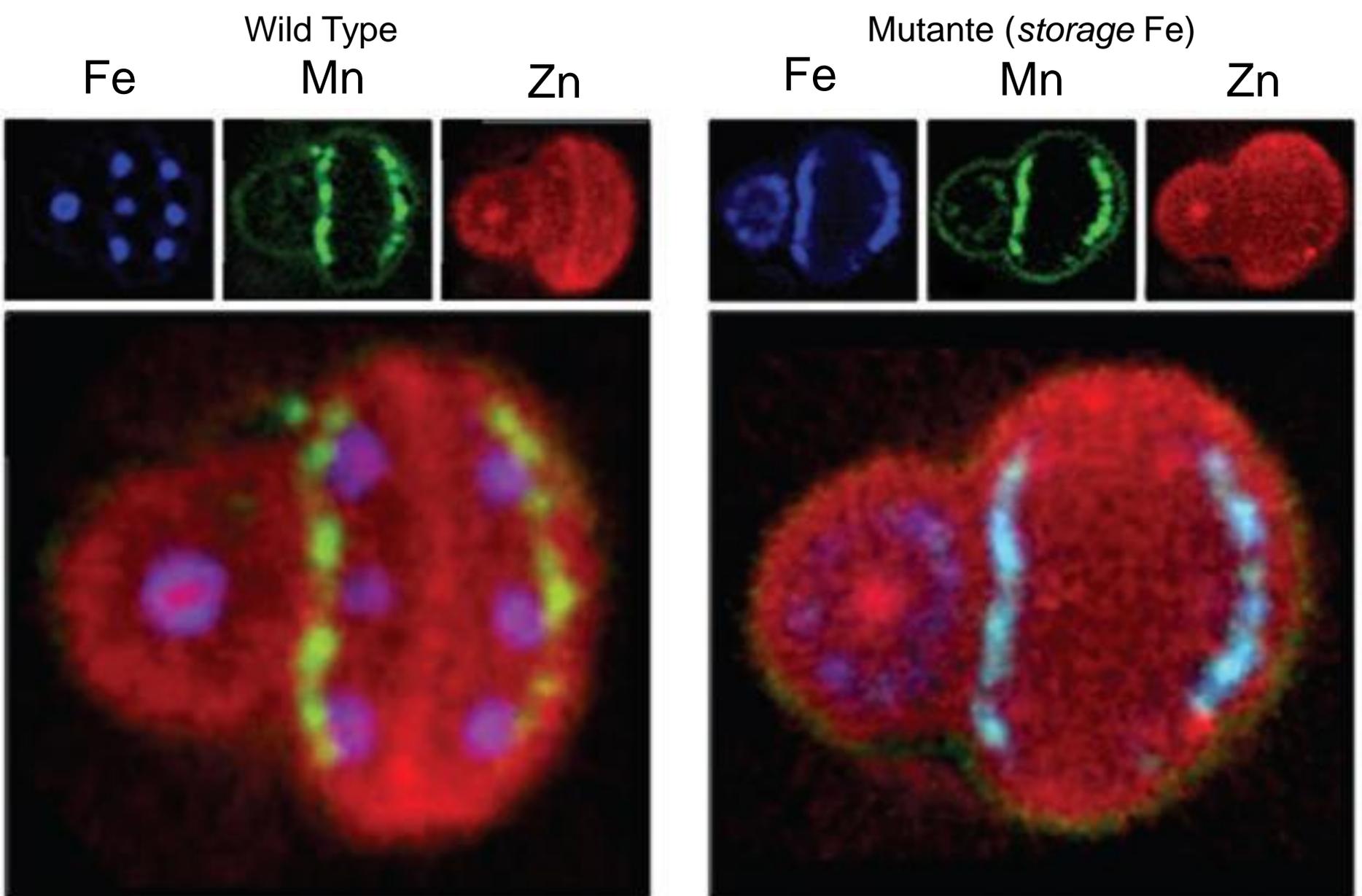
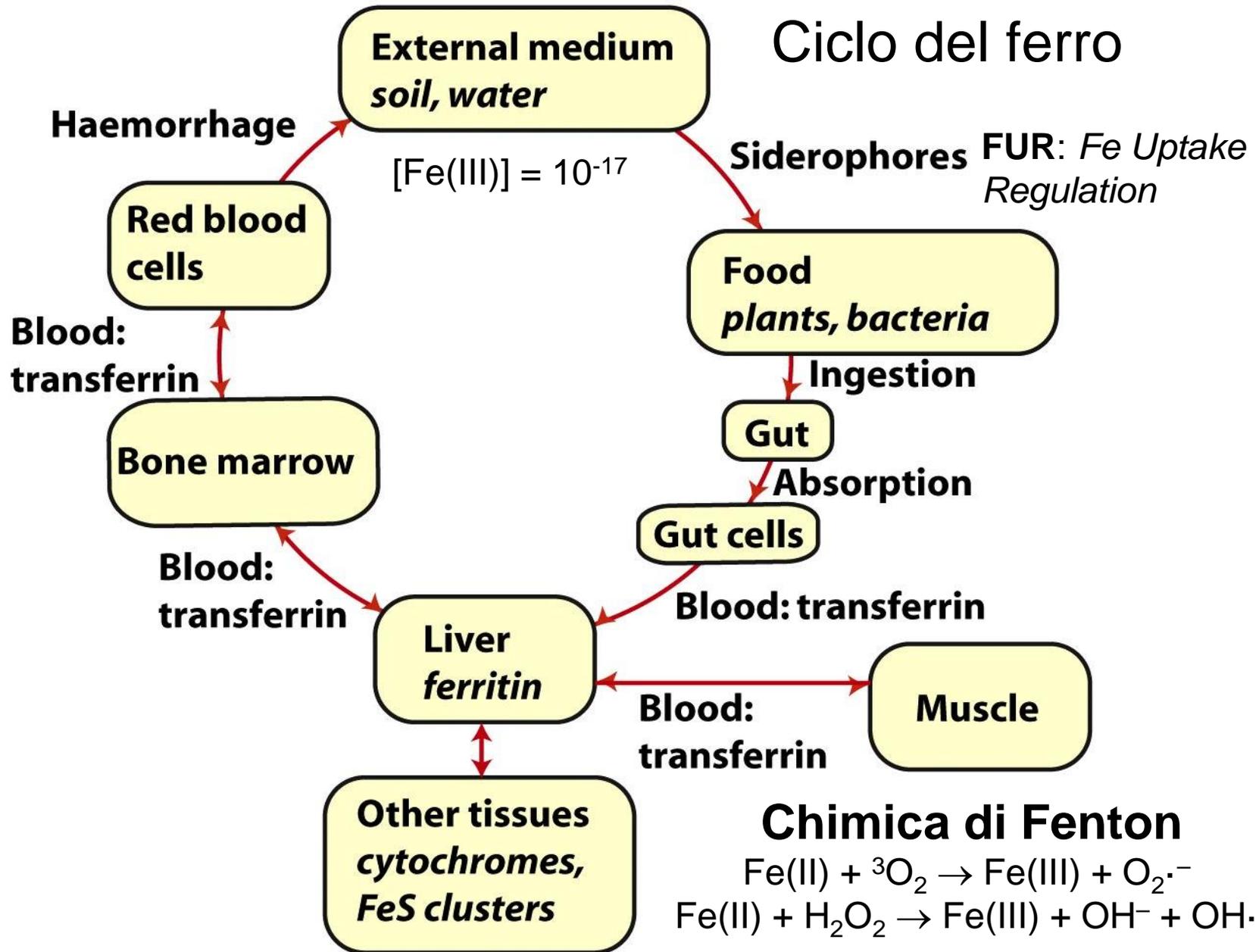


Omeostasi dei trace elements:
uptake, trasporto, *storage*....

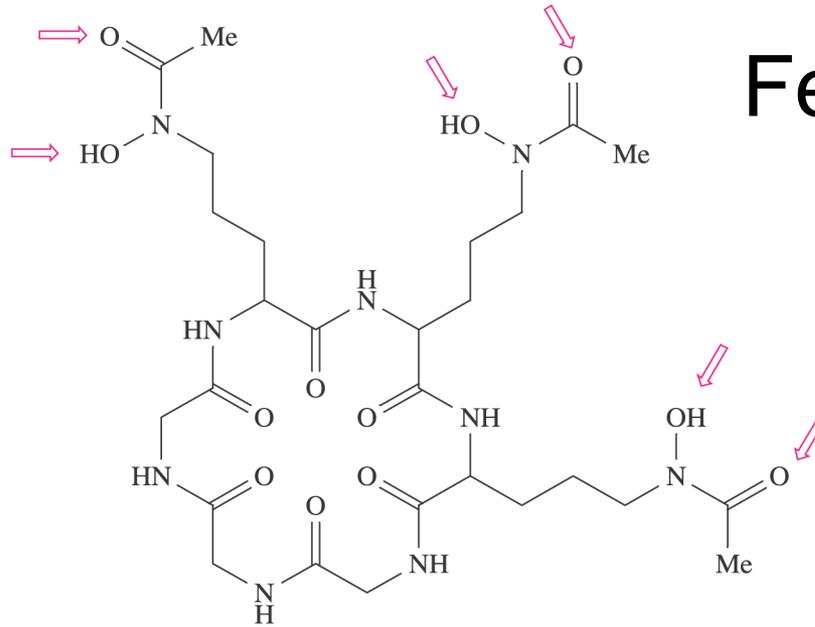


Microtomografia di fluorescenza ai raggi X

Ciclo del ferro



Siderofori
Idrossammati
(funghi, lievito)

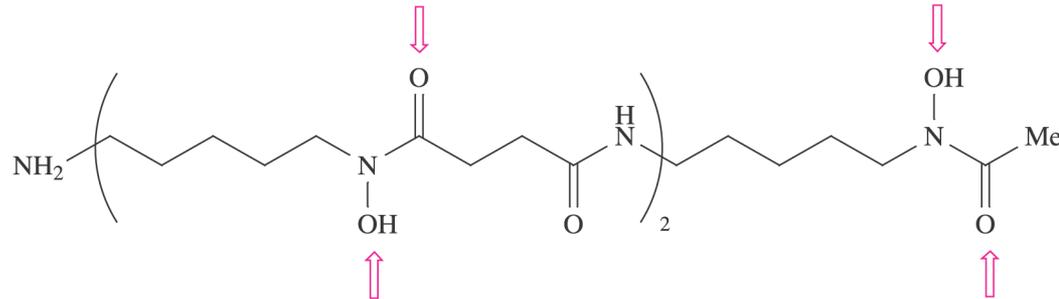


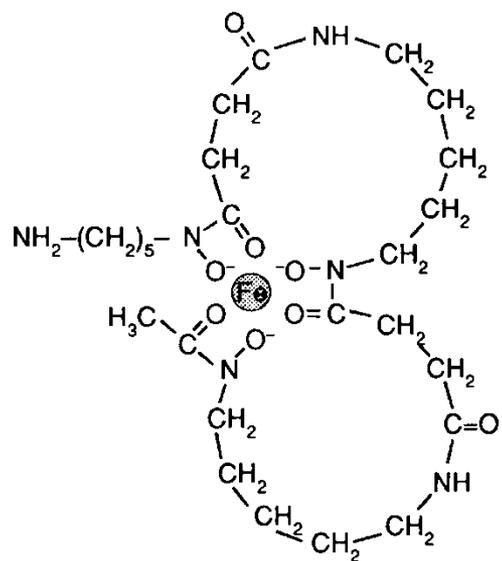
Fe(III) alto spi

desferricromo

d)

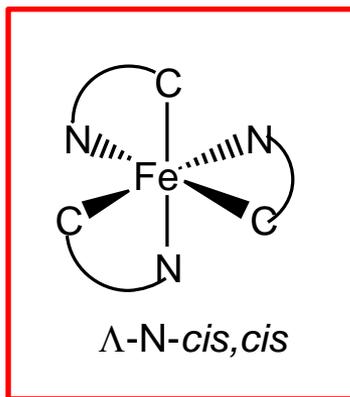
desferriossamina



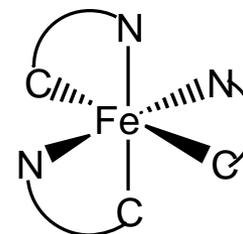


ferrioxamine B

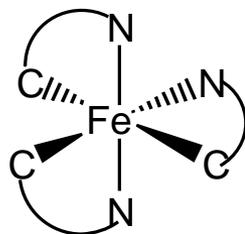
without Fe: deferrioxamine B



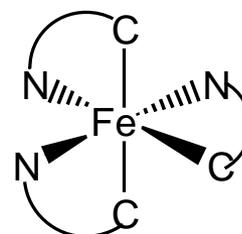
Λ -N-*cis,cis*



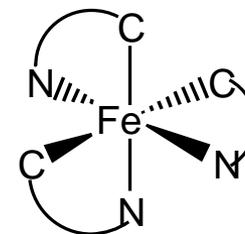
Λ -C-*trans,cis*



Λ -N-*trans,cis*



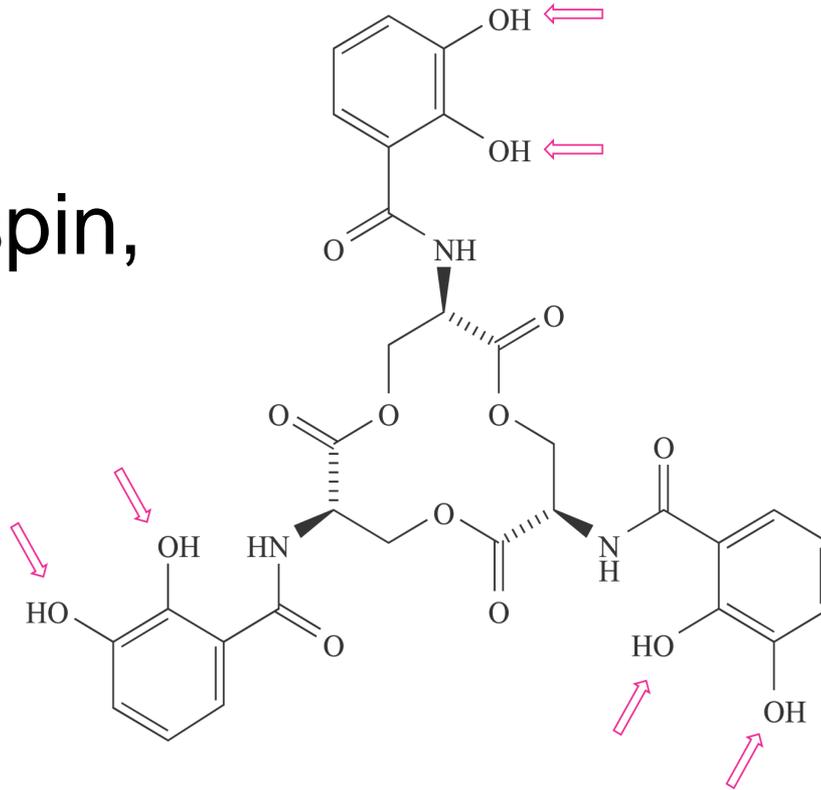
Λ -C-*cis,trans*



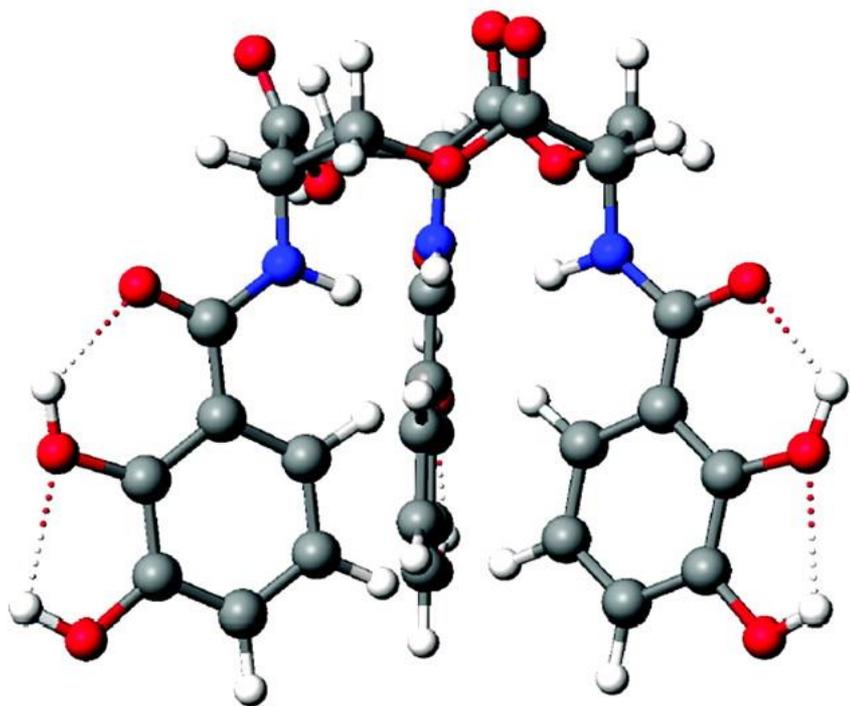
Λ -N-*trans,cis*

Siderofori catecolati (batteri)

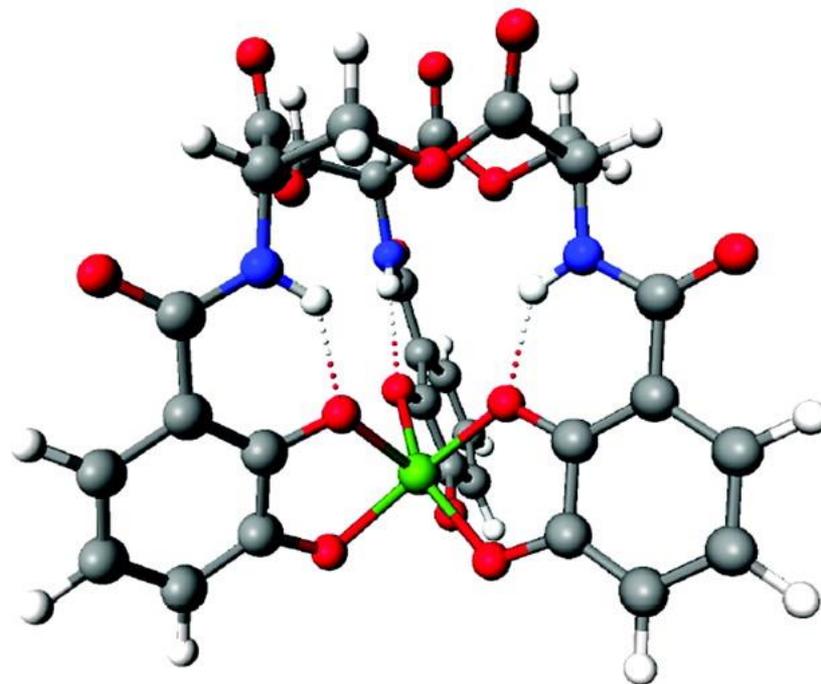
Fe(III) alto spin,
 $K_a = 10^{52}$



Enterobactina

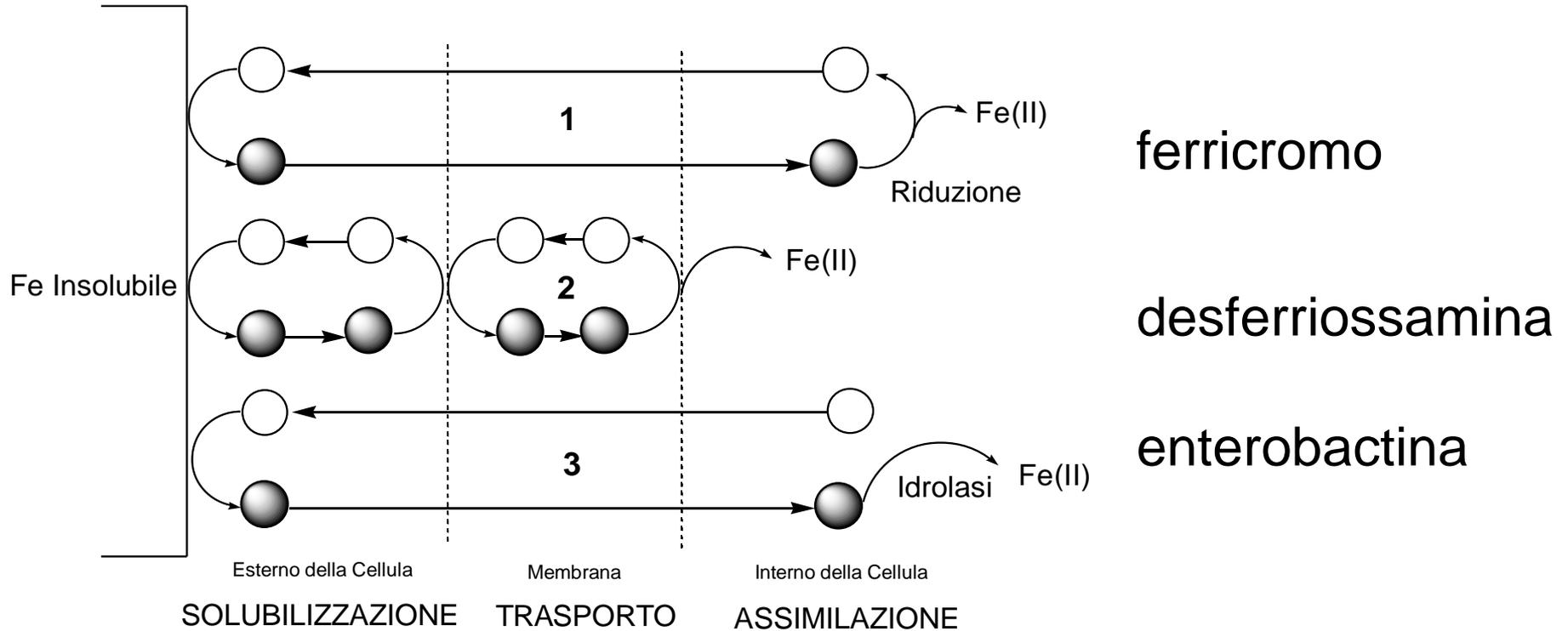


Modello di enterobactina
non coordinata



Complesso V(IV)-enterobactina
 Δ

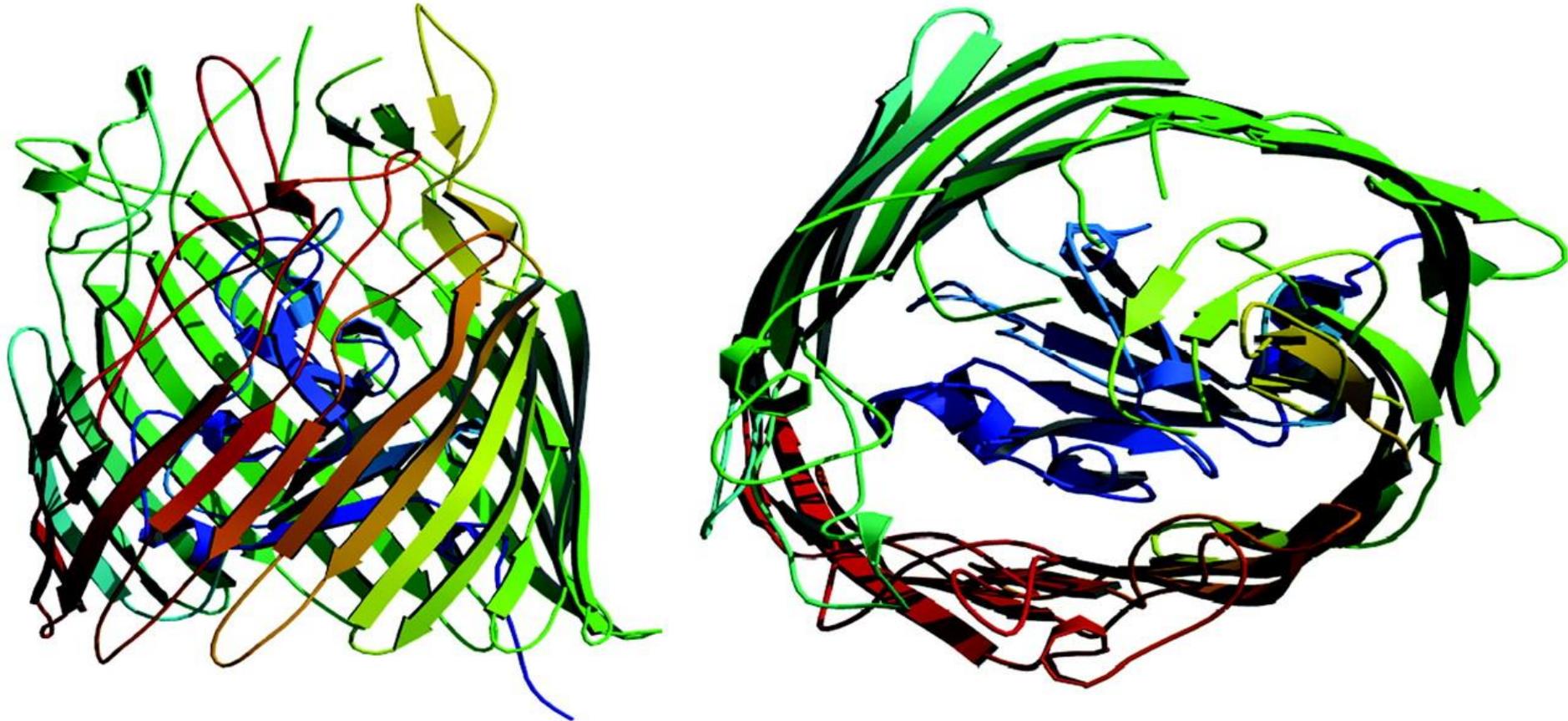
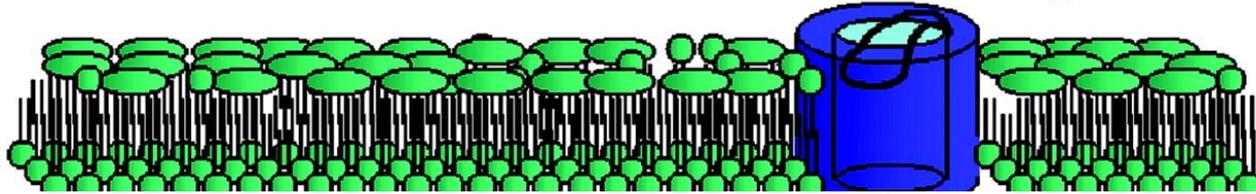
Meccanismi di trasporto trans-membrana



FepA: trasporto trans-membrana di Fe-enterobactina

OM

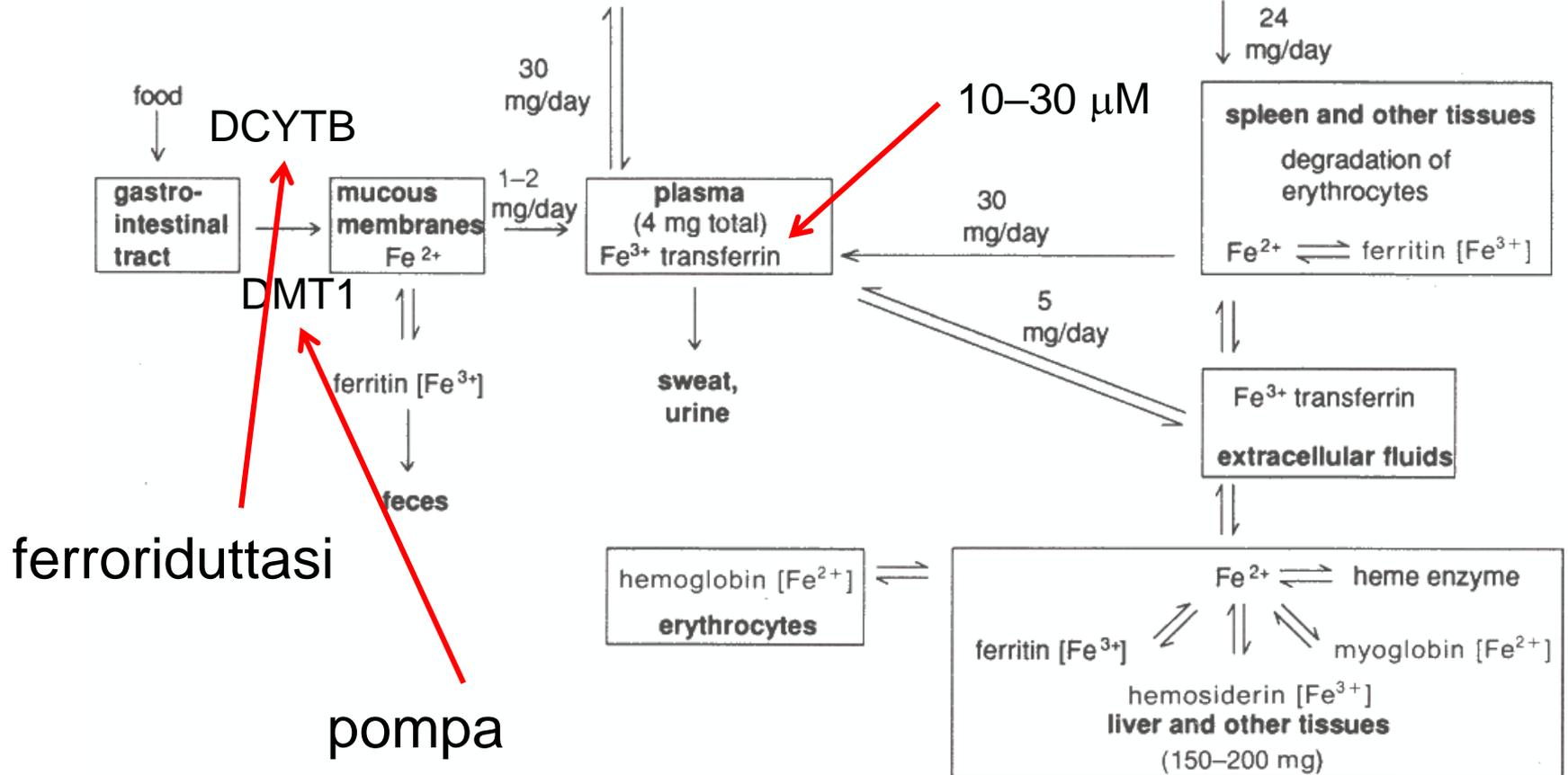
FepA



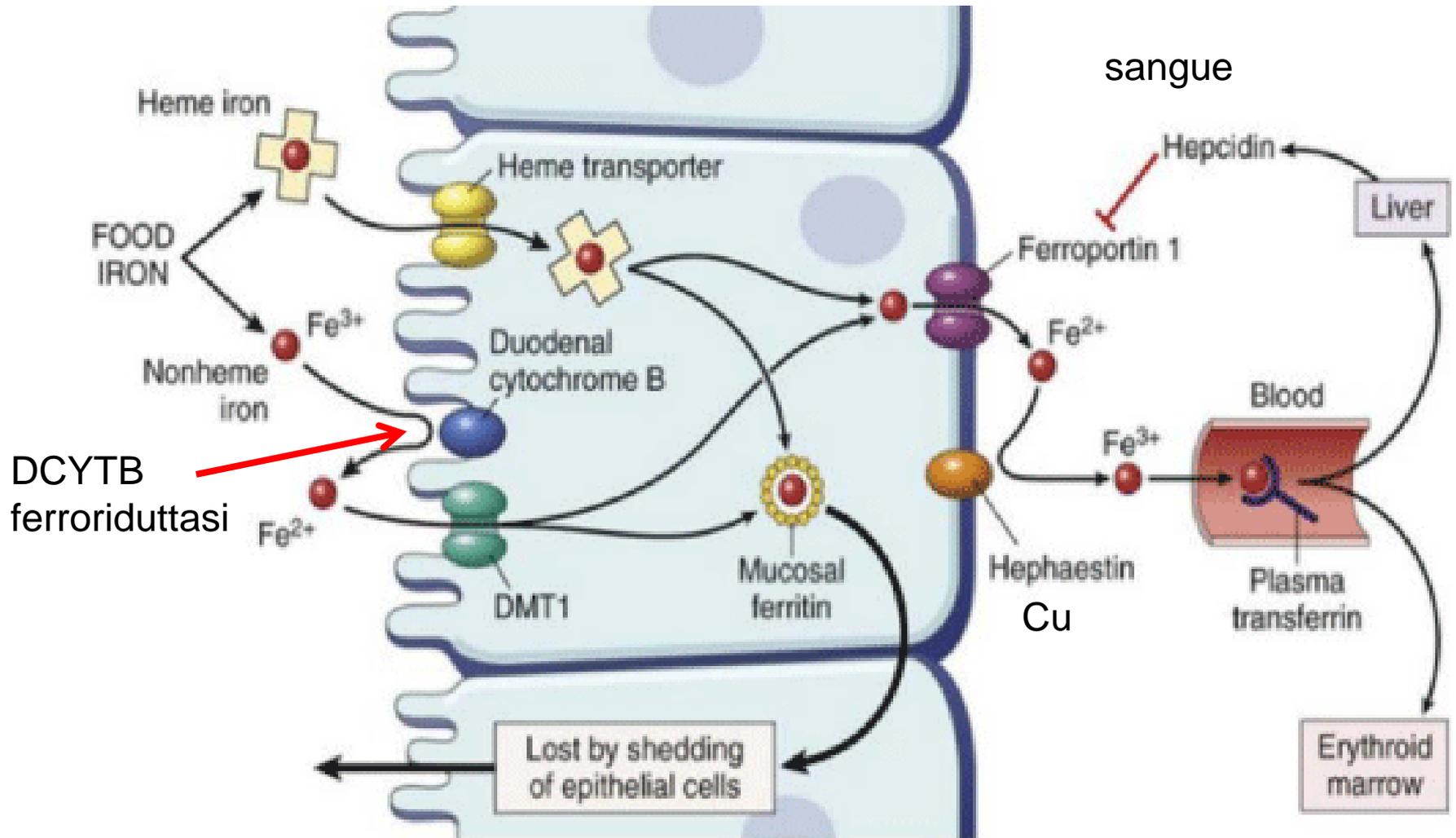
In blu la «gate protein» N-terminale

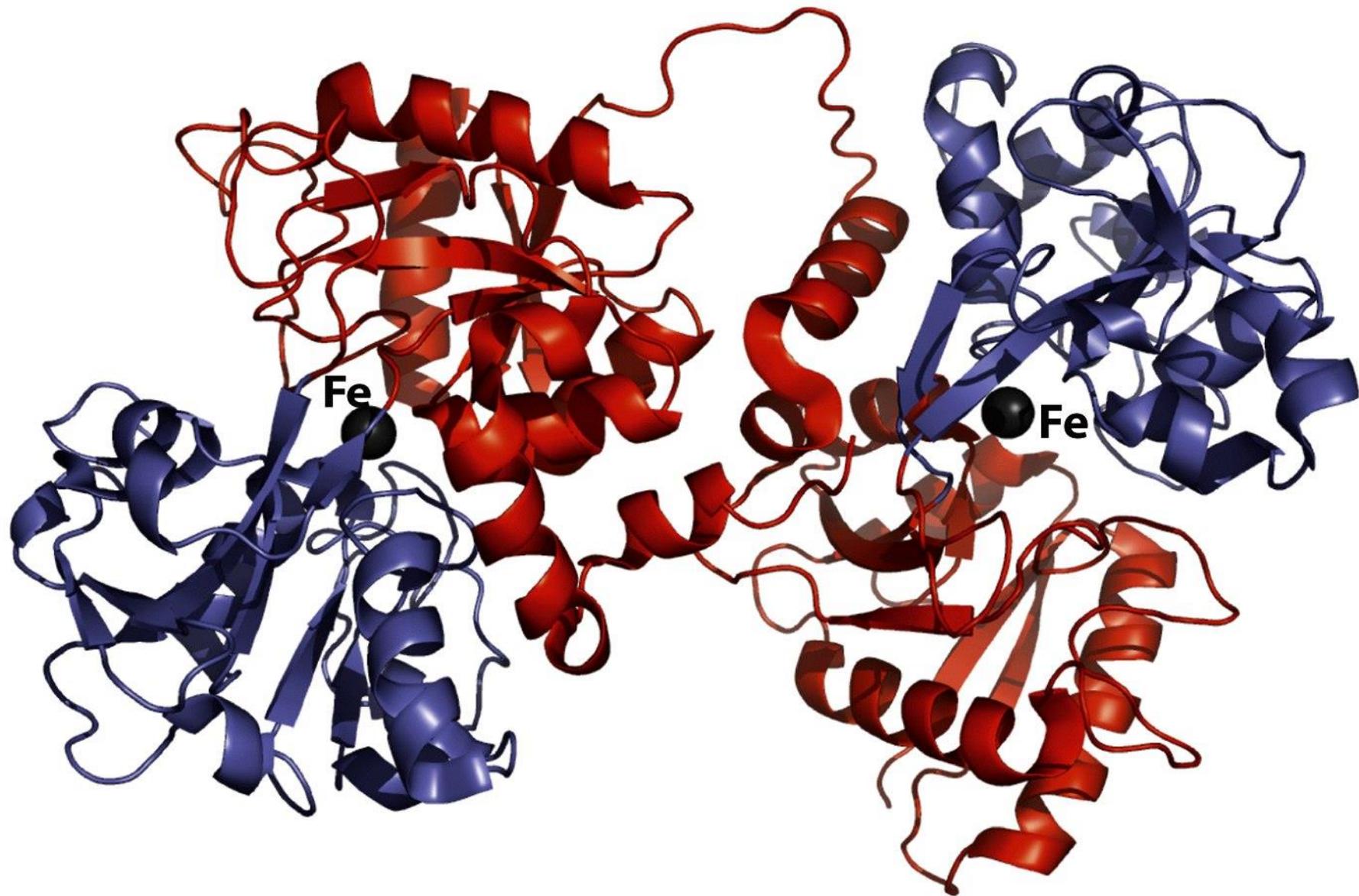
Midollo spinale

ferrochelatasi



Assorbimento del ferro nell'intestino e trasporto attraverso gli enterociti

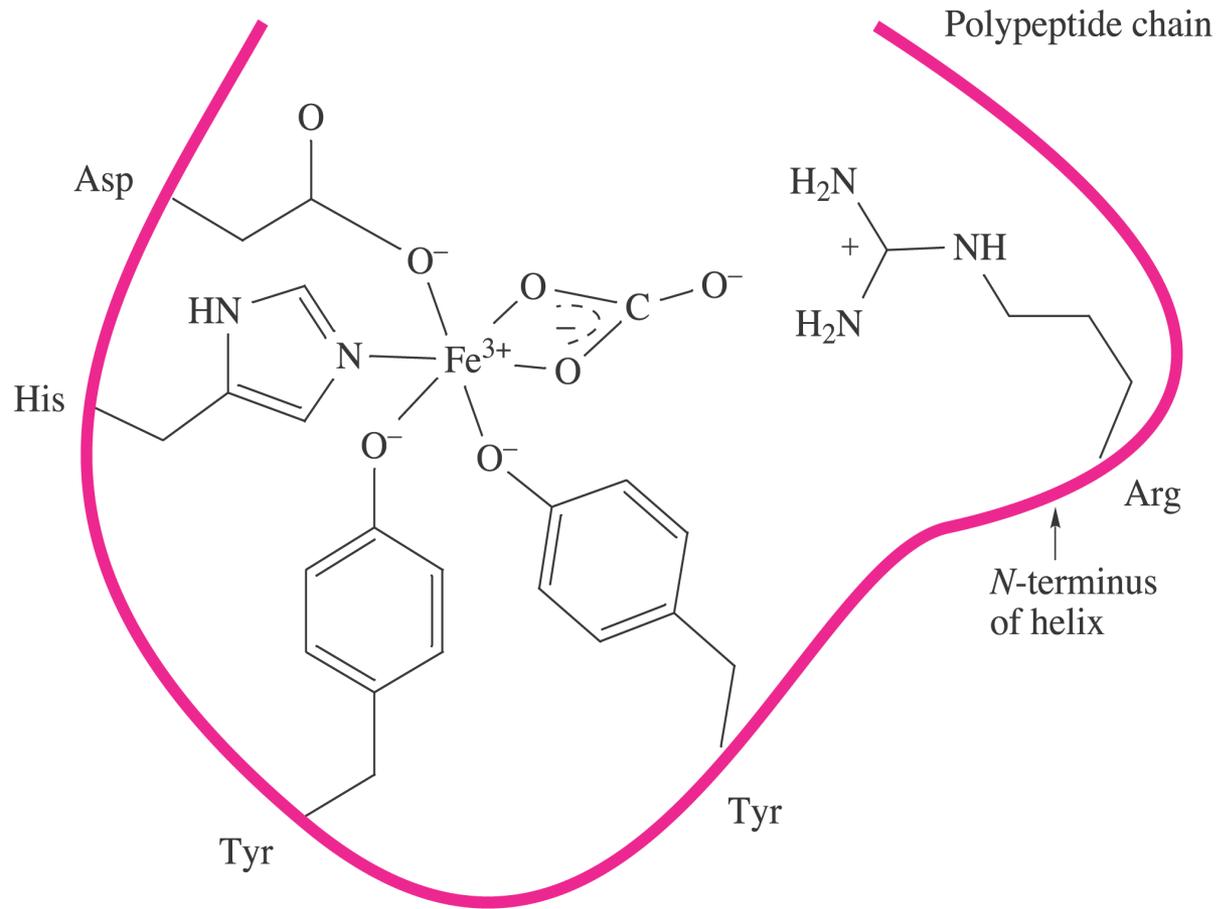




Transferrina

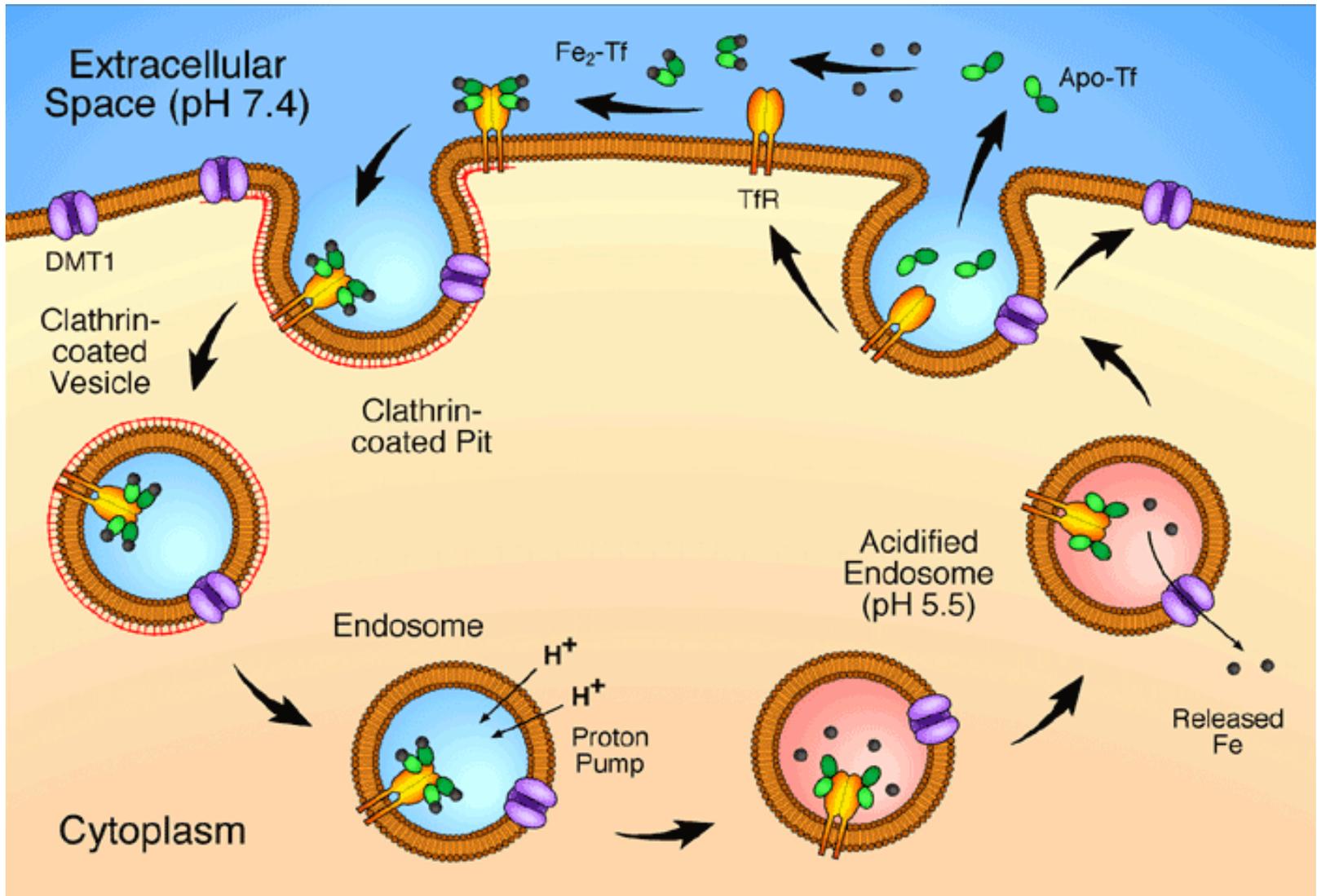
80 kDa

Sito di coordinazione del Fe nella transferrina

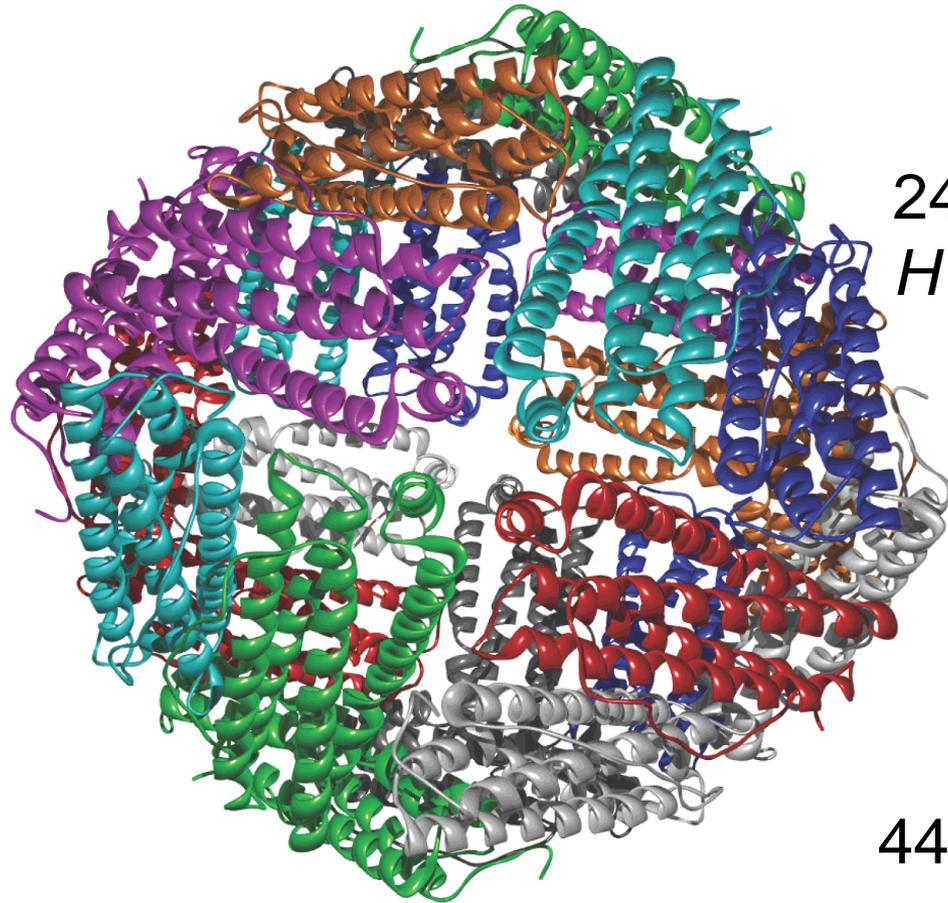
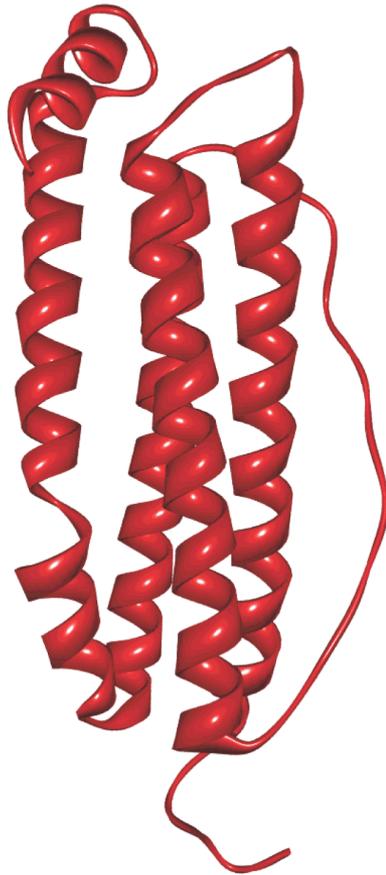


Sito di coordinazione del Fe nella transferrina

Ciclo della transferrina



Ferritina

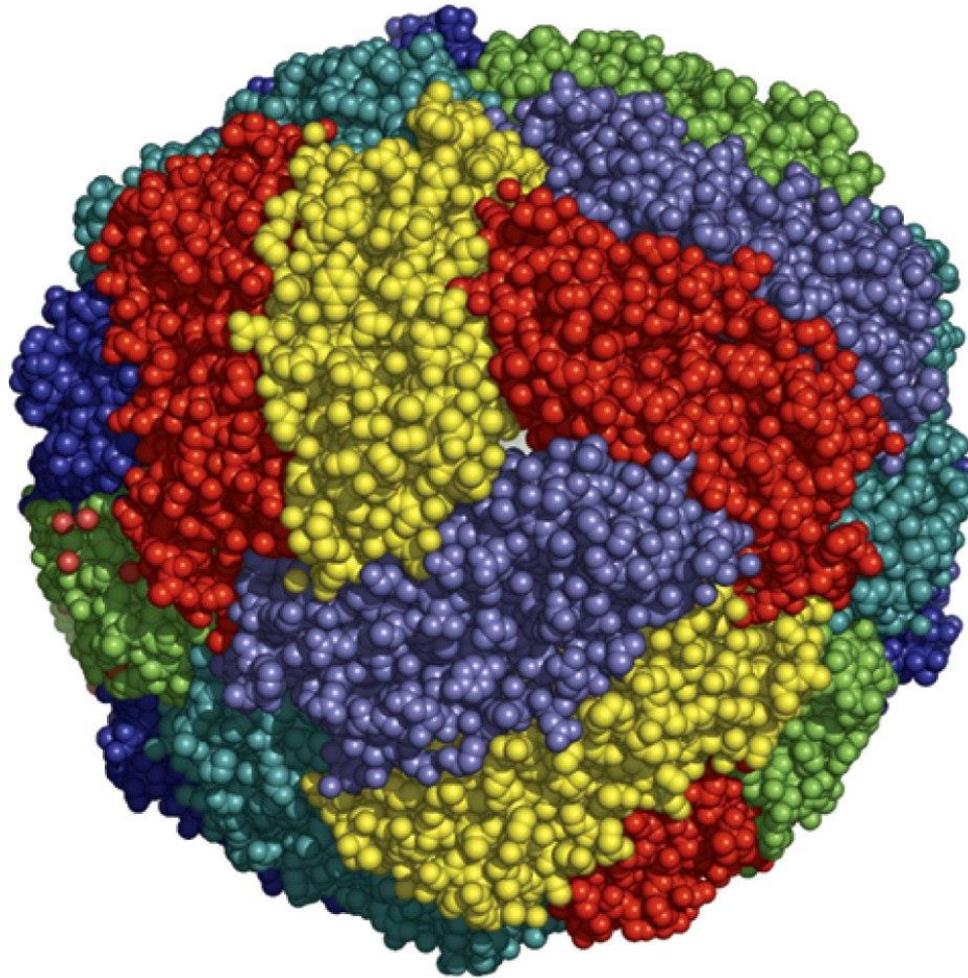


24 unità,
H e L

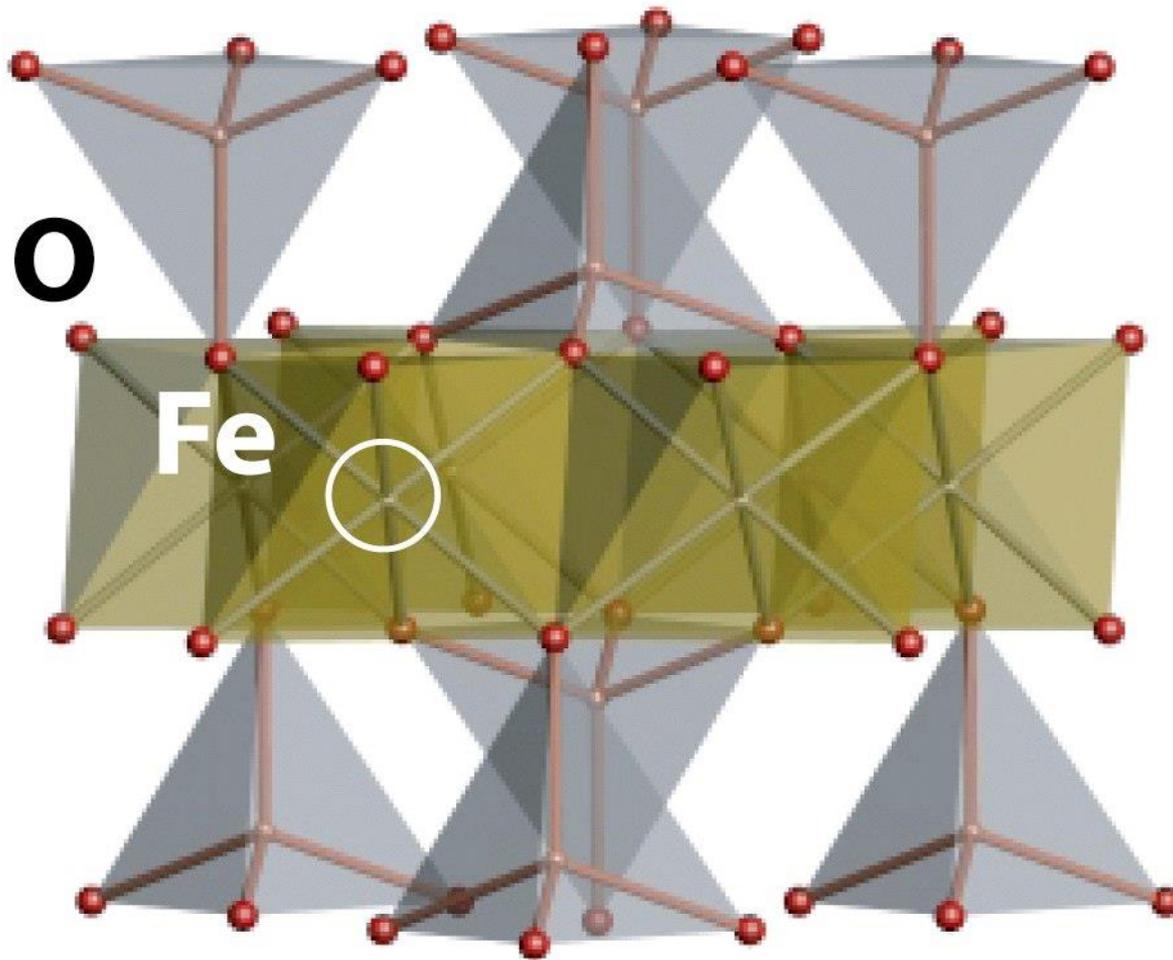
440 kDa

La *Heavy-chain ferritin* ha attività ferrossidasica
8 pori idrofilici con simmetria ternaria (*Fe in*)
6 pori idrofobici con simmetria quaternaria (*Fe out*)

In, 7.5nm

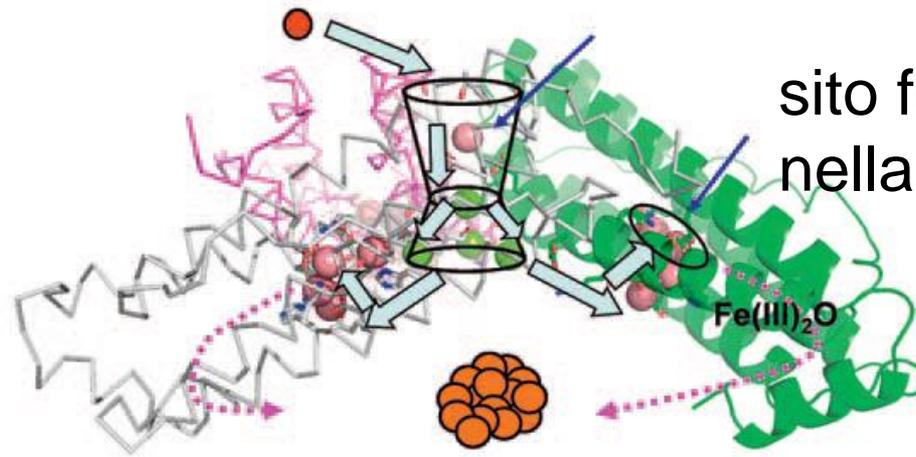
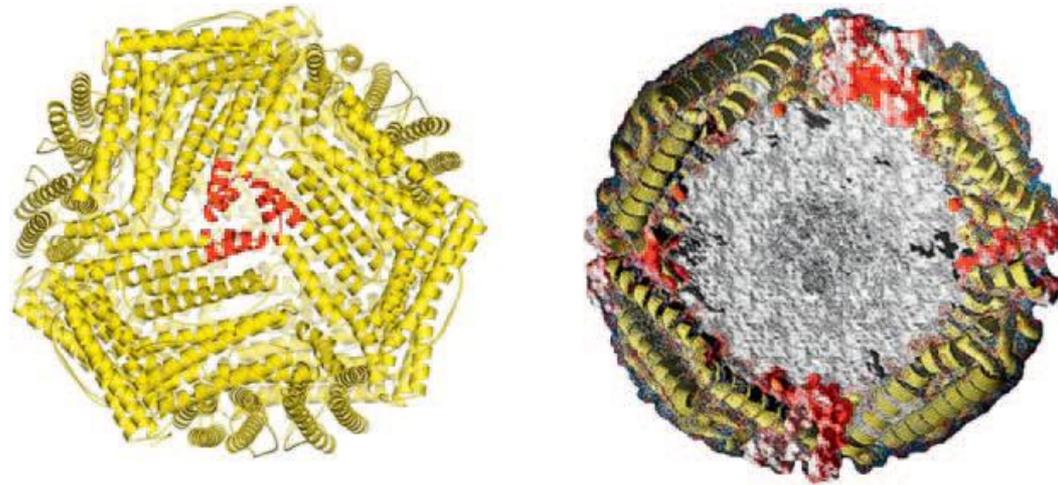


Out, 12 nm



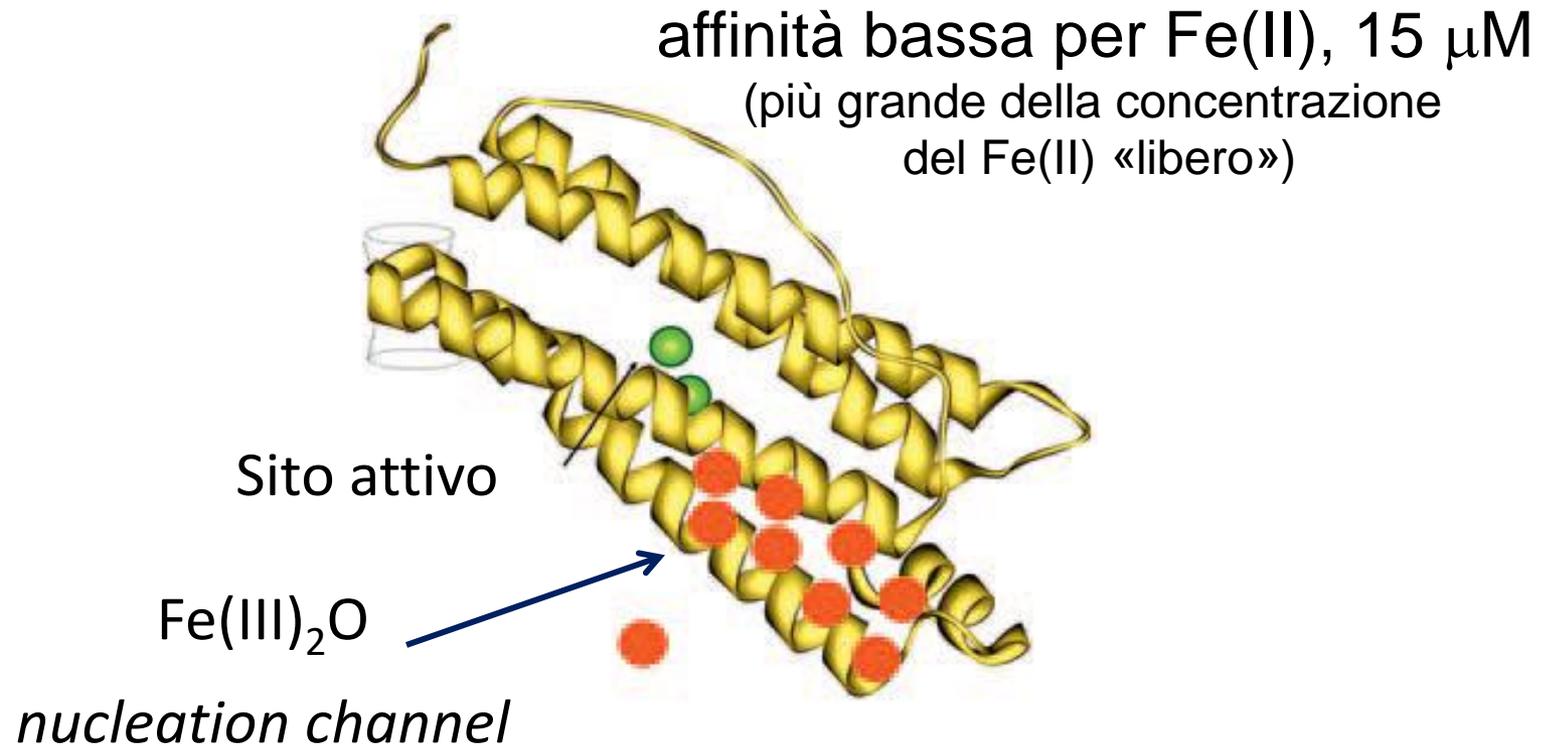
Ferrihydrite

Fino a 4500 atomi di Fe



sito ferrossidasico
nella *H*-ferritina

sito ferrossidasico



Ipotesi di proteine *chaperone* per il Fe(II) (e.g. PCPB1)

Struttura ai raggi X di un sito ferrossidasico

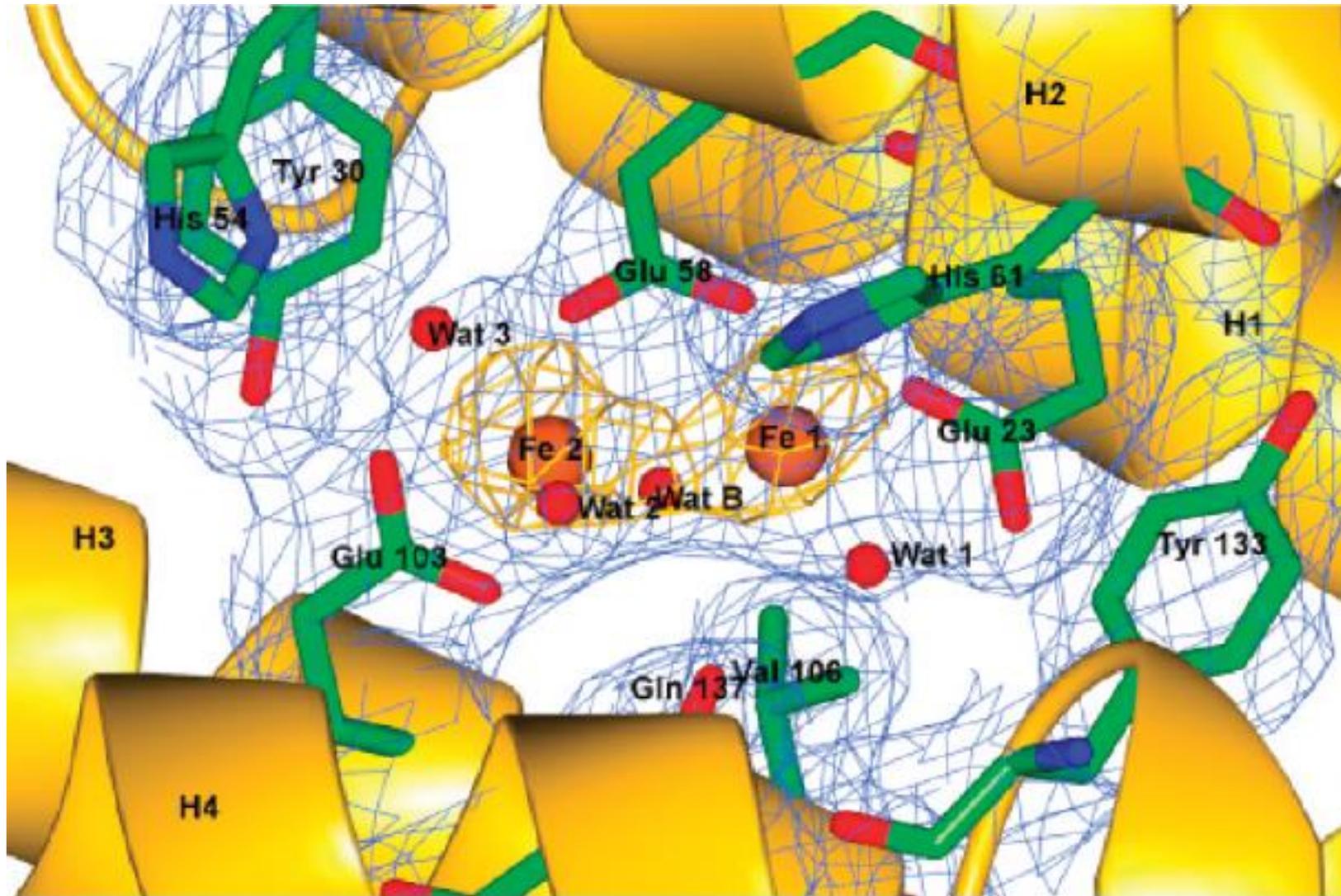
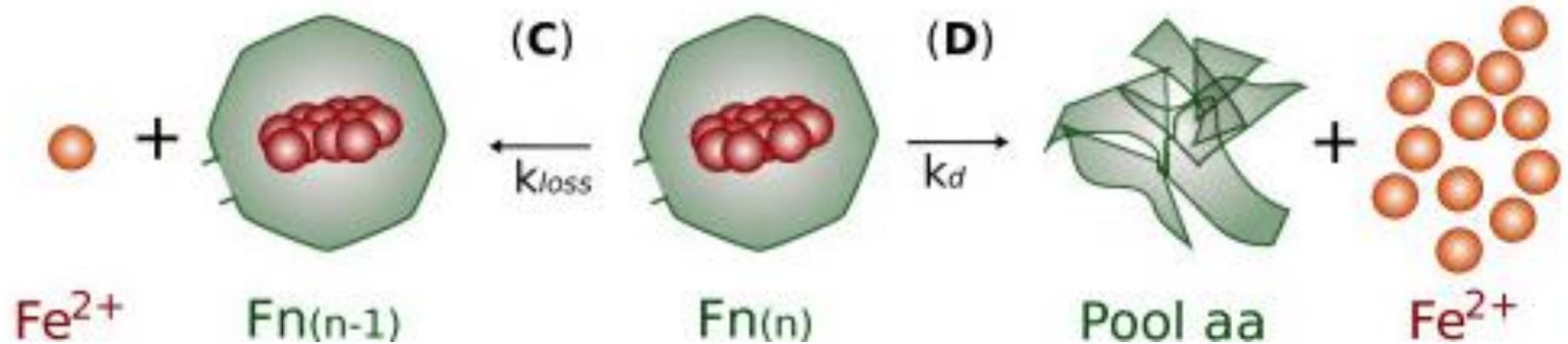


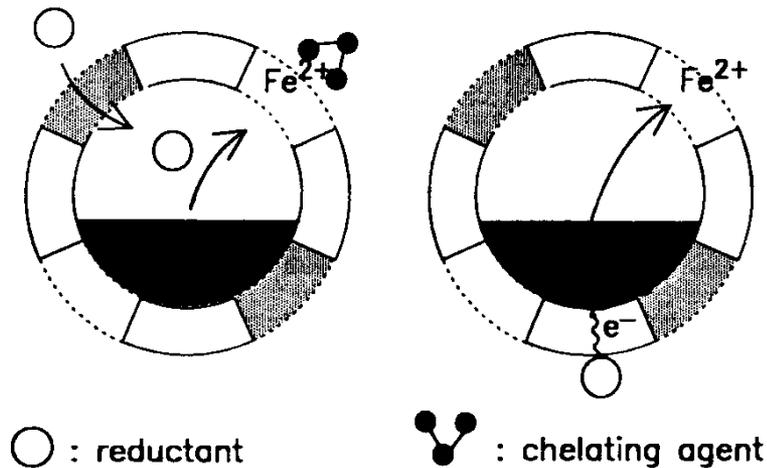


Immagine
TEM

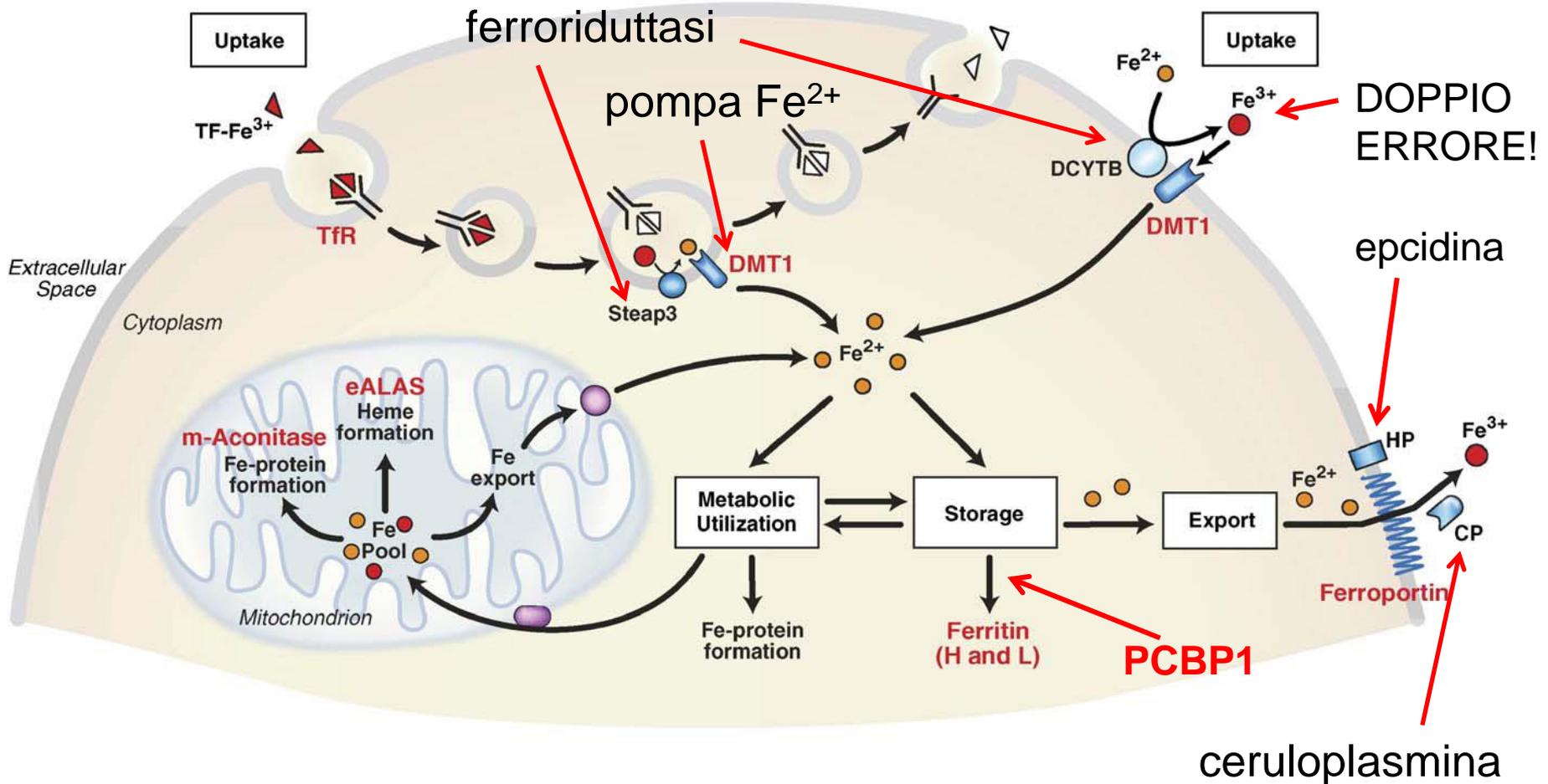
Rilascio del ferro



degradazione della proteina nei lisosomi?



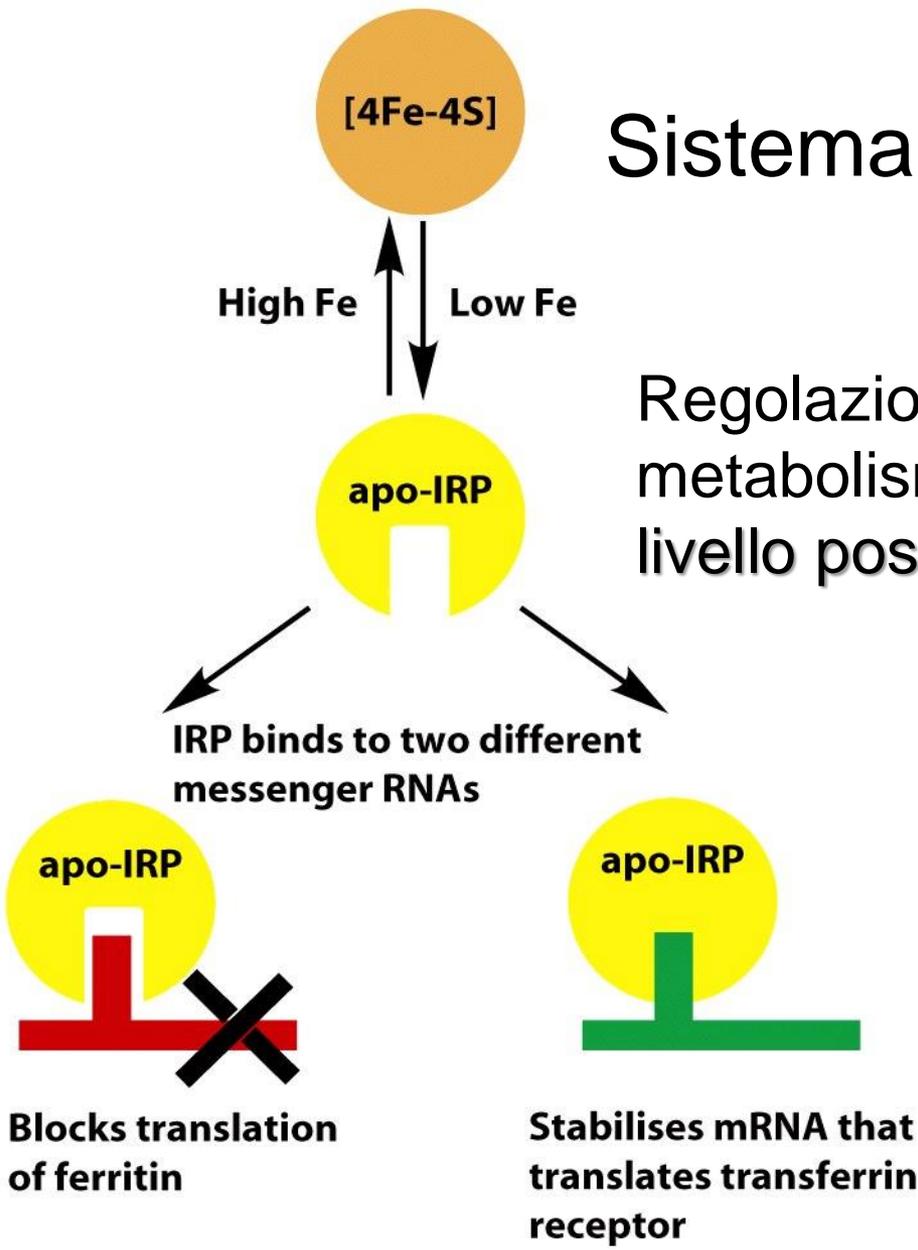
Omeostasi del ferro – Sistema IRP/IRE



IRP: Iron Regulatory Proteins

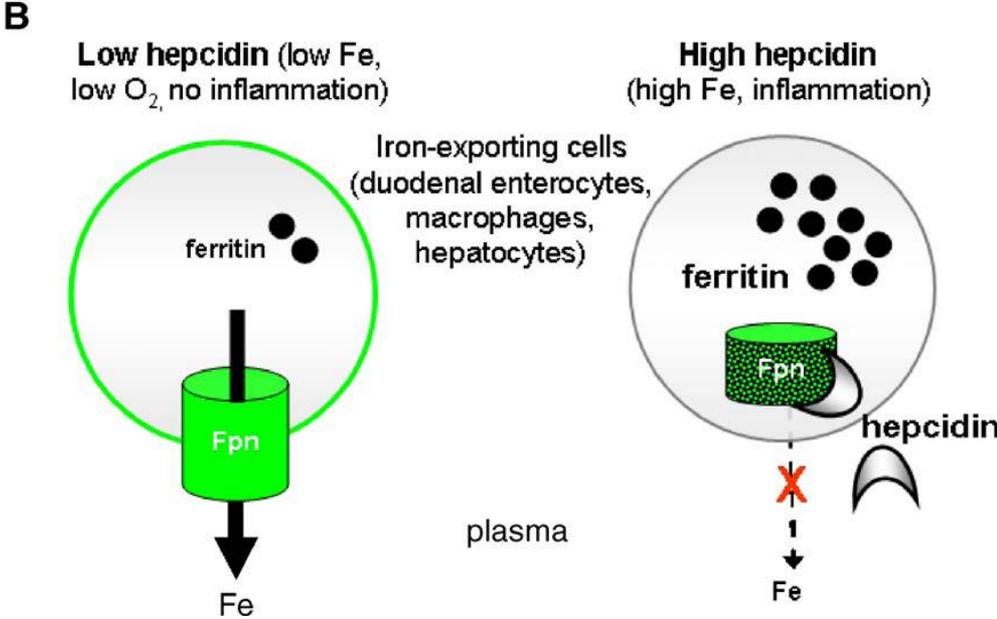
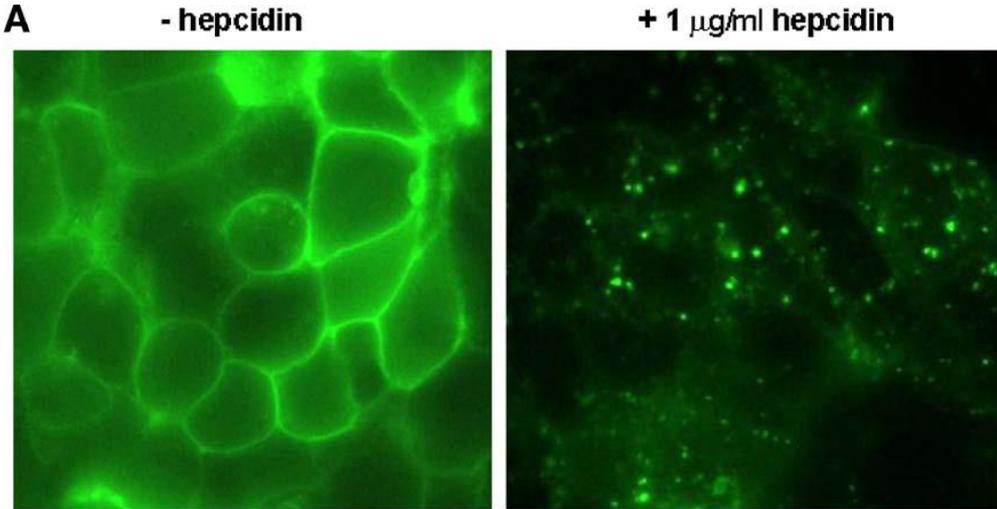
IRE: Iron Responsive Elements (mRNA)

Sistema IRP/IRE

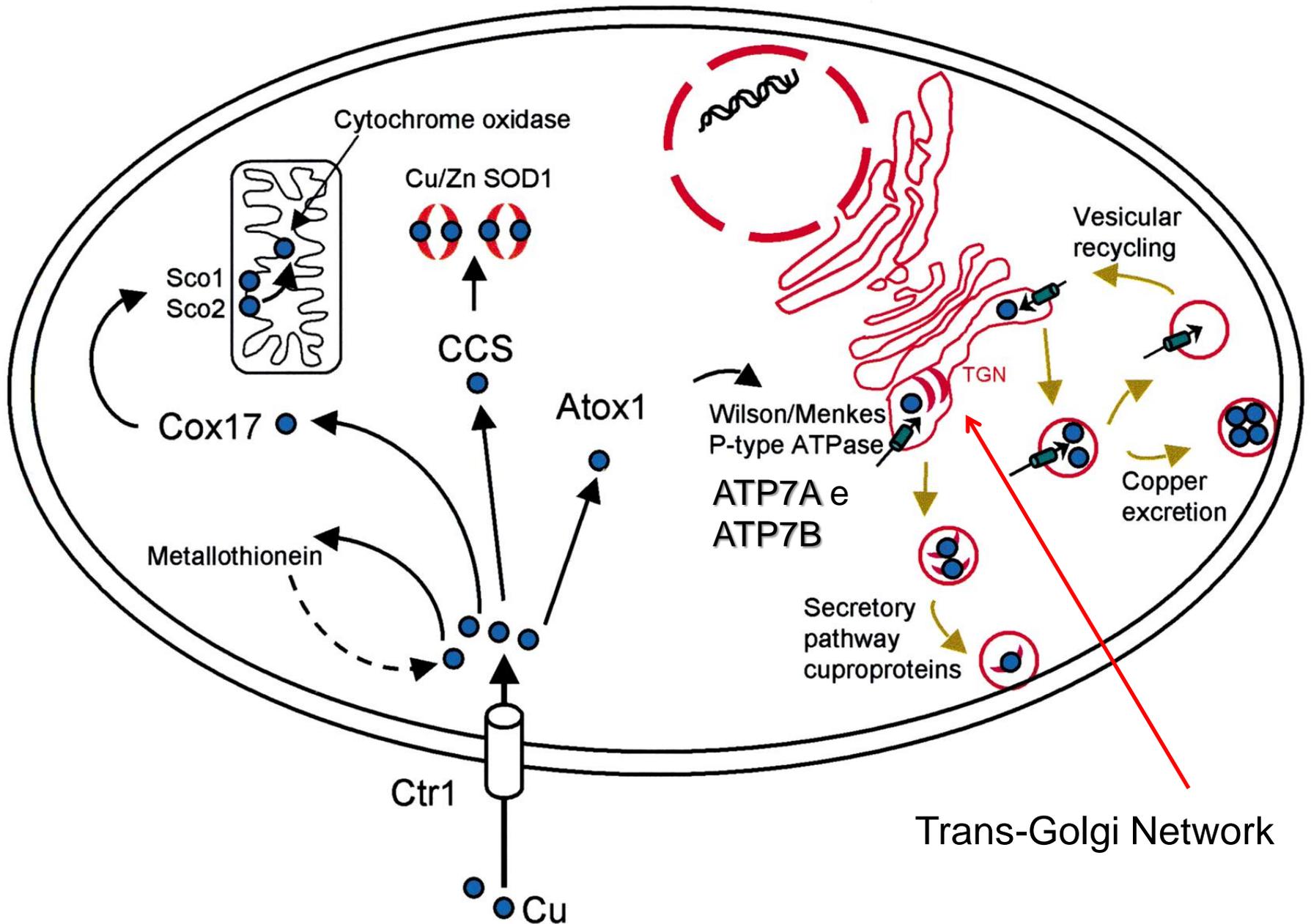


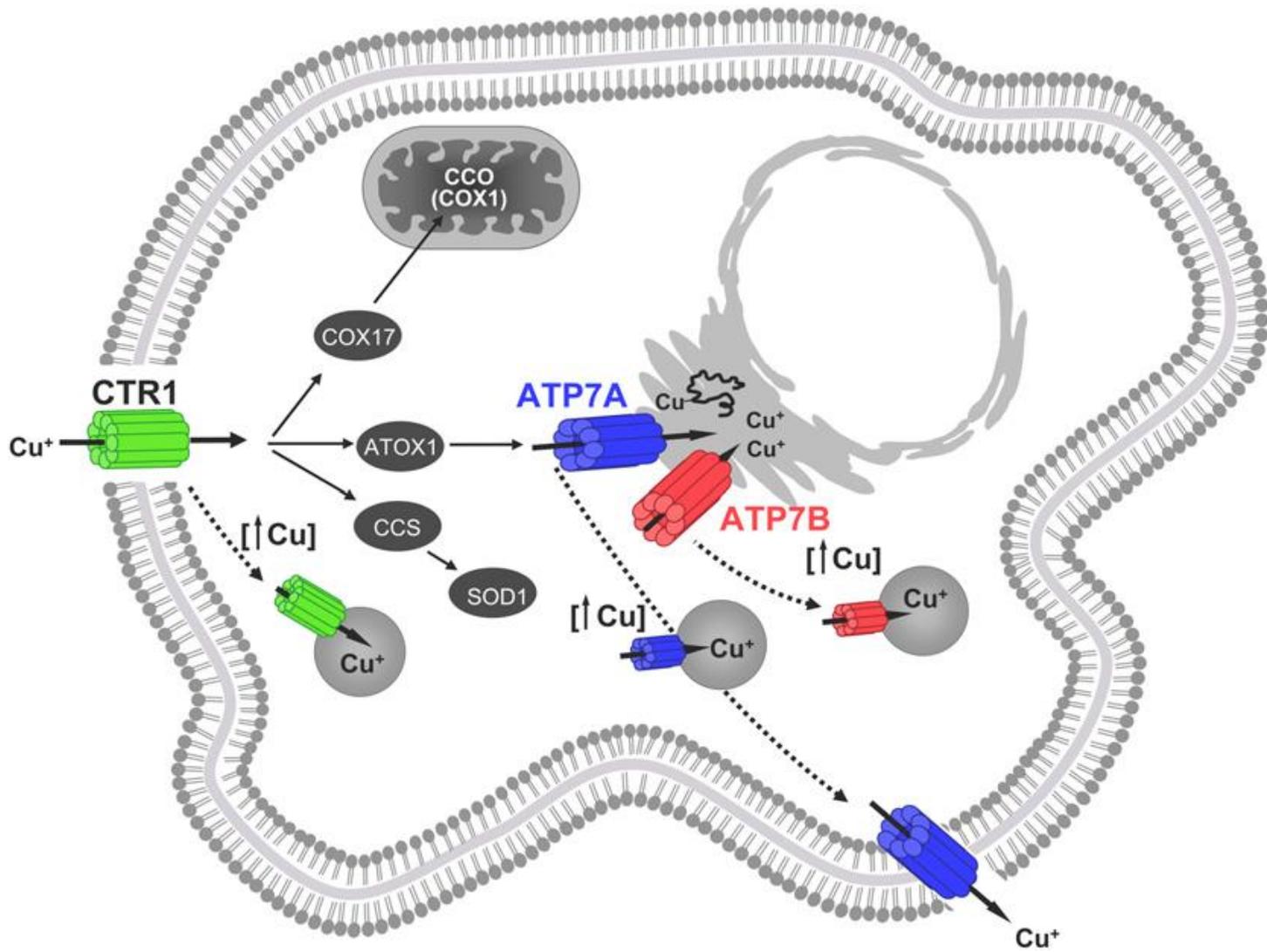
Regolazione del metabolismo del ferro a livello post-trascrizionale

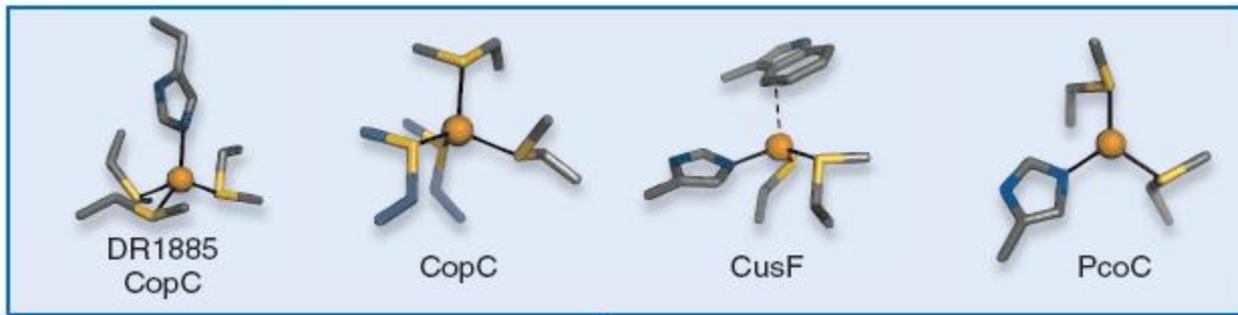
Export del ferro nel plasma regolato da epcidina



Omeostasi del rame

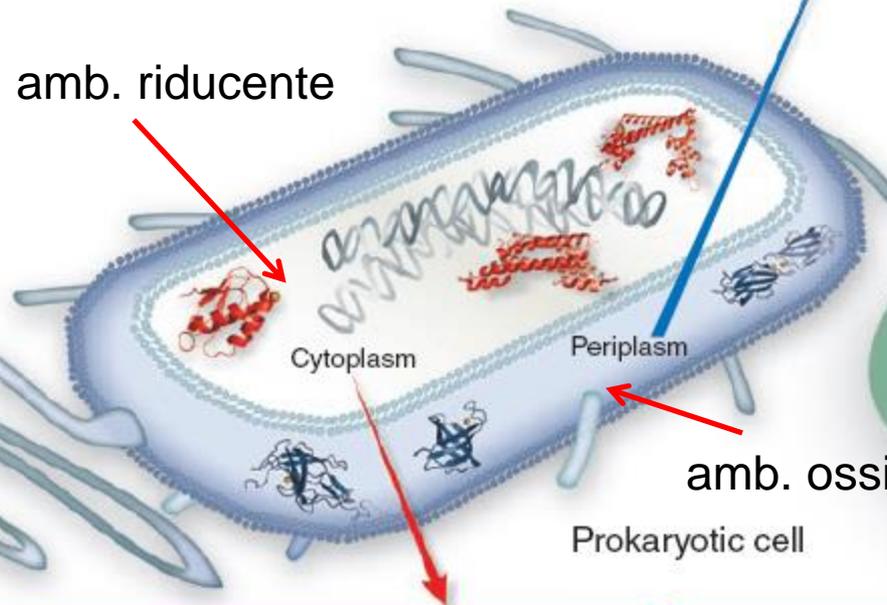






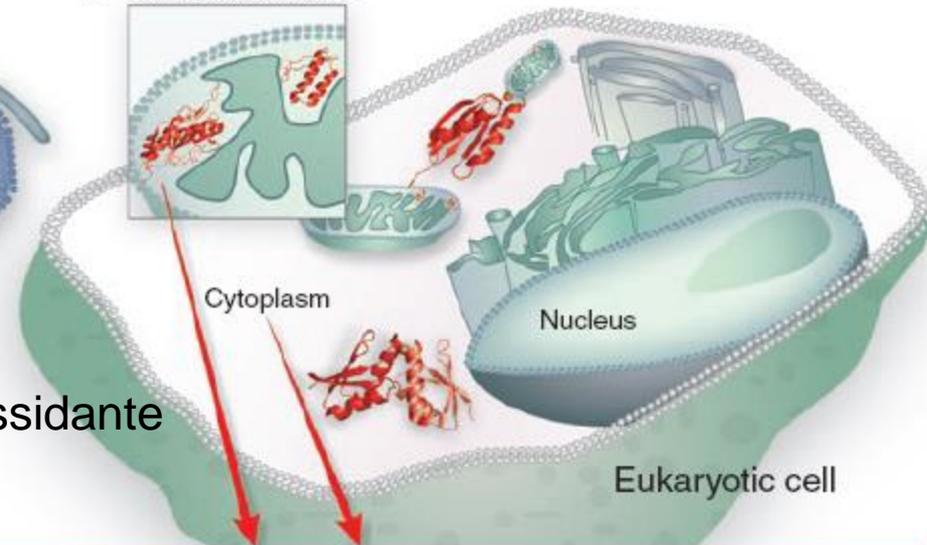
a

amb. riducente



b

Detail, mitochondrion



amb. ossidante

Prokaryotic cell

Eukaryotic cell



CopZ
CueR



CsoR



Atx1, Hah1
Ccc2, Mnk, Wnd
Cox17

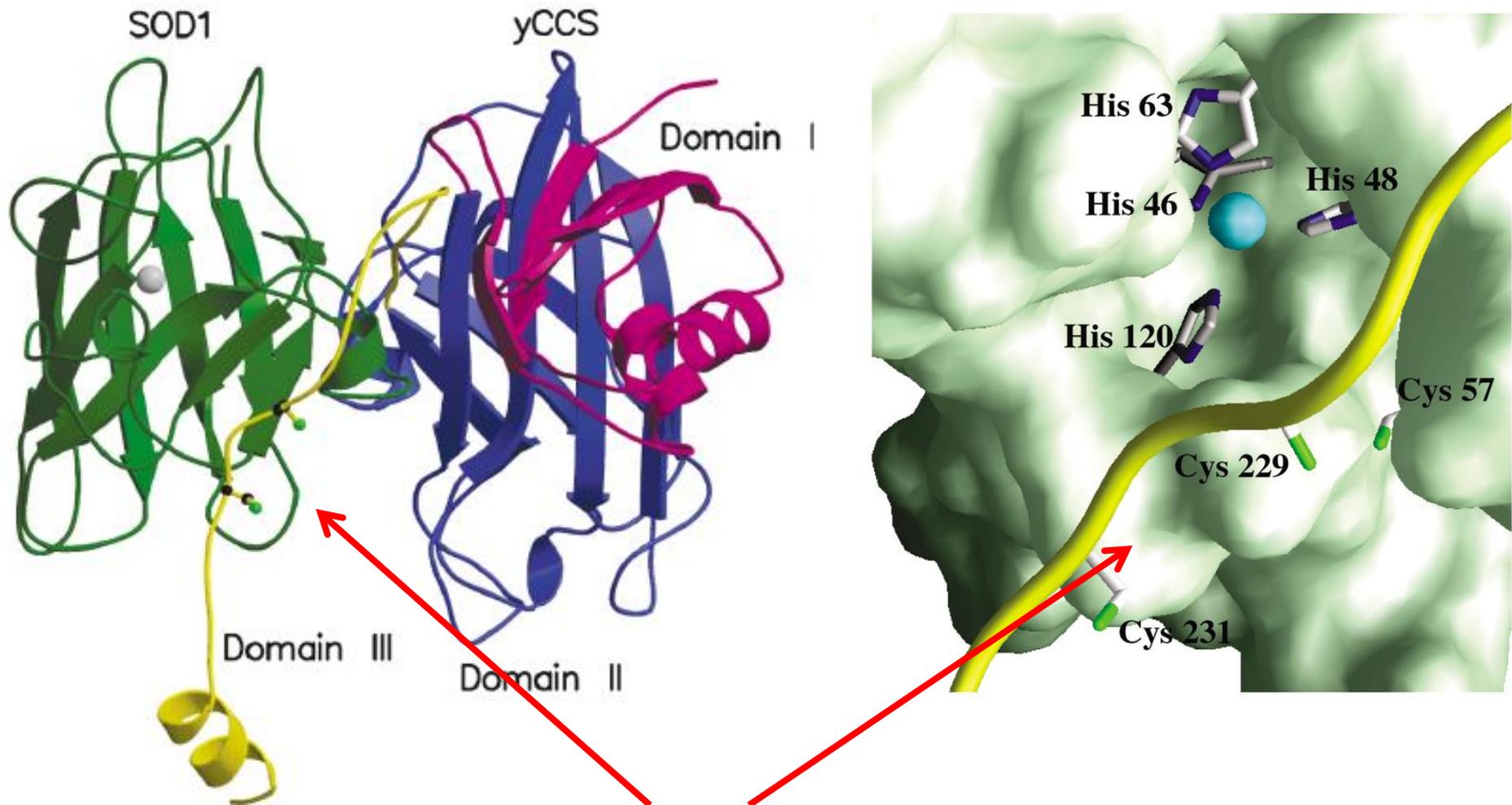


Hah1



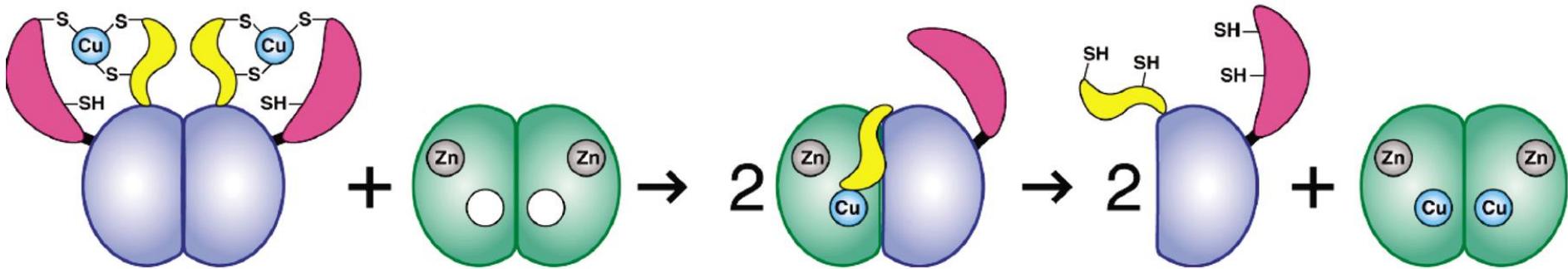
Sco1

CCS/Zn-SOD

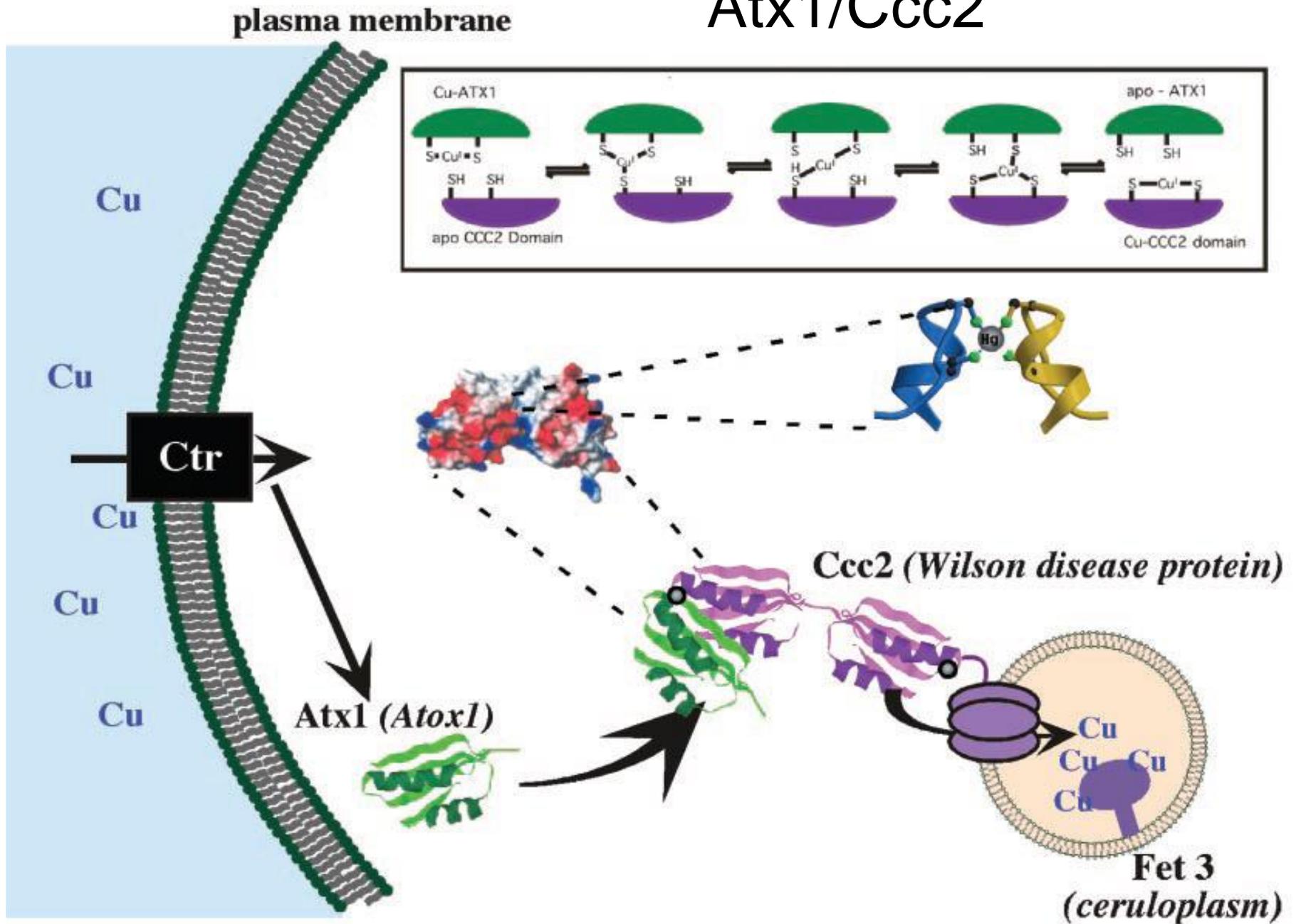


Sito di binding del Cu(I)

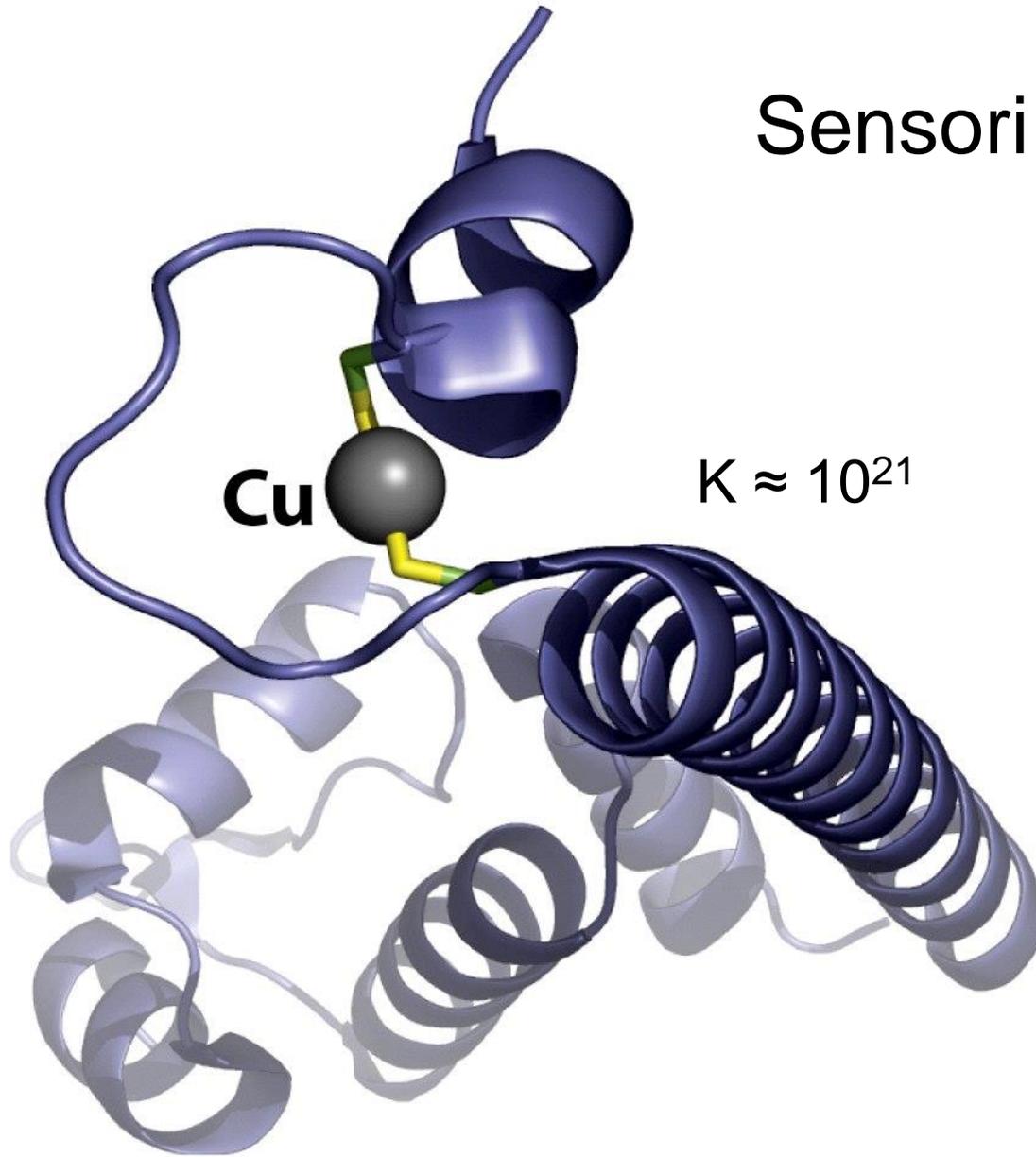
CCS/Zn-SOD



Atx1/Ccc2



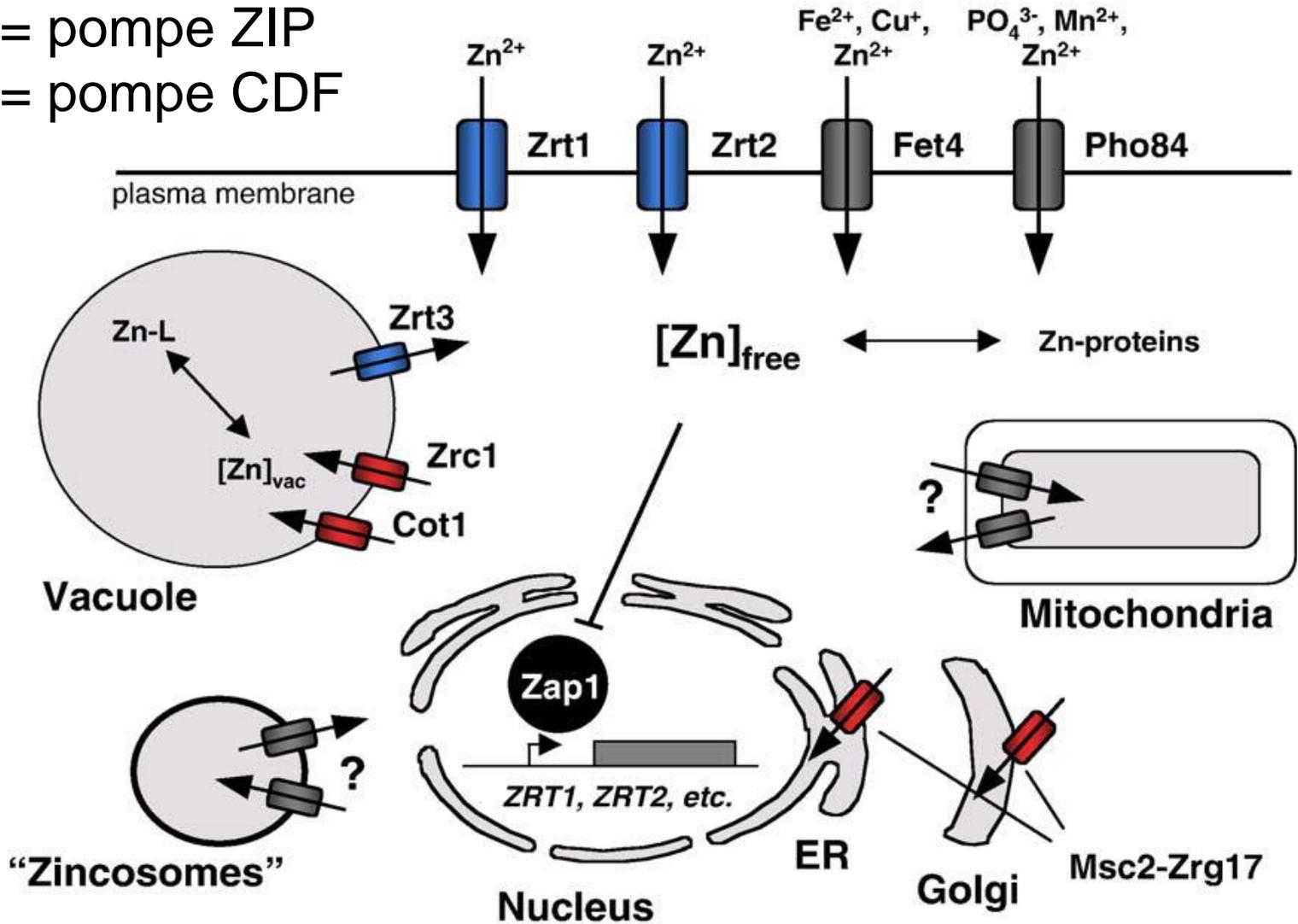
Sensori del Cu



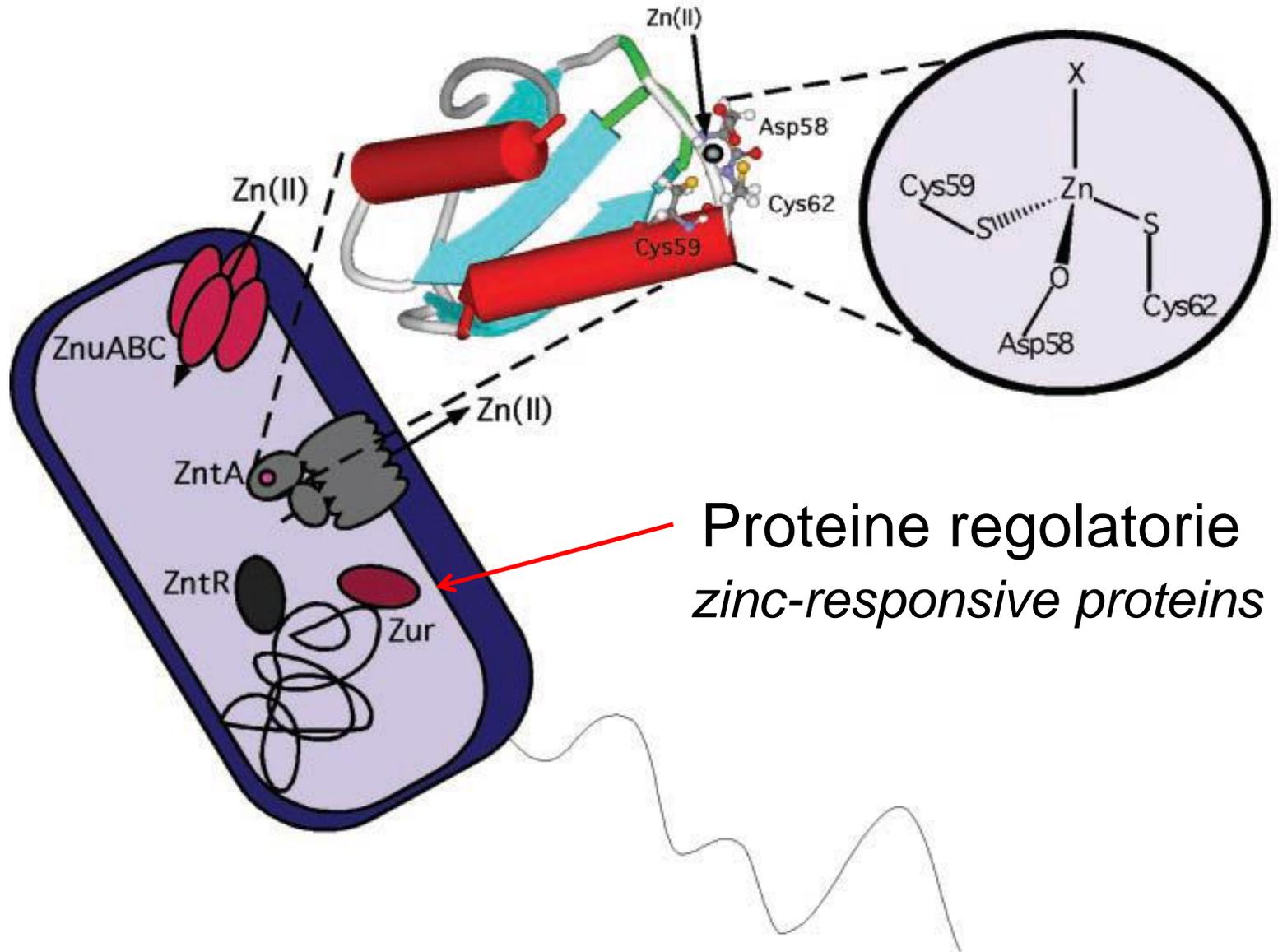
Fattore di trascrizione CueR (da *E. Coli*)

Omeostasi dello zinco in cellule eucariote

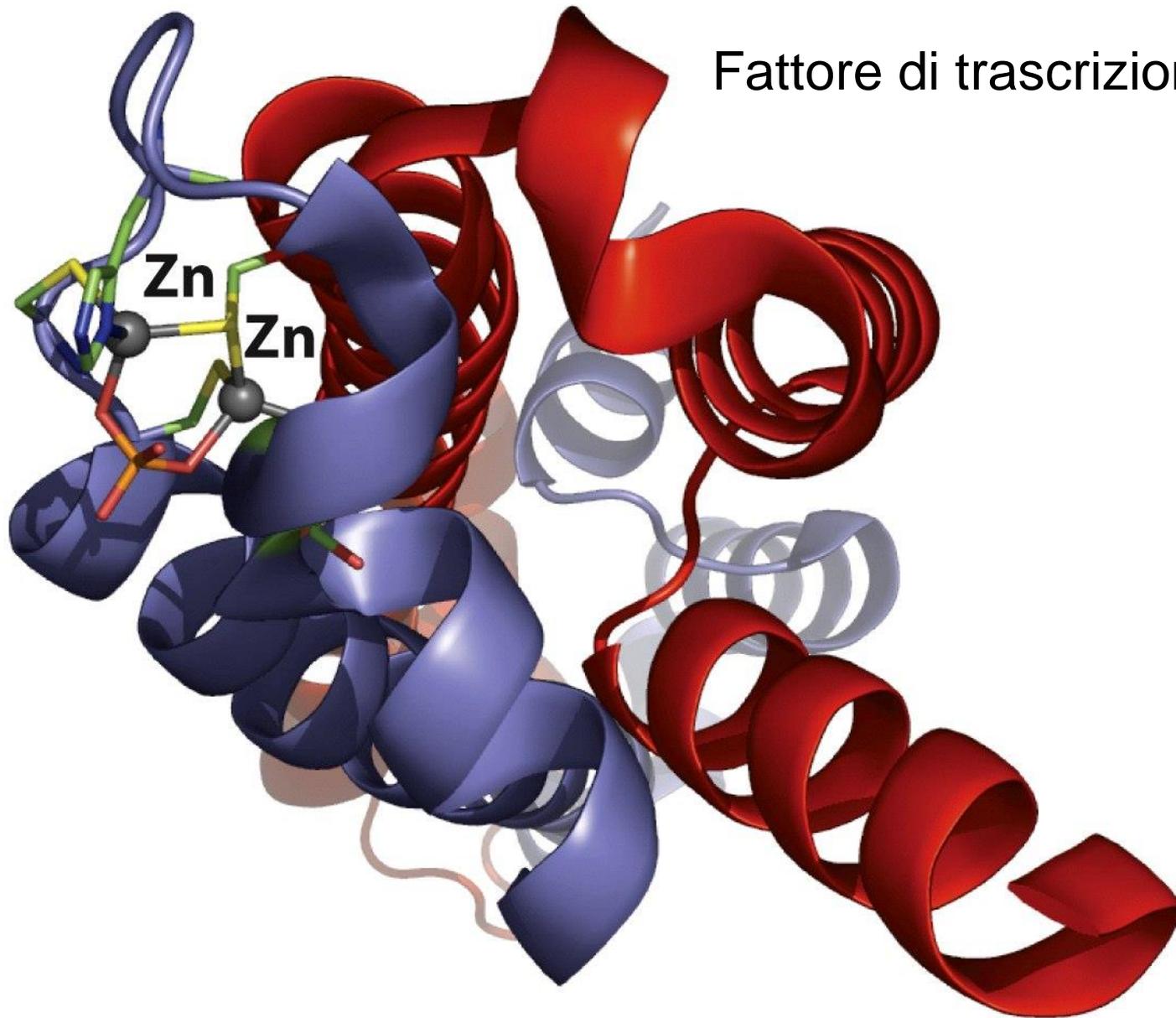
- = pompe ZIP
- = pompe CDF



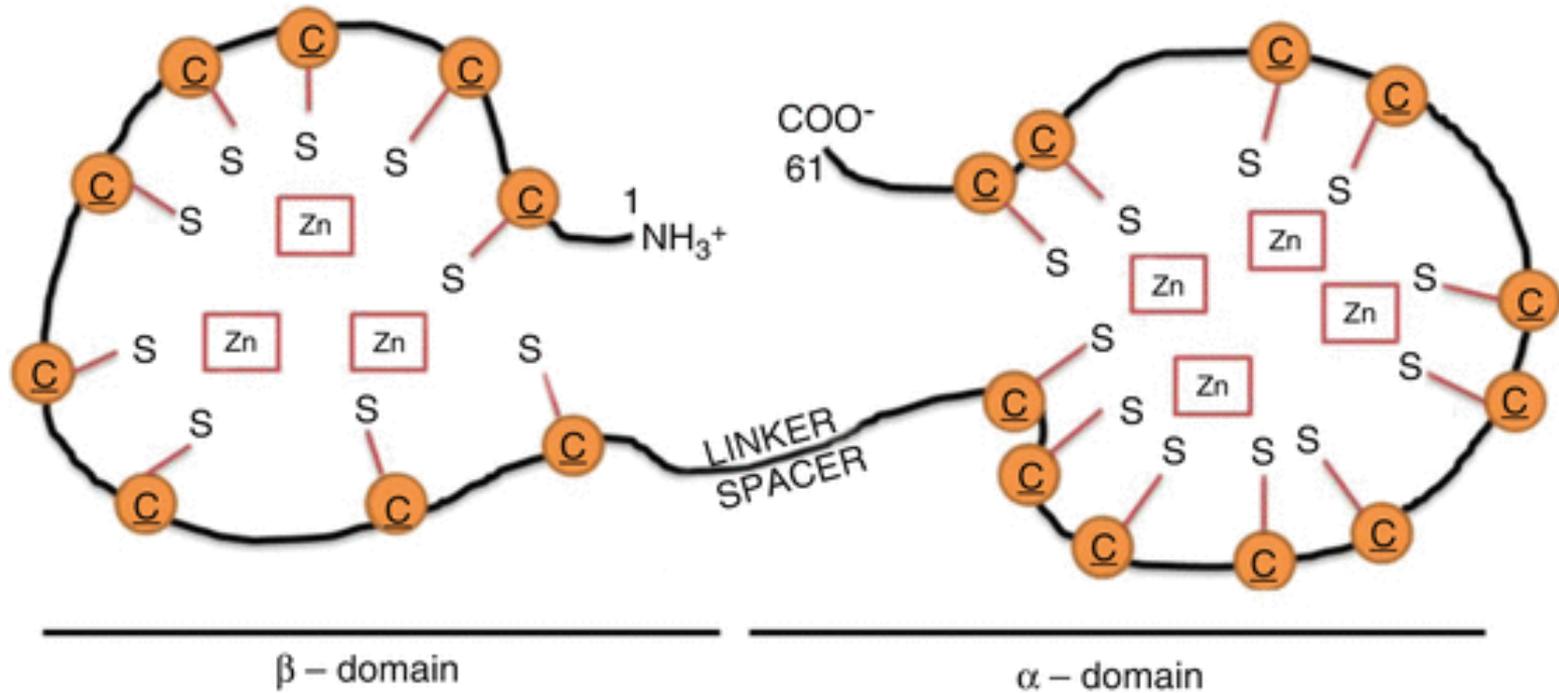
Omeostasi dello zinco nei batteri



Fattore di trascrizione ZntR



Metallotioneine



6 kDa,
ca. 60 a.a.
fino 30% cys

Metallotioneine

