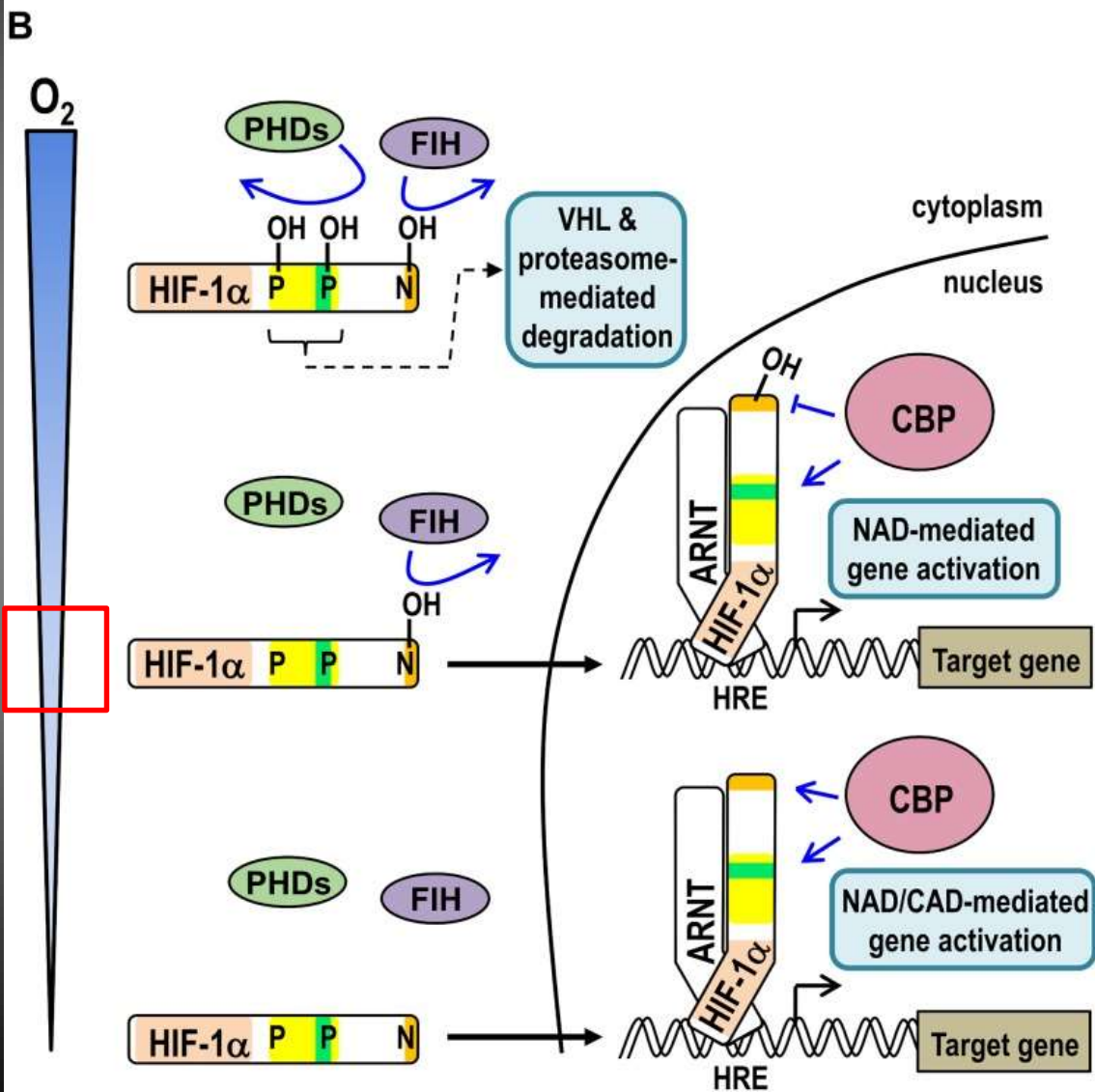
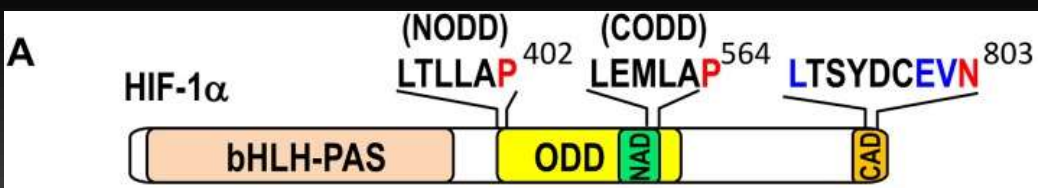
Regione 3'



1. Epo espressa in fegato, rene e tessuti che normalmente non esprimono Epo
2. Epo espresso nel fegato ma non nel rene → 400 bp-6 kb: sequenze regolatorie negative
3. Epo espresso nel fegato ma non nel rene → Entro le 9.5 kb: sequenze per l'espressione nel fegato
4. Epo espresso nel rene → 9.5-14 kb: sequenze per l'espressione nel rene

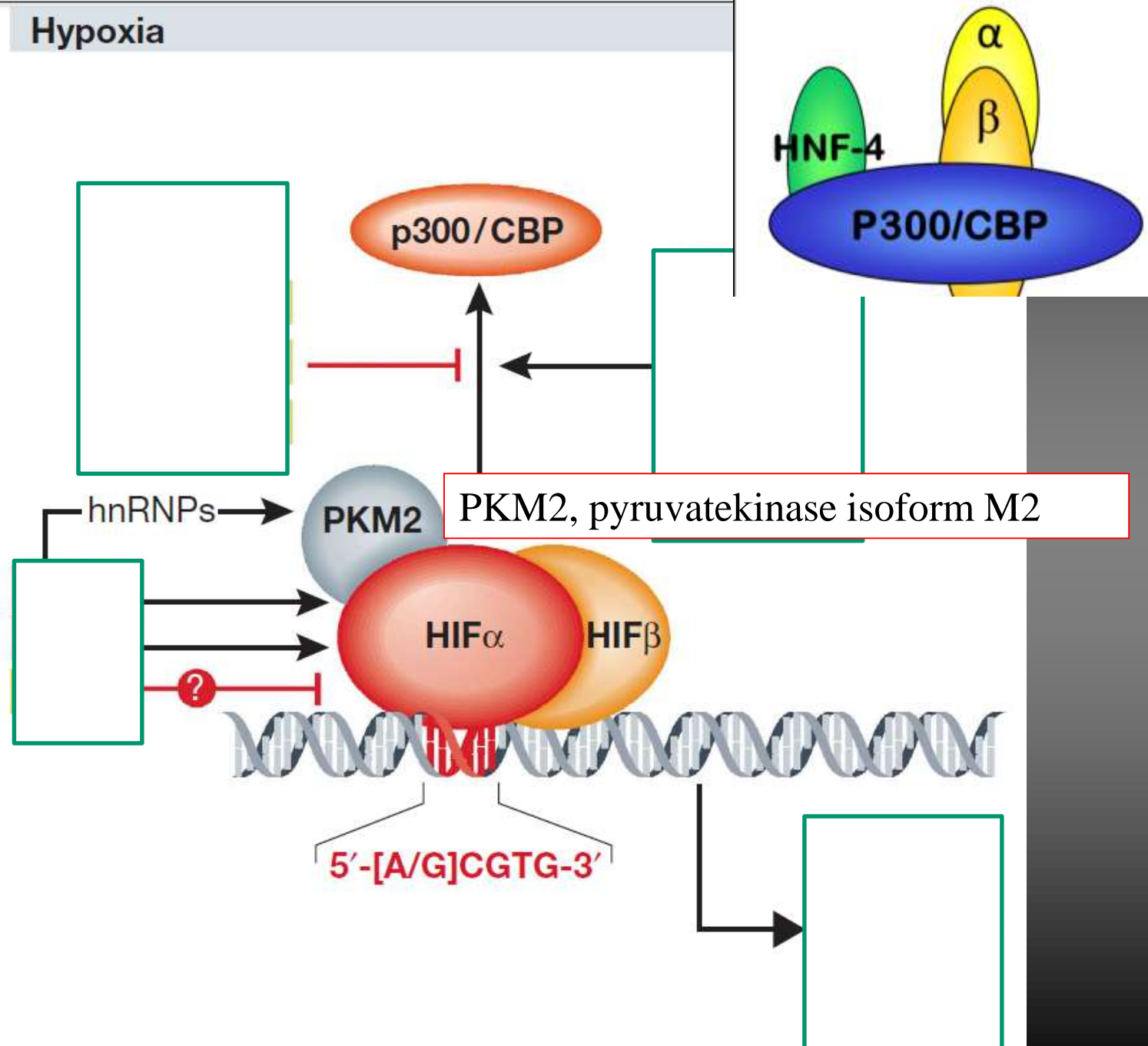
Asparaginyl hydroxylation (Asn N 803, CAD)
by Factor Inhibiting HIF (FIH)





Asparaginyl hydroxylation of N803 by FIH **inhibits binding** of the HIF1a CAD to coactivator p300/CBP

B Hypoxia



Pyruvate kinase (PK)

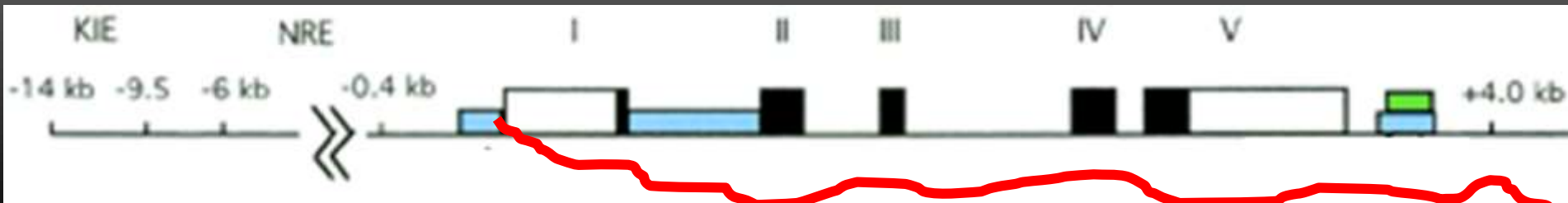
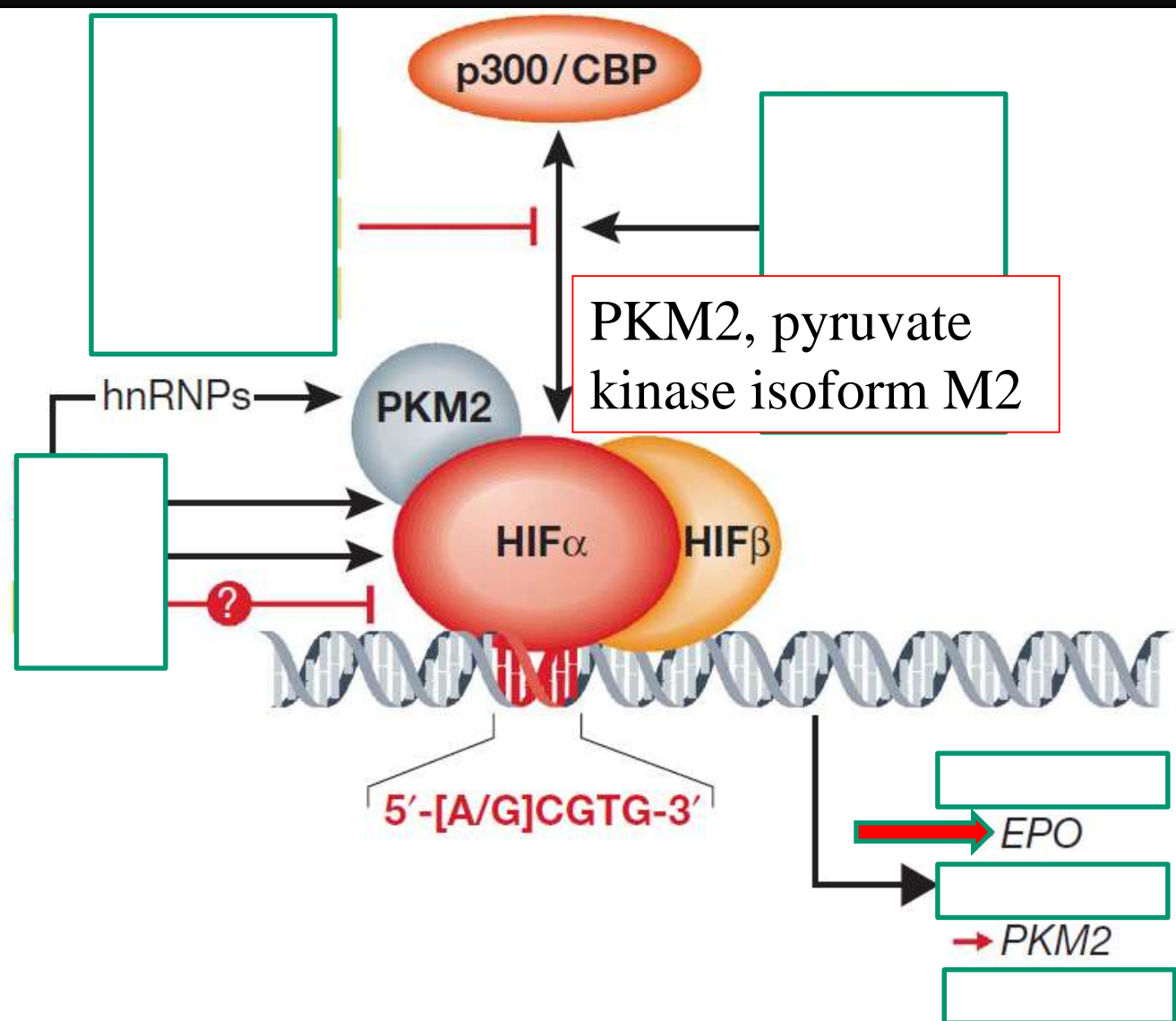
Enzima glicolitico e Fattore di trascrizione

The primary function of pyruvate kinase (PK) enzyme is to catalyze the transfer of a phosphate group (phosphoenolpyruvate PEP + ADP to Pyruvate + ATP)

There are four pyruvate kinase isoenzymes: **PKM2** is produced by alternative splicing of the PKM pre-mRNA, by **exon 10 inclusion**

PKM2 also interacts with HIF-1 α in the nuclei of hypoxic cells and enhances the recruitment of p300 to HRE sites and transactivation of HIF-1 α target genes!

HIF-1 α binds hypoxia response elements (HRE) within the first intron of human PKM2 that contains a HIF-1-binding site



ERITROPOIETINA (Epo)

- ✓ Ormone glicoproteico di 34 kDa (165 aa)
- ✓ Struttura a 4 α -eliche (A,B,C,D)
- ✓ Funzione: stimola l'eritropoiesi

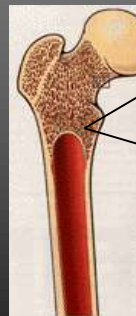


SINTESI

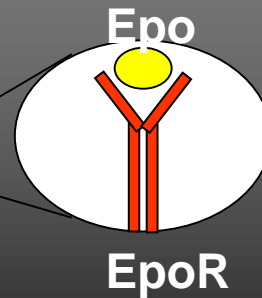
LEGAME CON IL RECETTORE



Reni

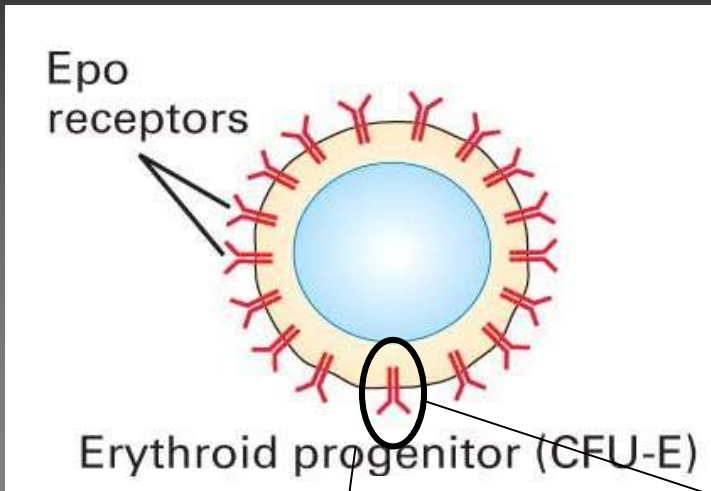


Midollo osseo



*PRODUZIONE DI
ERITROCITI*

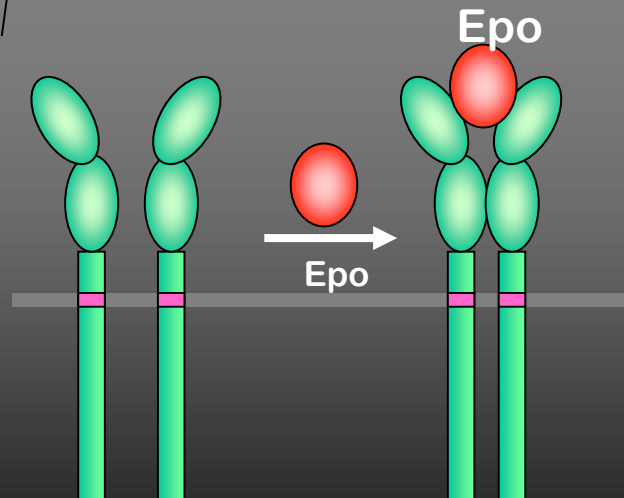
Il recettore dell'Epo (EpoR)



Glicoproteina
transmembrana

Monomero: 66
kDa (507 aa)

Famiglia dei recettori
delle citochine:

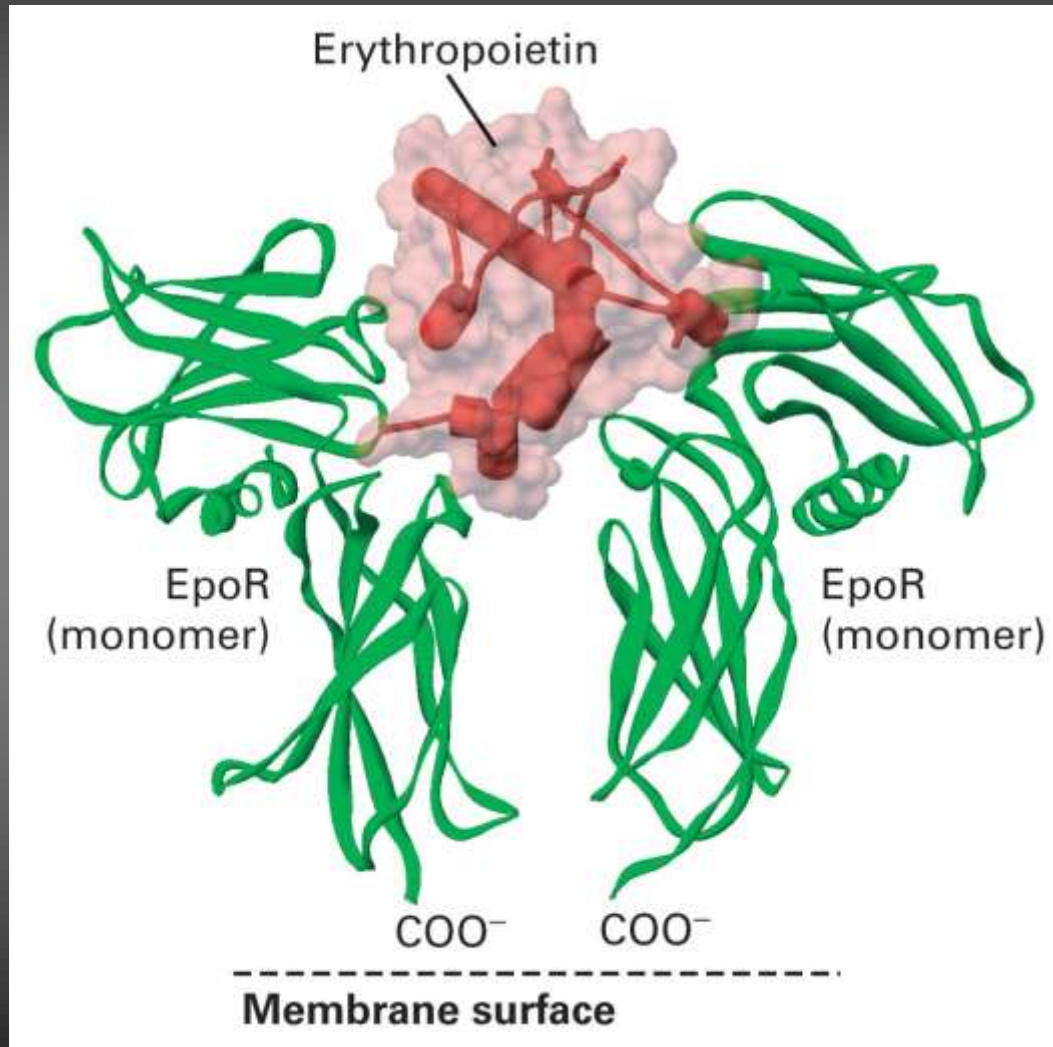


Legame del ligando

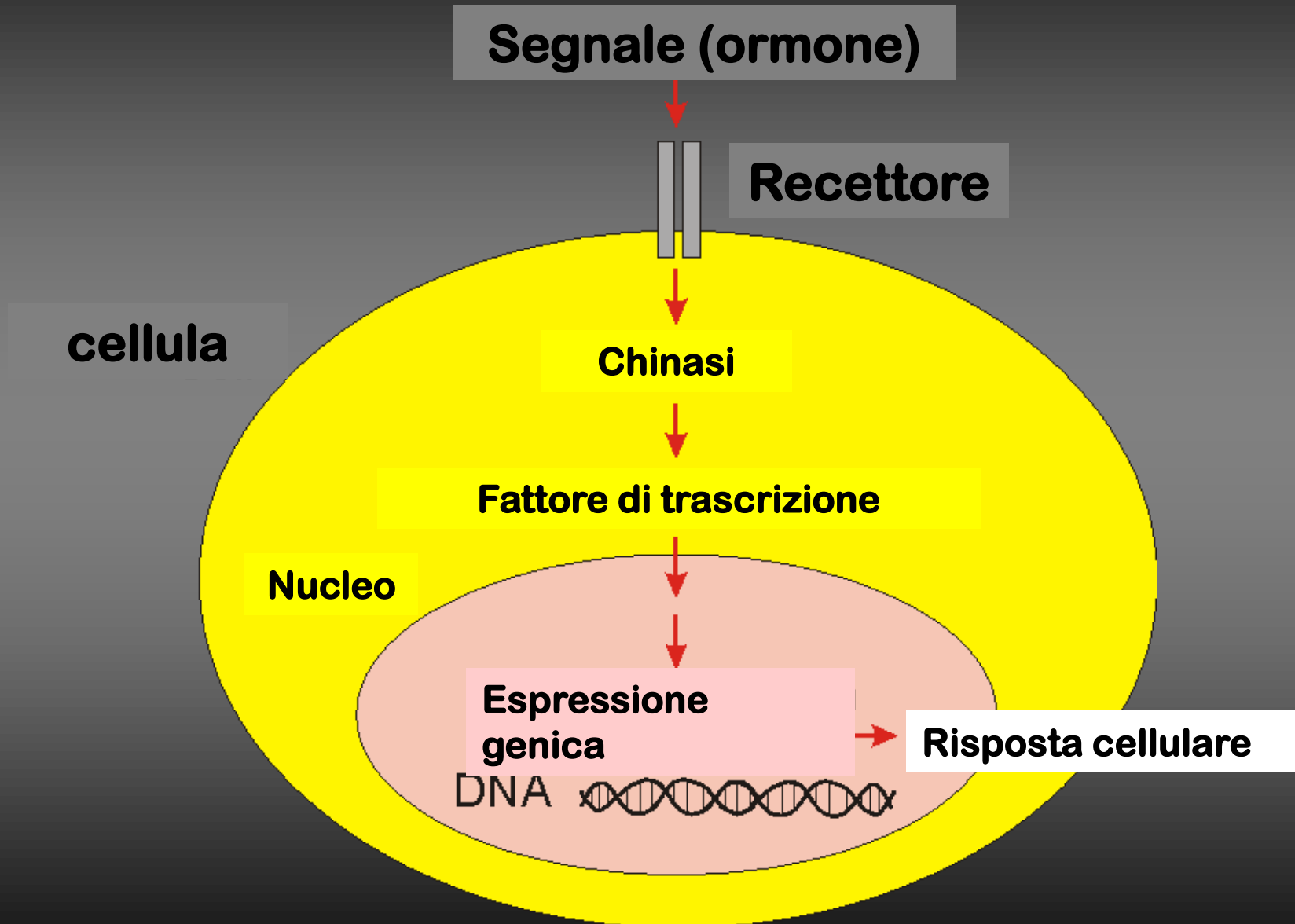
↓
Dimerizzazione

↓
Attivazione del
recettore

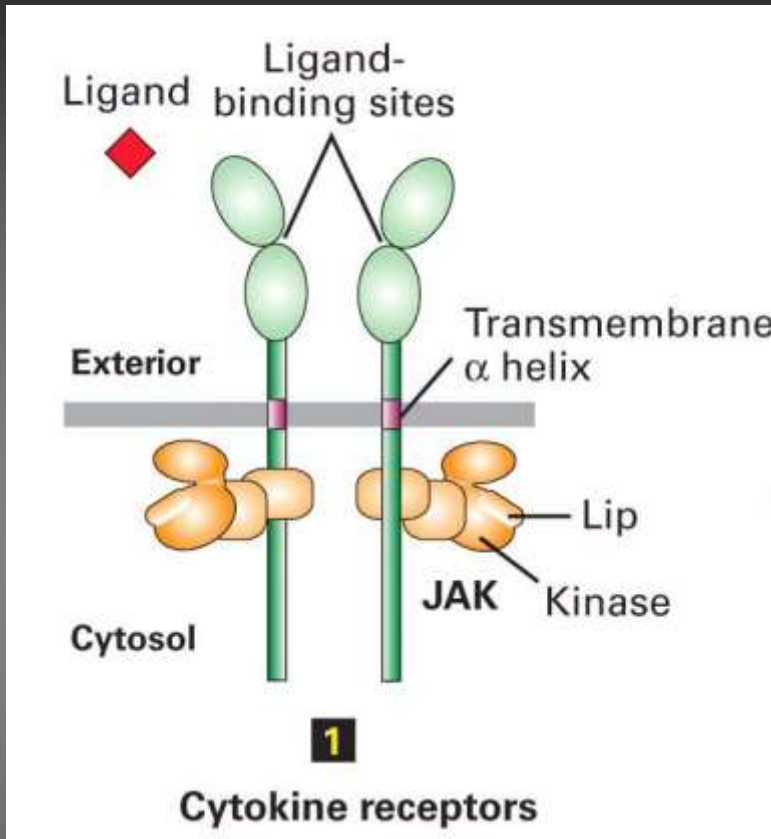
Erythropoietin-Epo Receptor complex



TRASDUZIONE DEL SEGNALE



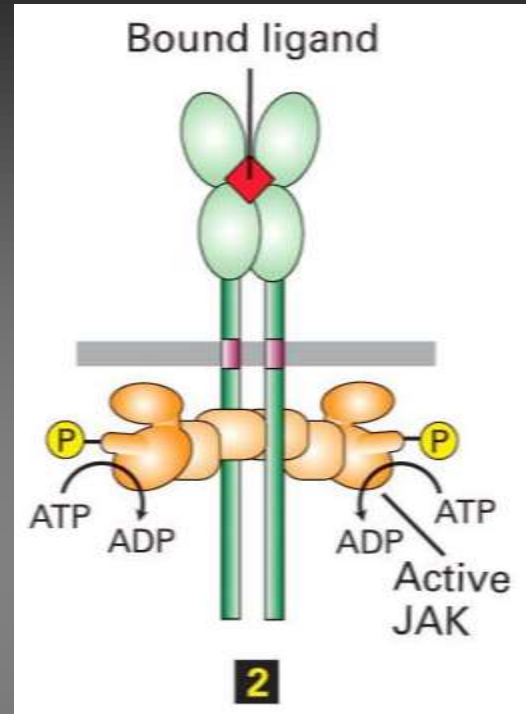
Trasduzione del segnale



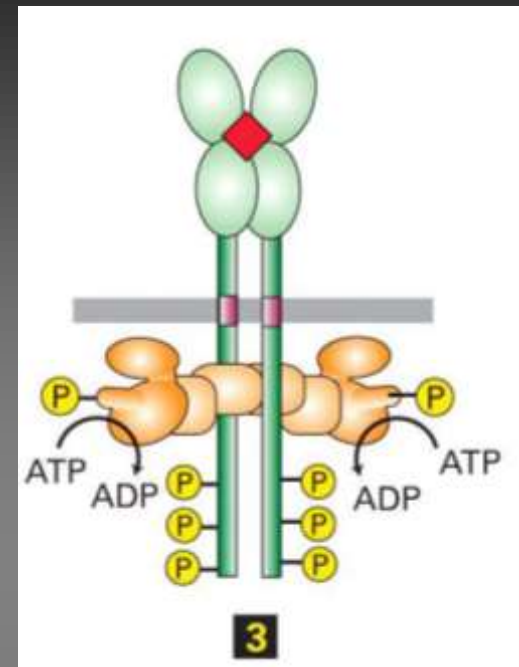
Dominio intracellulare privo di attività catalitica



Una JAK chinasi è associata al dominio citosolico di EpoR

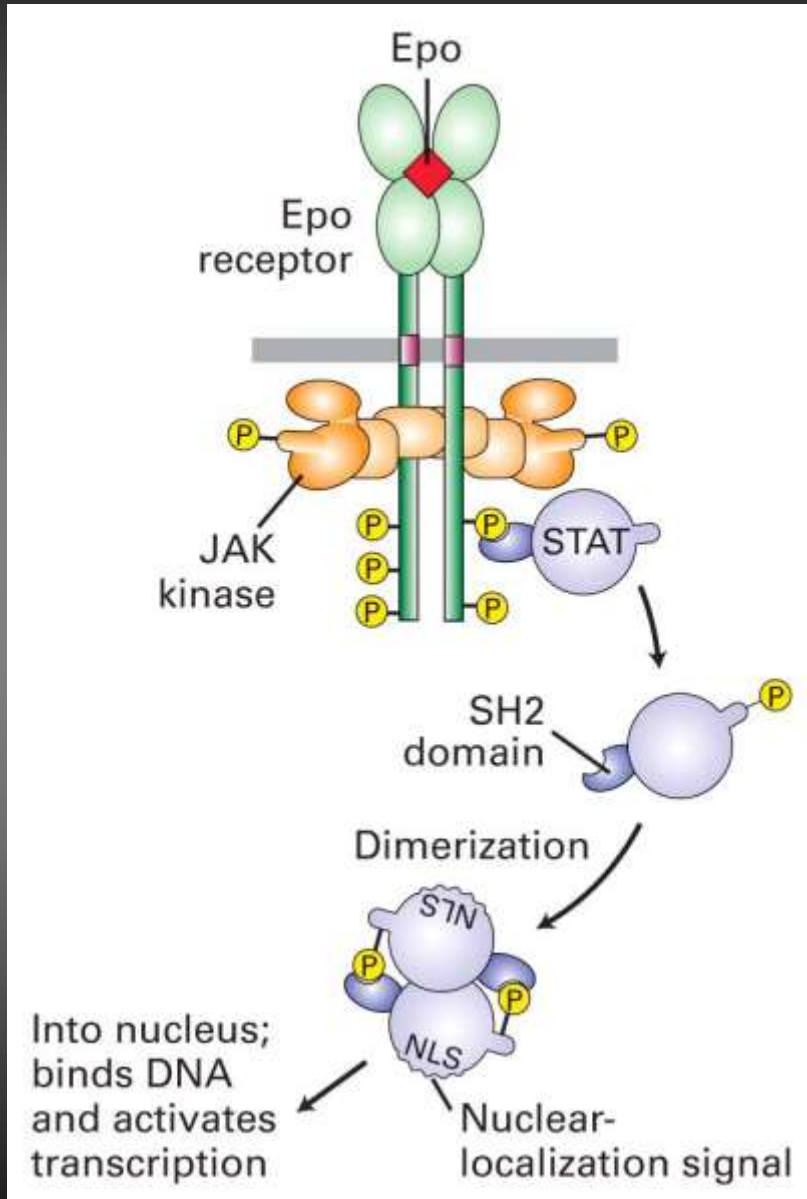


Dimerizzazione di EpoR
Fosforilazione di JAK e attivazione di JAK chinasi



JAK fosforila i residui di Tyr del dominio intracellulare di EpoR

Trasduzione del segnale



4) Legame di STAT ai residui di fosfo-Tyr di EpoR, mediante il dominio SH2 di STAT

5) Fosforilazione di STAT (fattore di trascrizione)

6) Dissociazione di STAT da EpoR e dimerizzazione di STAT

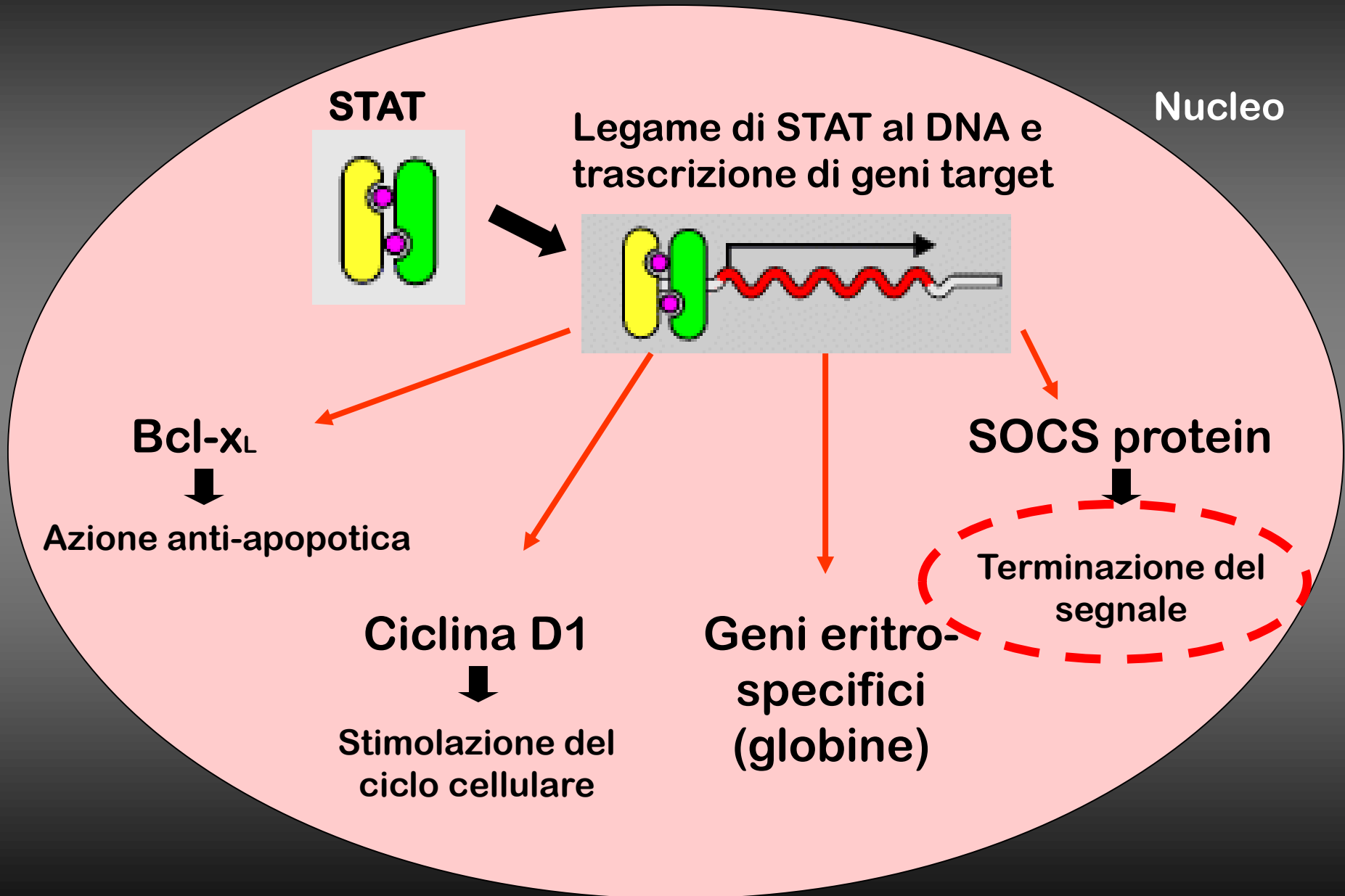


Esposizione di NLS (nuclear-localization signal)



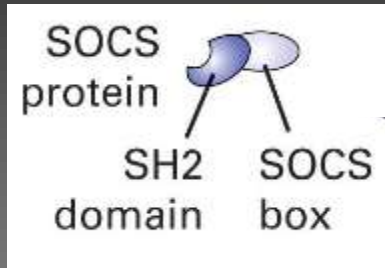
Spostamento di STAT al nucleo e legame a sequenze enhancer specifiche

Trascrizione di geni target



Terminazione del segnale

A lungo termine: *SOCS* proteins

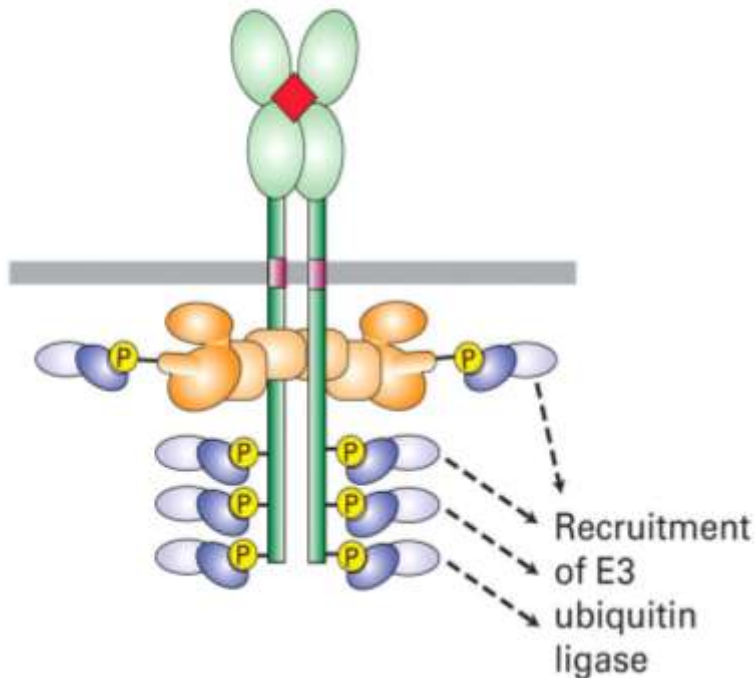


Struttura:

-1 dominio SH2

-1 dominio SOCS (SOCS box) →
richiama E3 ubiquitina ligasi

Signal blocking and protein degradation
induced by SOCS proteins



Meccanismo d'azione:

a) Il dominio SH2 si lega alle fosfo-Tyr del recettore: impedisce il legame di STAT

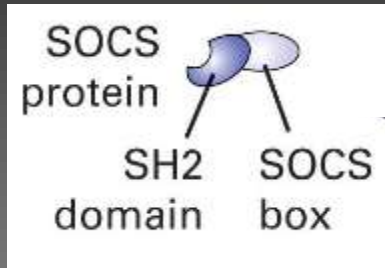
b) Il dominio SOCS richiama E3



Ubiquinizzazione e degradazione proteosomica di JAK

Terminazione del segnale

A lungo termine: *SOCS* proteins

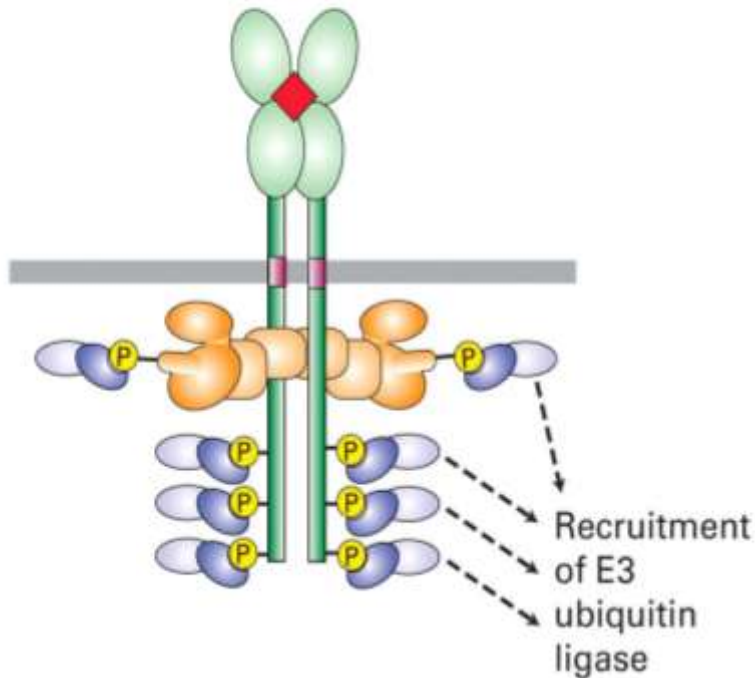


Struttura:

-1 dominio SH2

-1 dominio SOCS (SOCS box) →
richiama E3 ubiquitina ligasi

Signal blocking and protein degradation
induced by SOCS proteins



SOCS Box

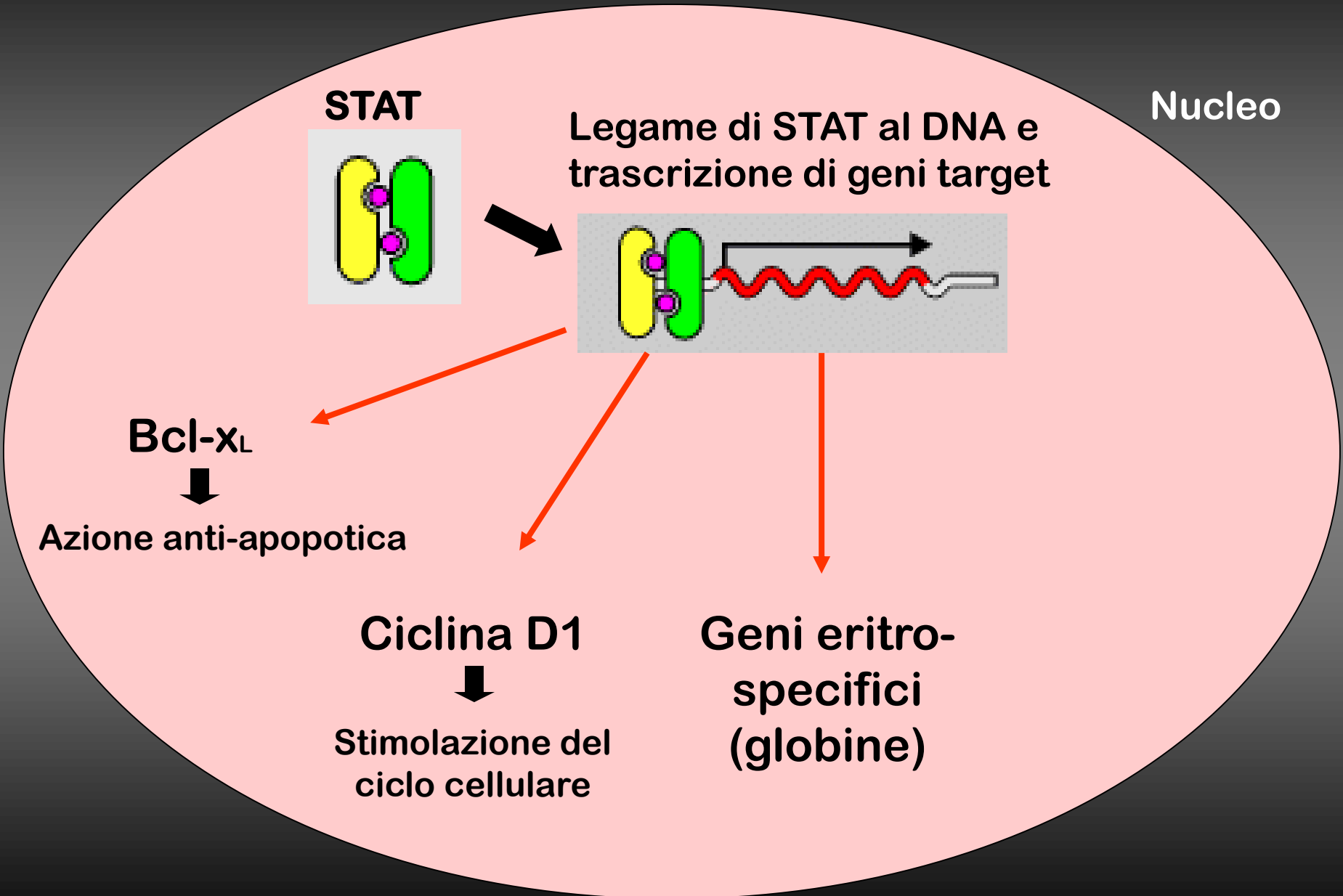
40-amino acid motif, which recruits
an **E3 ubiquitin ligase complex**
consisting of

the adapter **elongins B and C**

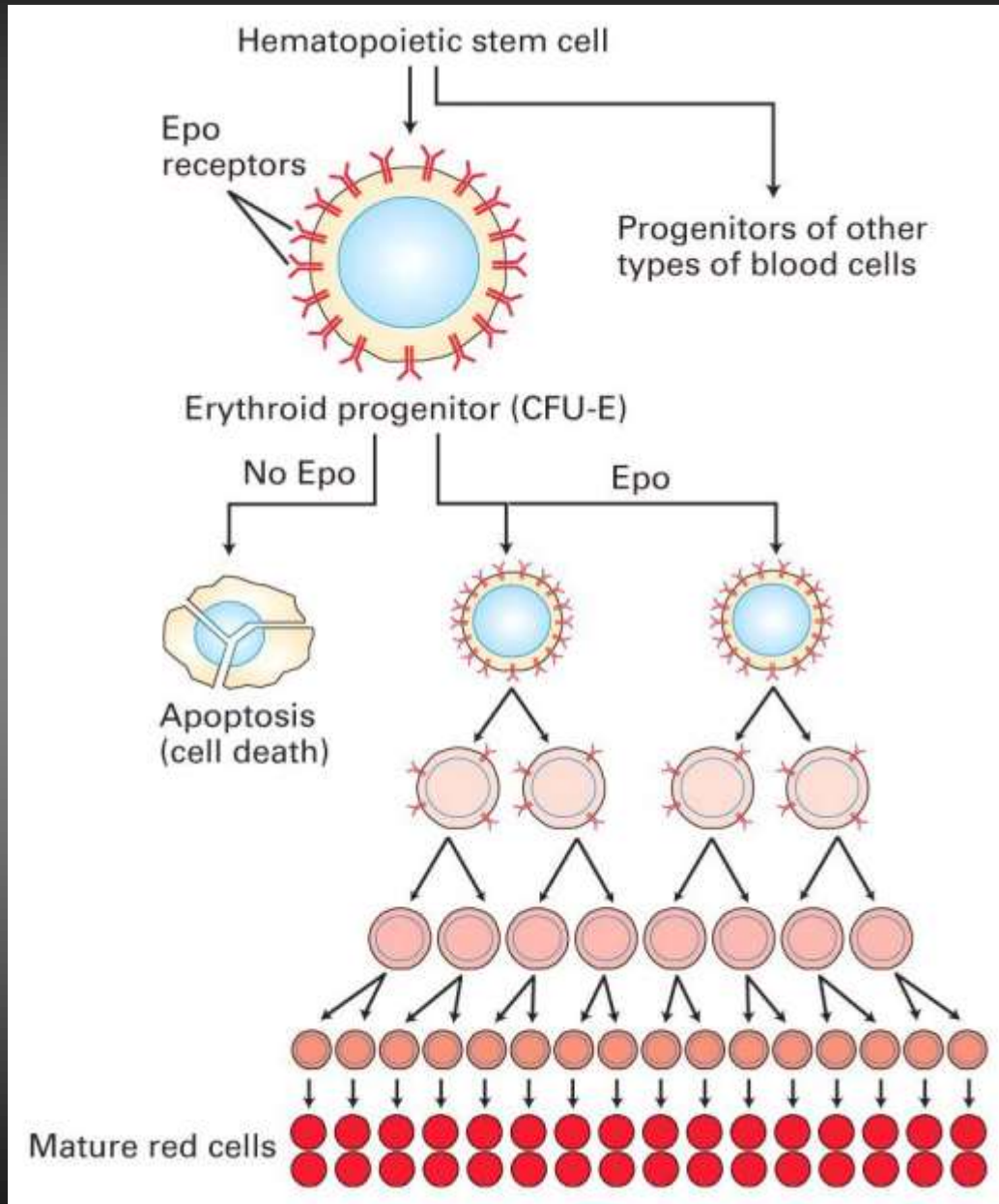
Rbx2

the scaffold protein **Cullin5**

Trascrizione di geni target

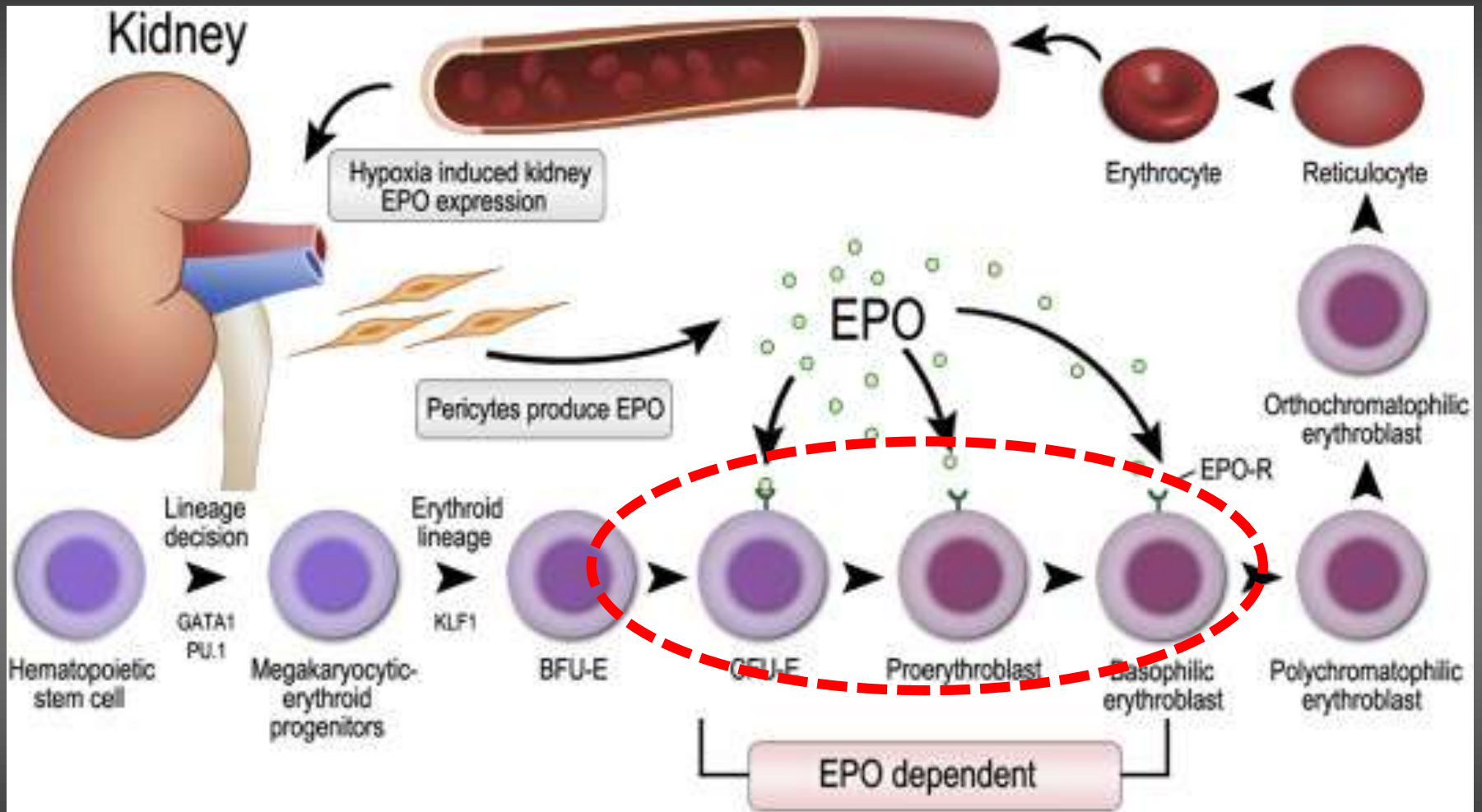


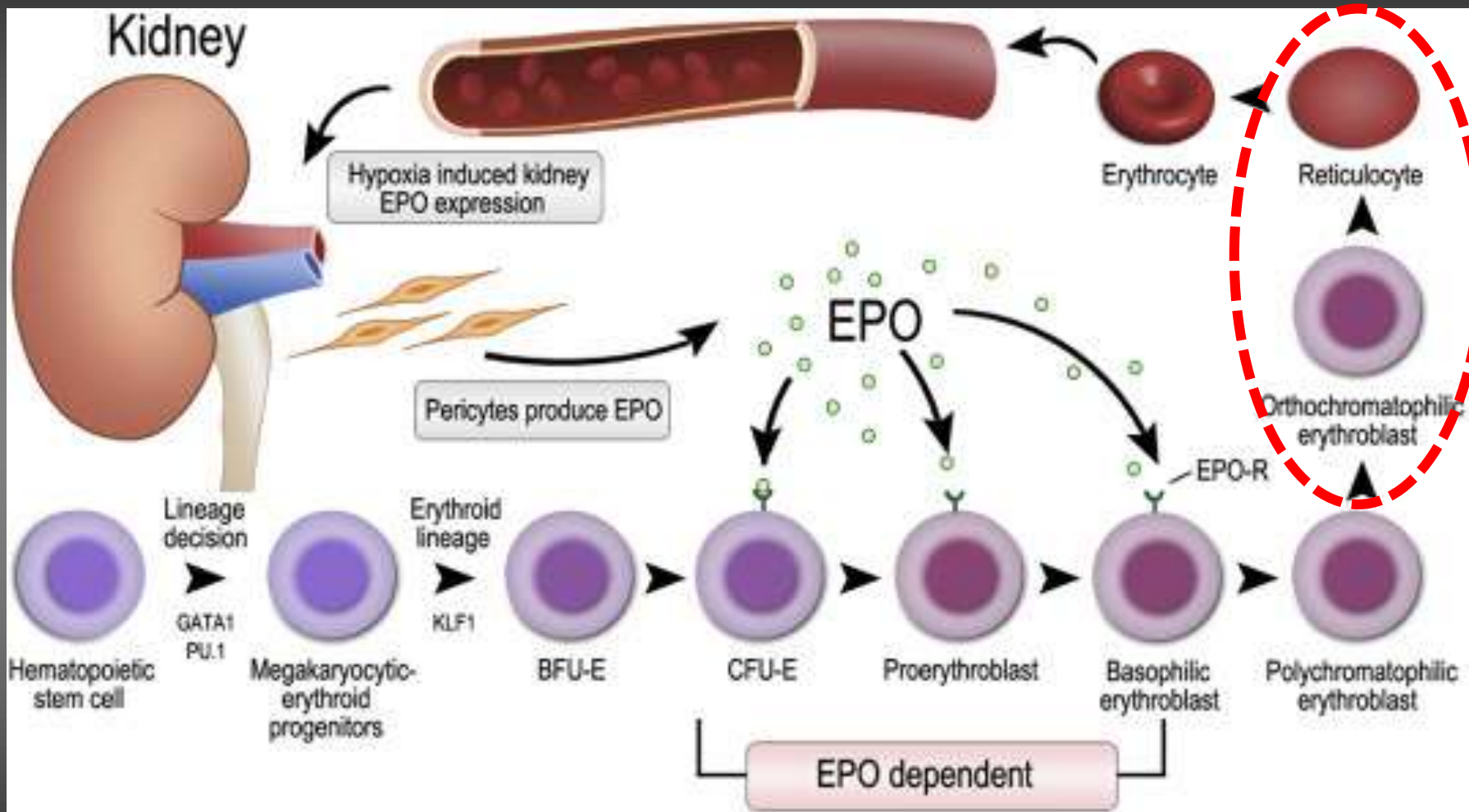
Ruolo dell'Epo nell'eritropoiesi



EpoR è espresso sulla superficie delle cellule eritroidi (massima espressione sulle CFU-E, diminuita sugli stadi più differenziati)

Epo agisce “salvando” dall’apoptosi le cellule progenitrici eritroidi, e stimolandone la maturazione





Epo

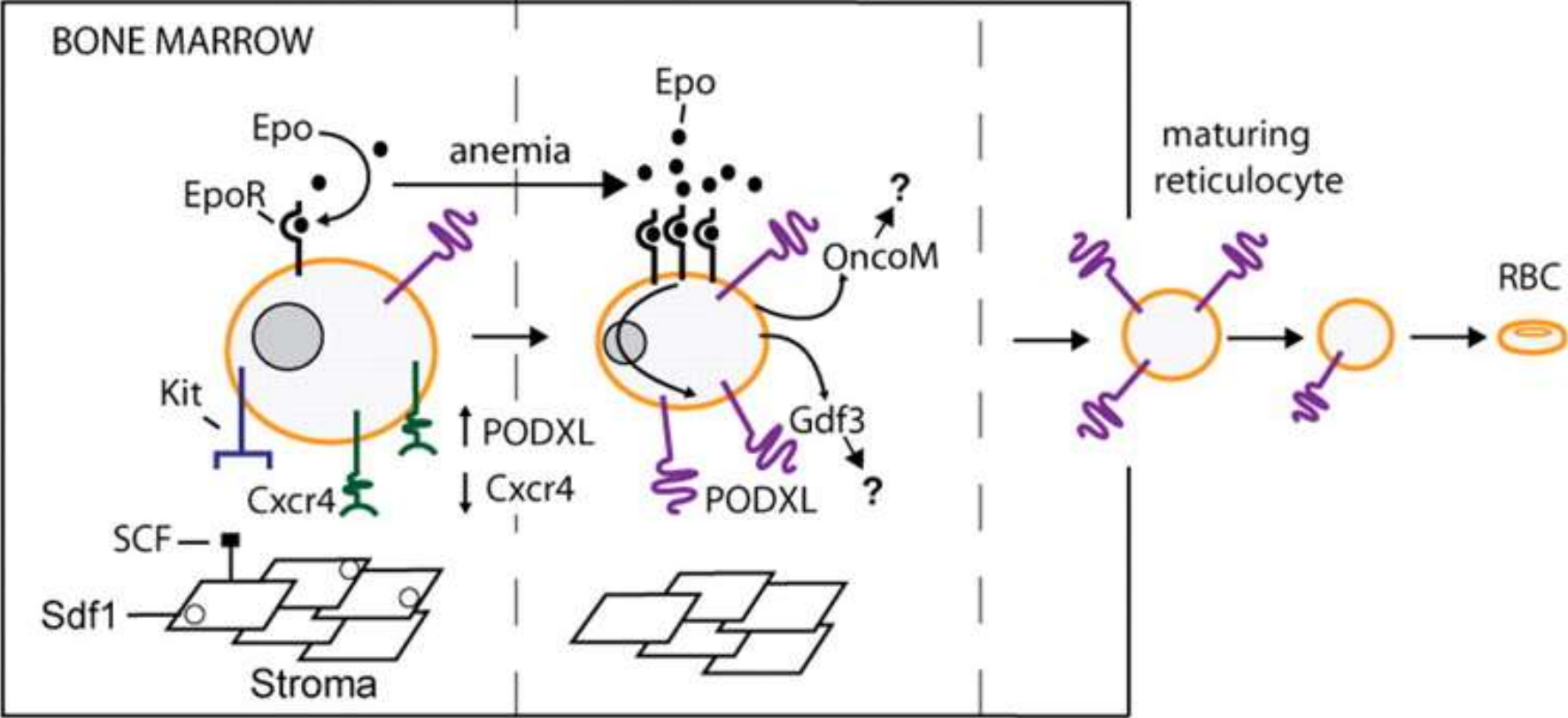
down-modulates adhesion factors:

Cxcr4 Chemokine receptor

up-modulates “releasing” factors:

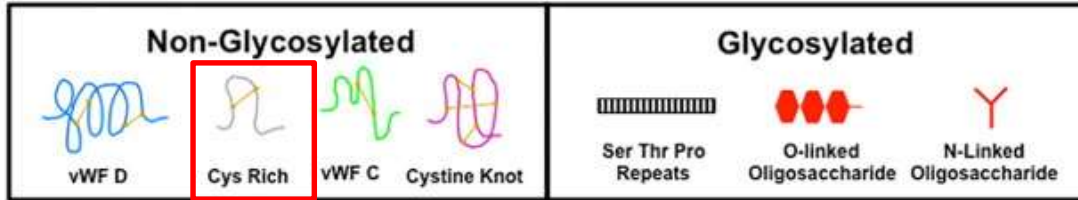
Podocalyxin like-1 (PODXL)

Erythropoietin modulation of podocalyxin and a proposed erythroblast niche

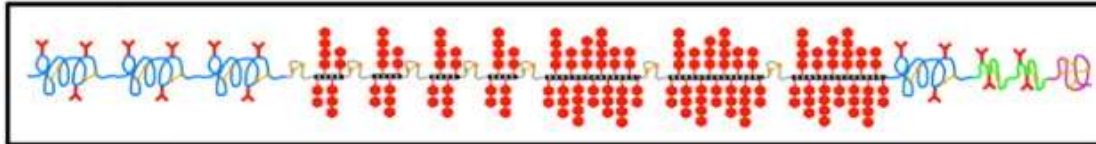


PODXL is a sulphated sialomucin, *antiadhesive*

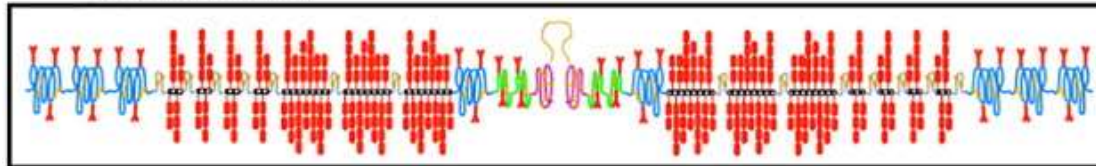
Mucin Domains



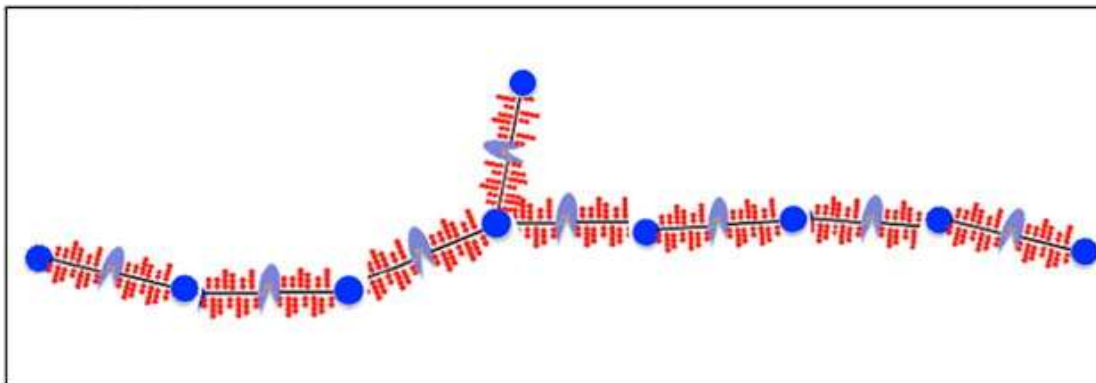
Mucin Monomer



Mucin Dimer



Mucin Multimer



Mucins

Central region - repeats
aa Ser Thr –
hundreds of O-linked
oligosaccharides

The cys residues participate in establishing disulfide linkages within and among mucin monomers.

Sialomucin - acid mucopolysaccharide containing sialic acid

