

# Post-translacijske modifikacije proteinov (PTM)

# PTM

- post-translacijske modifikacije so kovalentne kemijске modifikacije proteinov, do katerih pride po translaciji
- s temi modifikacijami se močno poveča raznolikost proteinov: iz ~23 000 genov -> tudi do 1 000 000 različnih proteinov
- okrog 5% genoma višjih evkariontov kodira encime, ki opravlja PTM (500 kinaz, 150 fosfataz, 500 proteaz, ...)

# Biološke funkcije PTM

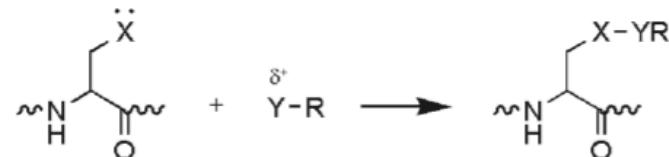
- z uvedbo novih kemijskih skupin se razširi repertoar funkcij nekega proteina
- aktivacija in inaktivacija encimov
- sprememba hidrofobnosti proteinov
- regulacija in prenos signalov
- razgradnja proteinov
- epigenetske spremembe DNA in organizacija kromosomov

...

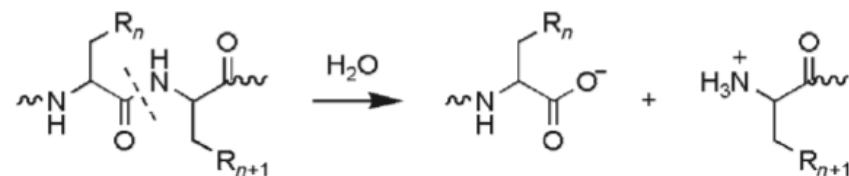
# Razdelitev PTM

- encimsko katalizirane kovalentne adicije različnih kemijskih spojin
  - razdelitev glede na aminokislino, ki se modificira
  - glede na kemijsko naravo skupine, ki se doda
  - glede na spremenjeno funkcijo PTM proteina
- proteolitična razgradnja proteinov, ki vpliva na lokalizacijo, aktivnost in življenjsko dobo proteina

1. Covalent modification



2. Cleavage of protein backbone

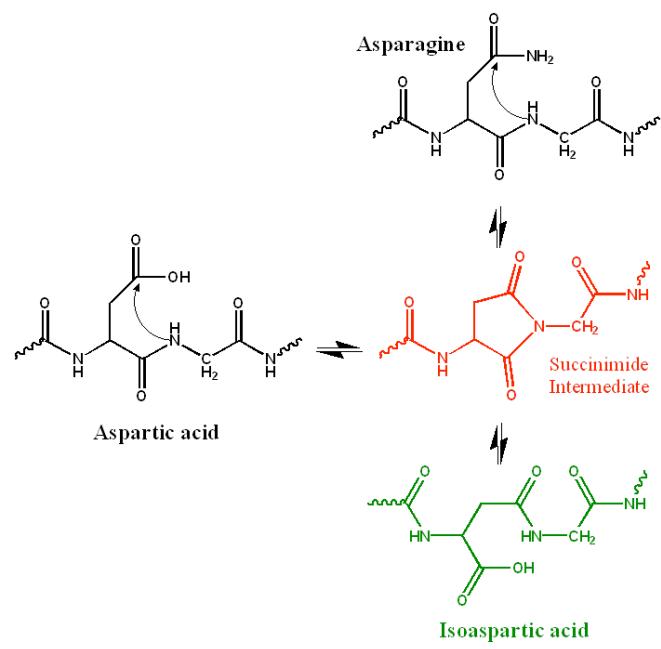


# PTM po aminokislinah

Residue	Reaction	Example
Asp	phosphorylation	protein tyrosine phosphatases; response regulators in two-component systems
	isomerization to isoAsp	
Glu	methylation	chemotaxis receptor proteins
	carboxylation	Gla residues in blood coagulation
	polyglycination	tubulin
	polyglutamylation	tubulin
Ser	phosphorylation	protein serine kinases and phosphatases
	O-glycosylation	notch O-glycosylation
	phosphopantetheinylation	fatty acid synthase
	autocleavages	pyruvamidyl enzyme formation
Thr	phosphorylation	protein threonine kinases/phosphatases
	O-glycosylation	

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	O-glycosylation	



# PTM po aminokislinah

Tyr	phosphorylation sulfation <i>ortho</i> -nitration TOPA quinone	tyrosine kinases/phosphatases CCR5 receptor maturation inflammatory responses amine oxidase maturation
His	phosphorylation  aminocarboxypropylation N-methylation	sensor protein kinases in two-component regulatory systems  diphthamide formation methyl CoM reductase
Lys	N-methylation  N-acylation by acetyl, biotinyl, lipoyl, ubiquityl groups  C-hydroxylation	histone methylation  histone acetylation; swinging-arm prosthetic groups; ubiquitin; SUMO (small ubiquitin-like modifier) tagging of proteins  collagen maturation
Cys	S-hydroxylation (S-OH) disulfide bond formation phosphorylation S-acylation S-prenylation protein splicing	sulfenate intermediates protein in oxidizing environments PTPases Ras Ras intein excisions

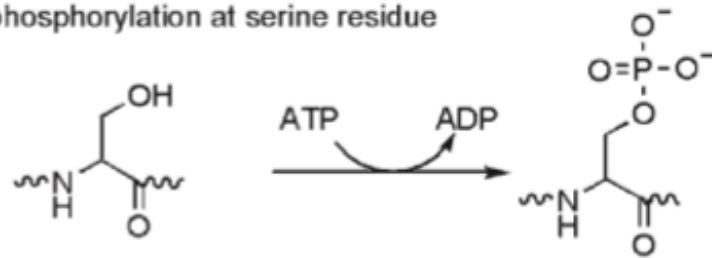
# PTM po aminokislinah

Met	oxidation to sulfoxide	Met sulfoxide reductase
Arg	N-methylation N-ADP-ribosylation	histones $G_{S\alpha}$
Asn	N-glycosylation N-ADP-ribosylation protein splicing	N-glycoproteins eEF-2 intein excision step
Gln	transglutamination	protein cross-linking
Trp	C-mannosylation	plasma-membrane proteins
Pro	C-hydroxylation	collagen; HIF-1 $\alpha$
Gly	C-hydroxylation	C-terminal amide formation

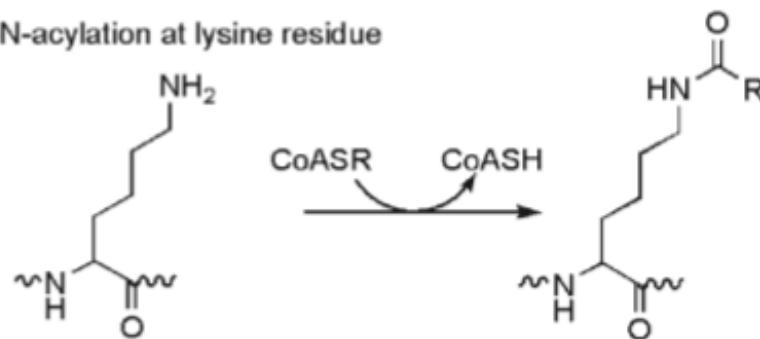
\*Ni znanih modifikacij Leu, Ile, Val, Ala, Phe

# Najpogostejše kovalentne adicije

O-phosphorylation at serine residue



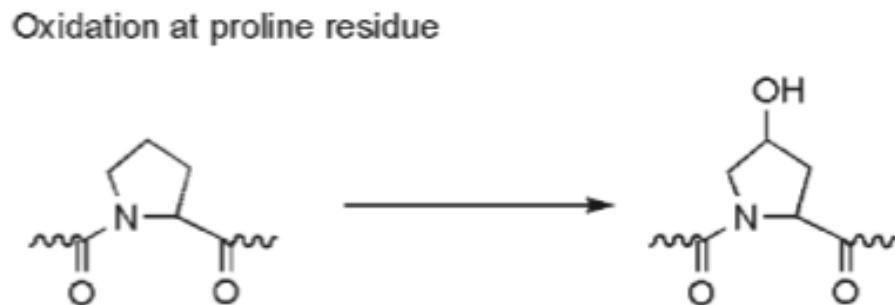
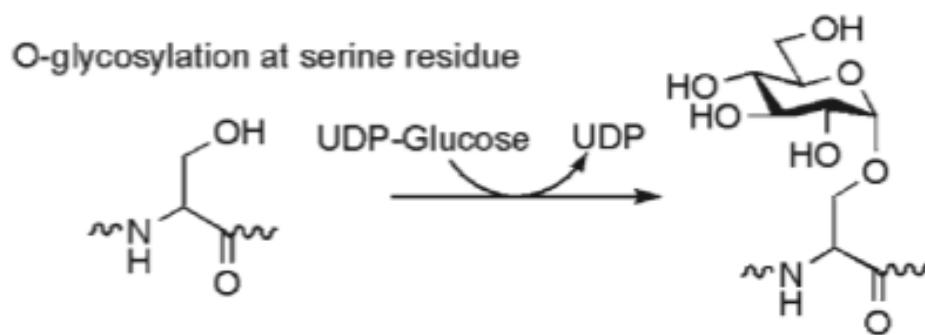
$\epsilon$ -N-acylation at lysine residue



$\epsilon$ -N-alkylation at lysine residue

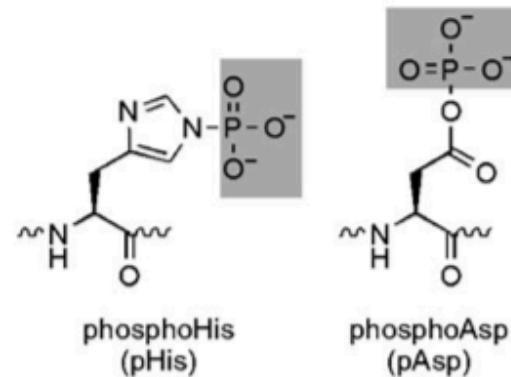
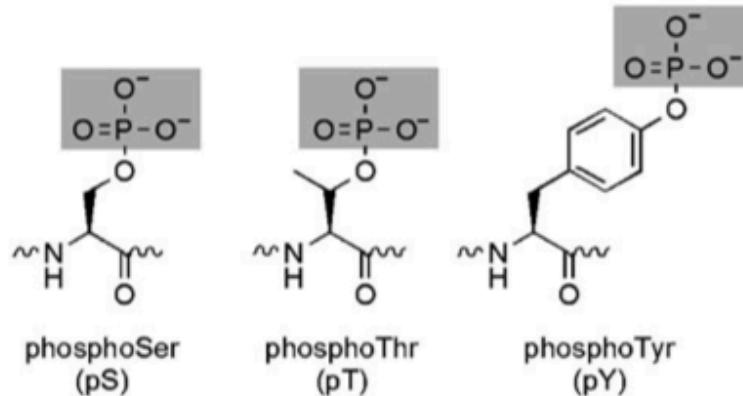


# Najpogostejše kovalentne adicije



# Fosforilacija

- sesalci pS, pT, pY
- bakterije in glive  
še pH in pD



# Fosforilacija vpliva na aktivnost encimov

- fosforilacijo proteinov katalizirajo **proteinske kinaze**
- defosforilacija je spontana ali pa jo katalizirajo **proteinske fosfataze**
- Največkrat se **fosforilirajo** hidroksilne skupine Ser, Thr ali Tyr

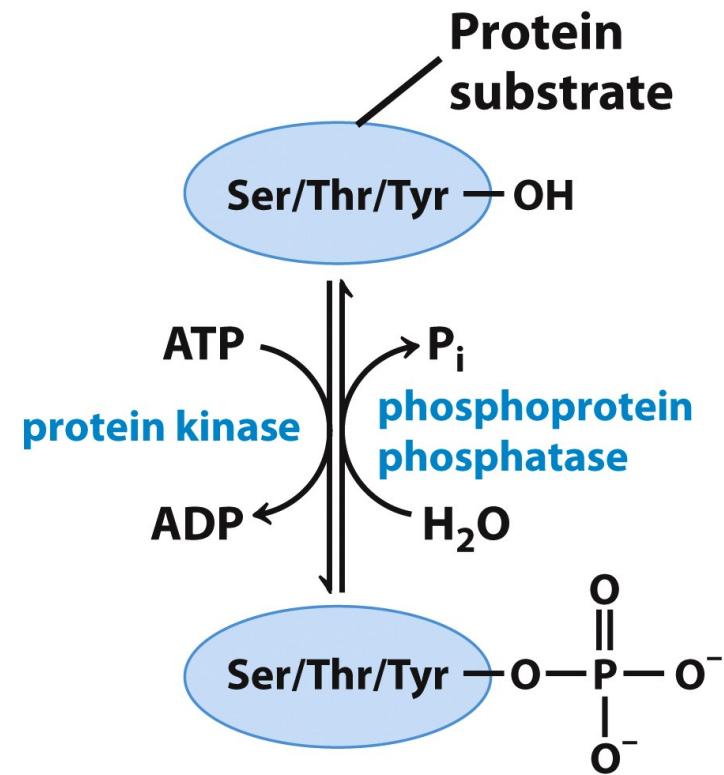
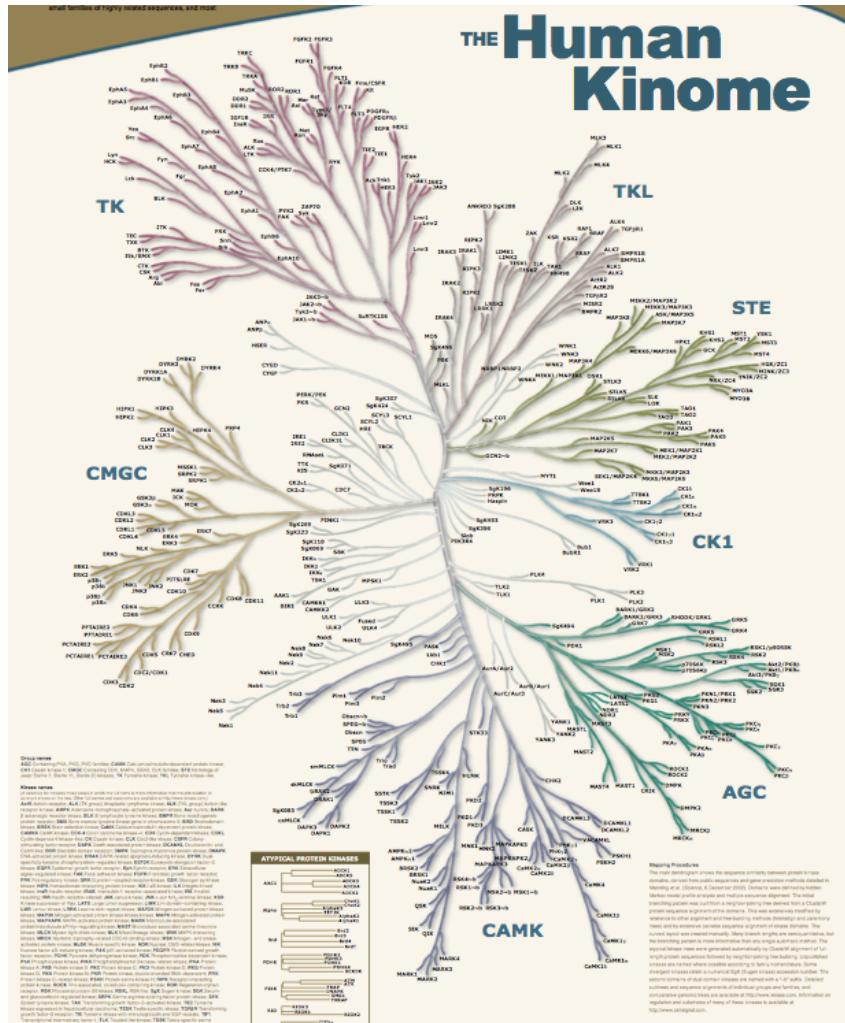
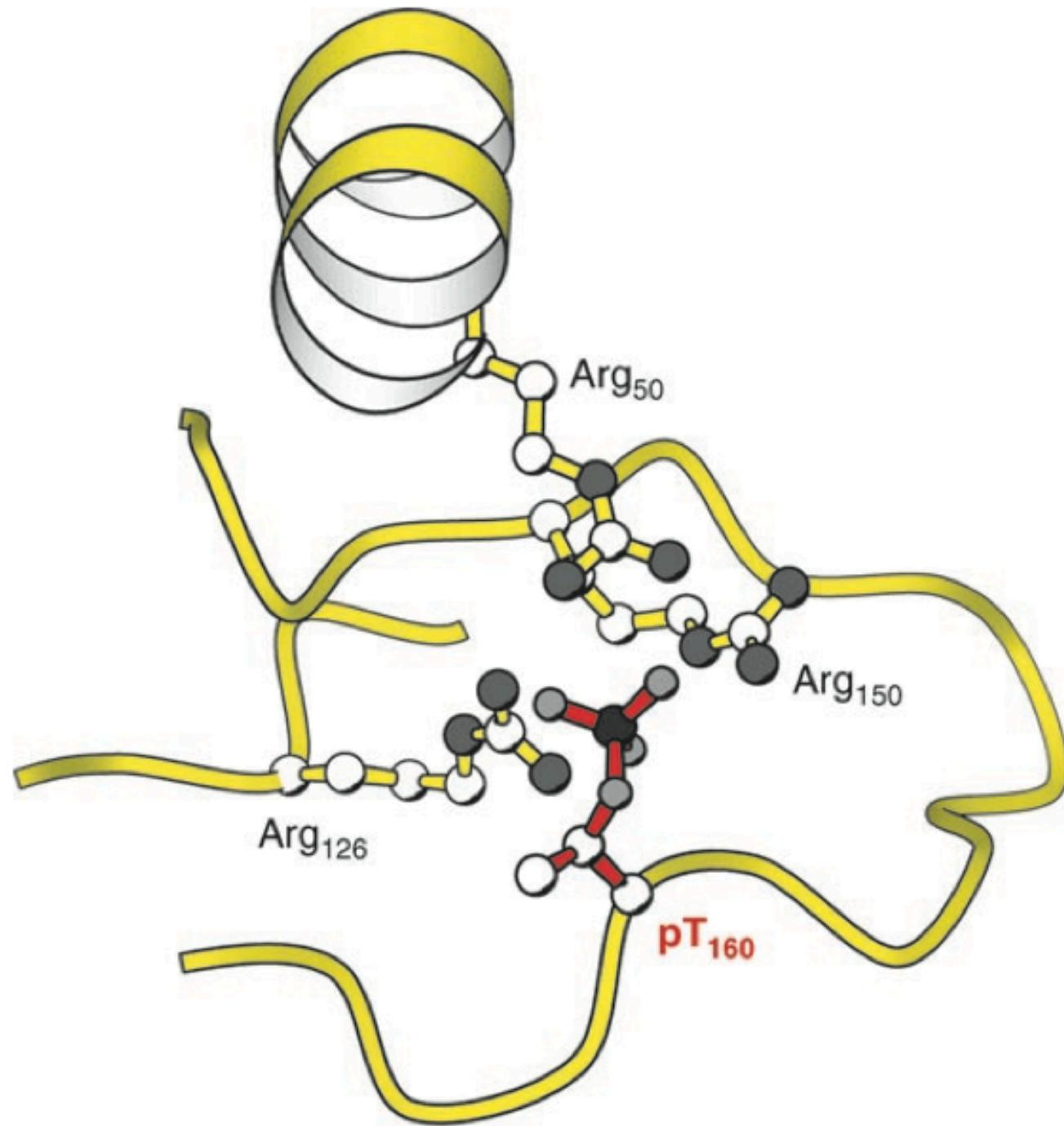


Figure 15-3  
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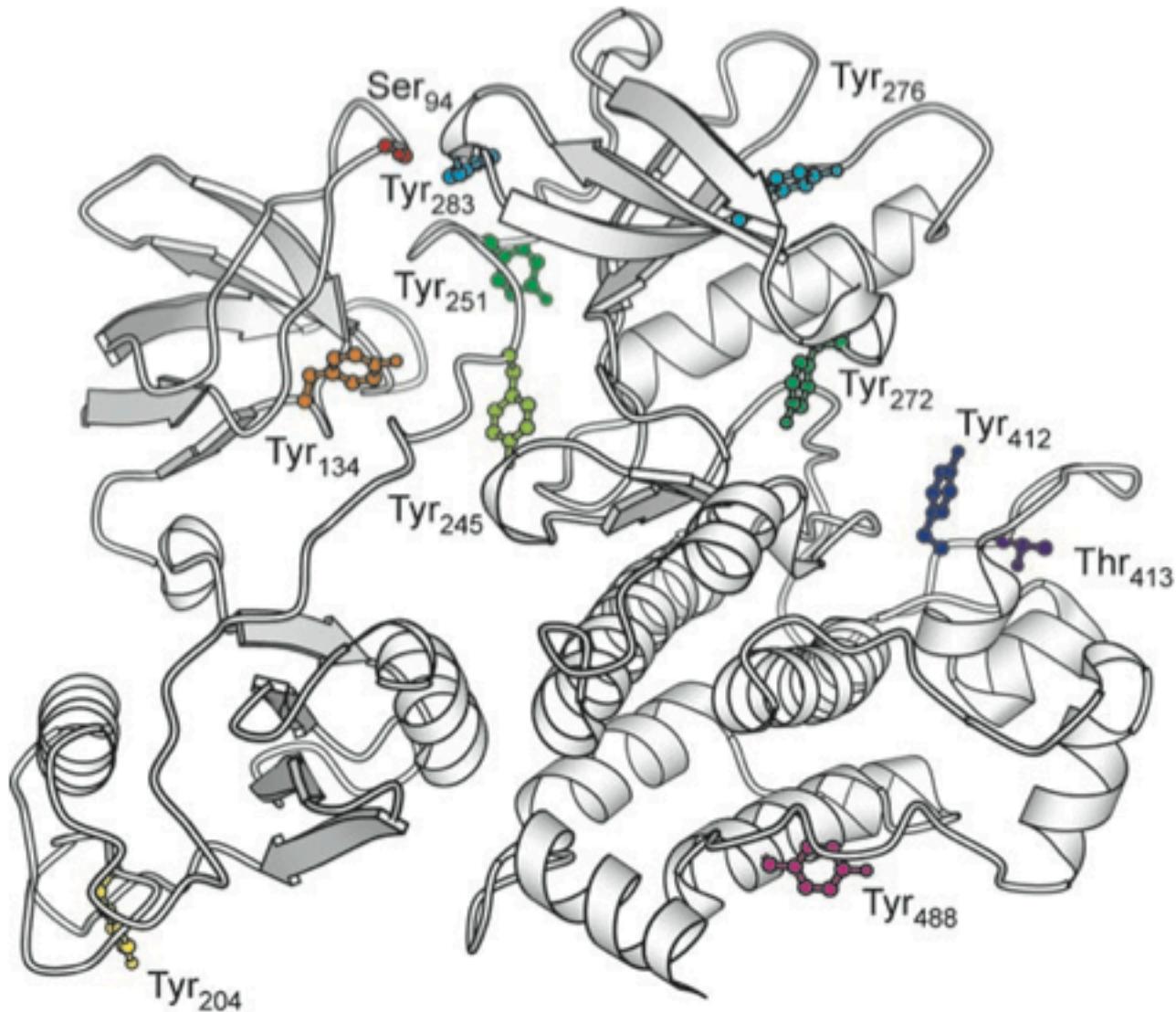
# Človeški kinom

- približno 500 različnih kinaz
  - veliko različnih fosforiliranih proteinov!!!
  - substrati so lahko fosforilirani tudi na več mestih (npr. Abl protein kinaza ima fosforiliranih 11 različnih aminokislin)





# Abl-kinaza



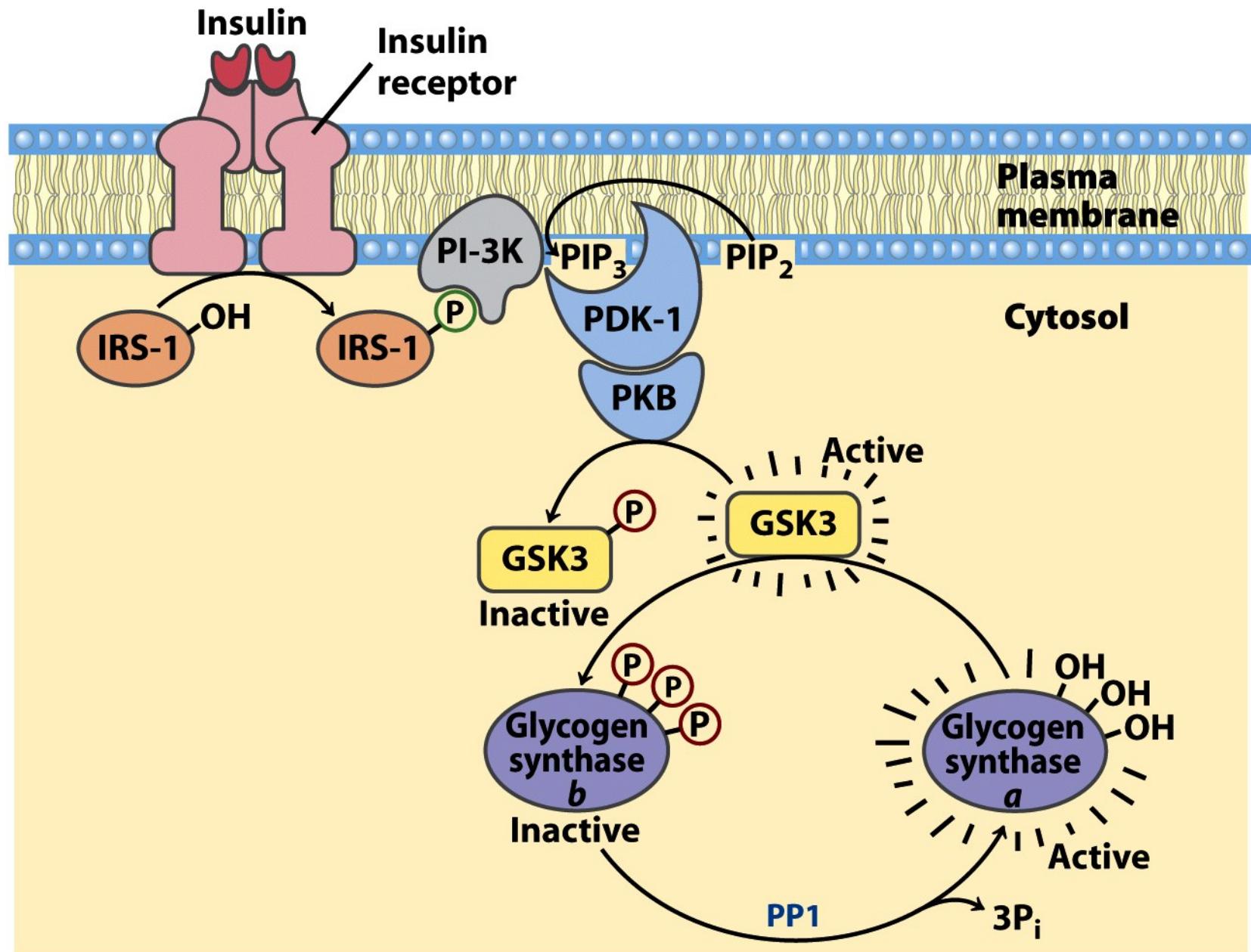


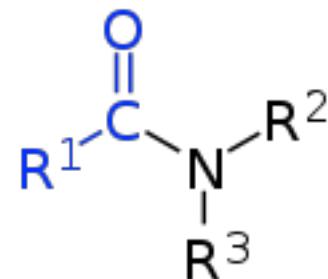
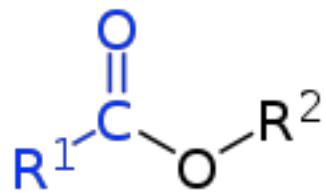
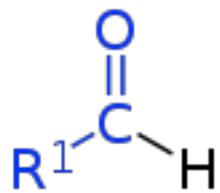
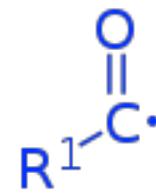
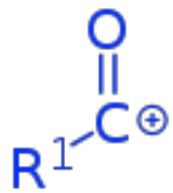
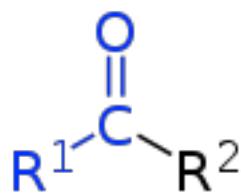
Figure 15-39

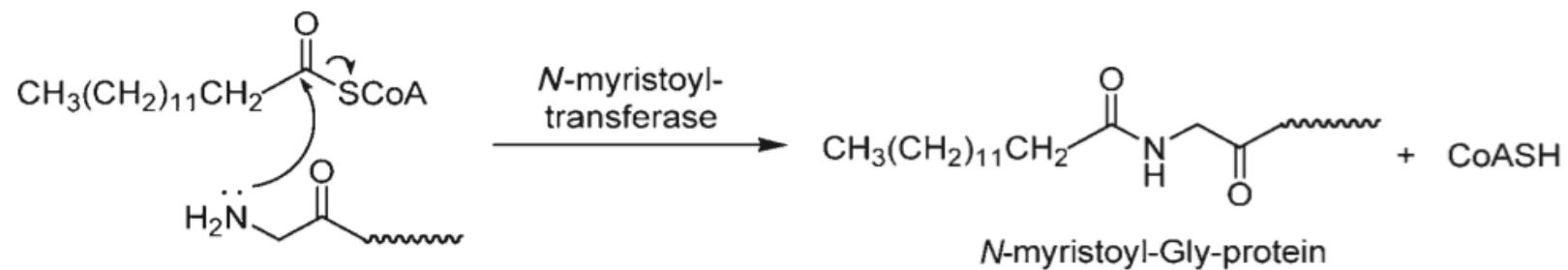
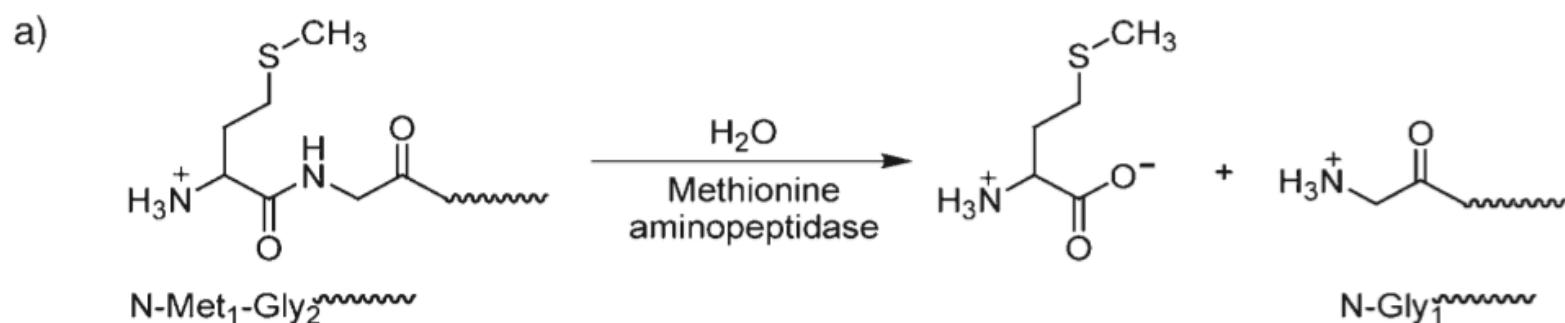
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fosfoproteína fosfatasa 1 (3x)

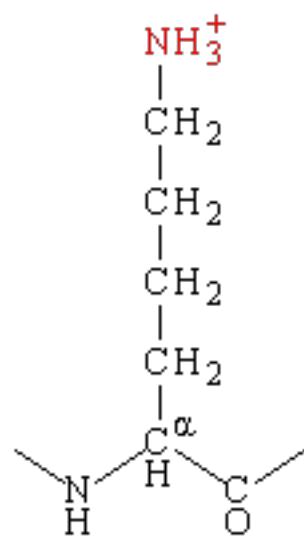
# Acilacija proteinov

- najpogosteje acetilacija (C2), npr. acetilacija histonov
- miristoilacija (C14) glicinskih N-začetkov
- palmitoilacija (C16) cisteinov (-S)



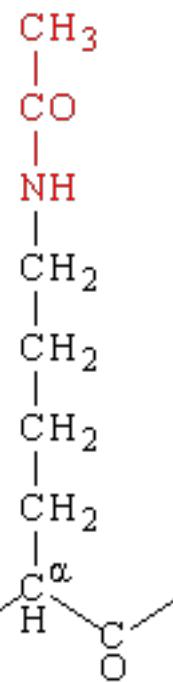


## Lysine

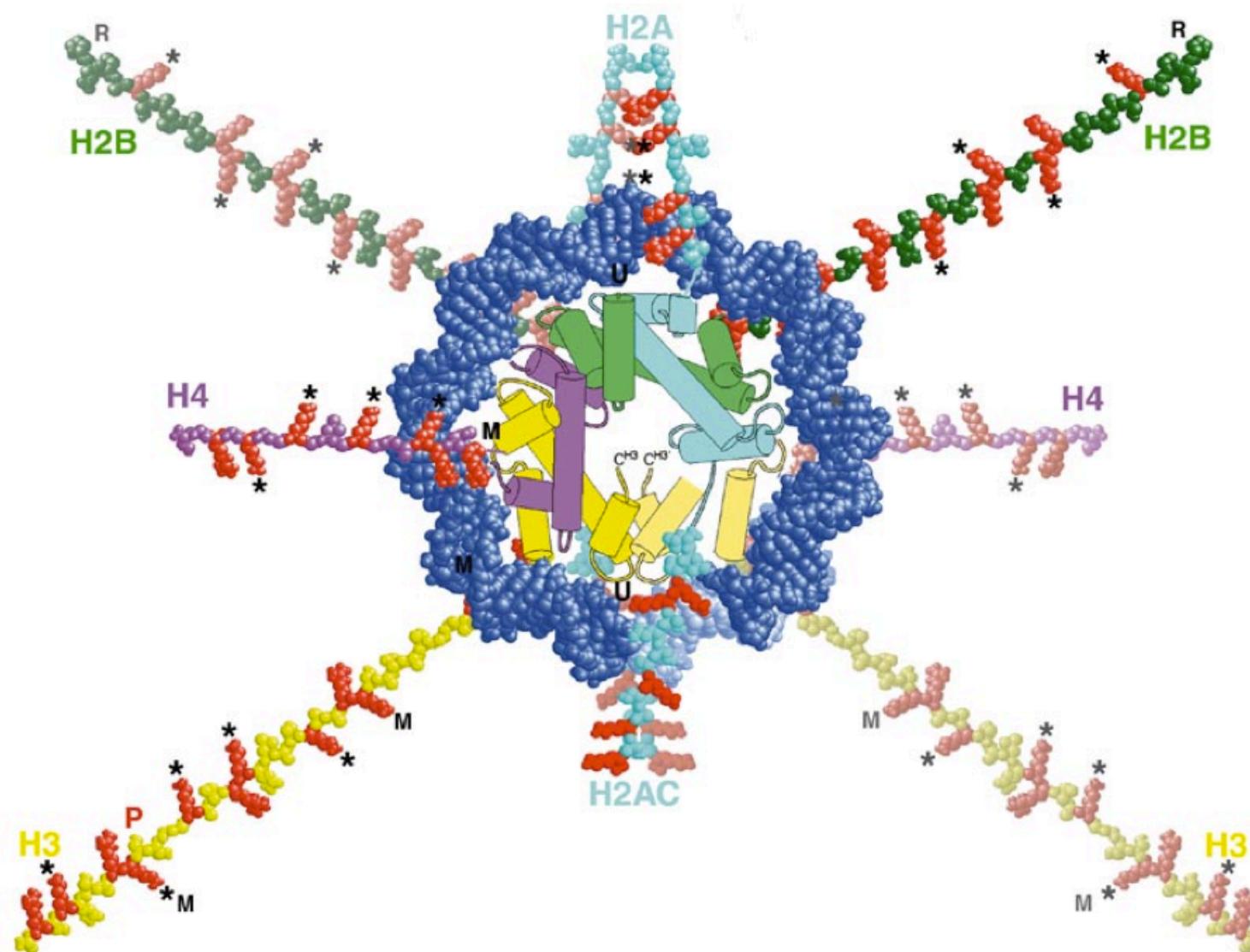


Acetylation  
by HATs

Deacetylation  
by HDs



# Acetilacija histonskih repov

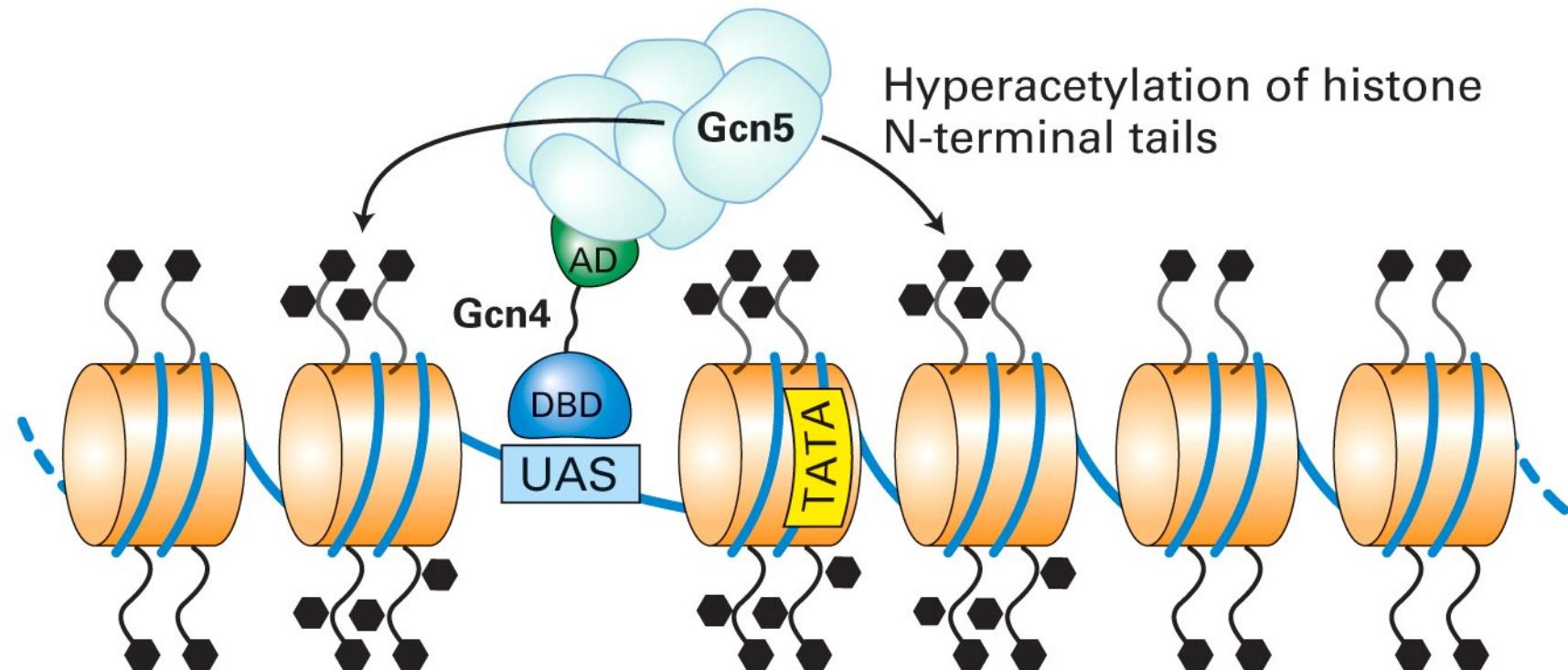


$14 \times 2 = 28$  potencialnih mest/oktamerno jedro

Wolffe and Hayes, NAR 27, 1999

# Aktivatorji regulirajo izražanje genov z acetilacijo histonov (kromatin se “odpre” - omogoči aktivacijo transkripcije)

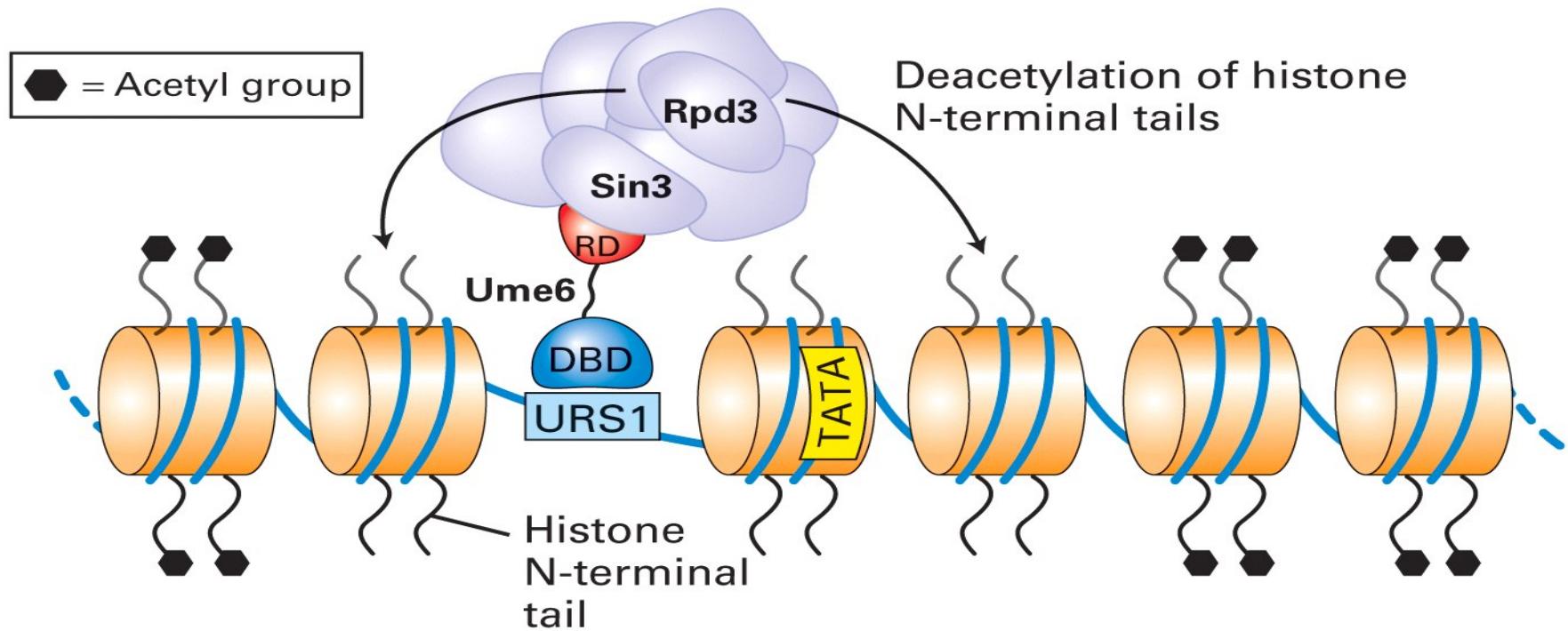
## (b) Activator-directed histone hyperacetylation



- The DBD of Activators like Gcn4 bind their Upstream Activating Sequence (UAS).
- Activation Domain (AD) attracts protein complexes containing histone acetylases (Gcn5)
- Subsequent acetylation of histone tails serve to open up chromatin.
- Thus HDACs and HATs are important global regulators of transcription

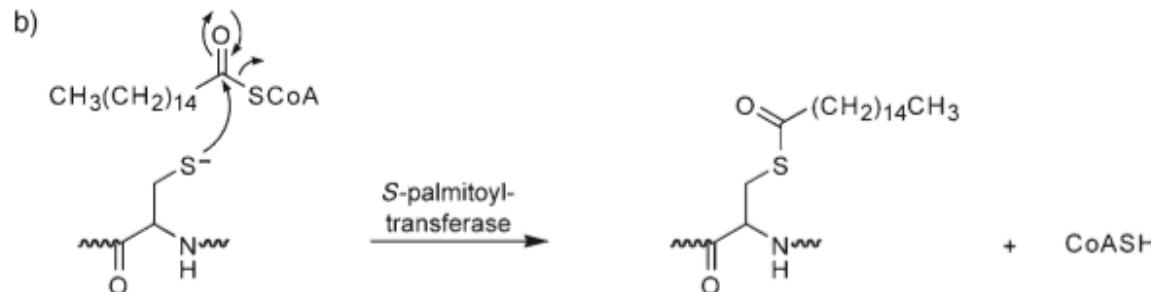
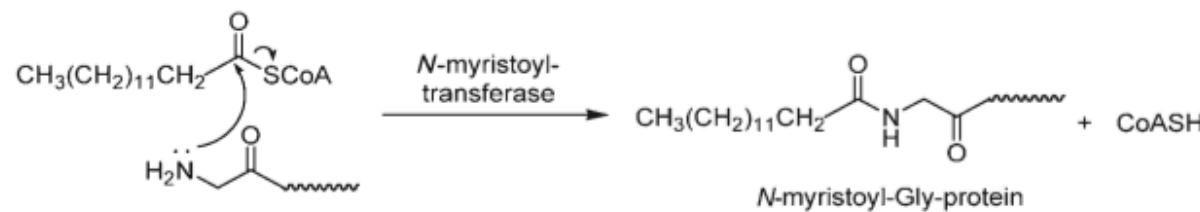
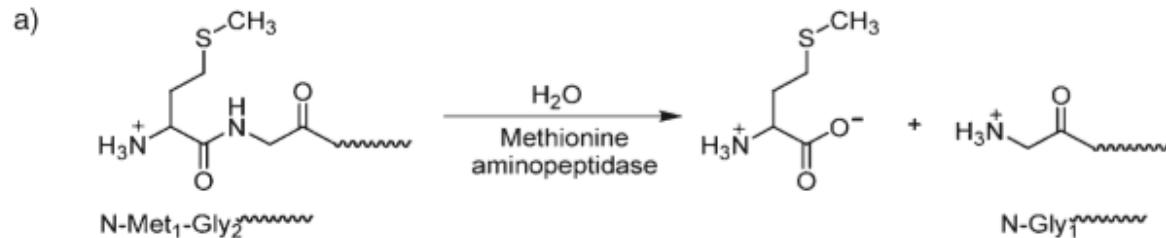
# Represorji regulirajo izražanje genov z deacetilacijo histonov (kromatin se “zapre”)

## (a) Repressor-directed histone deacetylation



- The DBD of repressors (like Ume6) bind a DNA element (URS1) and the Repression Domain (RD) recruits a protein complex containing a histone deacetylase like Rpd 3.
- The subsequent deacetylation of histone N-terminal tails results in chromatin condensation which promotes gene repression.

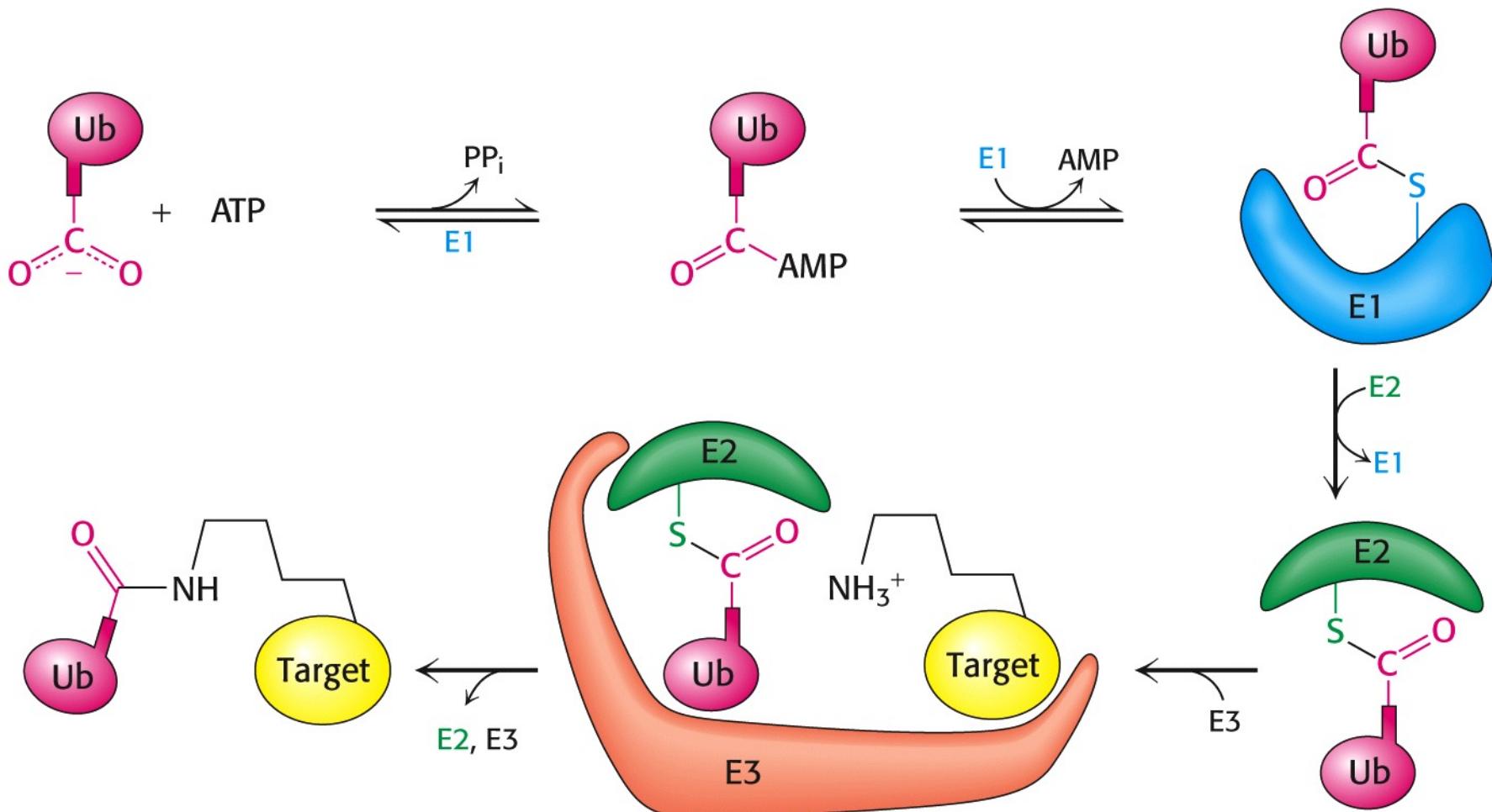
# N-miristoilacija in S-palmitoilacija

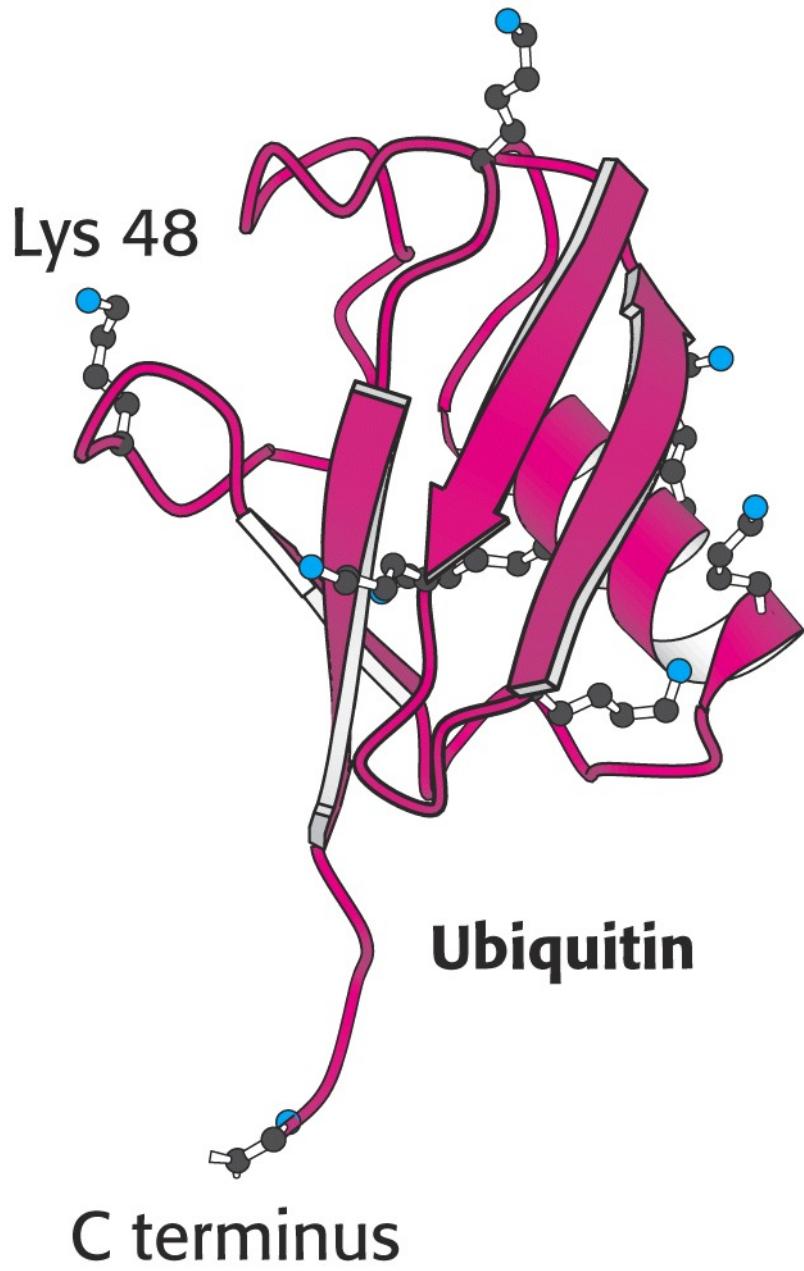


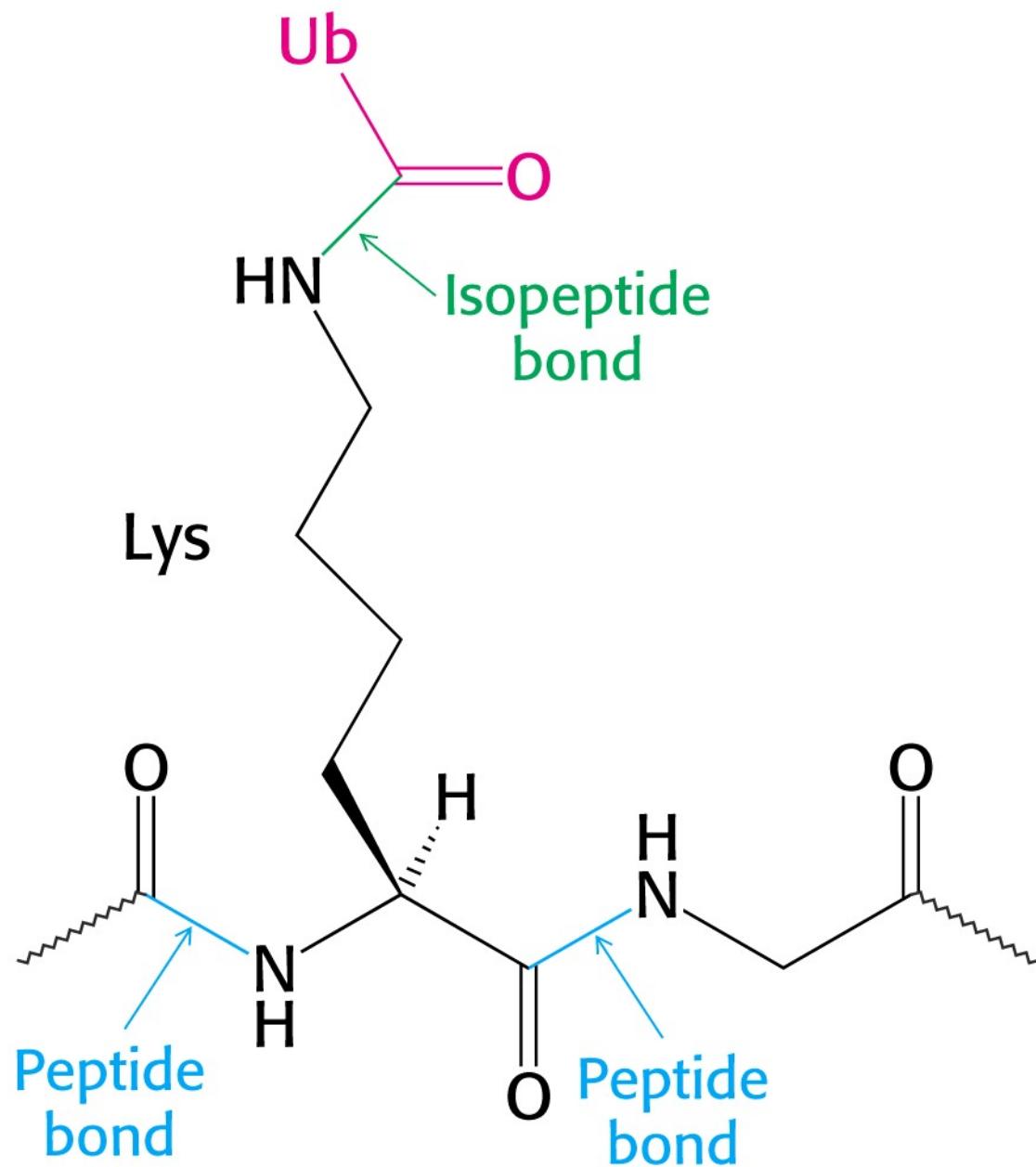
## sidro za membrano

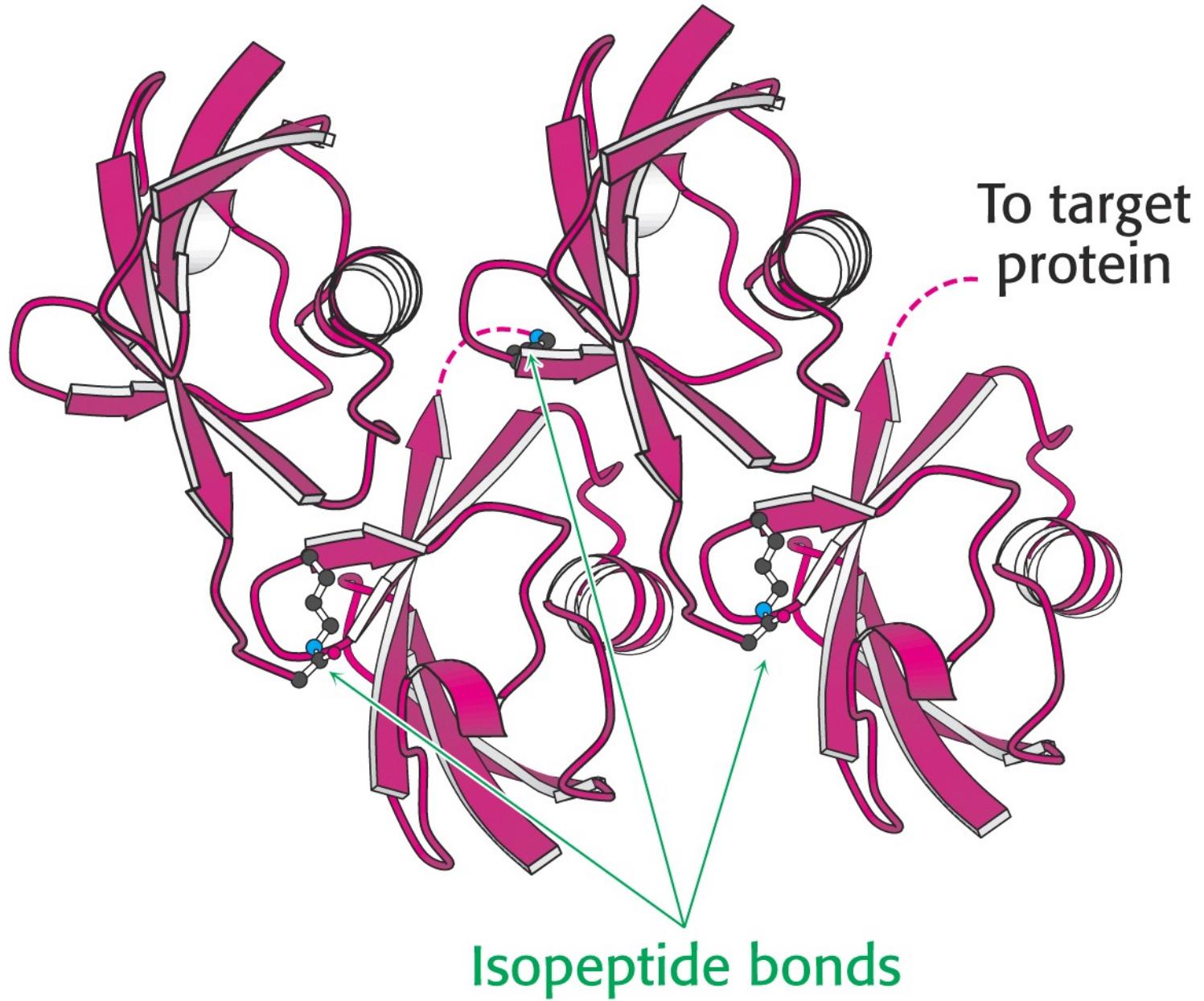
# Ubikvitinacija

Pripenjanje 76-AK dolgega ubikvitina preko njegovega C-konca na Lys



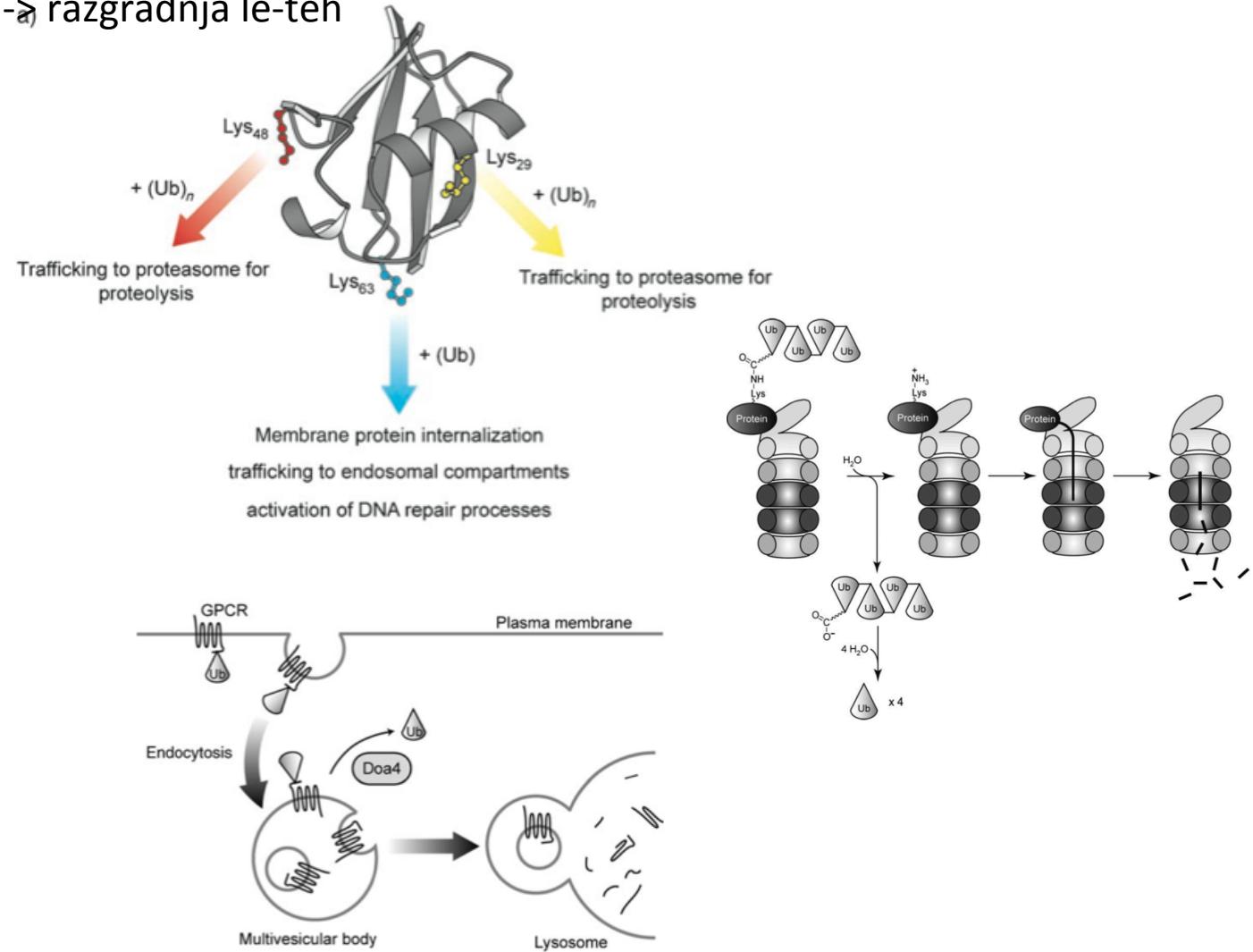






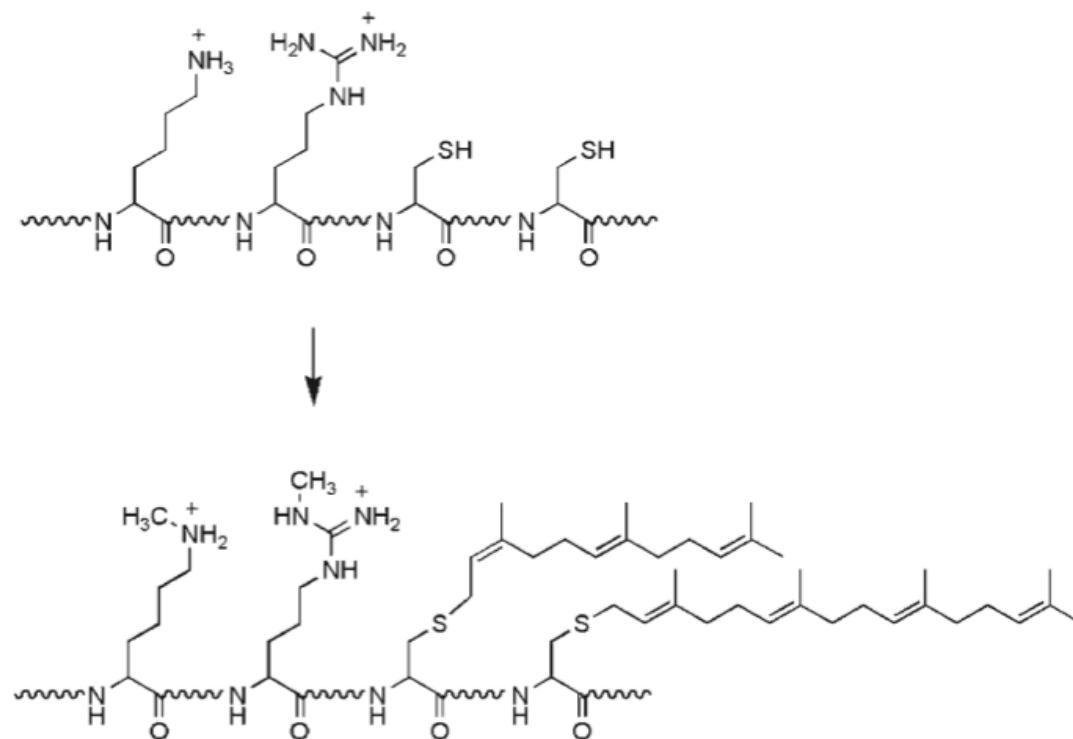
# Ubikvitinacija

Ubikvitinacija proteinov → razgradnja le-teh



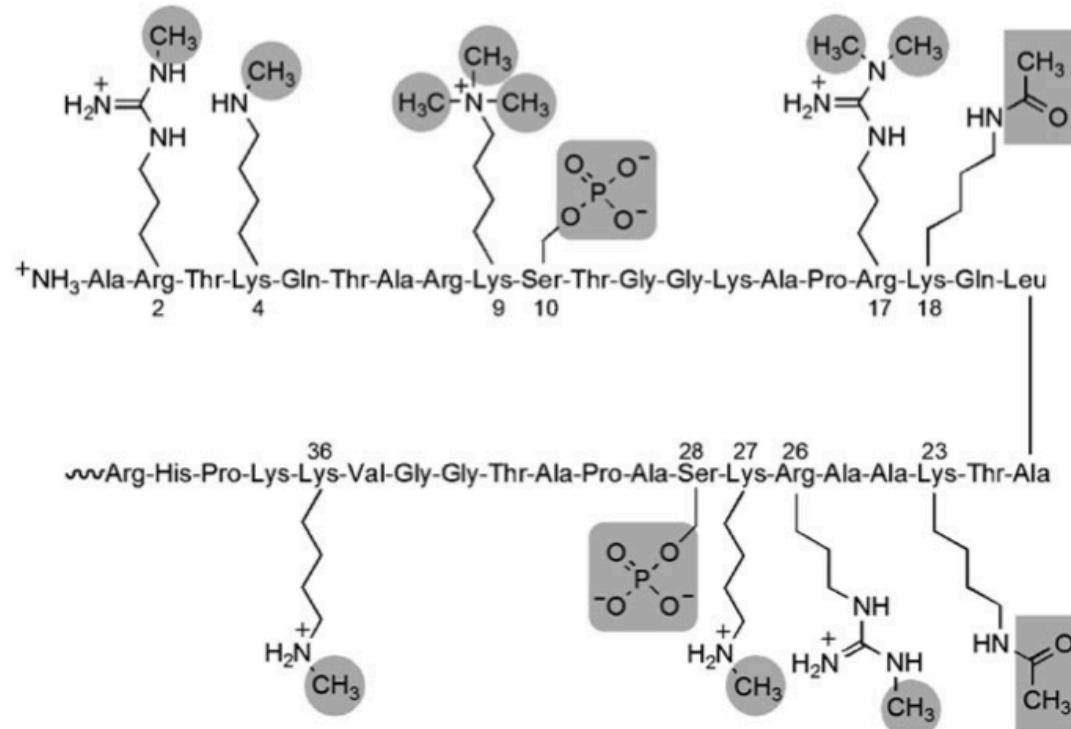
# Alkilacija proteinov

- najpogosteje se prenesejo C1 ter C15 in C20 izoprenske skupine
- poveča se hidrofobnost proteina



# Metilacija

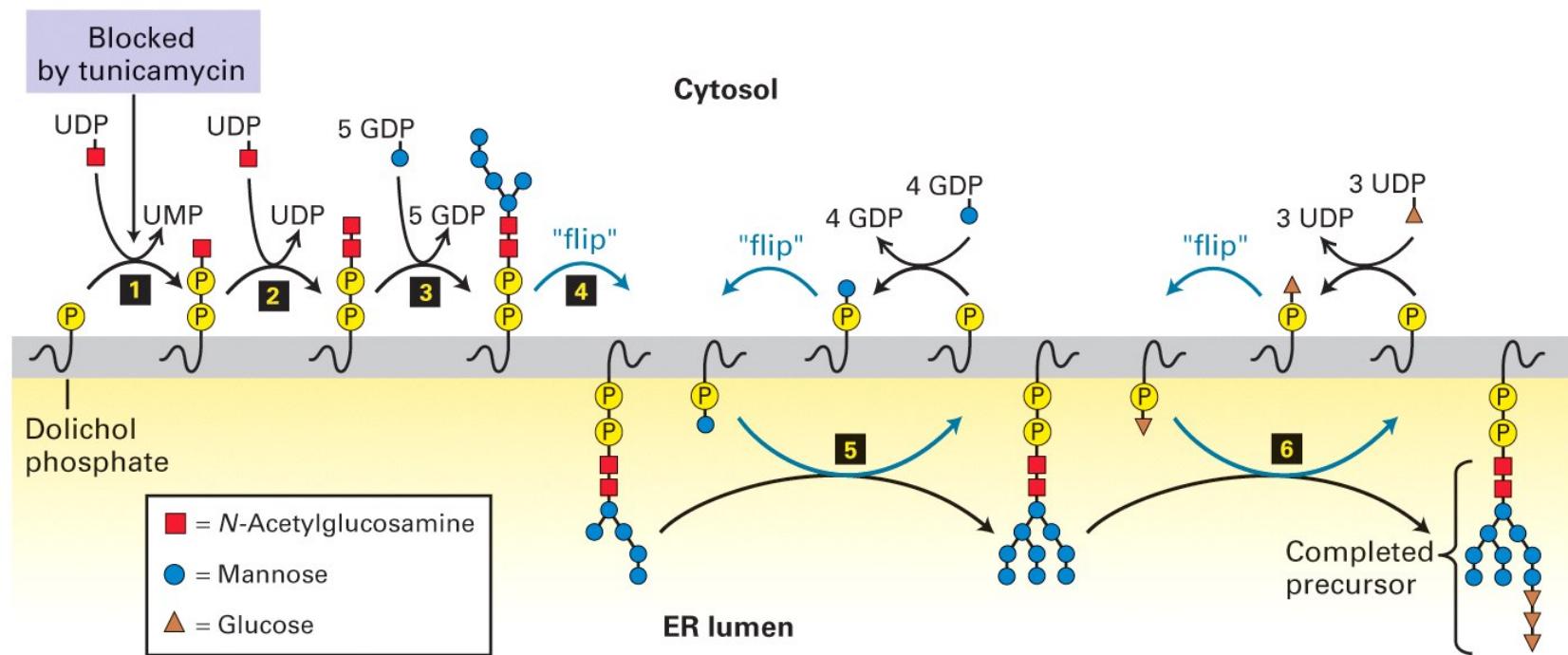
- N-metilacija Lys in Arg je najpogostejša, redkeje srečamo še C-, O- in S-metilacijo
- N-metilacija histonov Lys (mono-, di-, tri-metiliran), Arg (mono-, di-metiliran)- veliko kombinacij

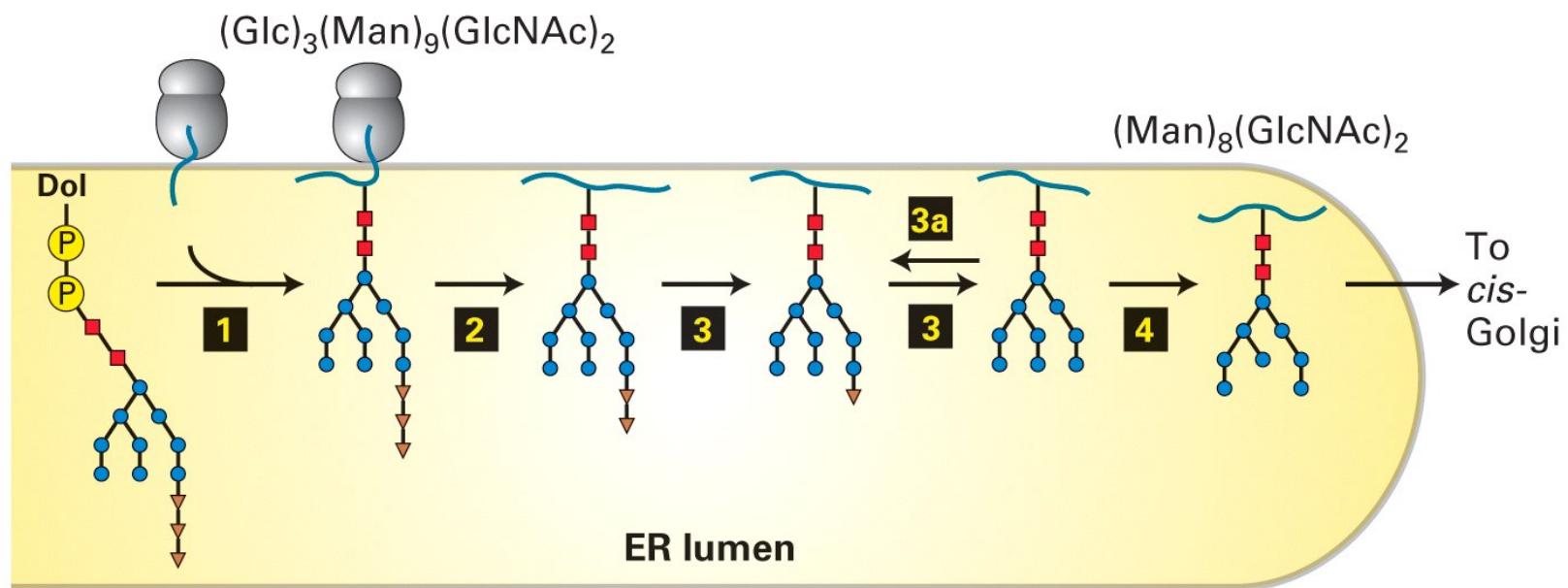
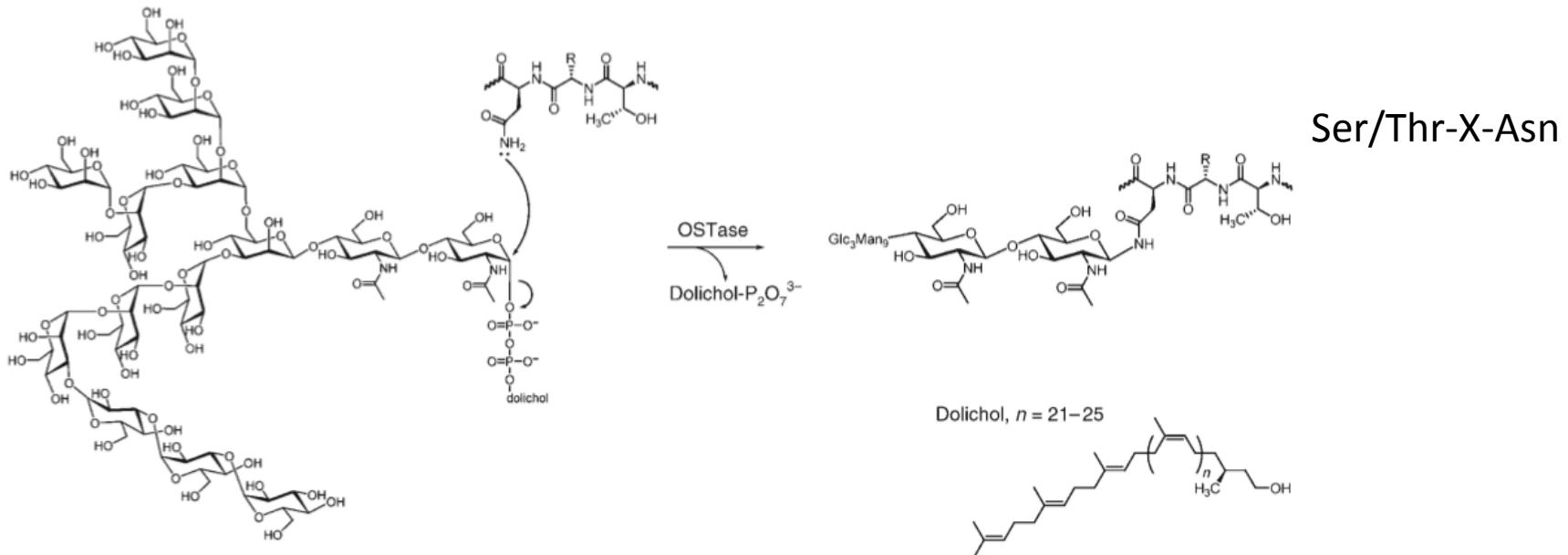


# Glikozilacija proteinov

- redko pri prokariontih, zelo pogosto pri evkariontih
- N-glikozilacija asparagina, skoraj vedno v sekvenci Ser/Thr-X-Asn, lahko pa tudi na Arg
- O-glikozilacija- na aminokisline z –OH skupino
- redko C-glikozilacija na Trp

# N-glikozilacija





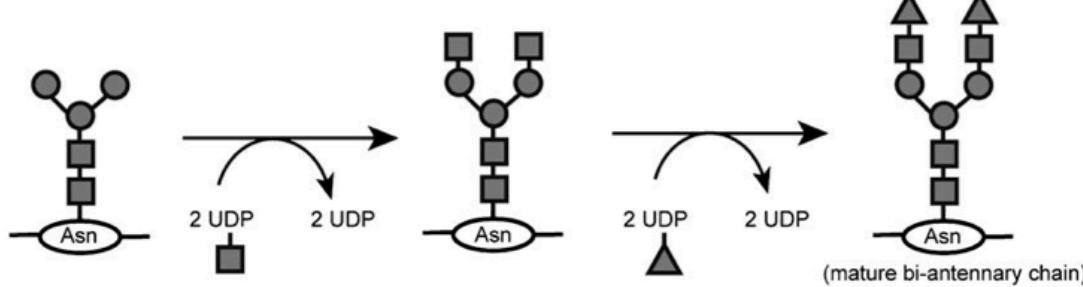
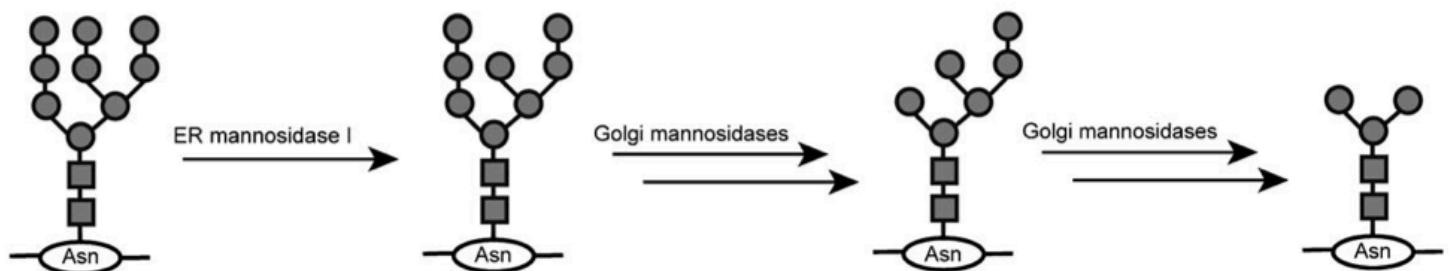
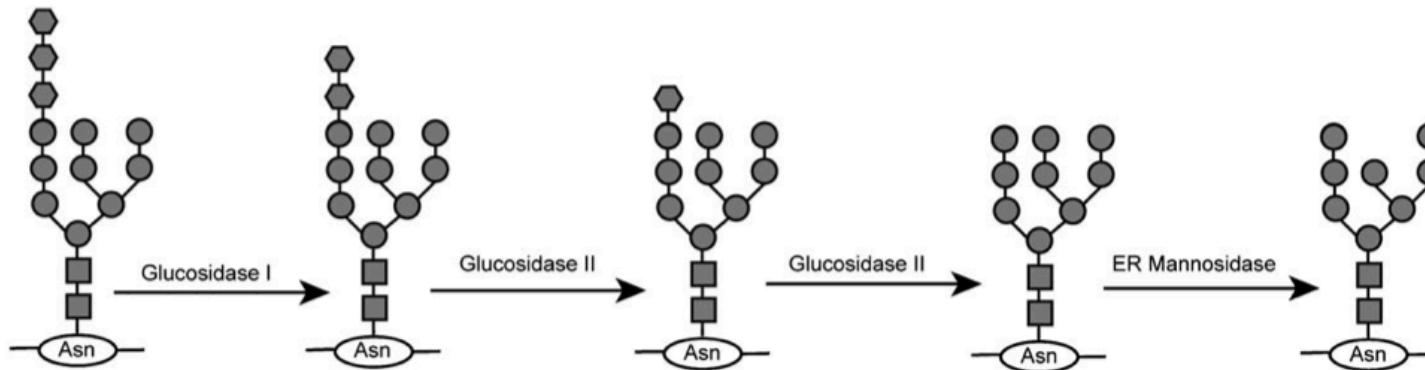
**Dol** = Dolichol

■ = *N*-Acetylglucosamine

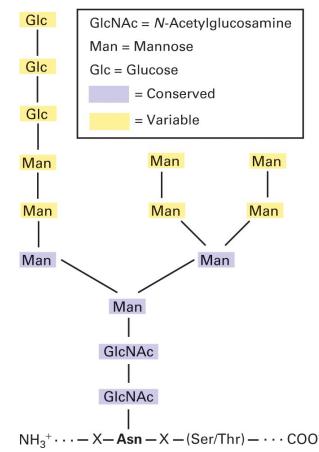
● = Mannose

▲ = Glucose

# N-glikozilacija

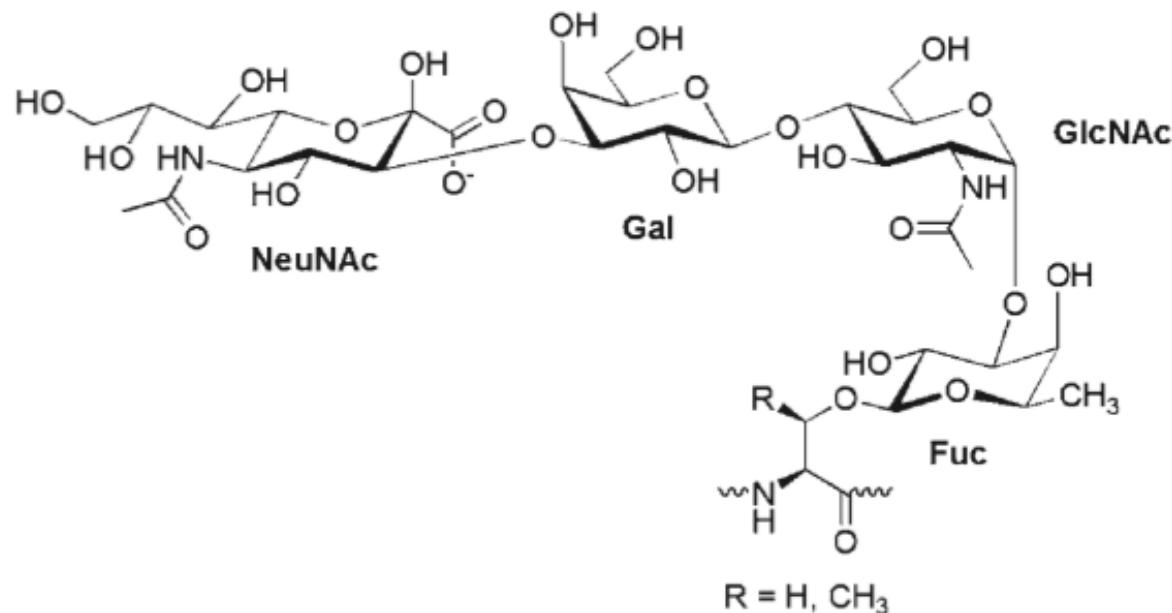


■ GlcNAc      ● Mannose      ▲ Galactose      ◊ Glucose

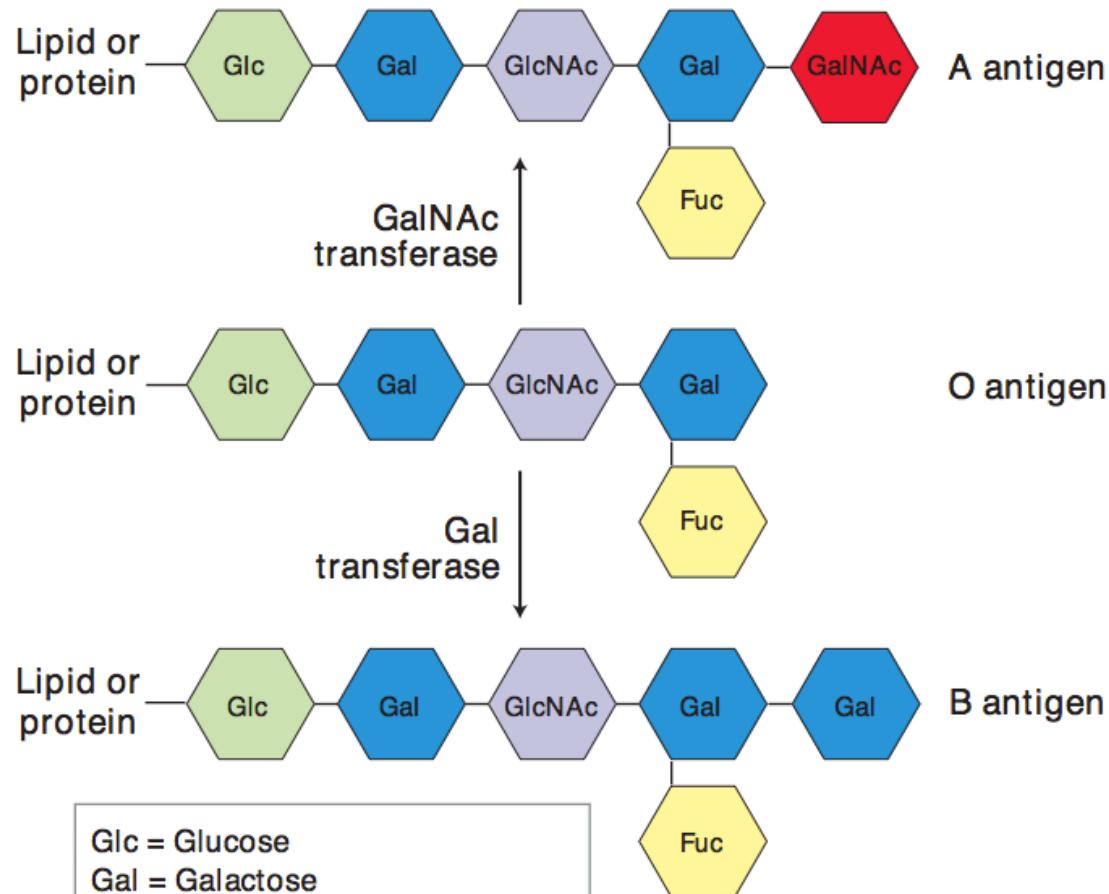


# O-glikozilacija

- največkrat krajše verige in manj kompleksne od N-glikozilacije, primer so antigeni krvnih skupin



# ABO antigeni

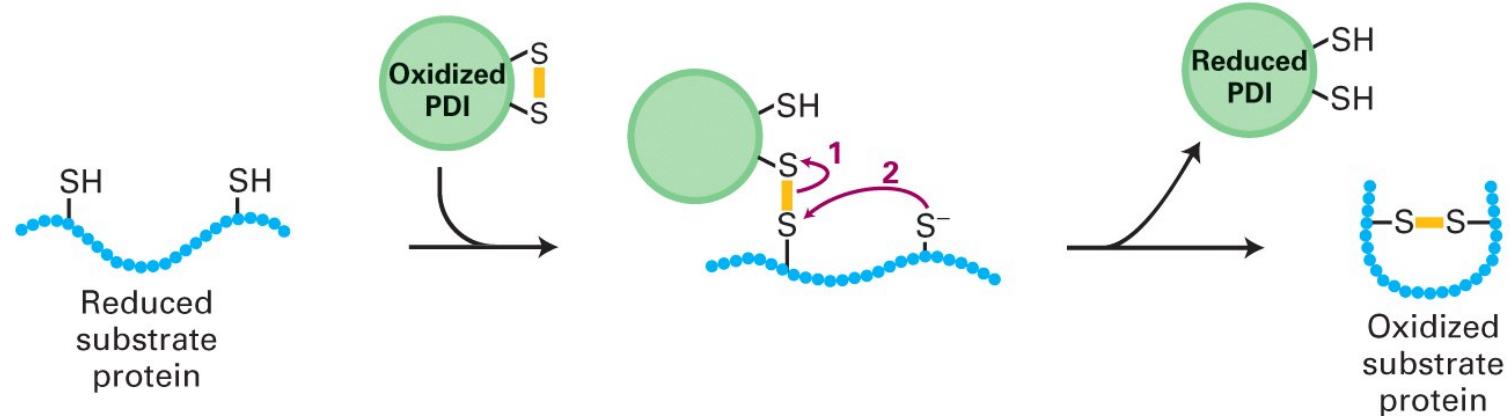


# Tvorba disulfidnih vezi

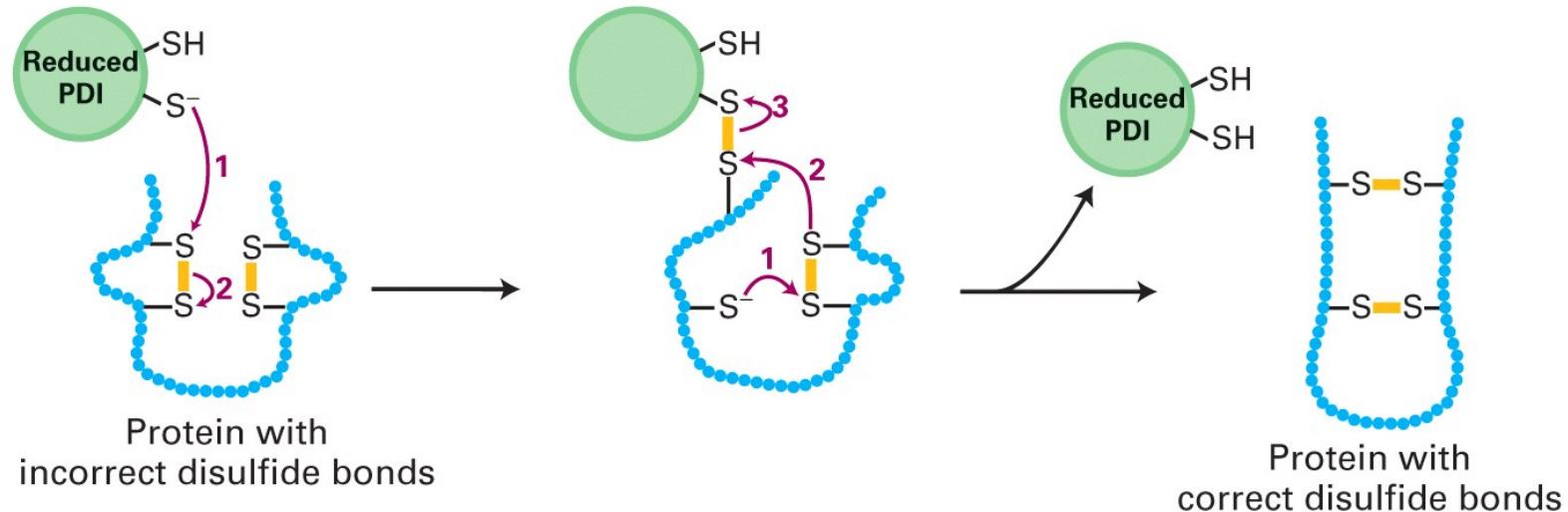
- v eukariontih je v citoplazmi in jedru redukcijsko okolje ( $\text{GSH}:\text{GSSG}=100:1$ , veliko tudi  $\text{NAD(P)H}$ )
- disulfidi stabilizirajo strukturo proteinov

# Tvorba disulfidnih vezi

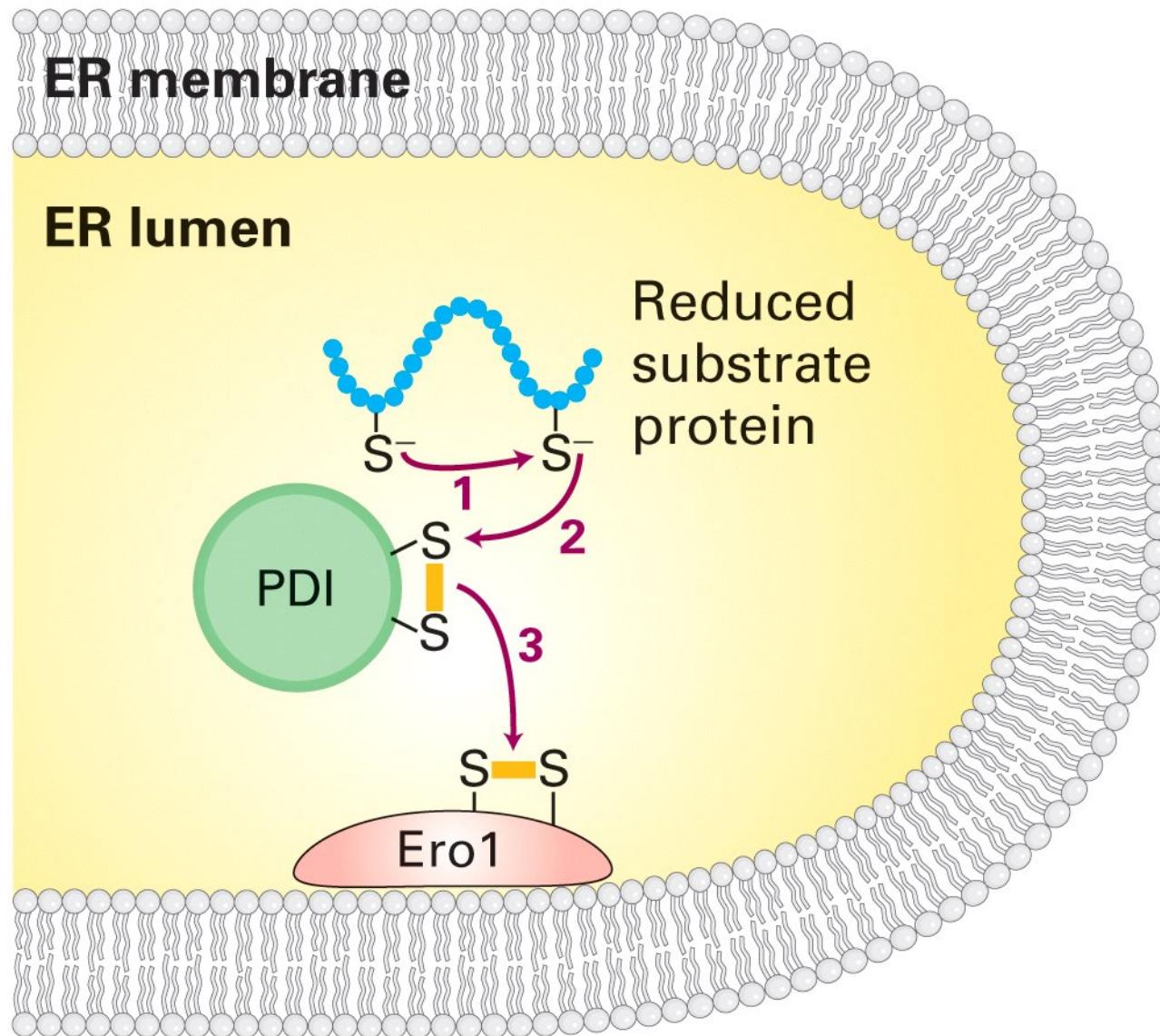
(a) Formation of a disulfide bond



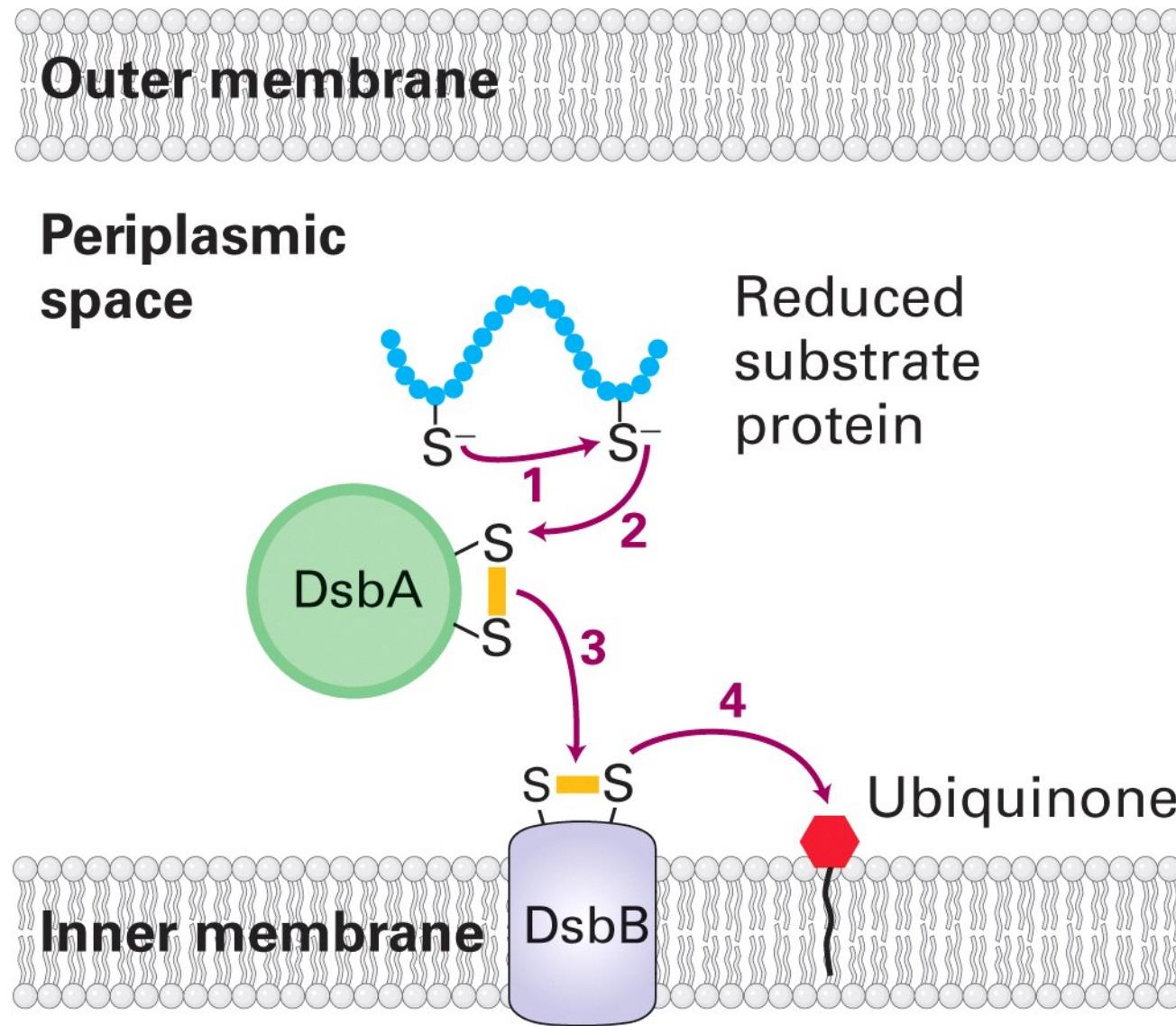
(b) Rearrangement of disulfide bonds



(a) Eukaryotes

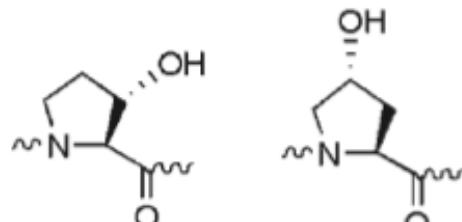


(b) Bacteria



# Hidroksilacija proteinov

- hidroksilacijo katalizirajo od železa odvisne monooksigenaze
- hidroksilacija kolagena (Gly-Pro-X/Gly-X-Hyp), ~30% vseh proteinov v telesu je kolagen
- HIF, Pro-hidroksilaza, raven O<sub>2</sub>, ubikvitinil ligaza,

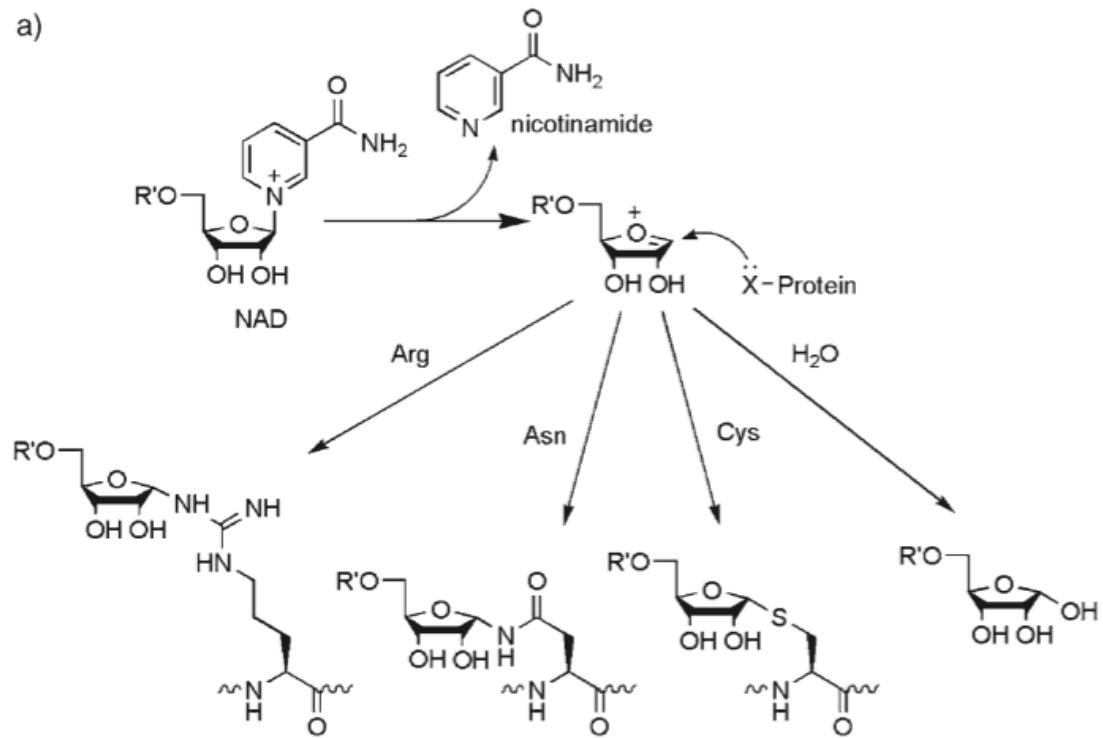


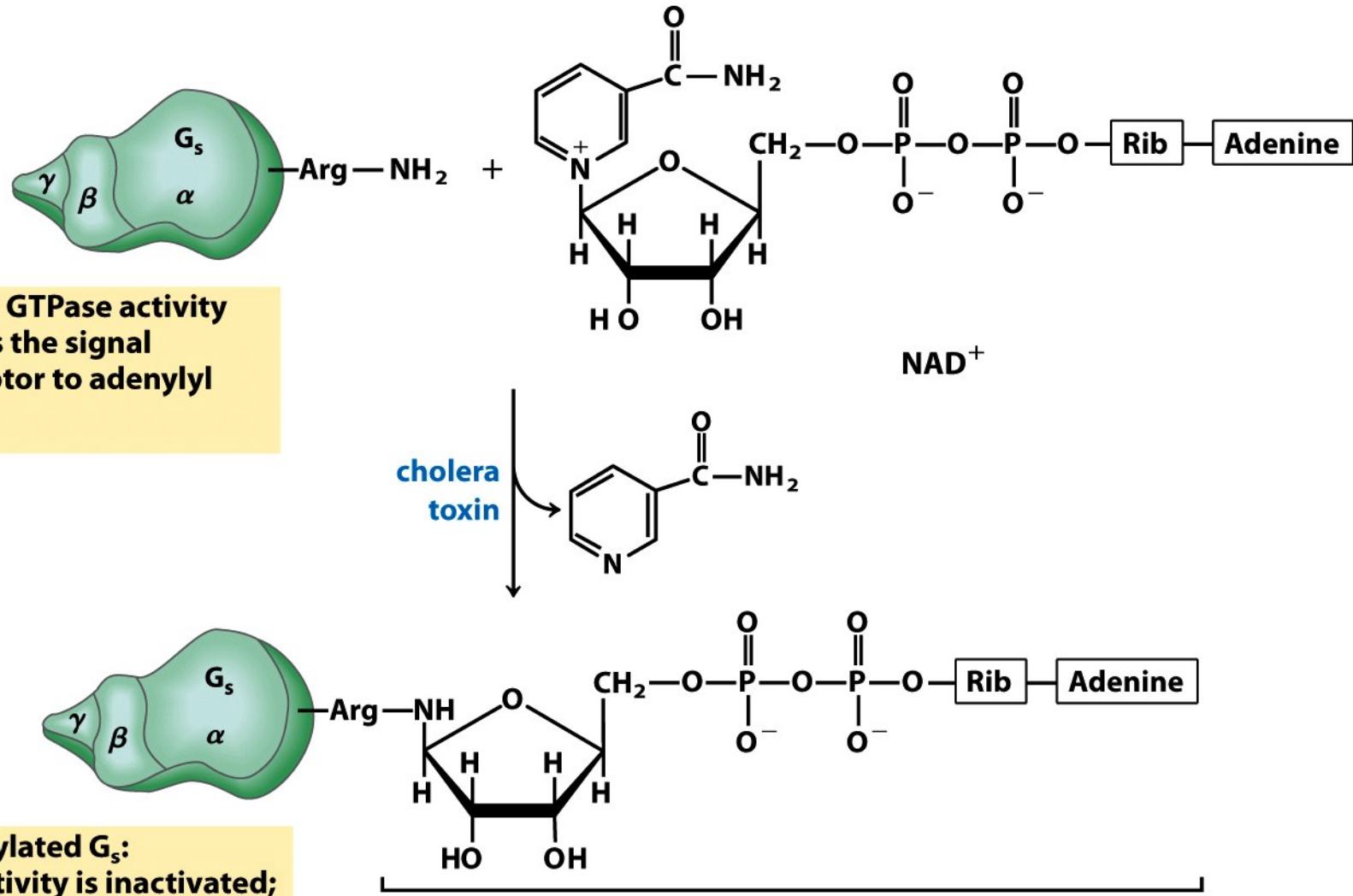
3-OH-Pro

# Modifikacije proteinov z bakterijskimi toksini

- cilj je onemogočiti obrambne mehanizme gostitelja
- ADP-ribozilacija, glukozilacija, deaminacija

a)





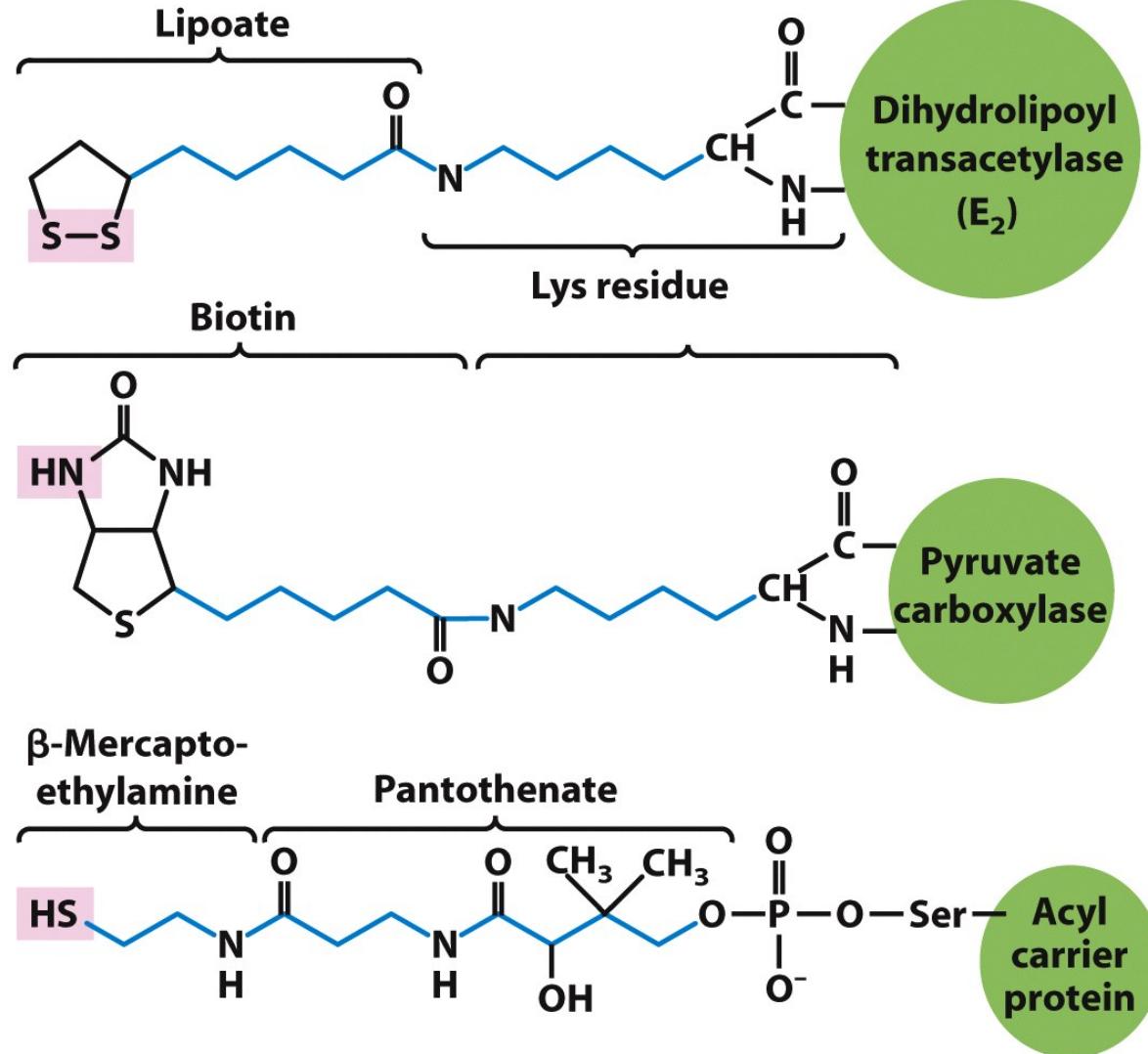
**Box 12-2 figure 5**

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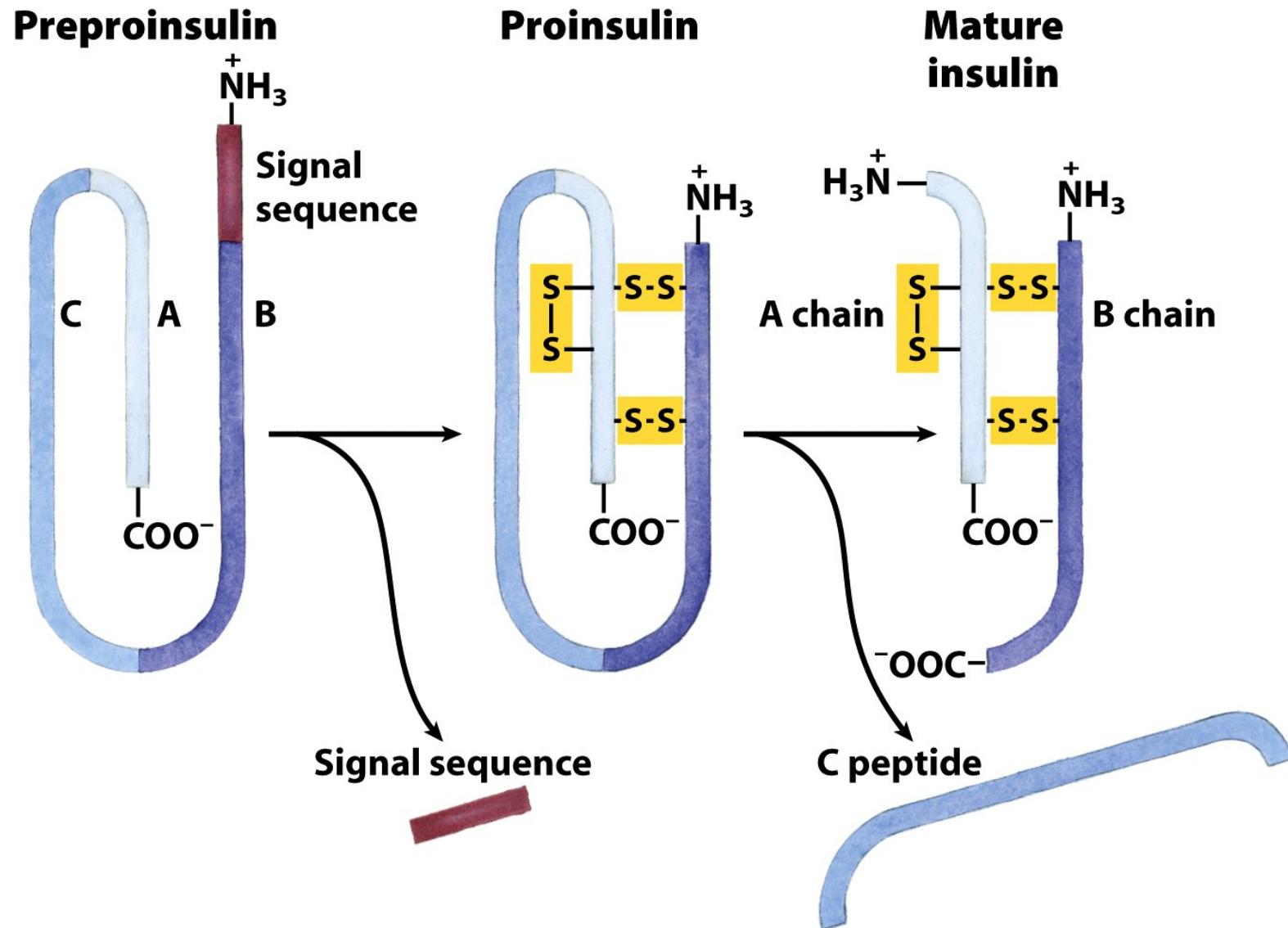
# Modifikacije s prostetičnimi skupinami

npr.



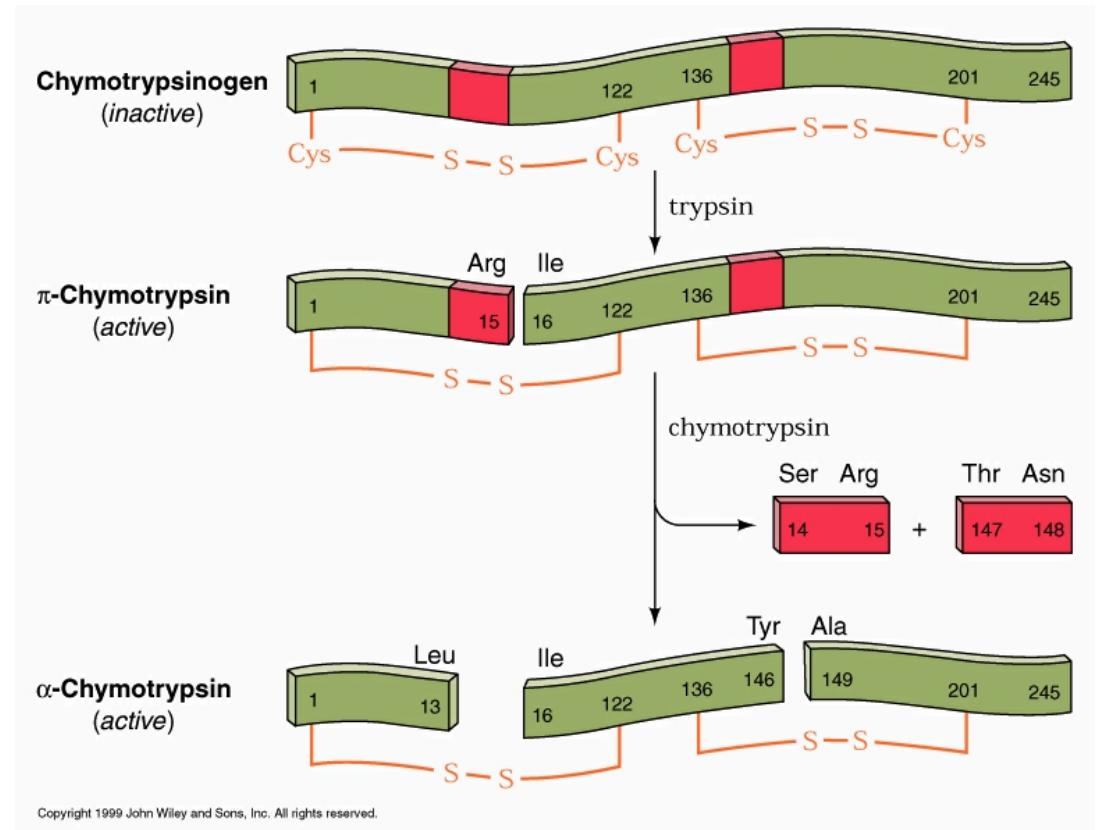
**Figure 16-17**  
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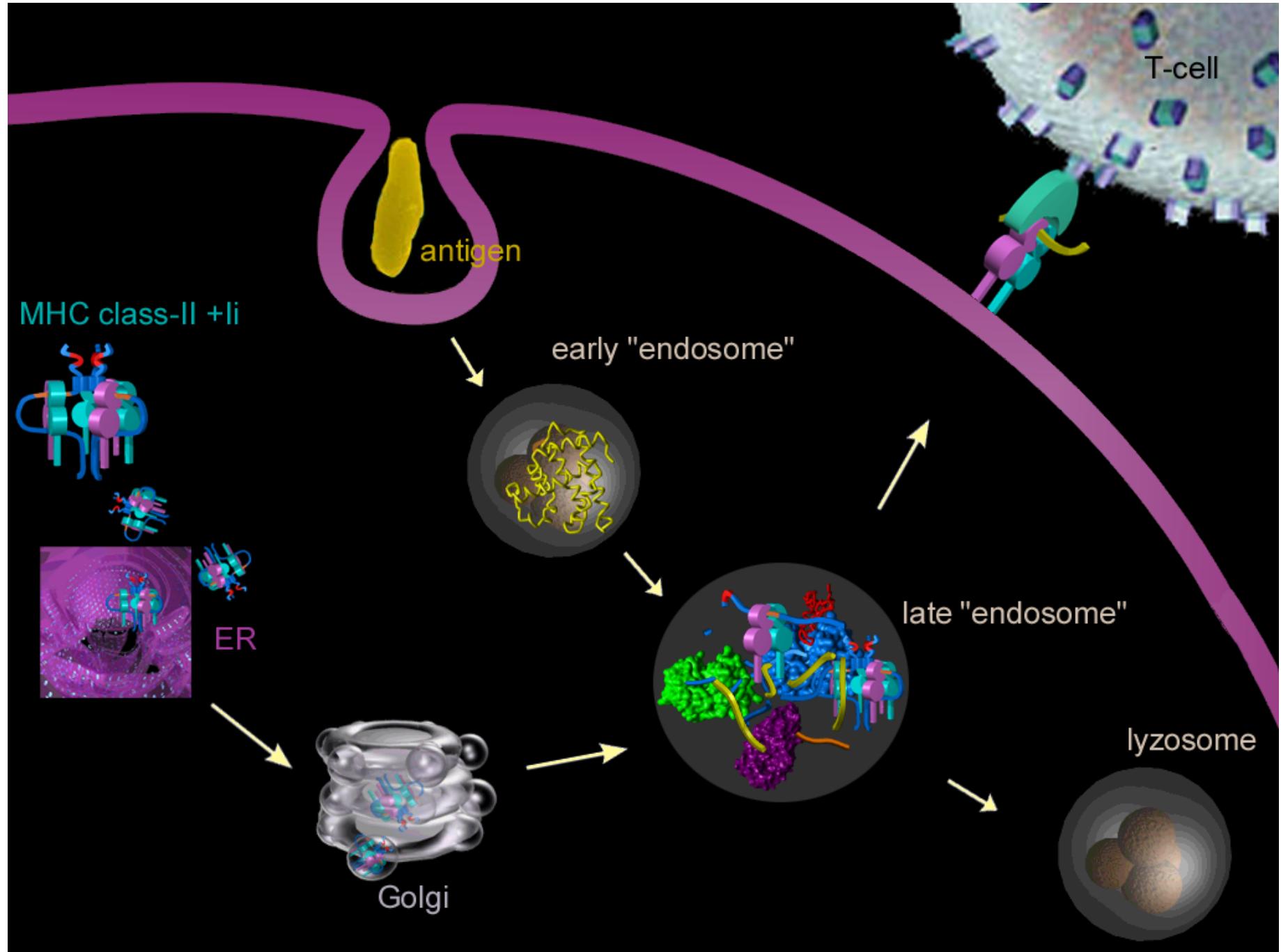
# Proteolitično procesiranje



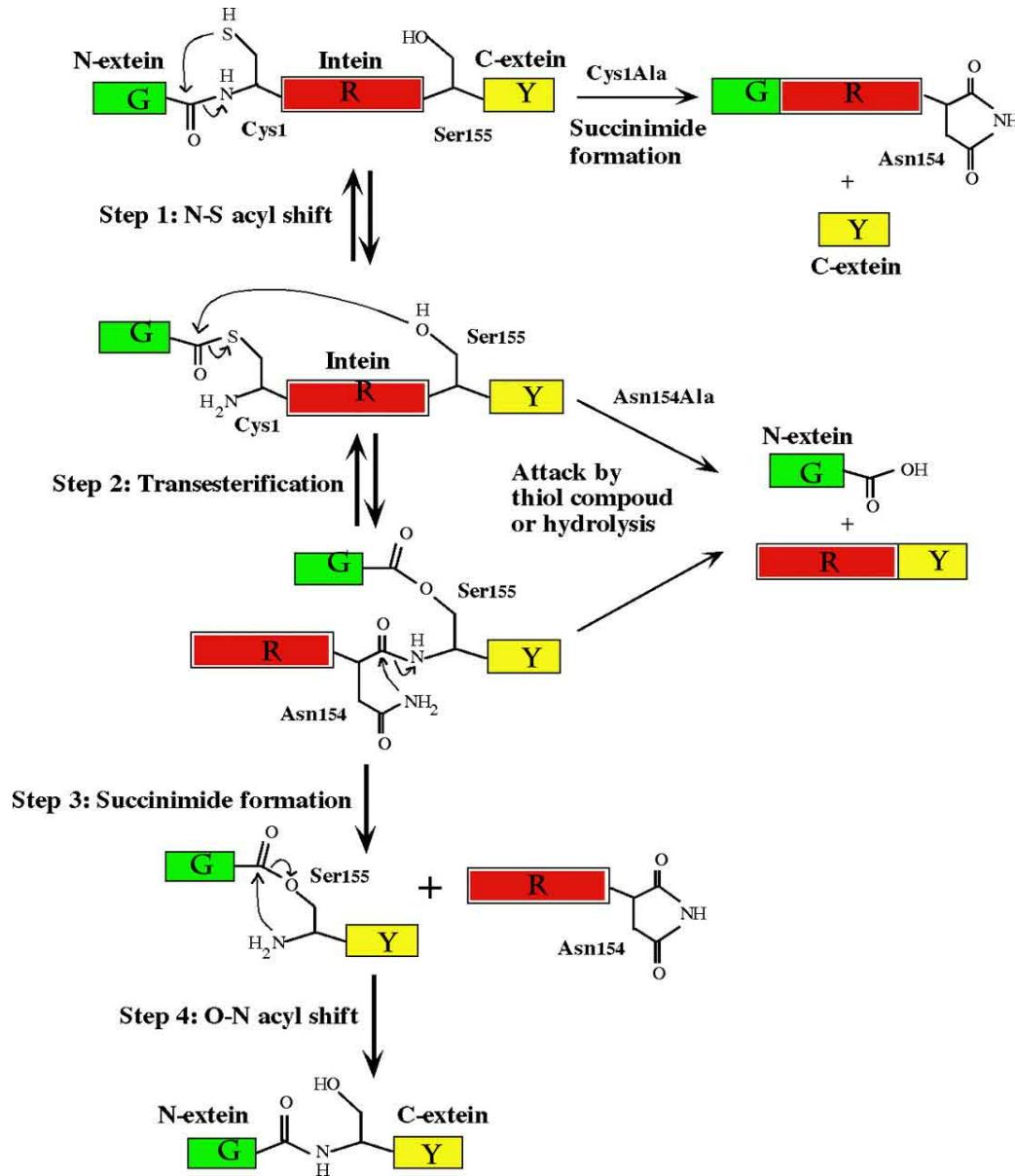
# Aktivacija proencimov

Proteinaze cepijo proencim na 1 ali več mestih.





# Proteinsko izrezovanje



- ❖ N-extein represents the N-terminal polypeptide segment that is retained
- ❖ C-extein represents the C-terminal segment that is retained
- ❖ the Intein is what is spliced out (much as a genomic DNA intron)
- ❖ Cys1, Asn154 and Ser155 represent conserved residues involved in the splicing reaction

# Protein Posttranslational Modifications: The Chemistry of Proteome Diversifications

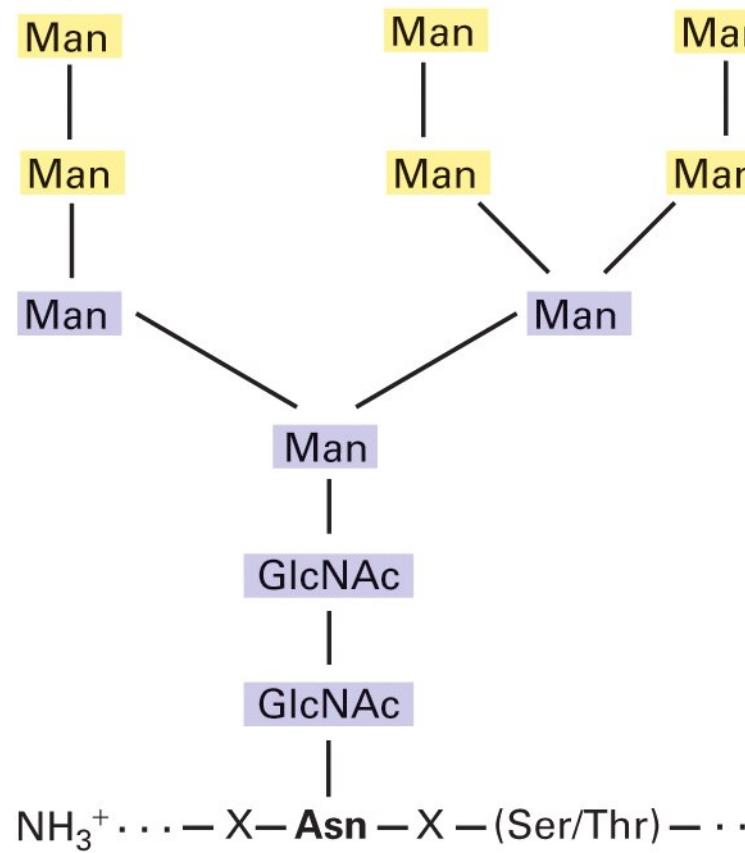
Christopher T. Walsh,\* Sylvie Garneau-Tsodikova, and Gregory J. Gatto, Jr.

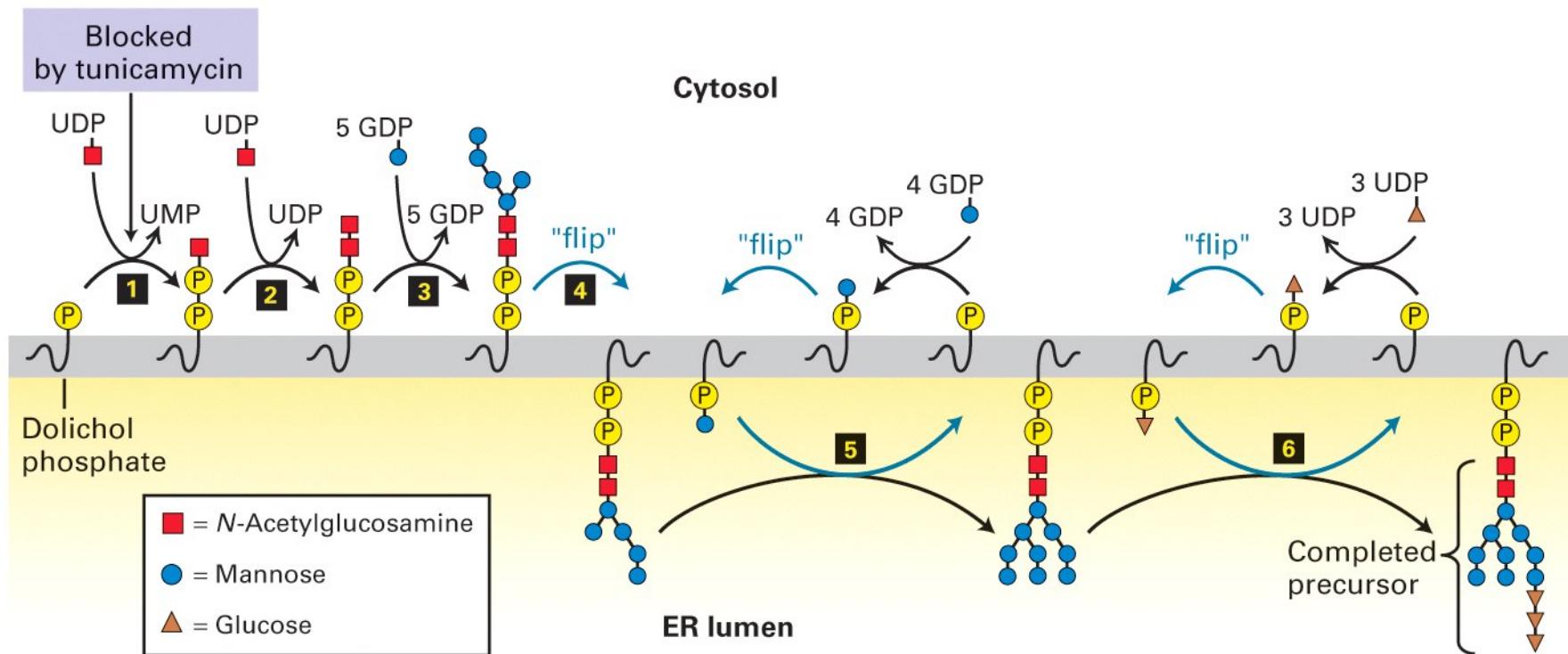
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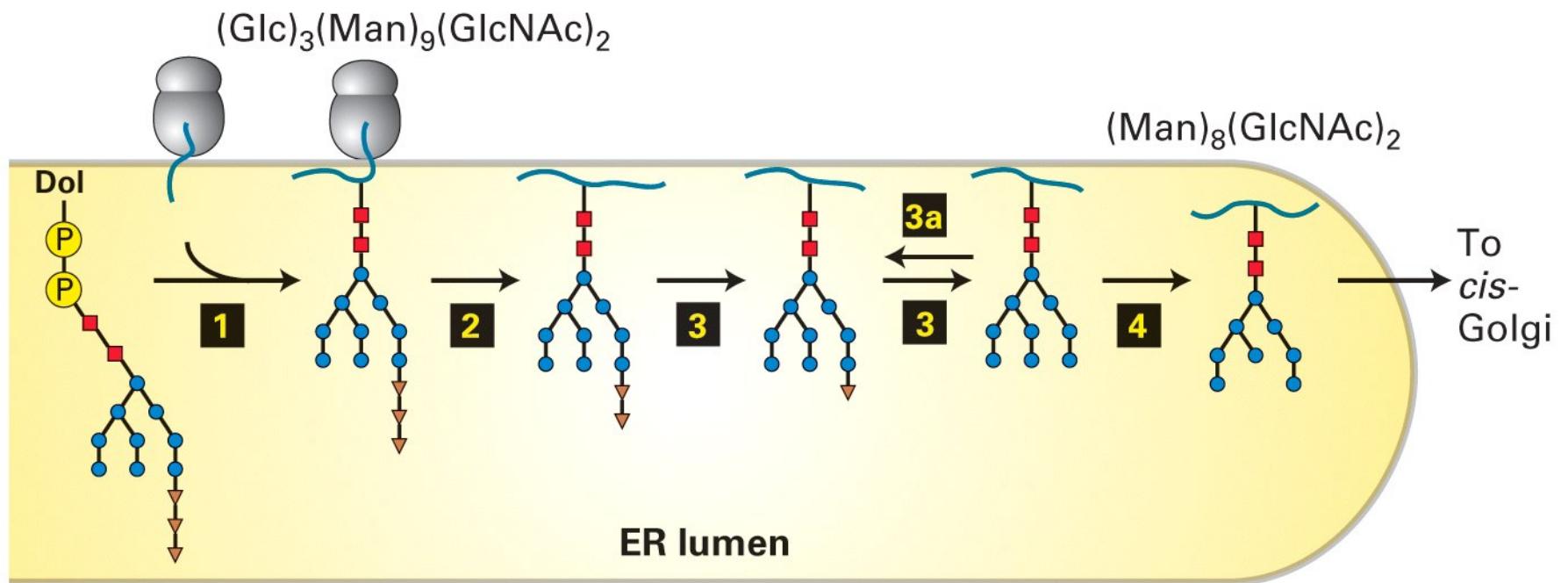
<http://bit.ly/K1IZfY>

Glc  
Glc  
Glc  
Man

GlcNAc = *N*-Acetylglucosamine  
Man = Mannose  
Glc = Glucose  
= Conserved  
= Variable





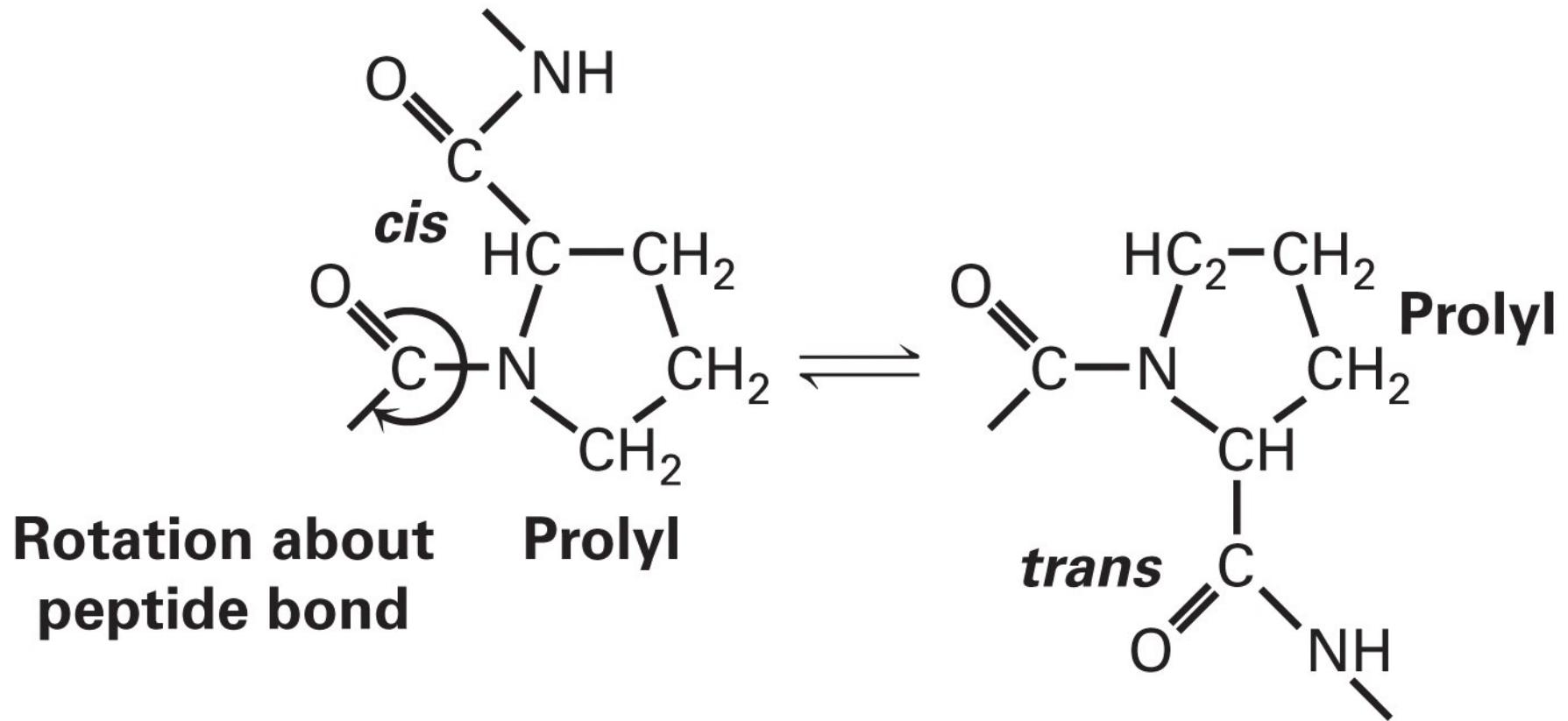


Dol = Dolichol

■ = *N*-Acetylglucosamine

● = Mannose

▲ = Glucose



Rotation about  
peptide bond