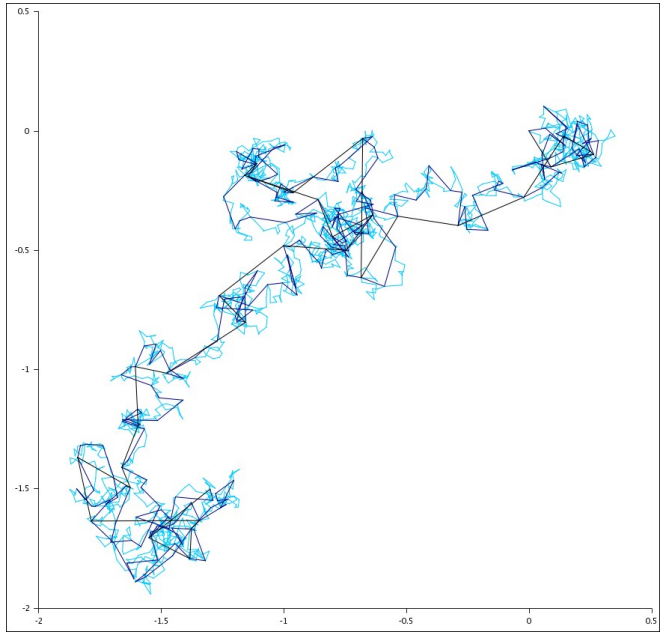
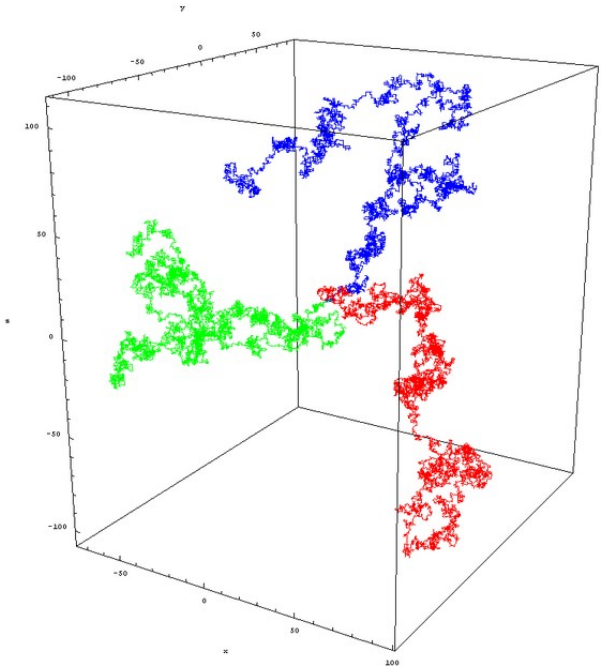
Protein Interactions *in vivo*

In one direction

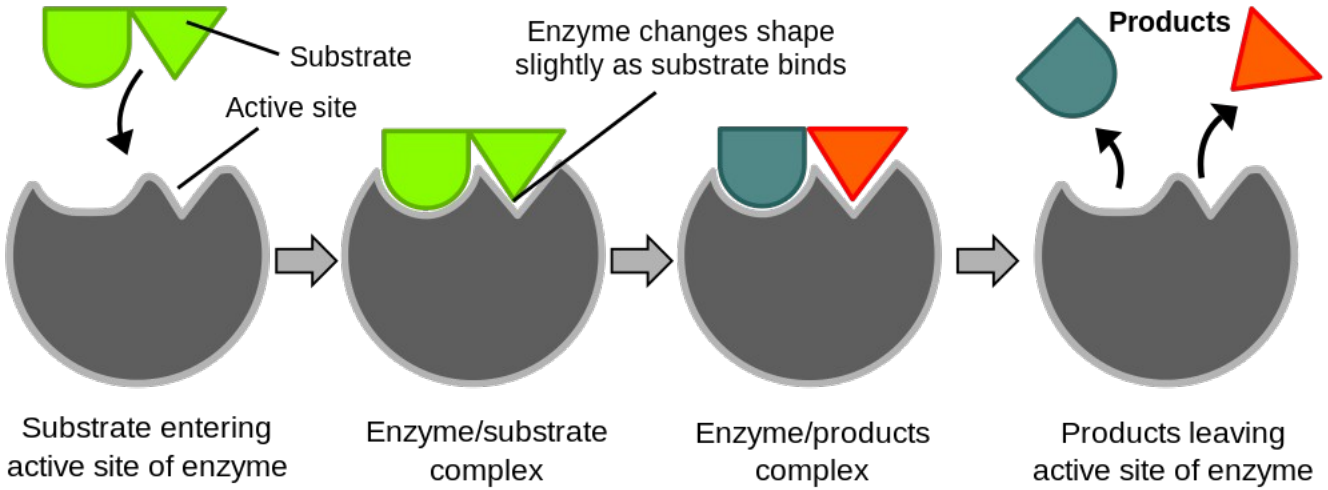




$$mv^2/2 = kT/2$$

$$v = (kT/m)^{1/2}$$

Protein Interactions *in vivo*

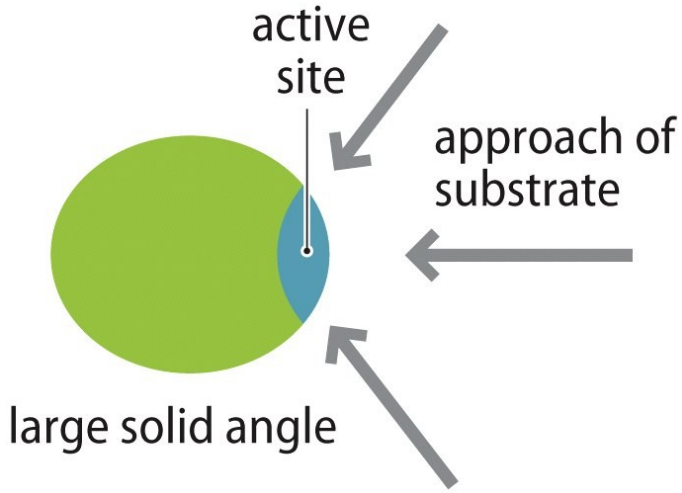


Σε μια χημική αντίδραση που είναι αρκετά γρήγορη

Ο ρυθμός ενός ενζύμου εξαρτάται από
το πόσο γρήγορα το υπόστρωμα μπορεί να διαχυθεί στην ενεργό θέση και το πόσο γρήγορα το προϊόν μπορεί να διαχυθεί έξω.

Αυτός ο ρυθμός είναι ανάλογος με τον ρυθμό διάχυσης-σύγκρουσης, ο οποίος με τη σειρά του εξαρτάται από το μέγεθος των μορίων και το ιξώδες του μέσου.

collision rate



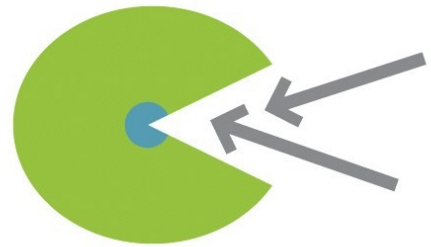


Figure 4.1 How Proteins Work (©2012 Garland Science)

k_{cat}/K_M is the catalytic efficiency. It is used to rank enzymes. A big k_{cat}/K_M means that an enzyme binds tightly to a substrate (small K_M), with a fast reaction of the ES complex.

k_{cat}/K_M is an apparent second order rate constant

$$v=k_{cat}/K_M[E]_0[S]$$

Kcat είναι η καταλυτική σταθερά για τη μετατροπή του υποστρώματος σε προϊόν

Km είναι η σταθερά Michaelis

- k_{cat}/K_M is the specificity constant. It is used to distinguish and describe various substrates.

TABLE 4.1 Values of k_{cat}/K_m for some enzymes

Enzyme	Substrate	k_{cat}/K_m ($M^{-1} s^{-1}$)
Acetylcholinesterase	Acetylcholine	1.5×10^8
Carbonic anhydrase	Carbon dioxide	8.3×10^7
Catalase	Hydrogen peroxide	4.0×10^8
Fumarase	Fumarate	1.6×10^8
Fumarase	Malate	3.6×10^7
Superoxide dismutase	Superoxide	2.8×10^9
Triosephosphate isomerase	Dihydroxyacetone phosphate	7.5×10^5
Triosephosphate isomerase	Glyceraldehyde 3-phosphate	2.4×10^8
Lysozyme	$(NAG\text{-}NAM)_3$	83
Glucose isomerase	Glucose	7.4

Abbreviation: NAG-NAM, *N*-acetylglucosamine–*N*-acetylmuramic acid disaccharide.

Table 4.1 How Proteins Work (©2012 Garland Science)

rate of diffusion

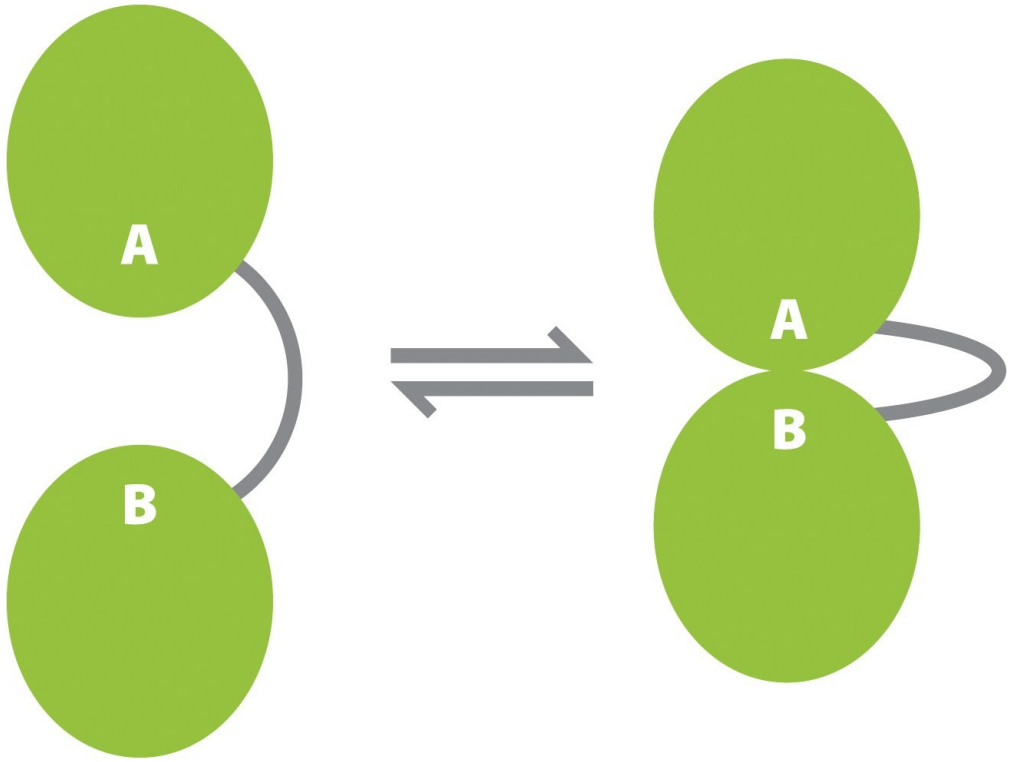


Figure 4.2 How Proteins Work (©2012 Garland Science)

Dielectric constant

$$F = q_1 q_2 / 4\pi\epsilon r^2,$$

ε είναι η διηλεκτρική σταθερά

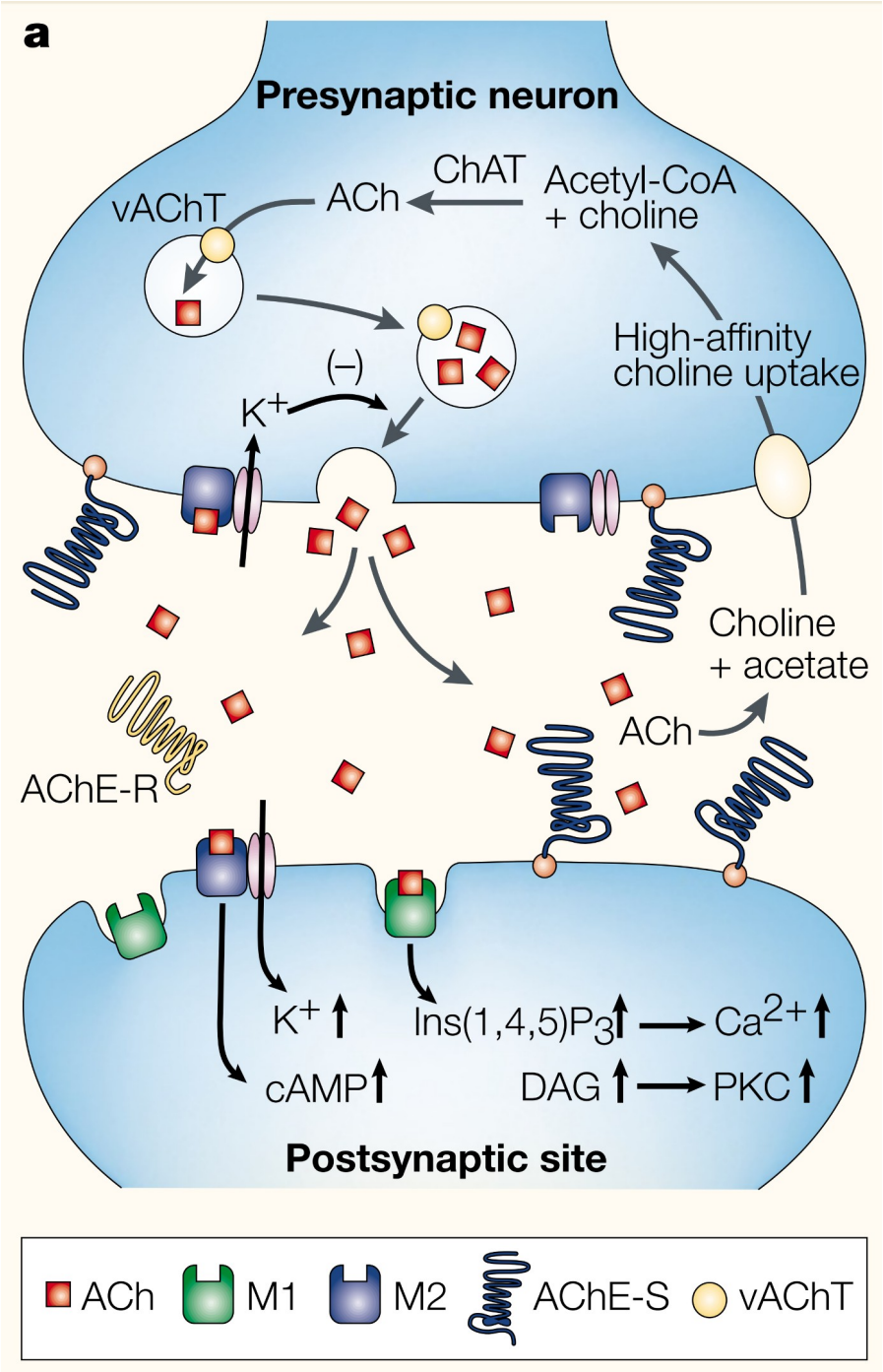
Ionic strength

$$\mu = \tfrac{1}{2} \sum z_i^2 C_i$$

Electrostatic screening

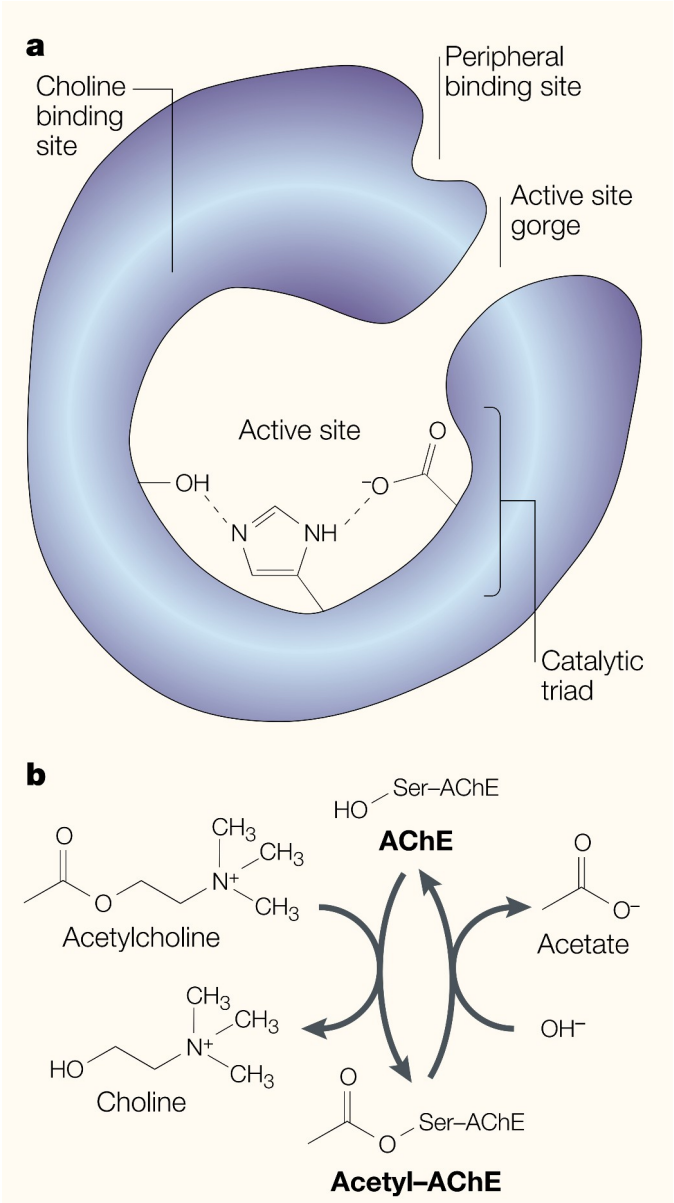
$$r = \left(\frac{\epsilon KT}{2N_0 e^2 \mu} \right)^{1/2}$$

Acetylcholinesterase



Collision rates

electrostatic orientational steering



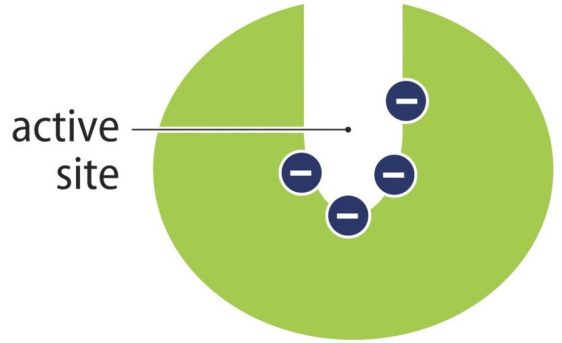


Figure 4.3 How Proteins Work (©2012 Garland Science)

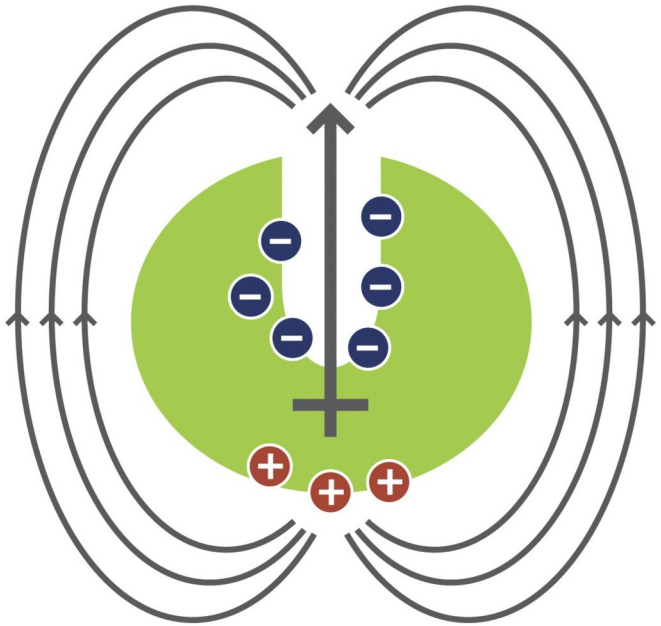


Figure 4.4 How Proteins Work (©2012 Garland Science)

Cytochrome c

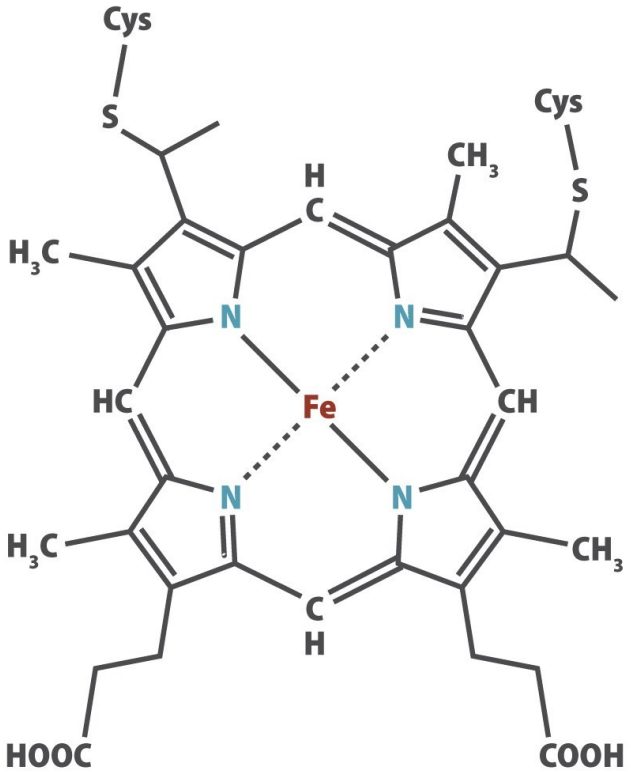


Figure 4.5.1 How Proteins Work (©2012 Garland Science)

Red basic
Green acidic

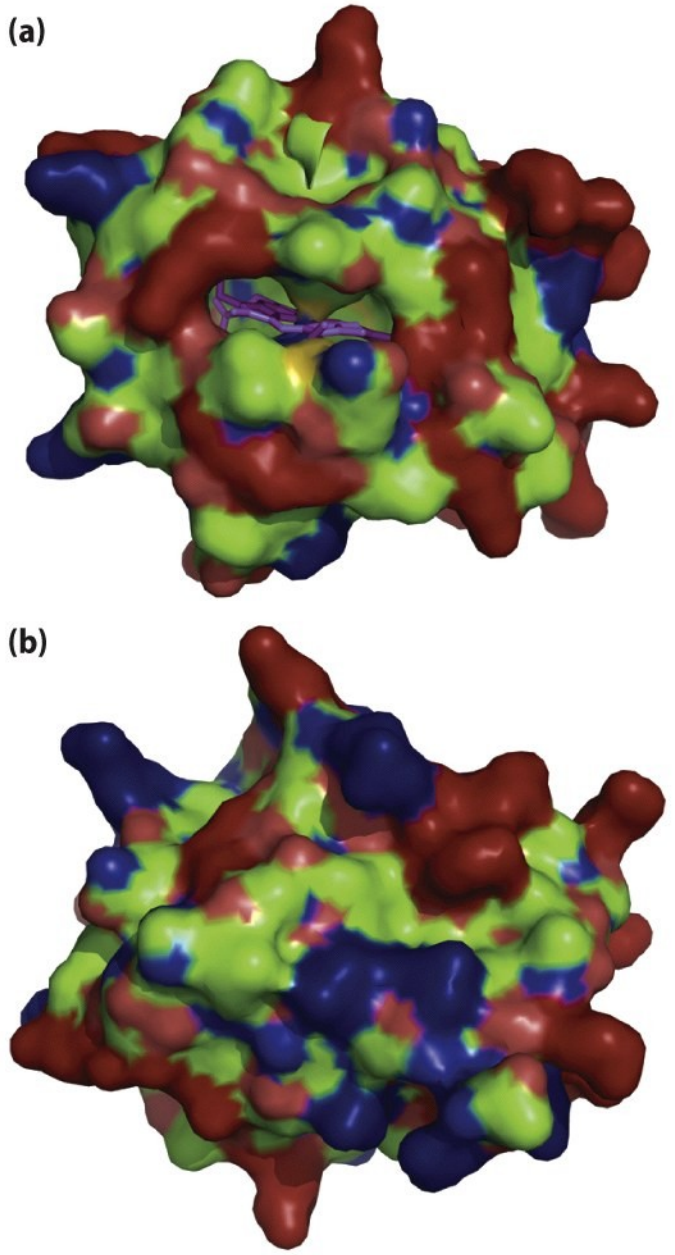
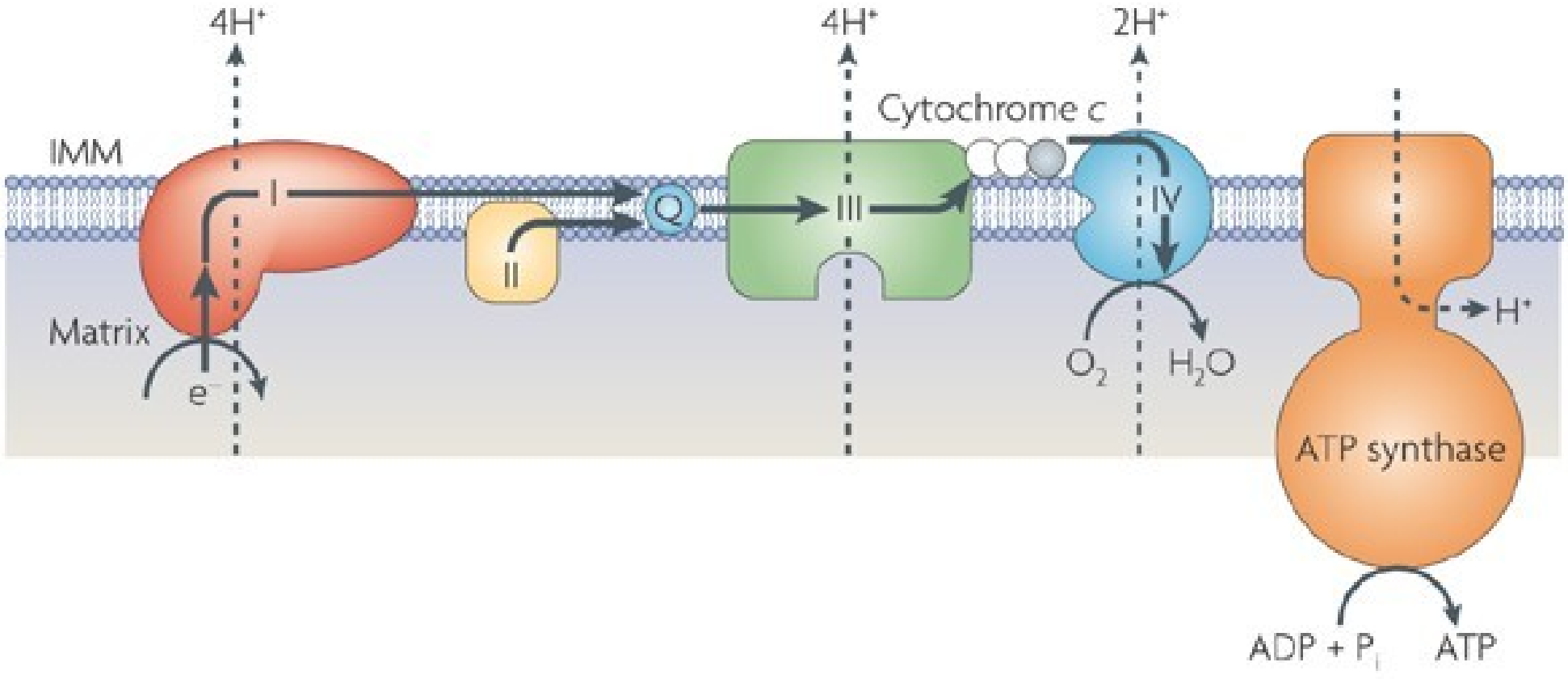


Figure 4.5 How Proteins Work (©2012 Garland Science)

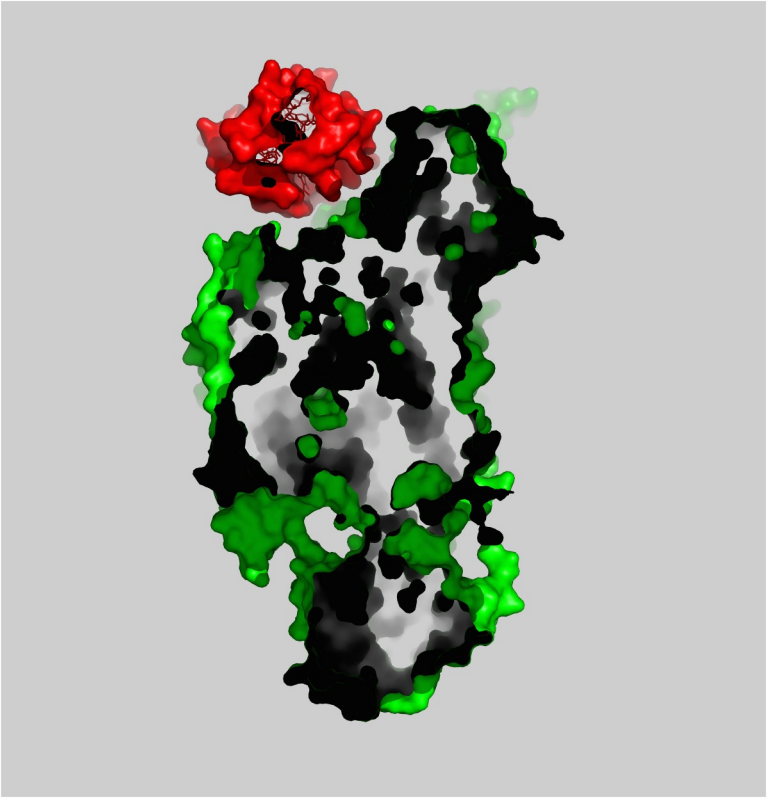
Cytochrome c

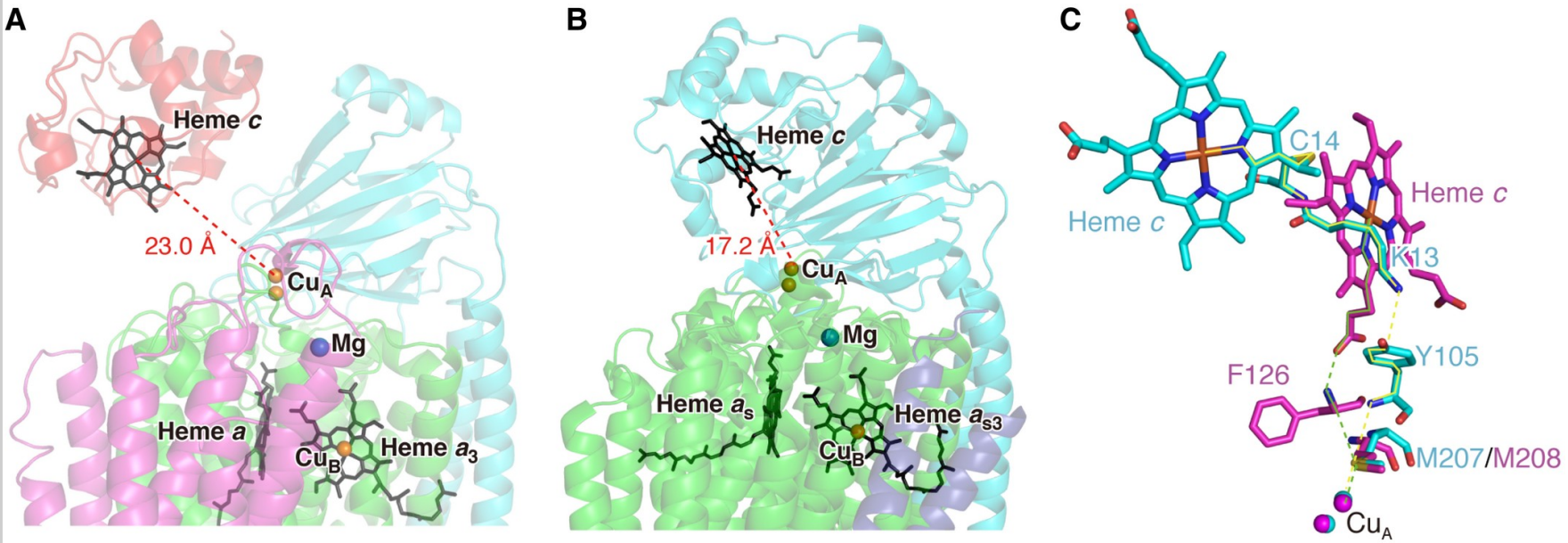
Electrostatic steering



ένας κρίσιμος μηχανισμός μέσω του οποίου το κυτόχρωμα c (cyt c) εντοπίζει και συνδέεται αποτελεσματικά με τους φυσιολογικούς του συνεργάτες, όπως η κυτόχρωμα c αναγωγάση (Σύμπλεγμα III) και η κυτόχρωμα c οξειδάση (Σύμπλεγμα IV), στον ενδομεμβρανικό χώρο των μιτοχονδρίων.

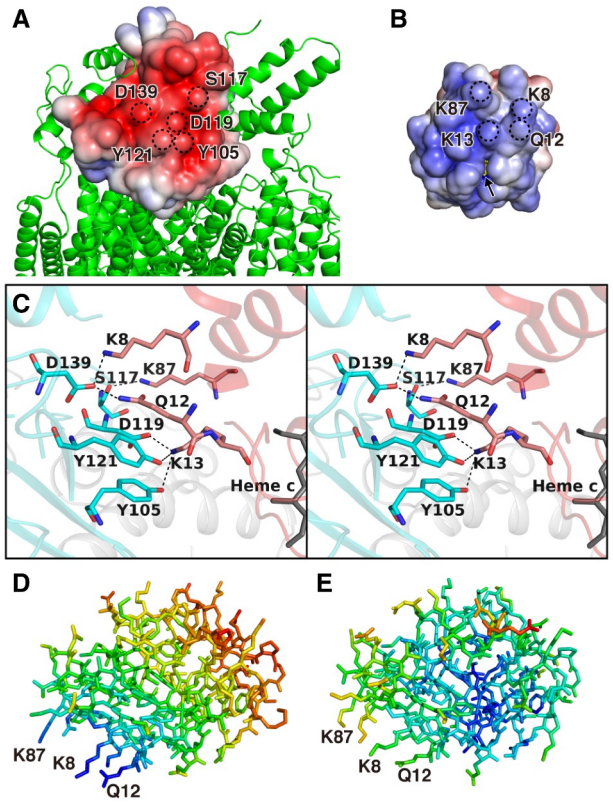
Complex structure of cytochrome c–cytochrome c oxidase reveals a novel protein–protein interaction mode

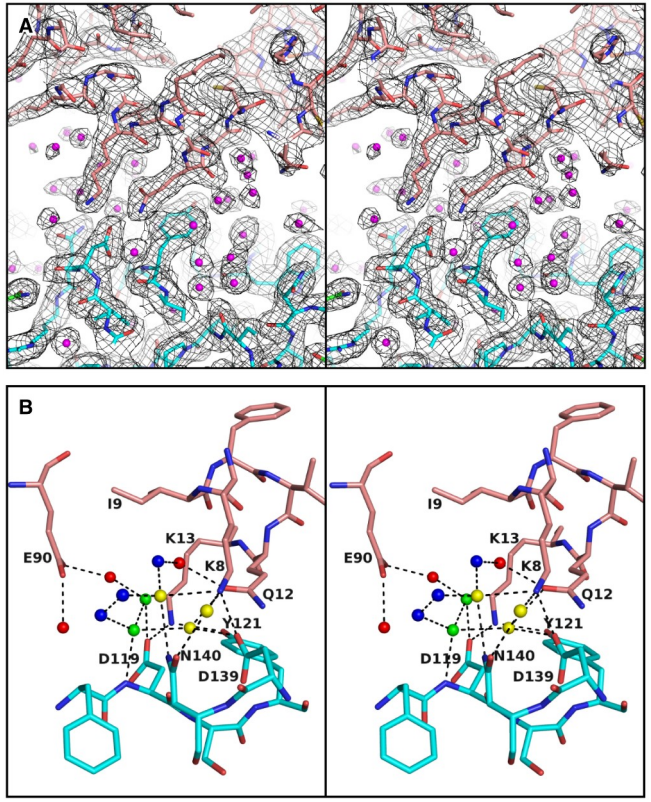




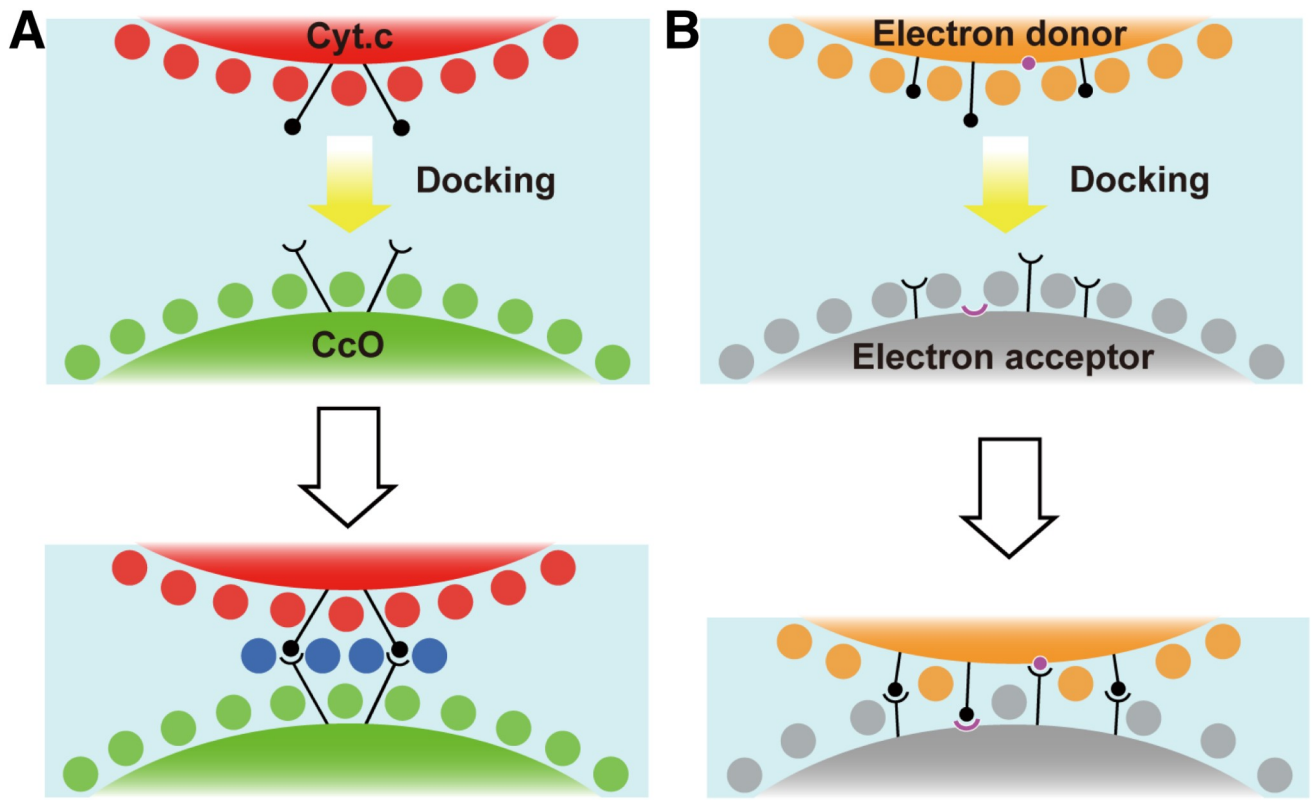
The EMBO Journal, Volume: 36, Issue: 3, Pages: 291-300, First published: 15 December 2016, DOI: (10.15252/embj.201695021)

Complex structure of cytochrome c–cytochrome c oxidase reveals a novel protein–protein interaction mode





The EMBO Journal, Volume: 36, Issue: 3, Pages: 291-300, First published: 15 December 2016, DOI: (10.15252/embj.201695021)


A
Cyt.c
Docking
CcO
B
Electron donor
Docking
Electron acceptor

Protein pIs

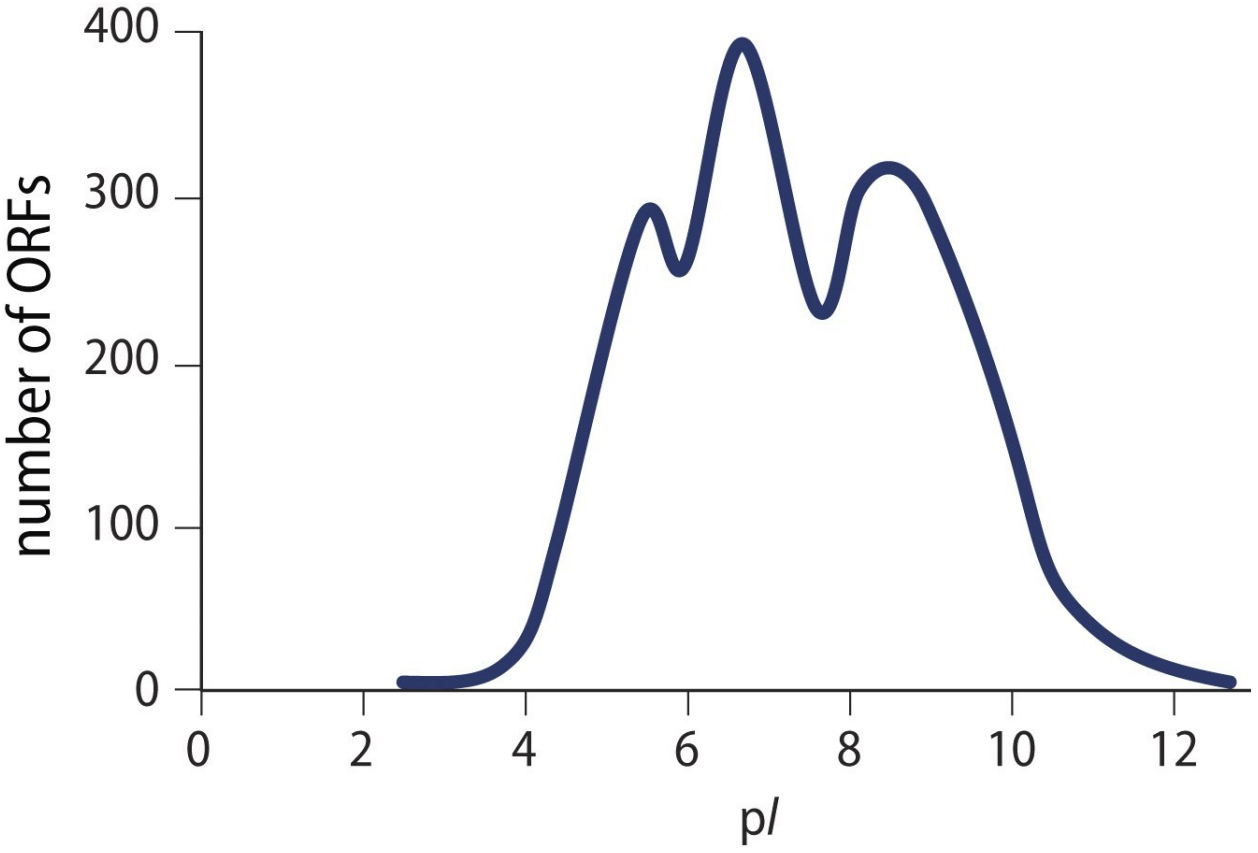


Figure 4.7 How Proteins Work (©2012 Garland Science)

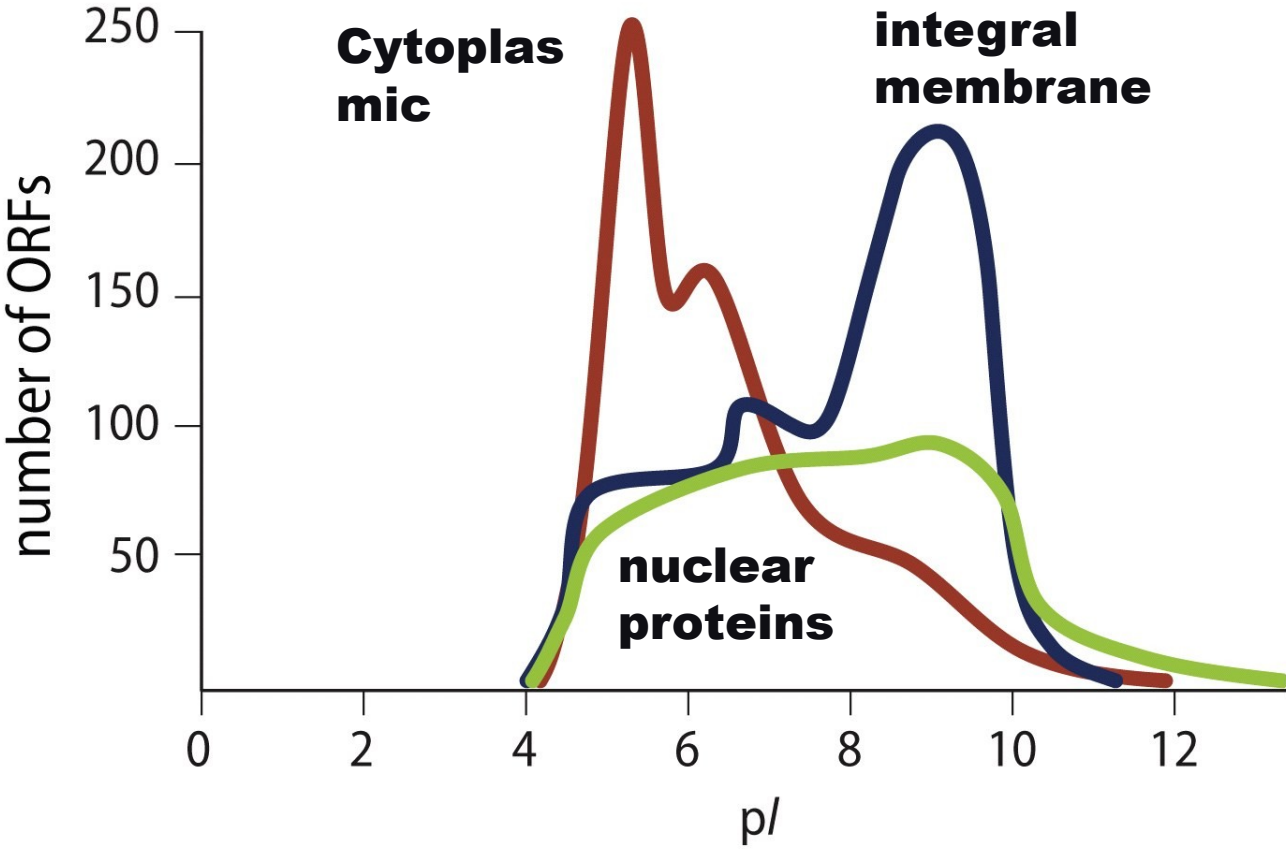


Figure 4.8 How Proteins Work (©2012 Garland Science)

σύμπλεγμα συνάντησης

encounter complex

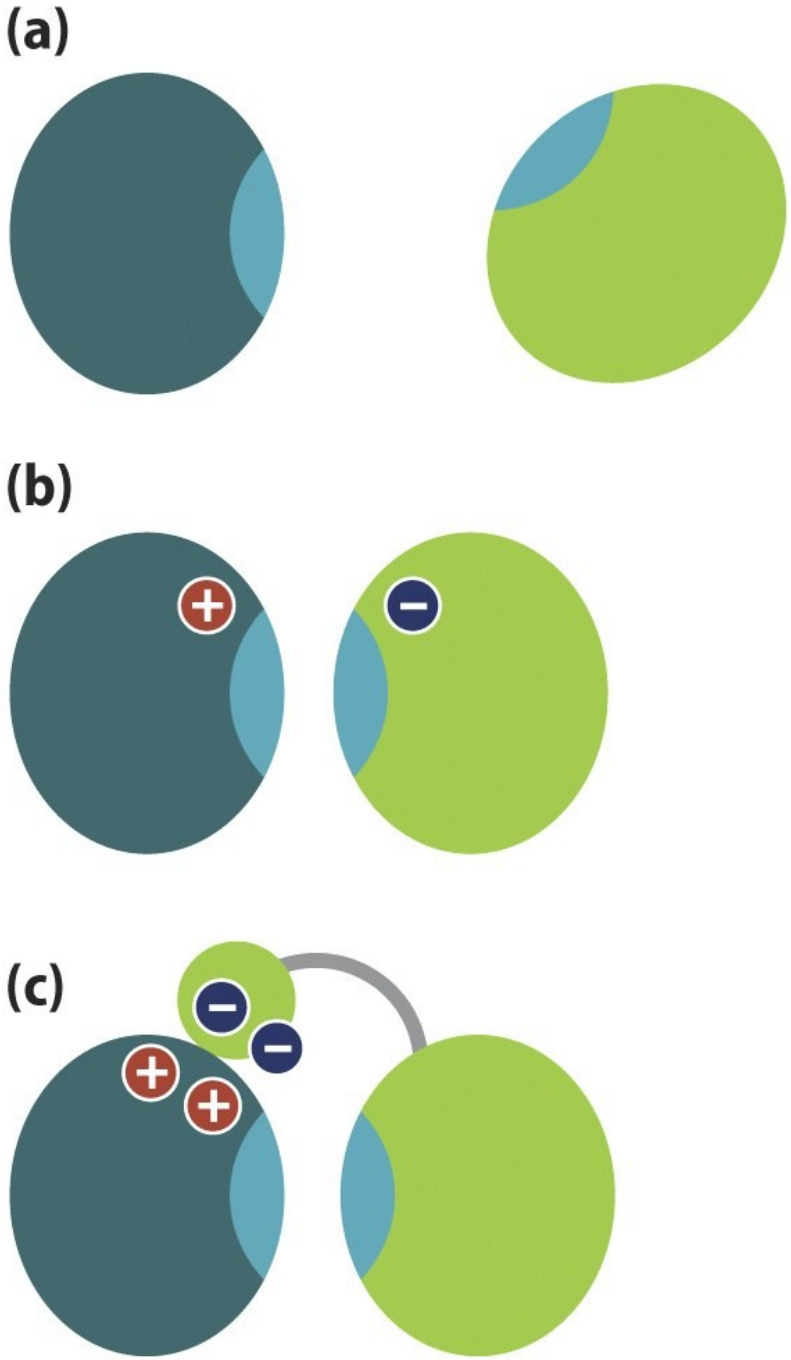
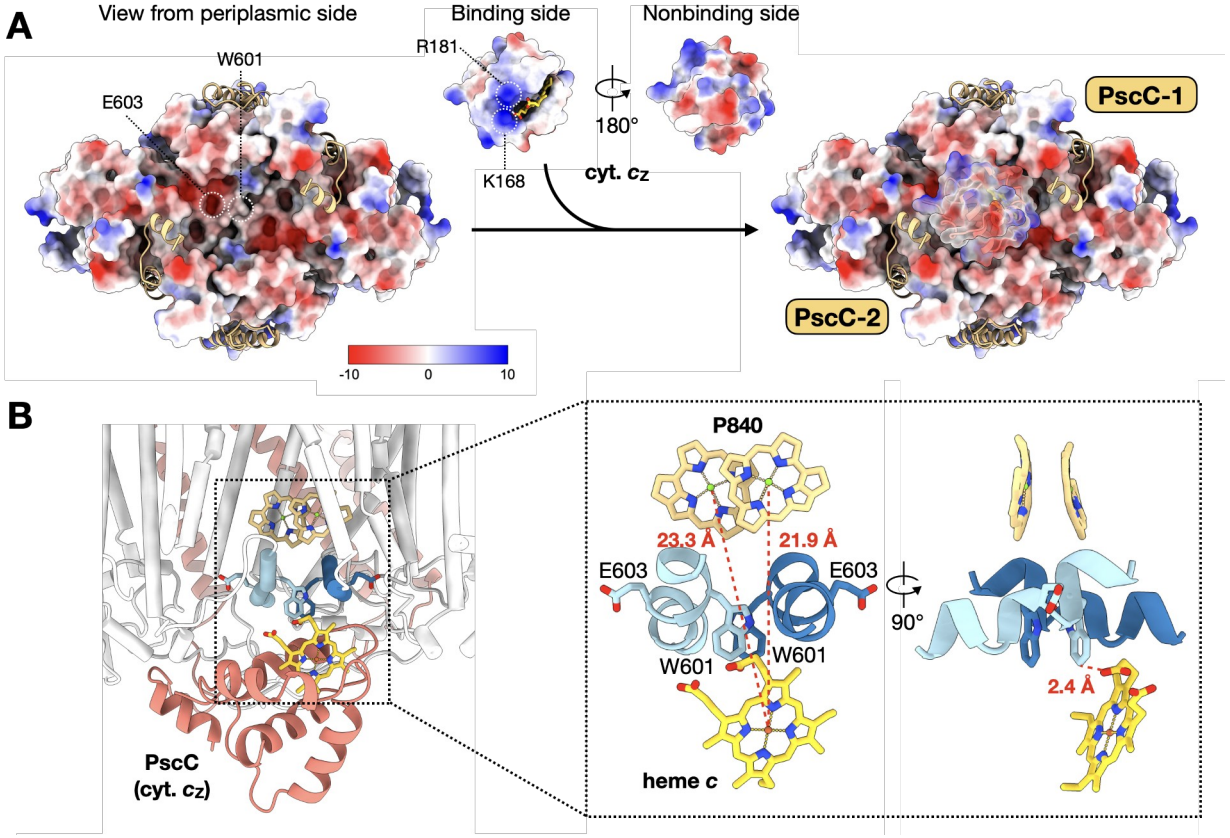
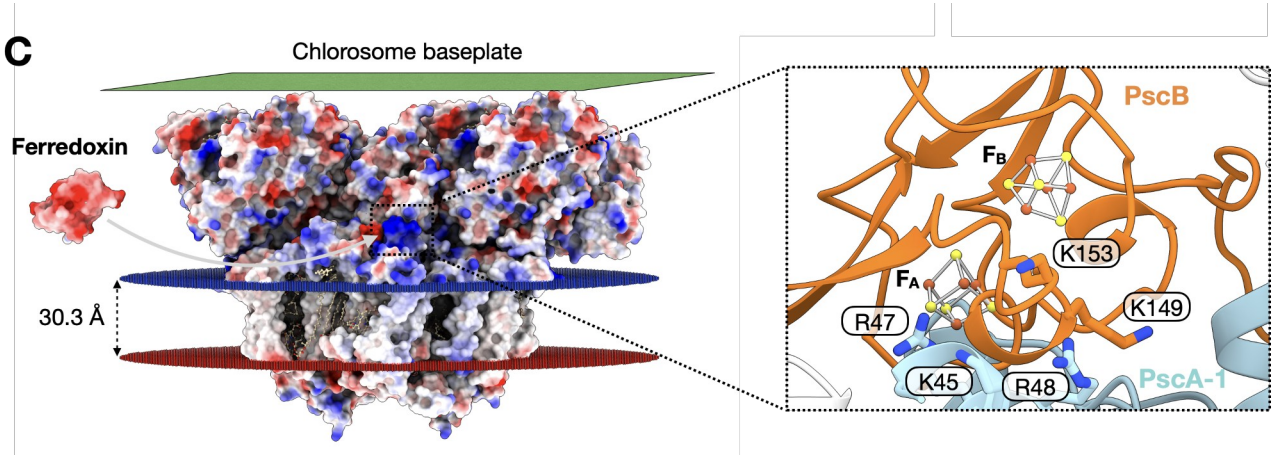


Figure 4.6 How Proteins Work (©2012 Garland Science)

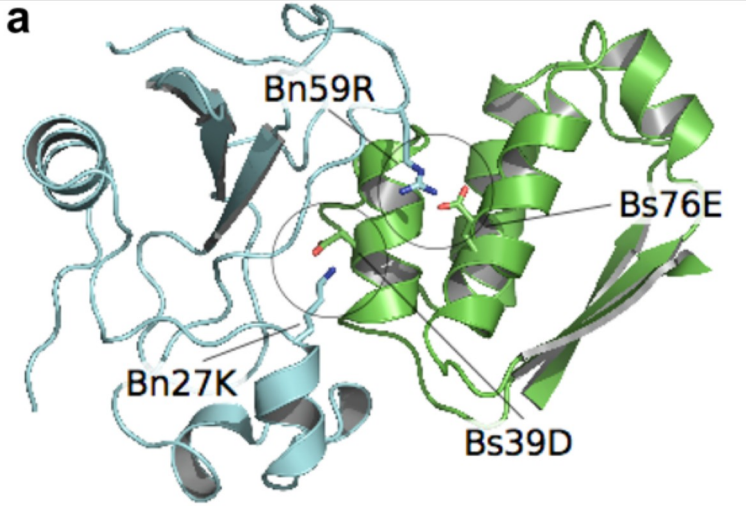
σύμπλεγμα συνάντησης

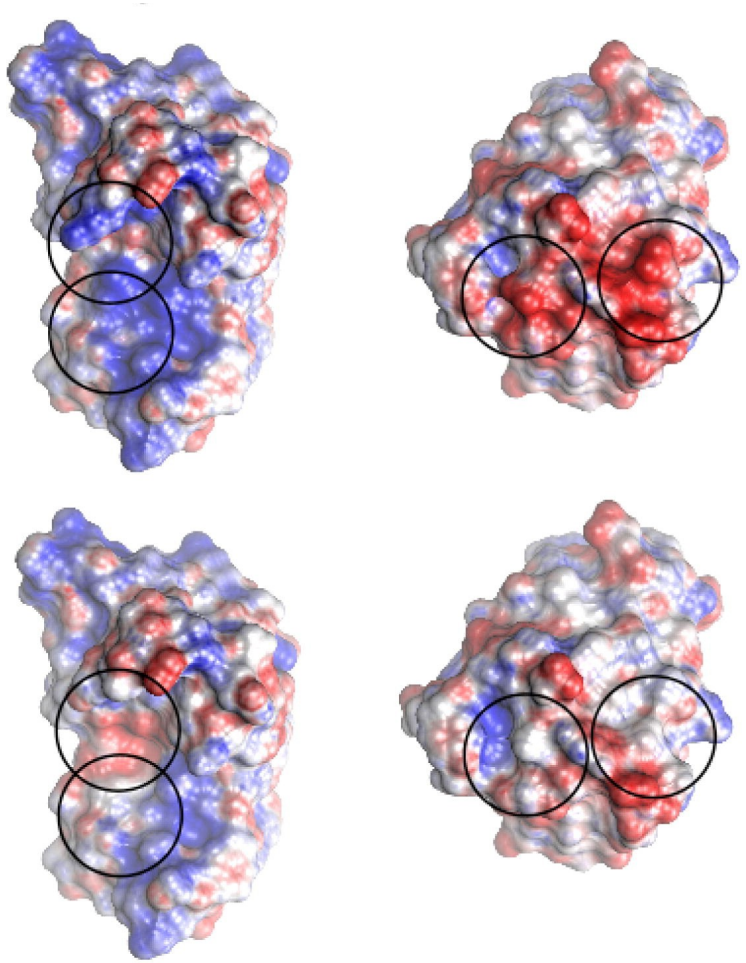




Xie, H., Lyratzakis,A et al. PNAS 2023

barnase with inhibitor barstar





M. Hoefling, K.E. Gottschalk /Journal of Structural Biology 171 (2010) 52–63

inside of a cell

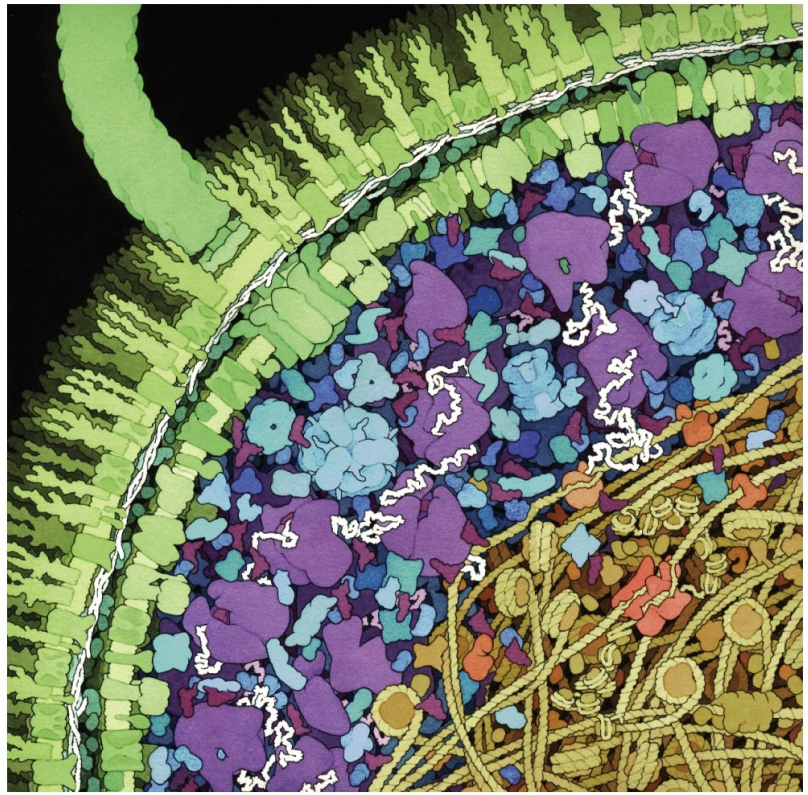


Figure 4.9 How Proteins Work (©2012 Garland Science)

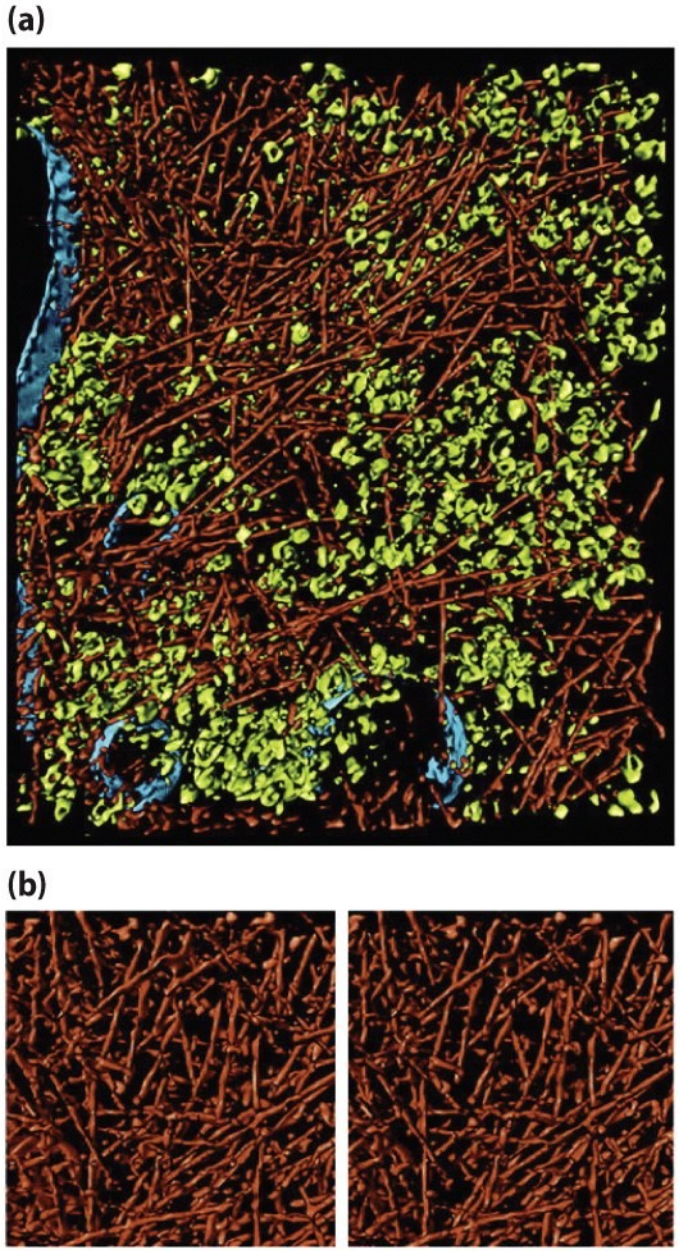


Figure 4.10 How Proteins Work (©2012 Garland Science)

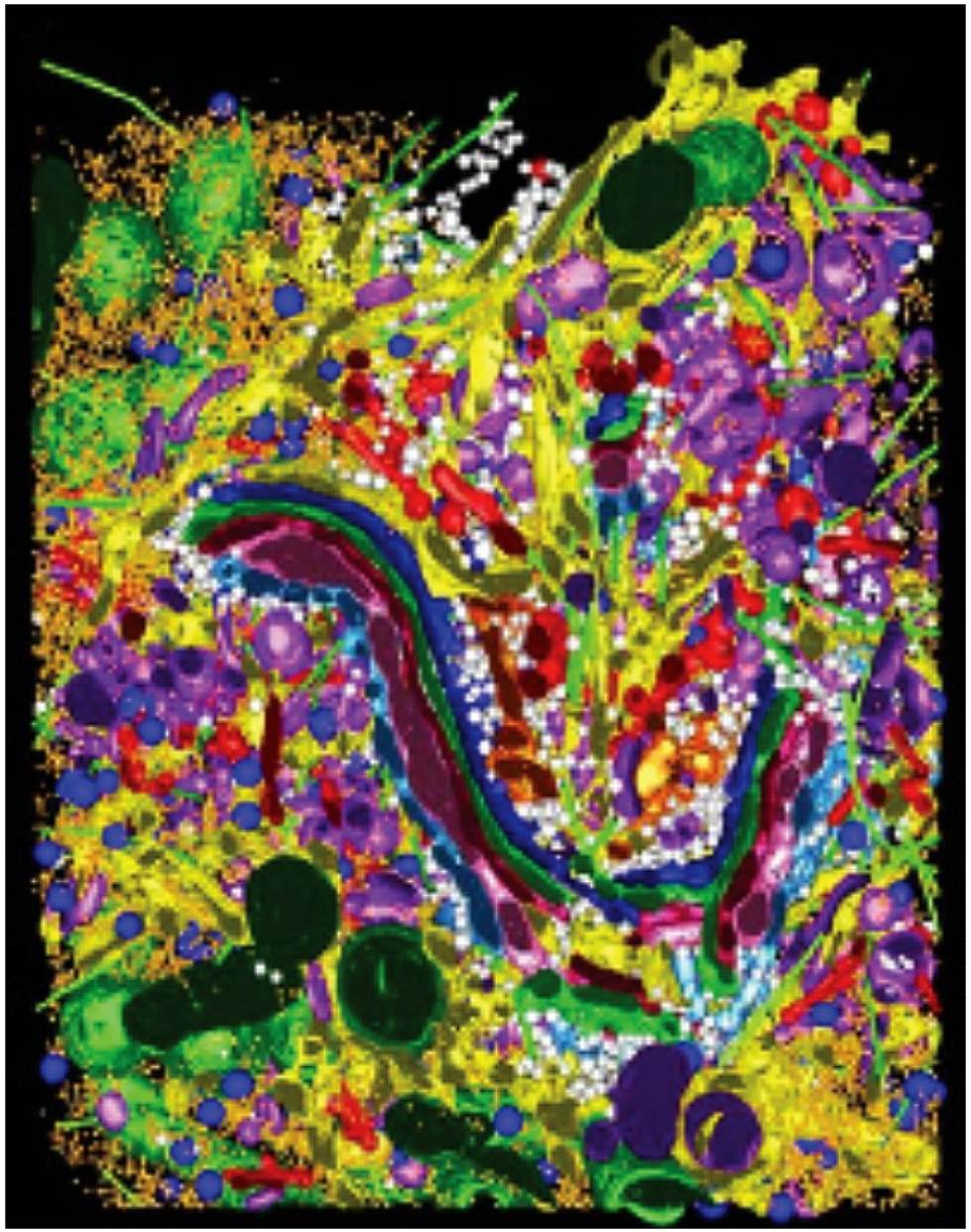
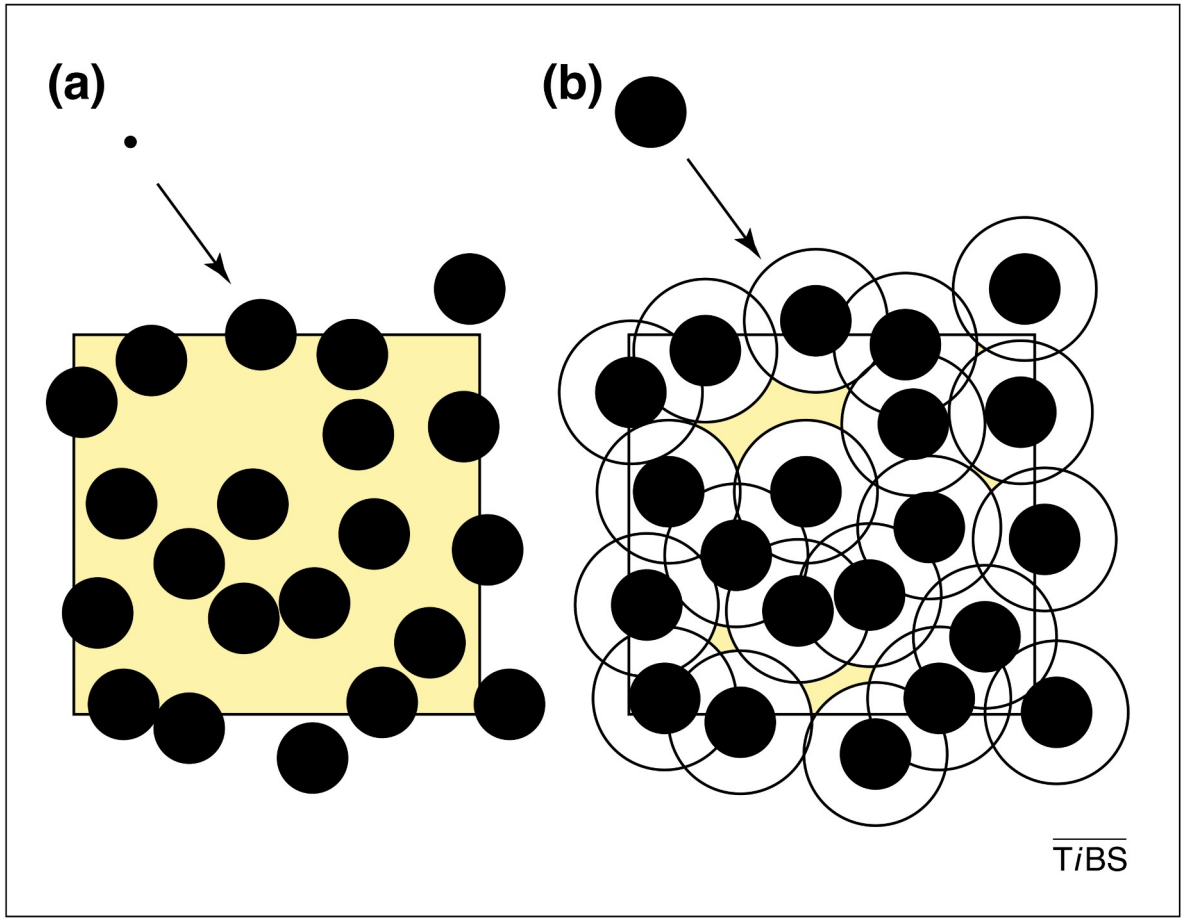


Figure 1.35 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

volume exclusion



TRENDS in Biochemical Sciences Vol.26 No.10 October 2001

relative sizes

The collision rate thus depends most critically on the size r_A of the diffusing molecule:

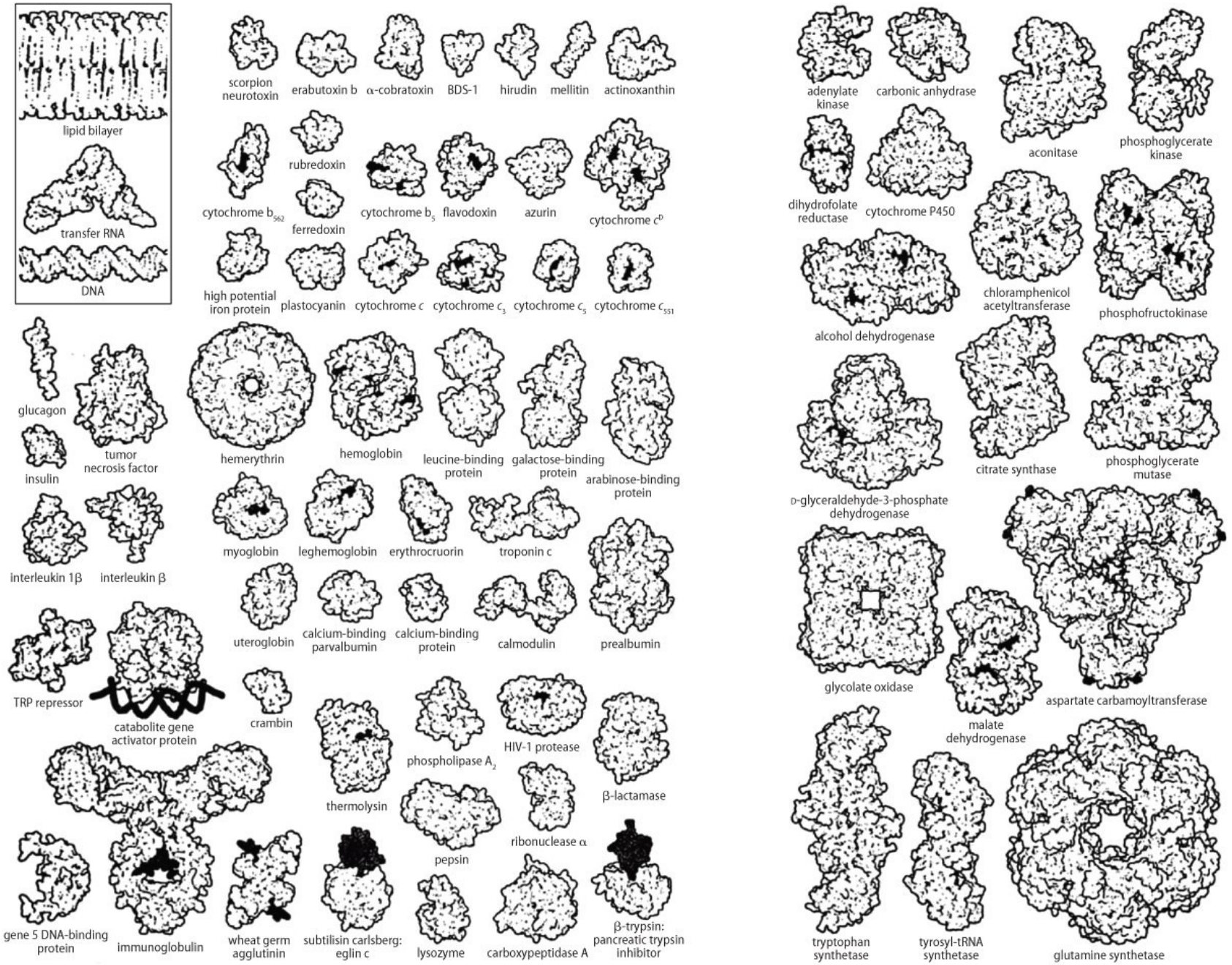
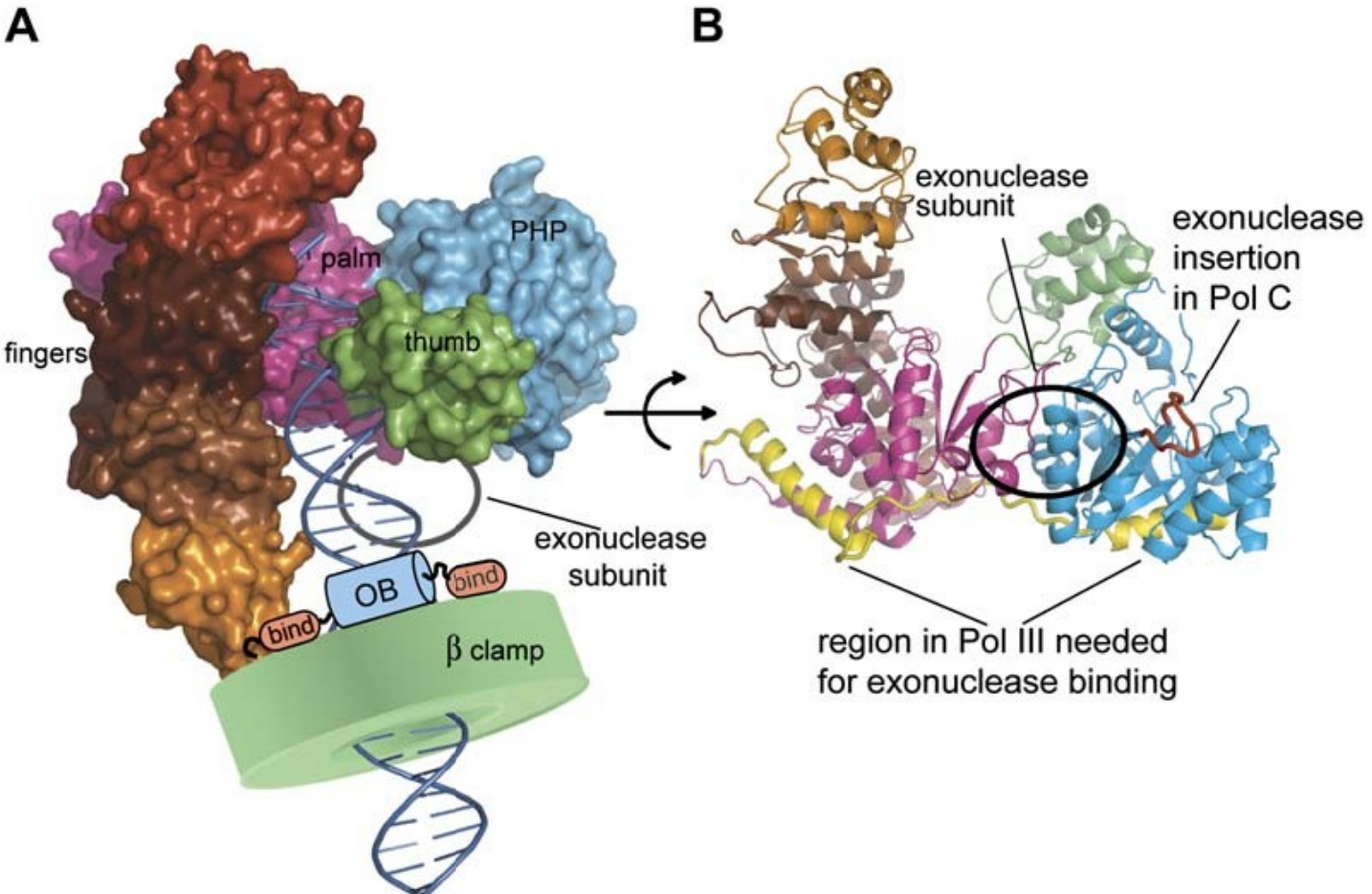
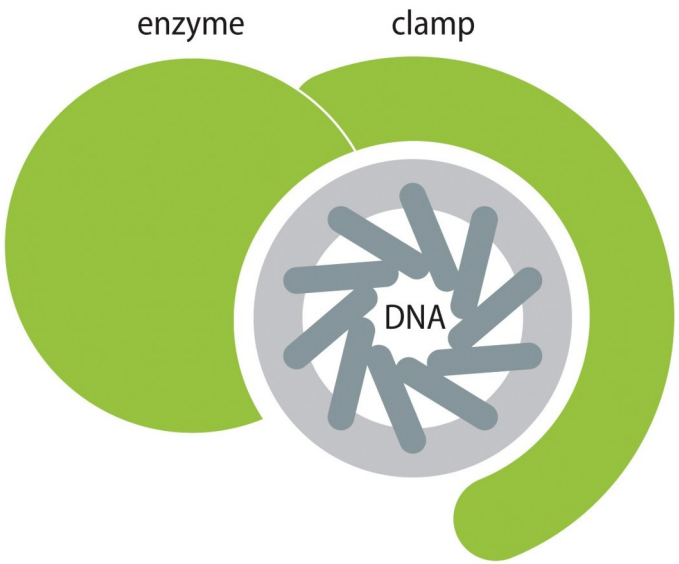


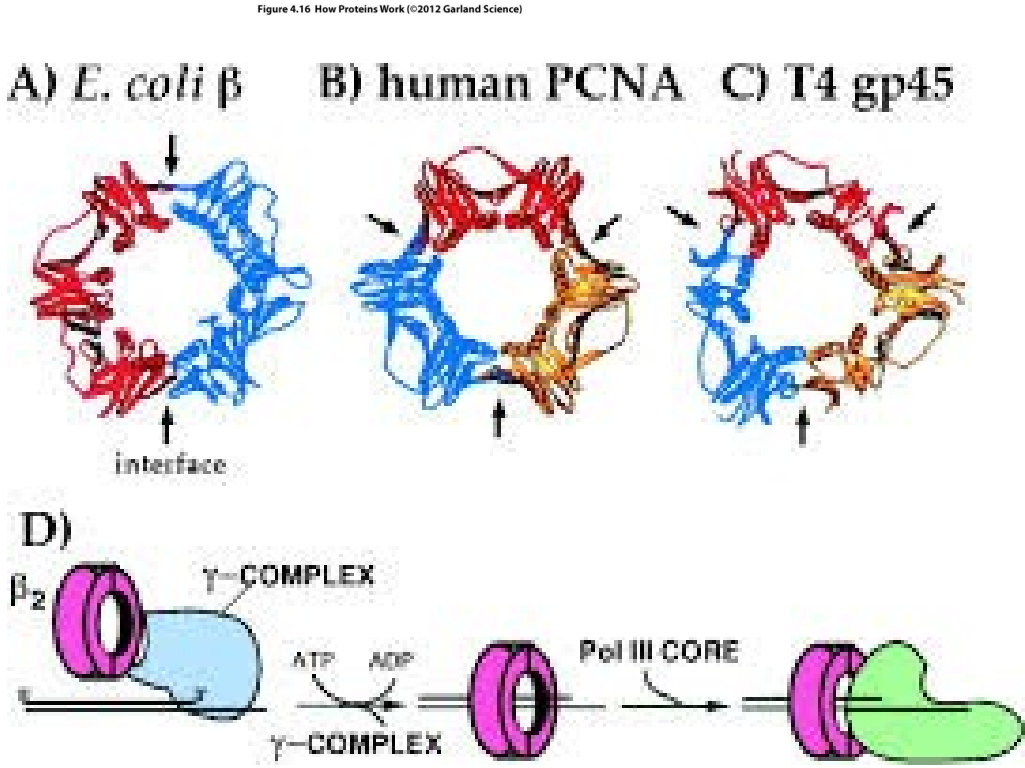
Figure 4.15 How Proteins Work (©2012 Garland Science)

Find the partner

Processivity decreases the off-rate from polymeric substrates







Glycogen

Table 1

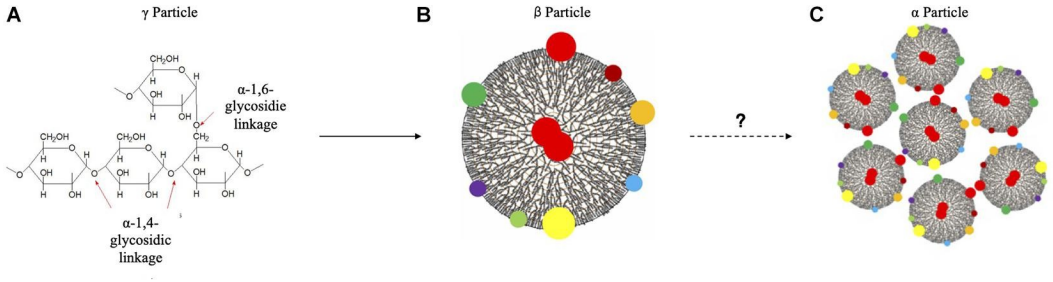
Overview of differences in glycogen levels and metabolism in brain, skeletal muscle, and liver

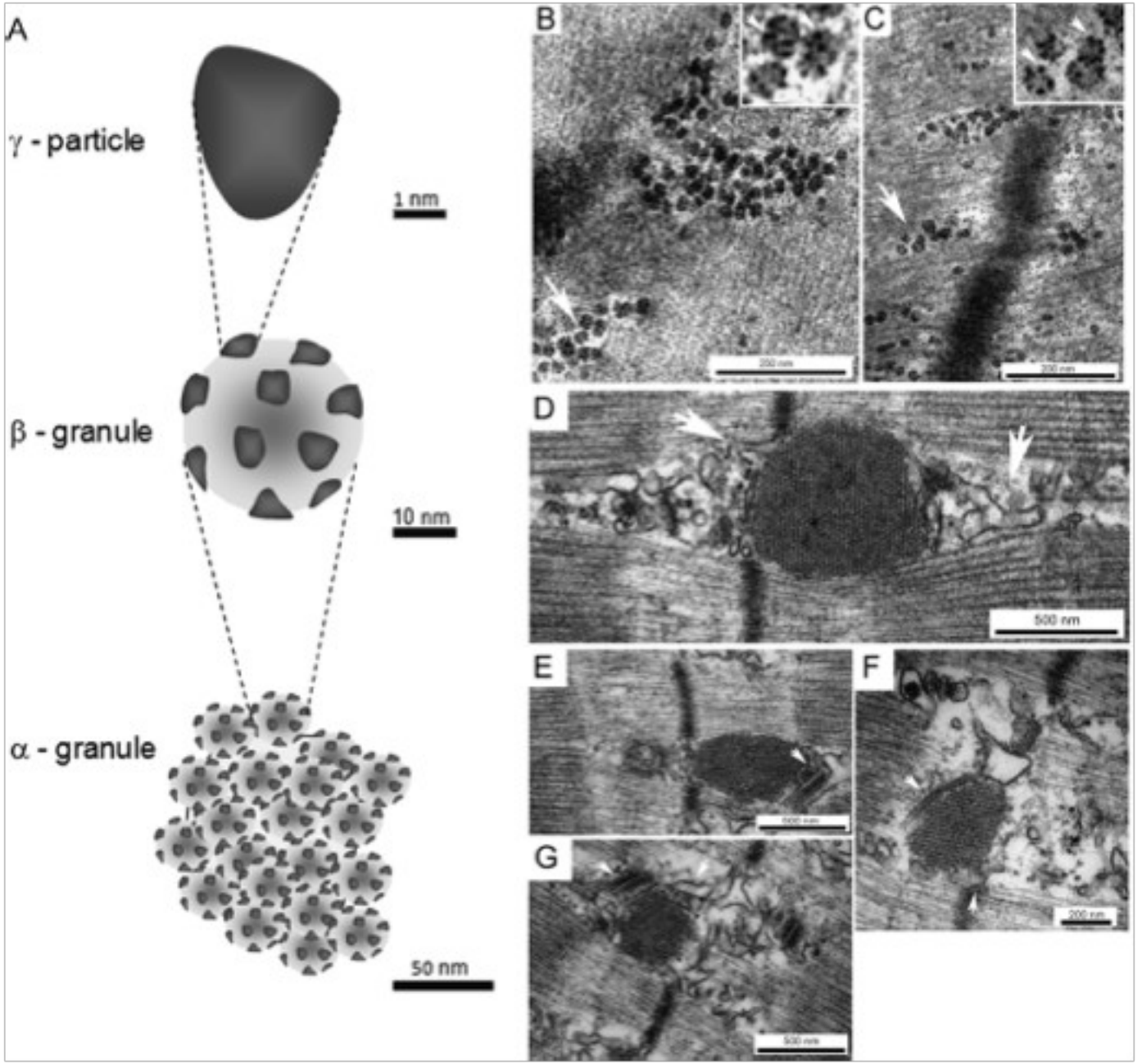
Specialization of different tissues and cells types has led to the diversification of glycogen metabolism regulation. An overview of the main differences in glycogen content, inter- and intracellular localization, and glycogen-related regulatory enzyme expression in brain, muscle, and liver are presented.

Attributes	Brain	Skeletal muscle	Liver
Average particle size (inner diameter, nm)	10–30	10–40	110–290
Glycogen concentration (human, μmol/g wet weight)	3–10	30–100	100–500
Estimated % of tissue weight	0.1	1–2	6–8
Estimated whole organ content (human, fed state, g)	0.5–1.5	100	400
Tissue localization	Regional variability. Gray matter > white matter	Muscle type-dependent. Type II > type I	Uniform
Cellular/subcellular localization	Cell-dependent, highest in astrocytes. Greater in areas with high synaptic density, primary branches and fine processes	Subsarcolemmal > myofibrillar	Hepatocytes, subcellular location modulated by metabolic conditions
Glycogenin isoform	GN1	GN1	GN2
Glycogen phosphorylase isoform	GPB GPM	GPM	PGPL
Glycogen synthase isoform	GS1	GS1	GS2

J. Biol. Chem. (2018) 293(19) 7089 –7098

Glycogen granule and the actin-rich spherical structures





Glycogen associated proteins

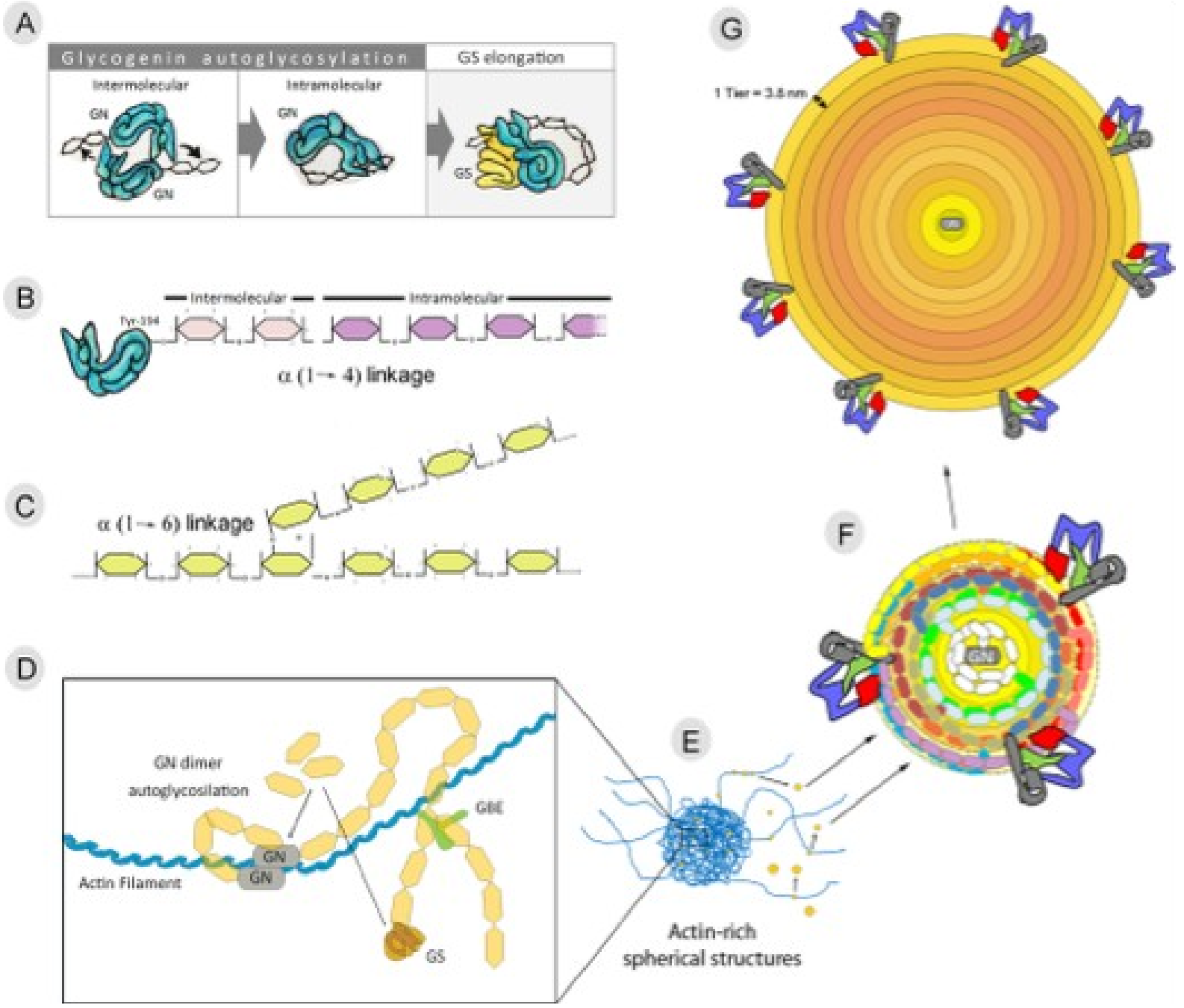
Primary proteins in the glycogen granule proteome and their interactions

List of main human glycosome-associated proteins as identified by name and UNIPROT identifier (ID) as well as primary interactions relevant to glycogen metabolism. Protein–protein interactions were derived from databases within UniProt (uniprot.org) (80), mainly The Biological General Repository for Interaction Datasets (BioGrid) (81) and the Protein Interaction Database and Analysis System (IntAct) (82). Abbreviations used are as follows: AMPK, 5′-AMP-activated protein kinase; EMP2A, laforin; GBE, branching enzyme; GDE, debranching enzyme; GN, glycogenin; GP, glycogen phosphorylase; GS, glycogen synthase; PhK, phosphorylase kinase; PP1, protein phosphatase; STDB1, starch-binding domain-containing protein 1; TRIM7, tripartite motif-containing protein.

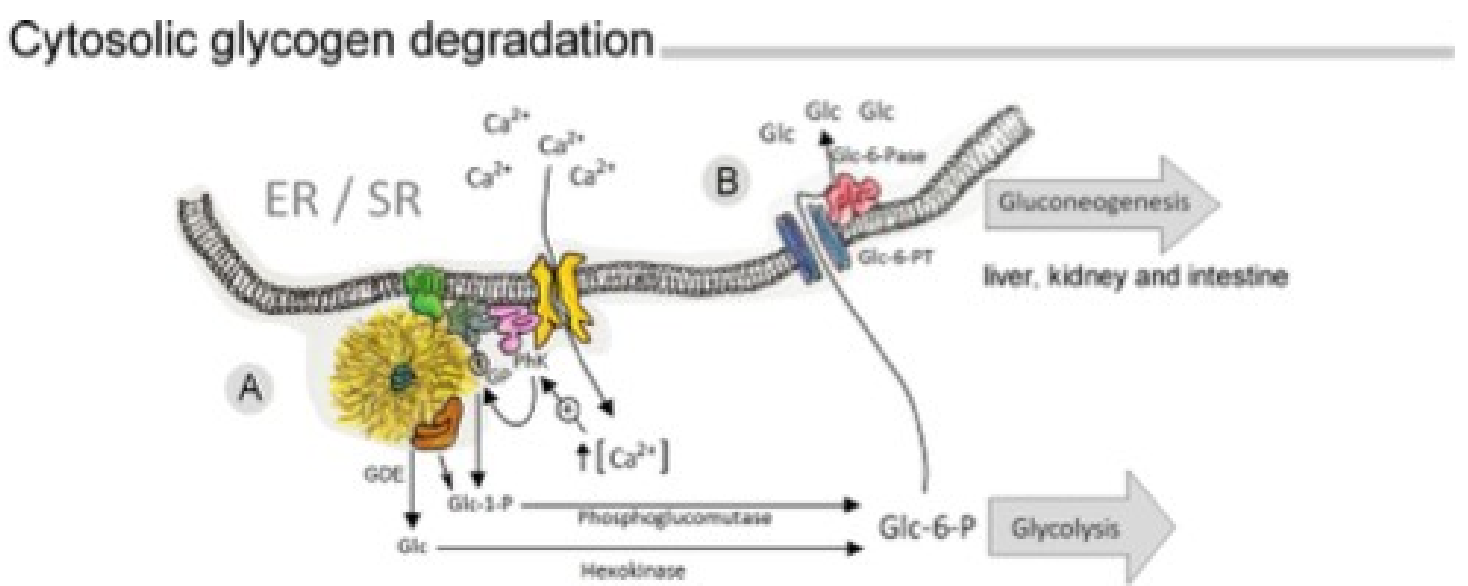
Protein	Role	UniProt ID	Key glycogen-related interactions
Glycogenin (GN)	Initiation	P46976 (GN1, muscle) O15488 (GN2, liver)	GS, AMPK, GBE, GP, STBD1, PP1 (PPP1R3C, PPP1CA, PPP1R5), TRIM7
Tripartite motif-containing protein (TRIM7, GNIP)	Initiation, regulation	Q9C029 (TRIM7)	GN
Glycogen synthase (GS)	Synthesis	P13807 (GS1, muscle) P54840 (GS2, liver)	GN, AMPK, GBE, PP1 (PP1R3B, PPP1R3C, PPP1CA), STBD1, KAPCA, CSK21, MAPKAPK2, GSK3, PAST, laforin, MLP3B/3C, DYRK
Glycogen branching enzyme (GBE)	Synthesis	Q04446	GP, GS, GN, STBD1, GBE, VAPA
Glycogen phosphorylase (GP)	Degradation	P11217 (PYGM, muscle) P11216 (PYGB, brain) P06737 (PYGL, liver)	AMPK, PKC, GBE1, PP2, MAPKAPK2, PP1
Glycogen debranching enzyme (GDE, AGL)	Degradation	P35573	AMPK, PP1, malin, AMPK, STBD1
Malin (E3 ubiquitin-protein ligase NHLRC1)	Ubiquitin ligase	Q6VVB1	Laforin, GS, PP1, GDE, AMPK
5′-AMP-activated protein kinase (AMPK)	Kinase	P54646 (α2) Q9Y478 (β1) O43741 (β2)	Laforin, PP1 (PPP2CA, PPP2R1B), PHKG2, CAMK, GN
Laforin (EPM2A)	Carbohydrate phosphatase, ubiquitin ligase	O95278	AMPK, PP1 (PPP1R3C, PPP1R3D), GSK3B, STBD1, GS, malin,
Protein phosphatase 1 (PP1) and targeting subunits	Phosphatase, main regulatory and catalytic subunits	PP1	AMPK, laforin, GSK3B, GN, GS
		Q16821 (PPP1R3A, GM) Q86X16 (PPP1R3B, GL) Q0VCR4 (PPP1R3C, PTG) O95685 (PPP1R3D, PPP1R6) P67775 (PPP2CA) P62136 (PPP1CA) P30154 (PPP2R1B)	
Phosphorylase kinase (PhK)	Kinase	P15735 (γ, liver, testis) Q16816 (γ, muscle)	AMPK, PP1 (PPP1R3B), GP
Starch-binding domain- containing protein 1 (STBD1)	Cargo receptor for glycogen	O95210	GDE, GBE, PP1, malin, GN, GS, AMPK, GP, MLP3B/3C

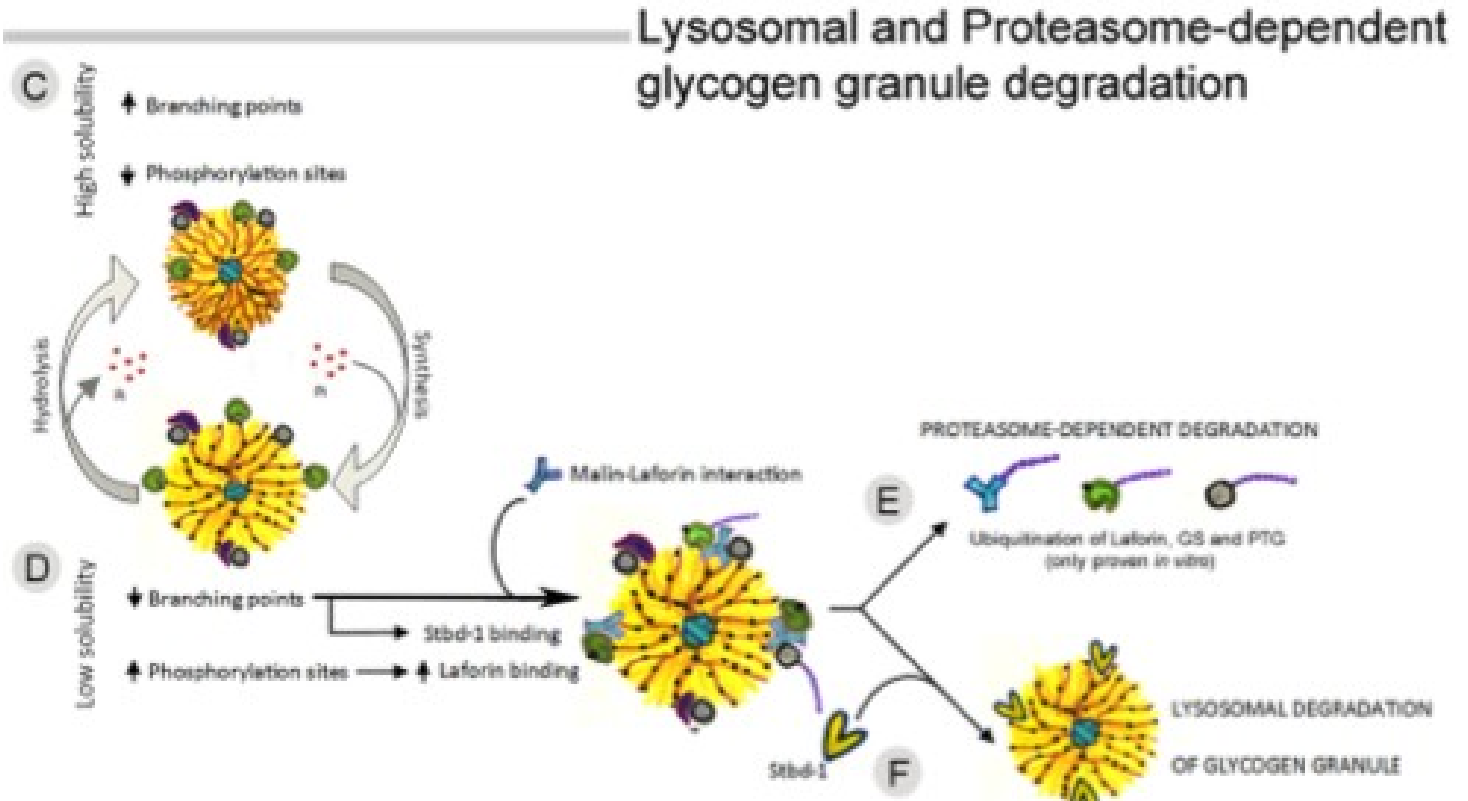
Find the partner

glycogen synthase (GS)
glycogen-branching enzyme (GBE)



Find the partner

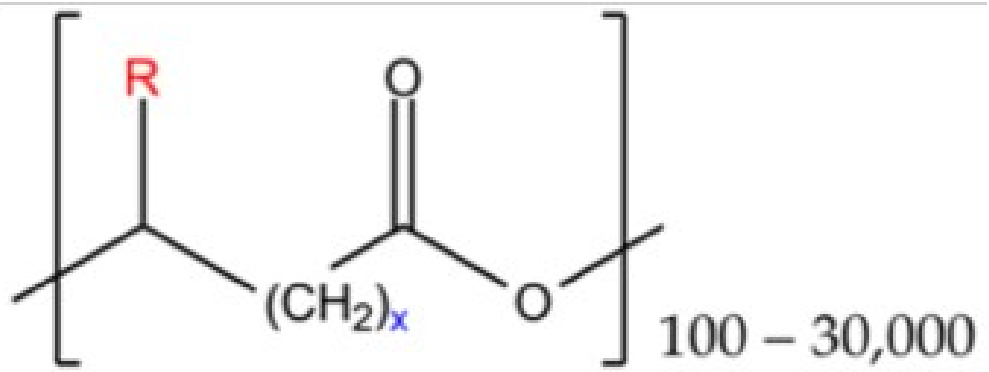




Plastics

Plastic	Applications	Usage Time	Degradation Time *
PET (Polyethylene terephthalate)	Bottles and other plastic containers	1–3 years	500–1000 years
HDPE (high-density polyethylene)	Pipelines, bottles	5–35 years	250–5000 years
LDPE (low-density polyethylene)	Plastic wrappers and bags	1–3 years	150 years
PVC (Polyvinyl chloride)	Pipelines and other uses in construction	35 years	>1000 years
PP (Polypropylene)	Textiles, packaging, automotive components	5–15 years	50–800 years
PHAs (Polyhidroxyalkanoates)	Bags, packaging, medical implants	-	<1 year

The general structure of PHAs

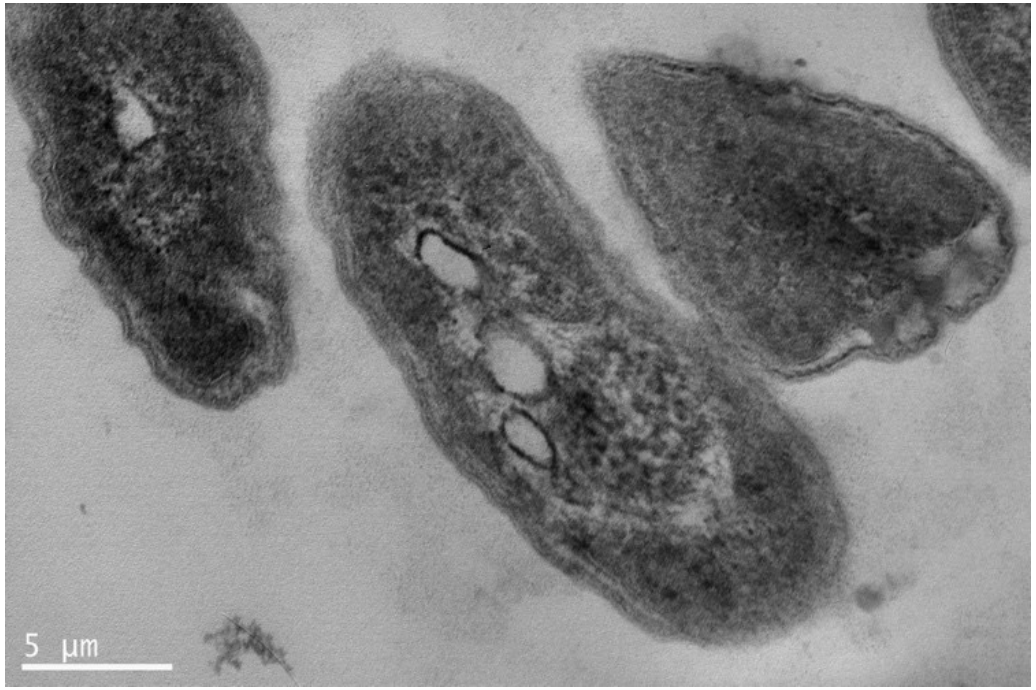


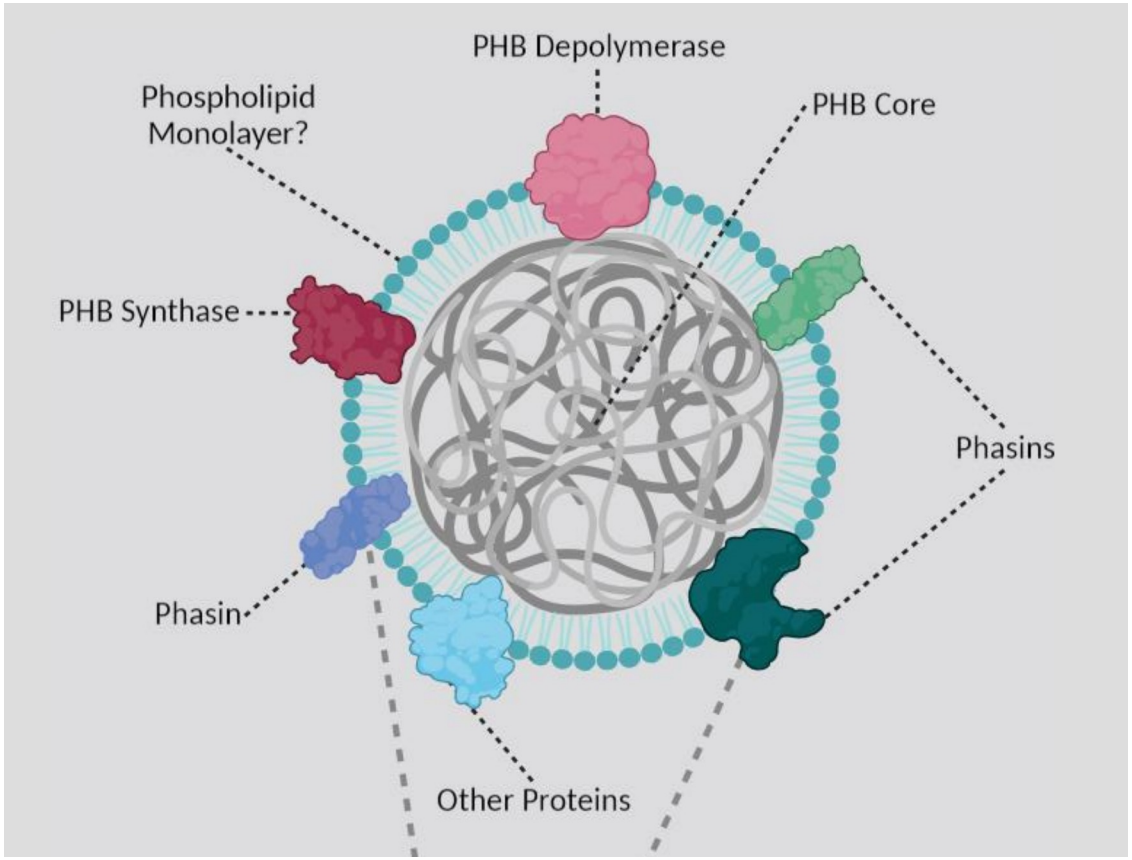
Similar properties to conventional plastics

- Accumulated in the form of granules in microorganisms, as a type of carbon storage
- PHB is the most studied PHA

Chain	x	R	Carbon	PHA	Abbreviation
Short	1	Hydrogen	C_3	Poly(3-hydroxypropionate)	P(3HP)
		Methyl	C4	Poly(3-hydroxybutyrate)	P(3HB)
		Ethyl	C_5	Poly(3-hydroxyvalerate)	P(3HV)
	2	Hydrogen	C_4	Poly(4-hydroxybutirate)	P(4HB)
		Methyl	C_5	Poly(4-hydroxyvalerate)	P(4HV)
	3	Hydrogen	C_5	Poly(5-hydroxyvalerate)	P(5HV)
Medium	1	Propyl	C_6	Poly(3-hydroxyhexanoate)	P(3HHx)
		Butyl	C_7	Poly(3-hydroxyheptanoate)	P(3HHp)
		Pentyl	C_8	Poly(3-hydroxyoctanoate)	P(3HO)
		Hexyl	C_9	Poly(3-hydroxynonanoate)	P(3HN)
		Heptyl	C_{10}	Poly(3-hydroxydecanoate)	P(3HD)
		Octyl	C_{11}	Poly(3-hydroxyundecanoate)	P(3HUD)
		Nonyl	C_{12}	Poly(3-hydroxydodecanoate)	P(3HDD)
		Decyl	C_{13}	Poly(3-hydroxytridecanoate)	P(3HTD)
		Undecyl	C_{14}	Poly(3-hydroxytetradecanoate)	P(3HTTD)
	2	Ethyl	C_6	Poly(4-hydroxycarpoate)	P(4HC)
	3	Methyl	C_6	Poly(5-hydroxycarpoate)	P(5HC)
		Ethyl	C_7	Poly(4-hydroxyheptanoate)	P(4HH)
Long	1	Dodecyl	C_{15}	Poly(3-hydroxypentadecanoate)	P(3HPD)
		Tridecyl	C_{16}	Poly(3-hydroxyhexadecanoate)	P(3HHxD)
		Pentadecyl	C_{18}	Poly(3-hydroxyoctadecanoate)	P(3HOD)

Find the partner

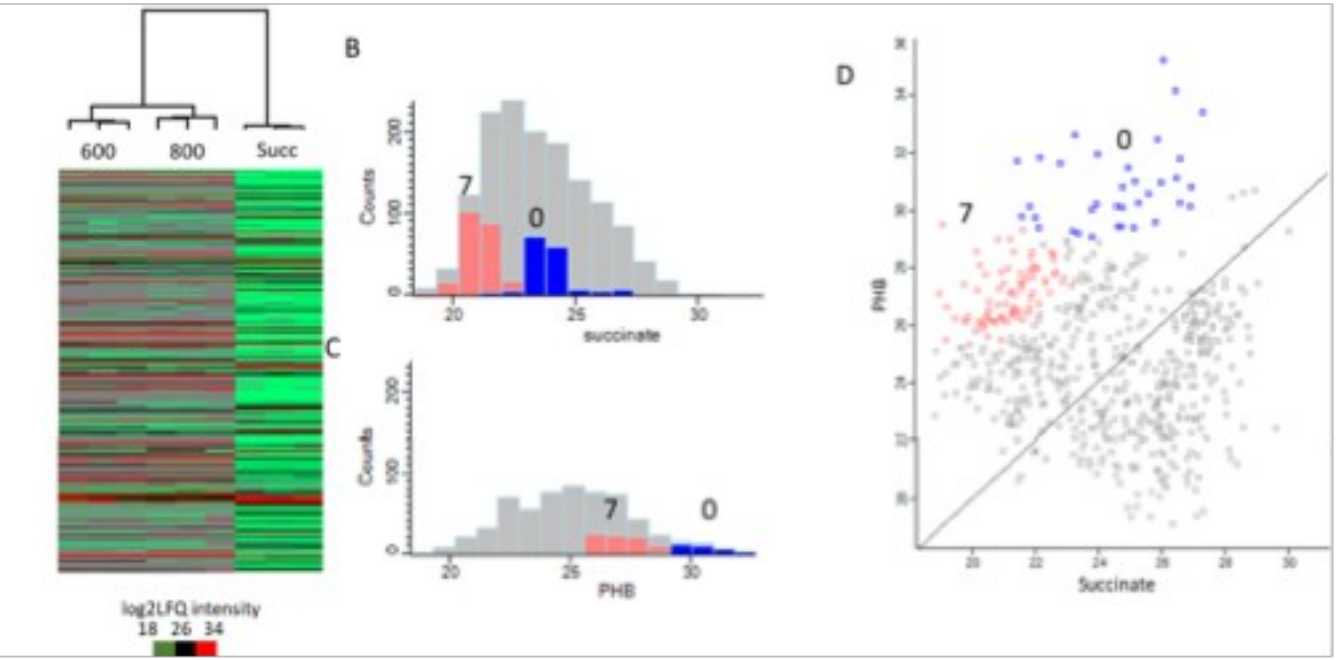


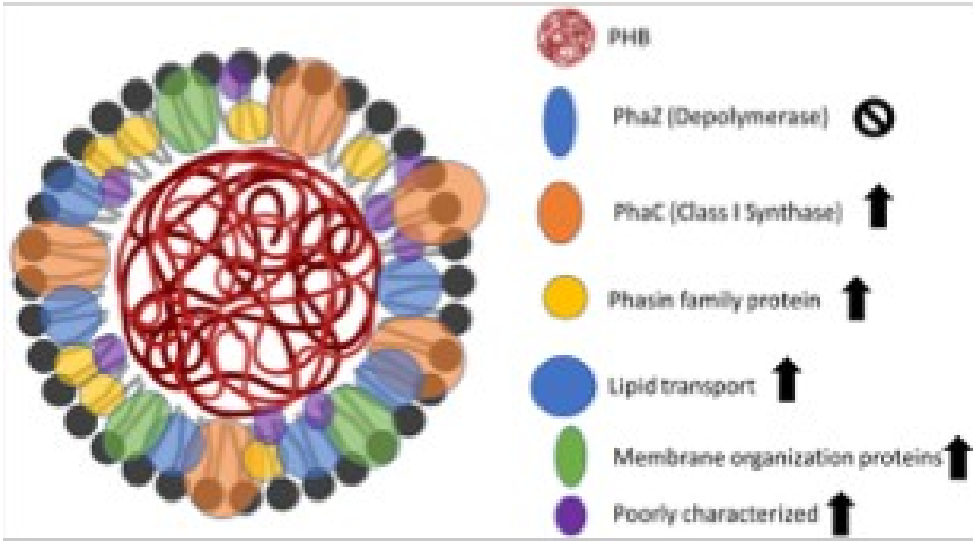


I. Kanavaki, A. Drakonaki, E.D. Geladas, A. Spyros, H. Xie, G. Tsiotis,
Polyhydroxyalkanoate (PHA) Production in Pseudomonas sp. phDV1 Strain Grown on Phenol as Carbon Sources., Microorganisms. 9 (2021).

A Drakonaki, E Mathioudaki, ED Geladas, E Konsolaki, N Vitsaxakis,, N & Tsiotis, G. Production of Polyhydroxybutyrate by Genetically Modified *Pseudomonas* sp. phDV1: A Comparative Study of Utilizing Wine Industry Waste as a Carbon Source Microorganisms 11 (6), 1592

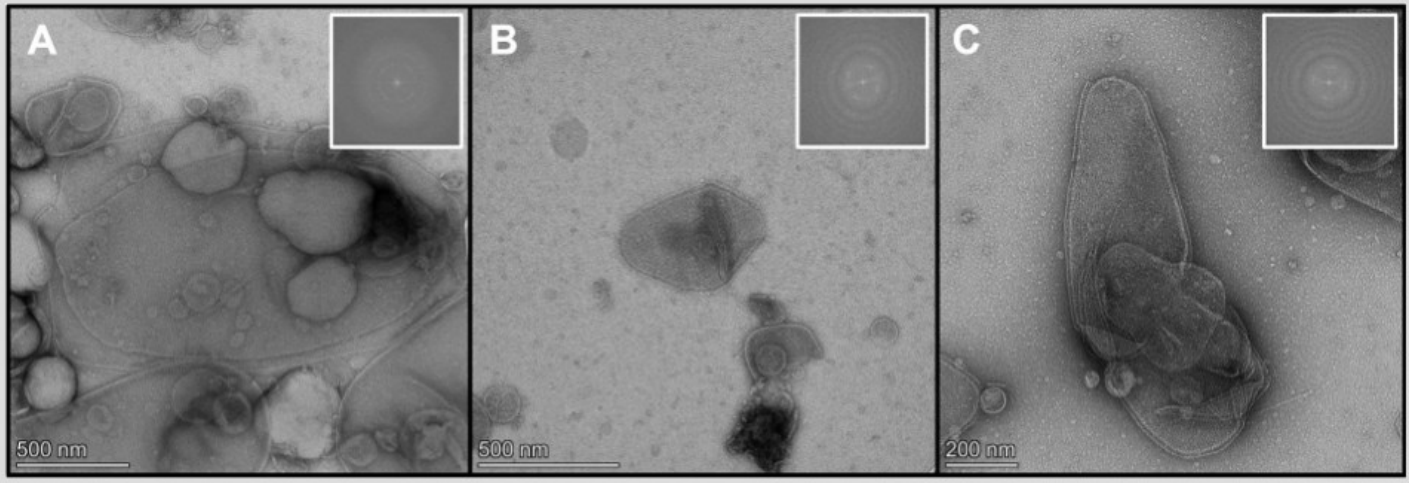
Carbonosomes





Geladas, E.D.; Lyratzakis, A.; Drakonaki, A.; Gkikas, G.; Tsiotis, G. Isolation and Characterization of Carbonosomes from Pseudomonas sp. phDV1 Grown Using Phenol as Carbon Source. Microorganisms 2025, 13, 369. https://doi.org/10.3390/microorganisms13020369

Negative-Stain TEM

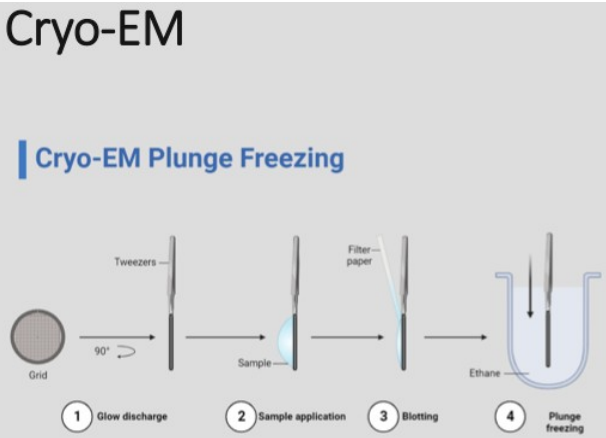


WT **ΔphaR** **ΔphaZ**

(Jendrossek et al., 2007, Applied and Environmental Microbiology)

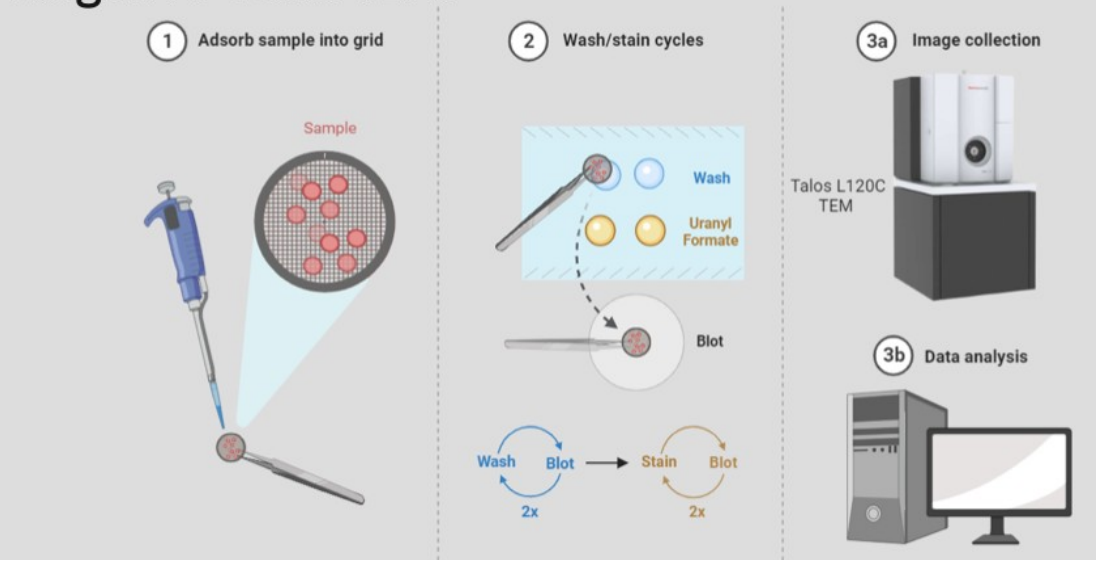
22

Cryo-EM

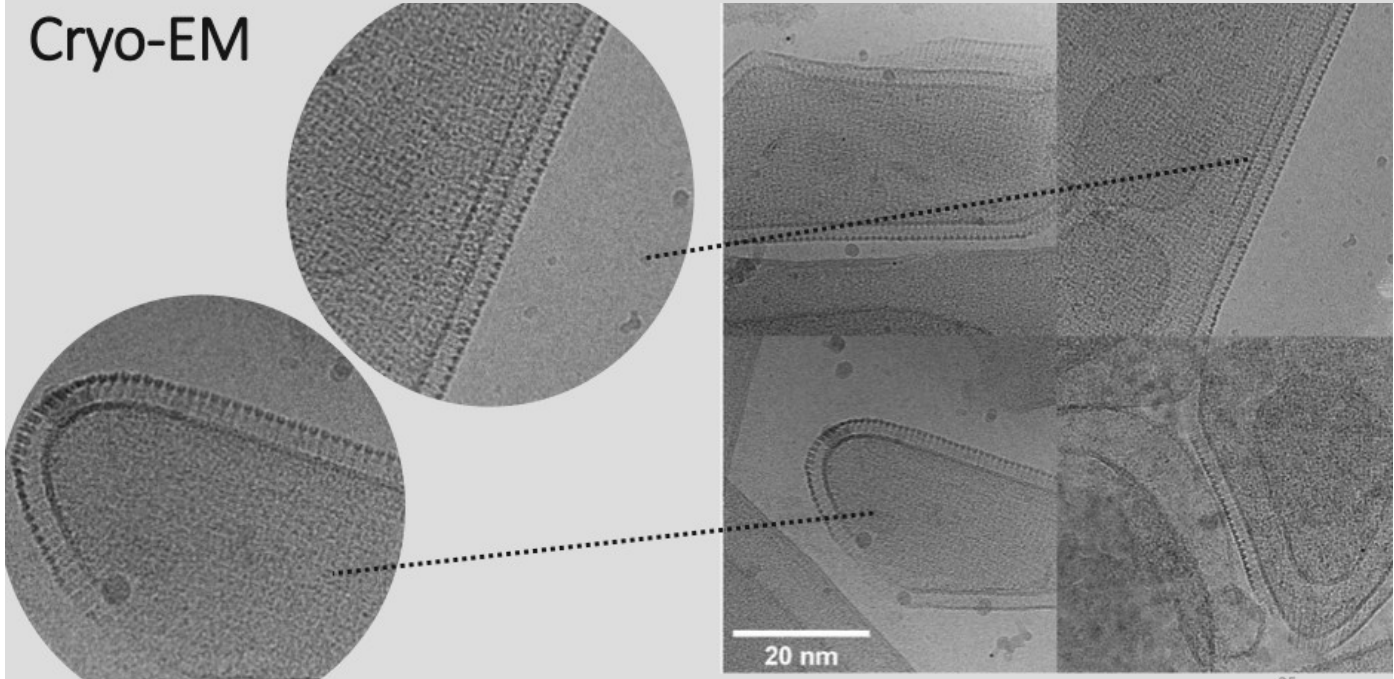


Krios G4 Cryo-TEM

Negative-Stain TEM



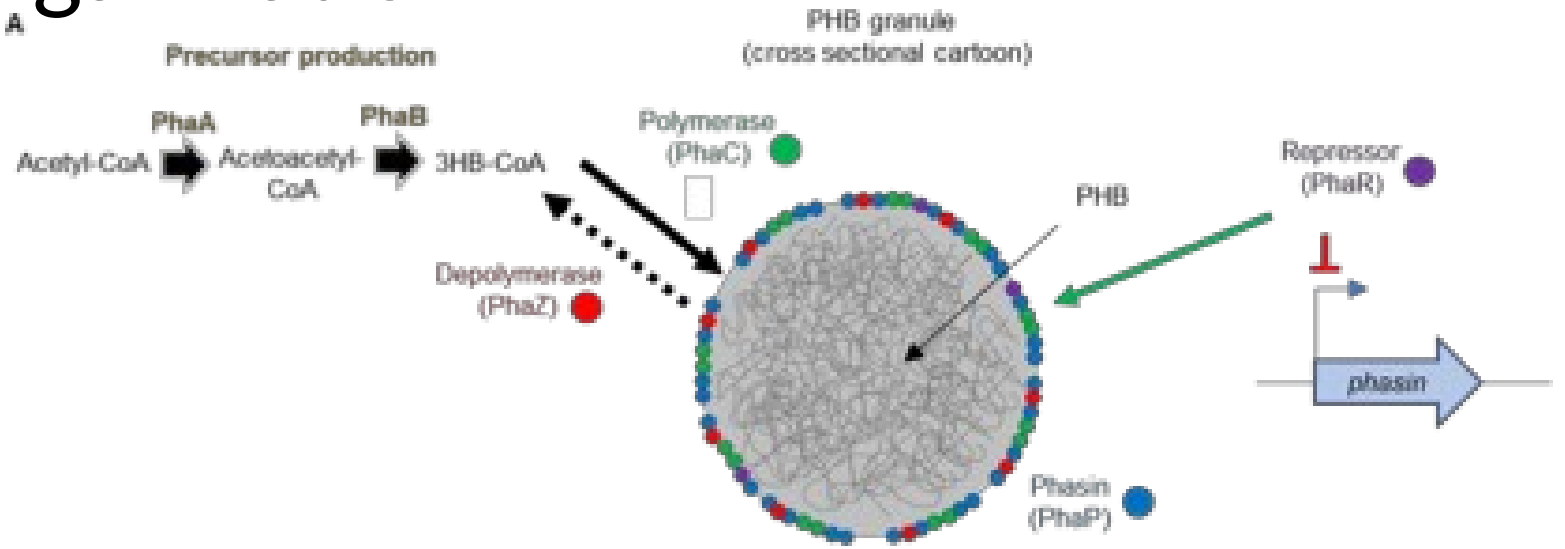
Cryo-EM

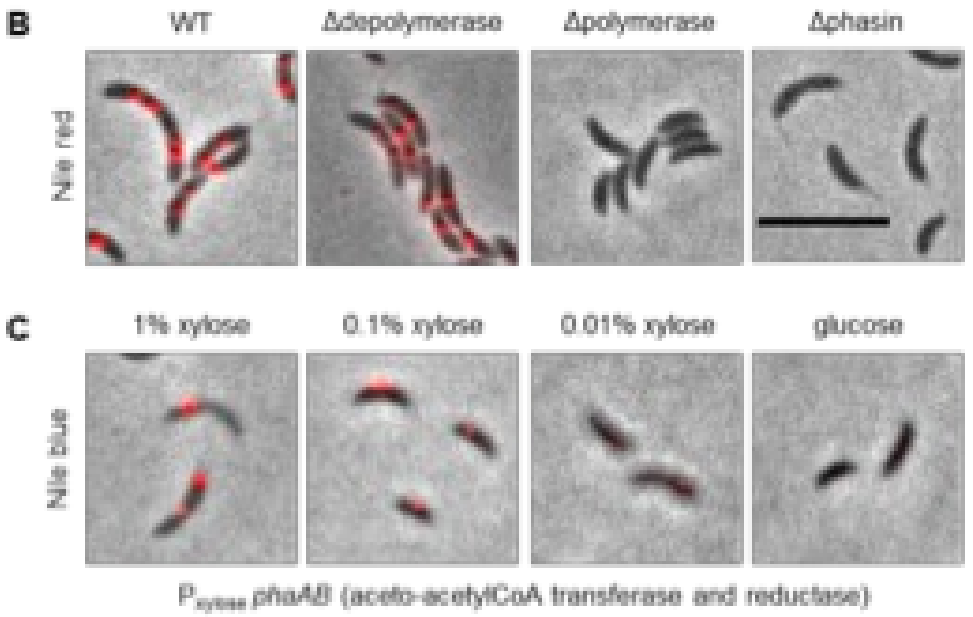


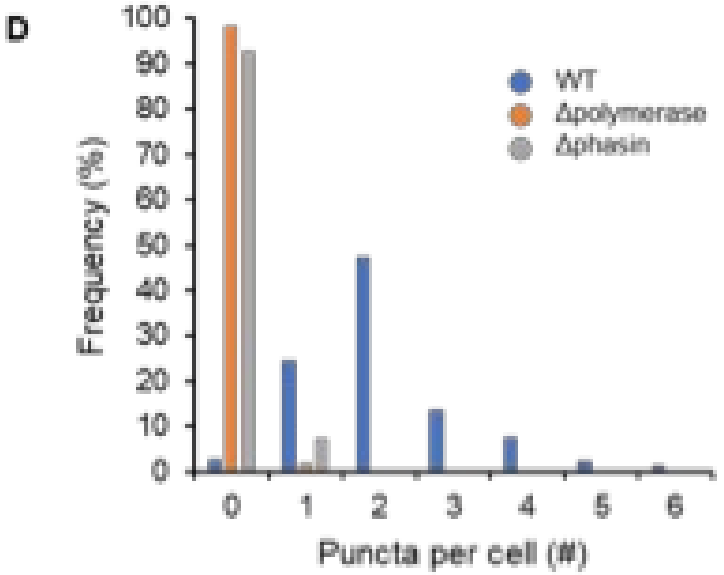
25

Geladas, E.D. Master Thesis UoC, 2023

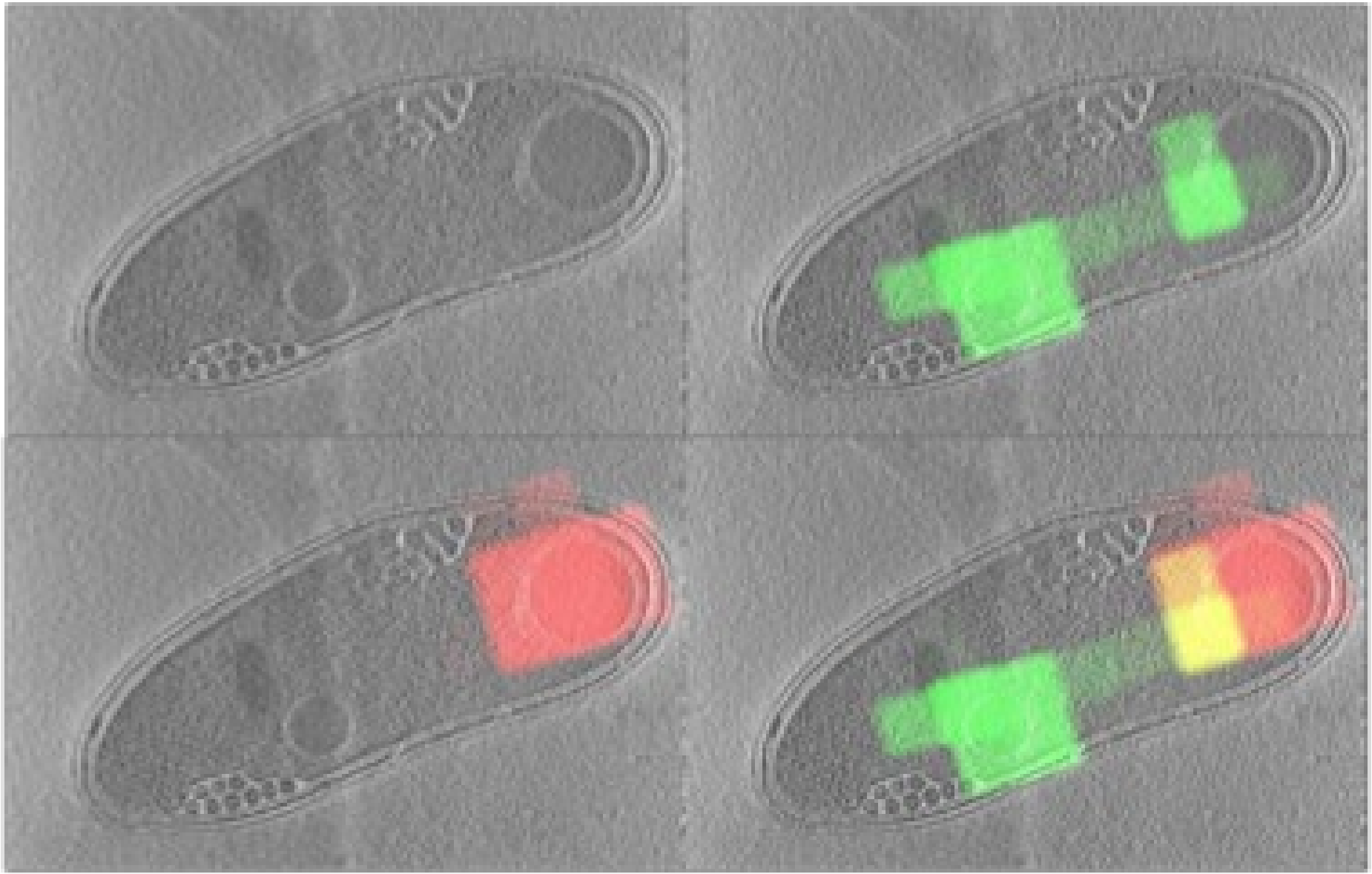
PHB granule organization



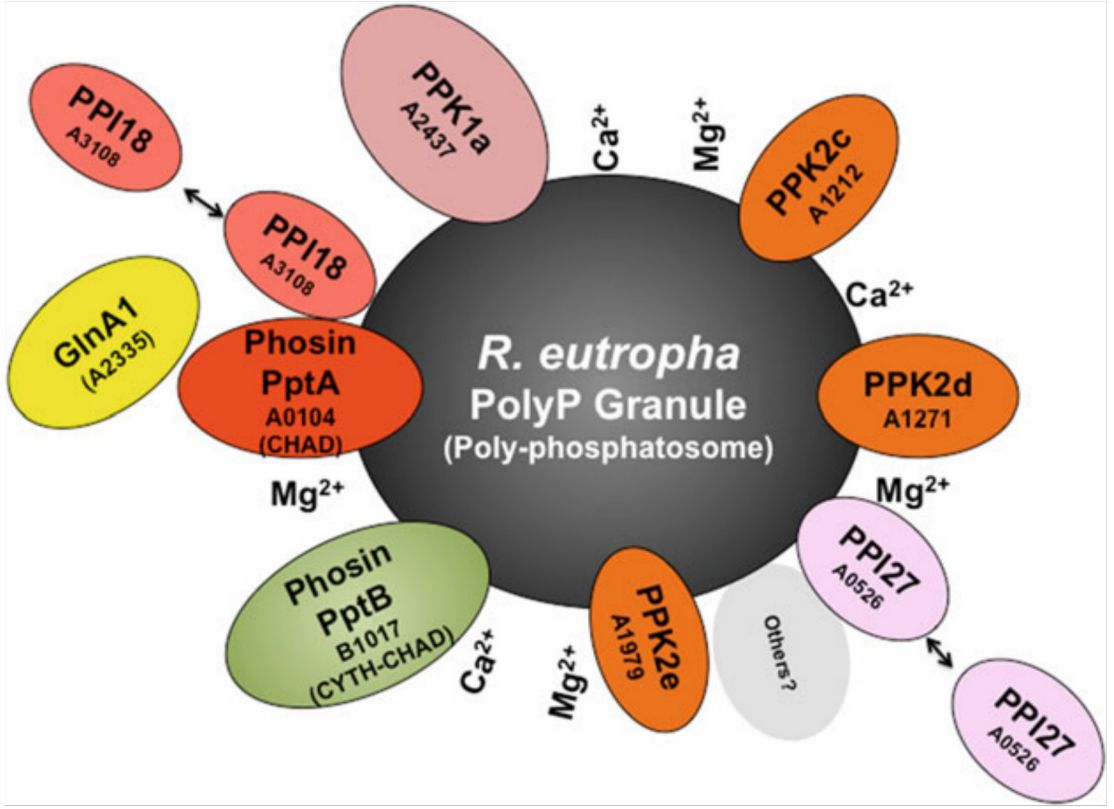




PHB granules

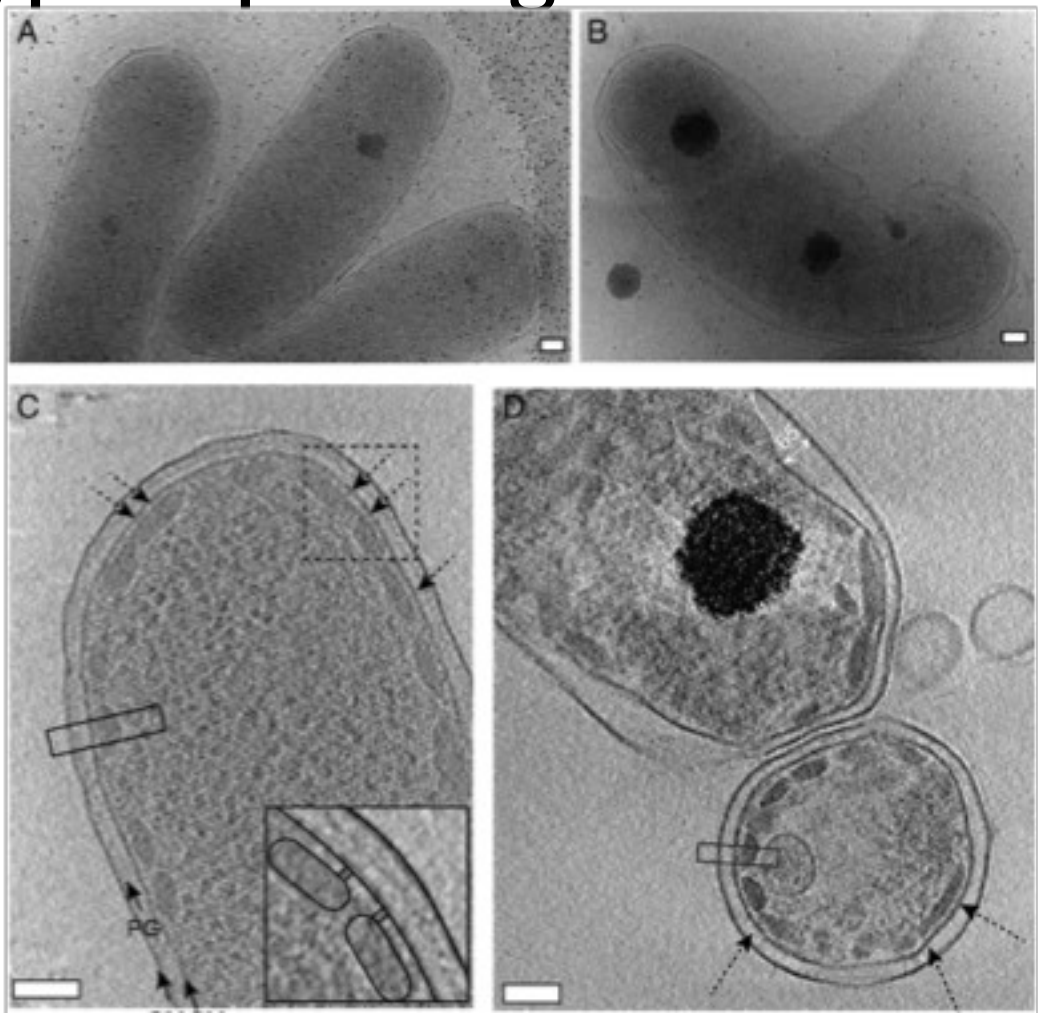


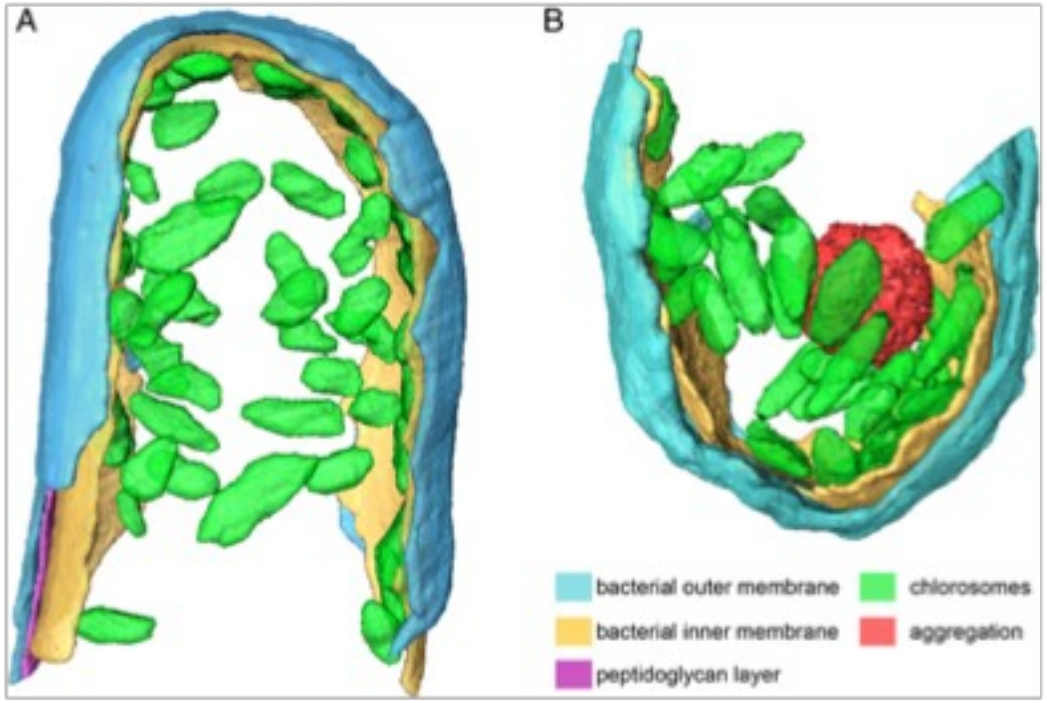
Find the partner



Polyphosphate (polyP) is a linear polymer of phosphate residues linked by energy-rich phospho-anhydride bonds.

Polyphosphate granules





M. Kudryashev et al. / Biochimica et Biophysica Acta 1837 (2014) 1635–1642

Polyphosphate granules

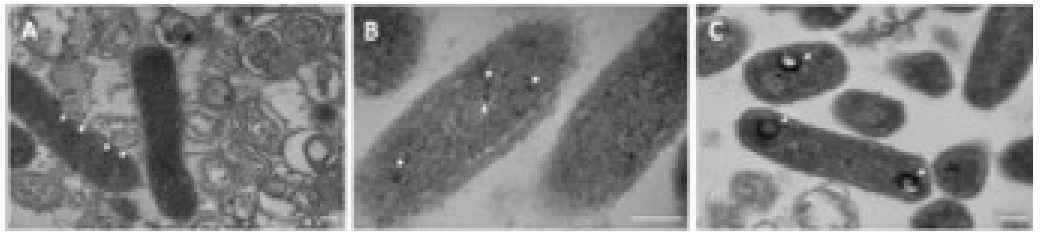
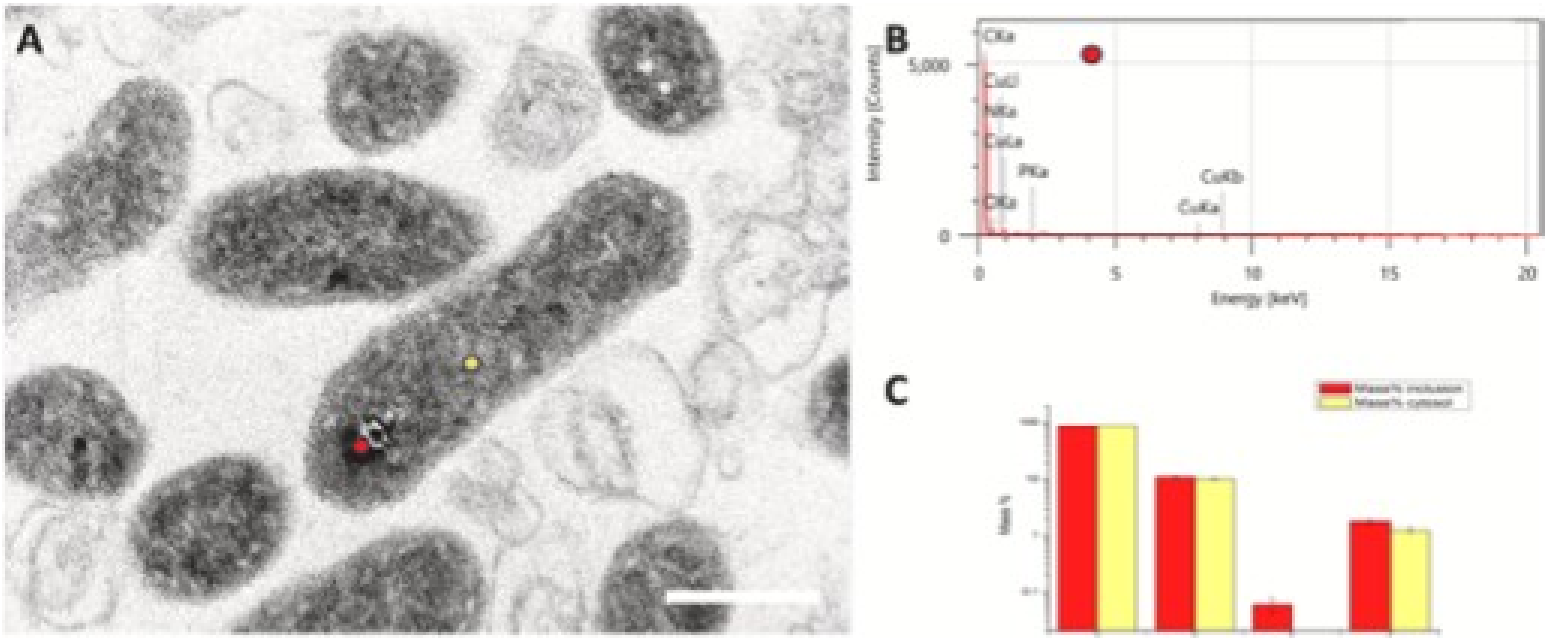
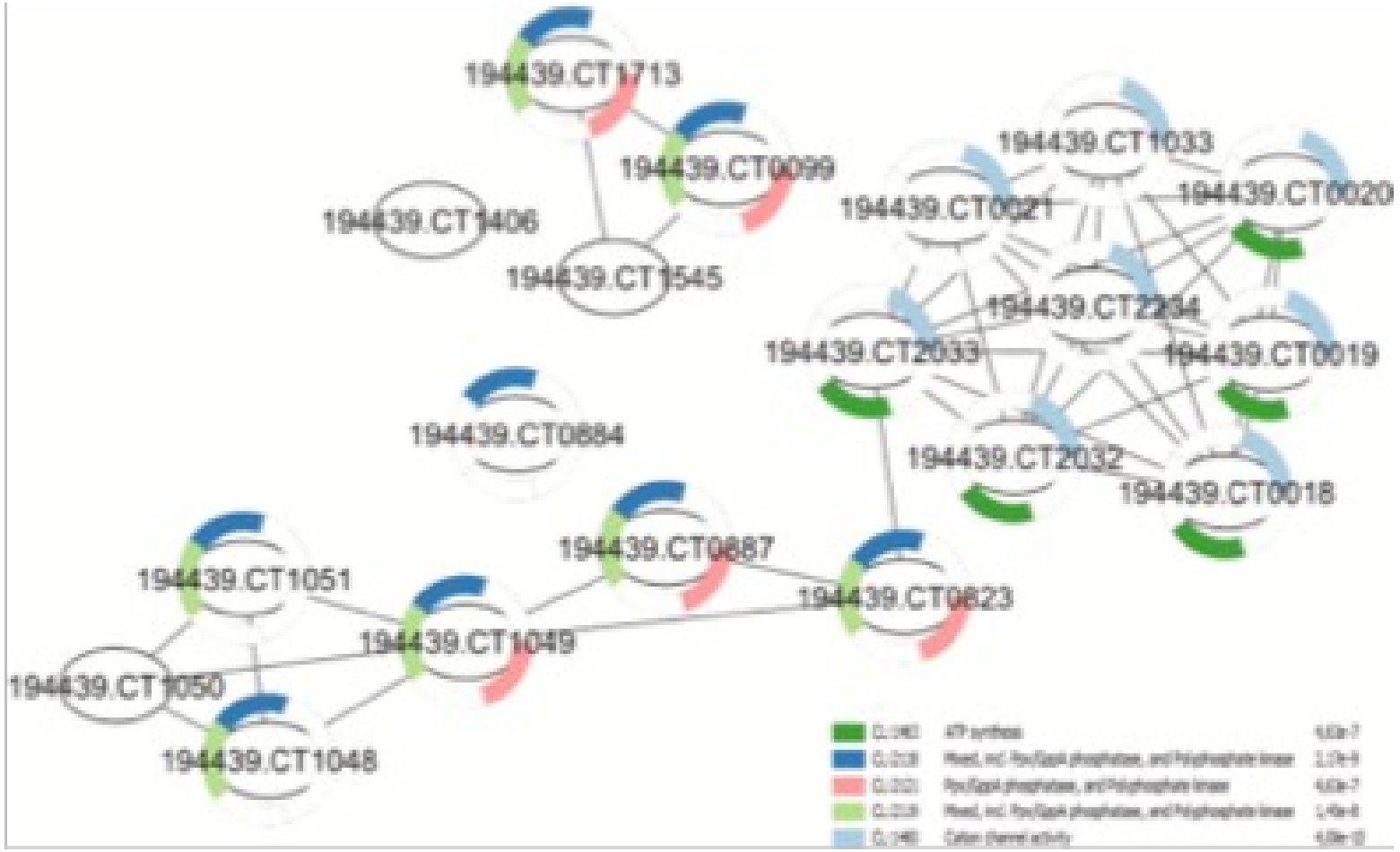


Fig. 2. TEM micrographs of thin sections from A) 10 PI, B) 20 PI and C) 40 PI, the arrows indicate the electron-rich inclusions (bar: 200 nm).



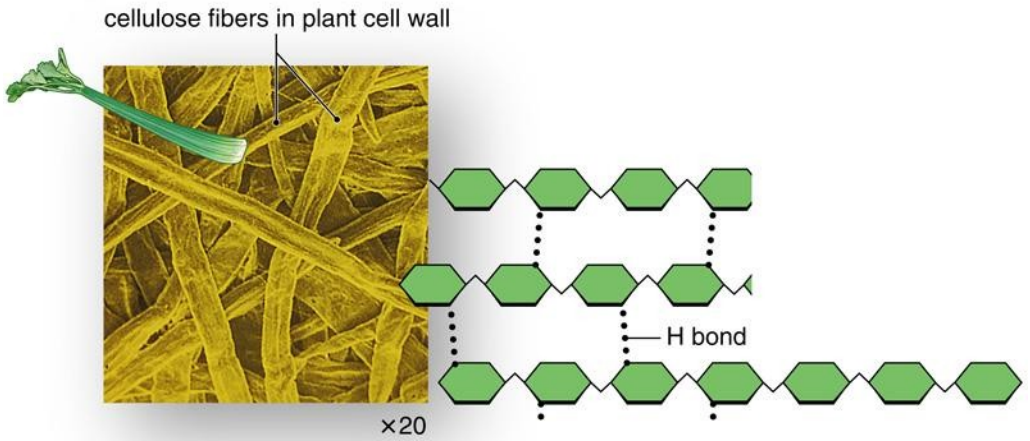
Lytatzakis et al., BBA - General Subjects 1868 (2024) 130718

Polyphosphate granules

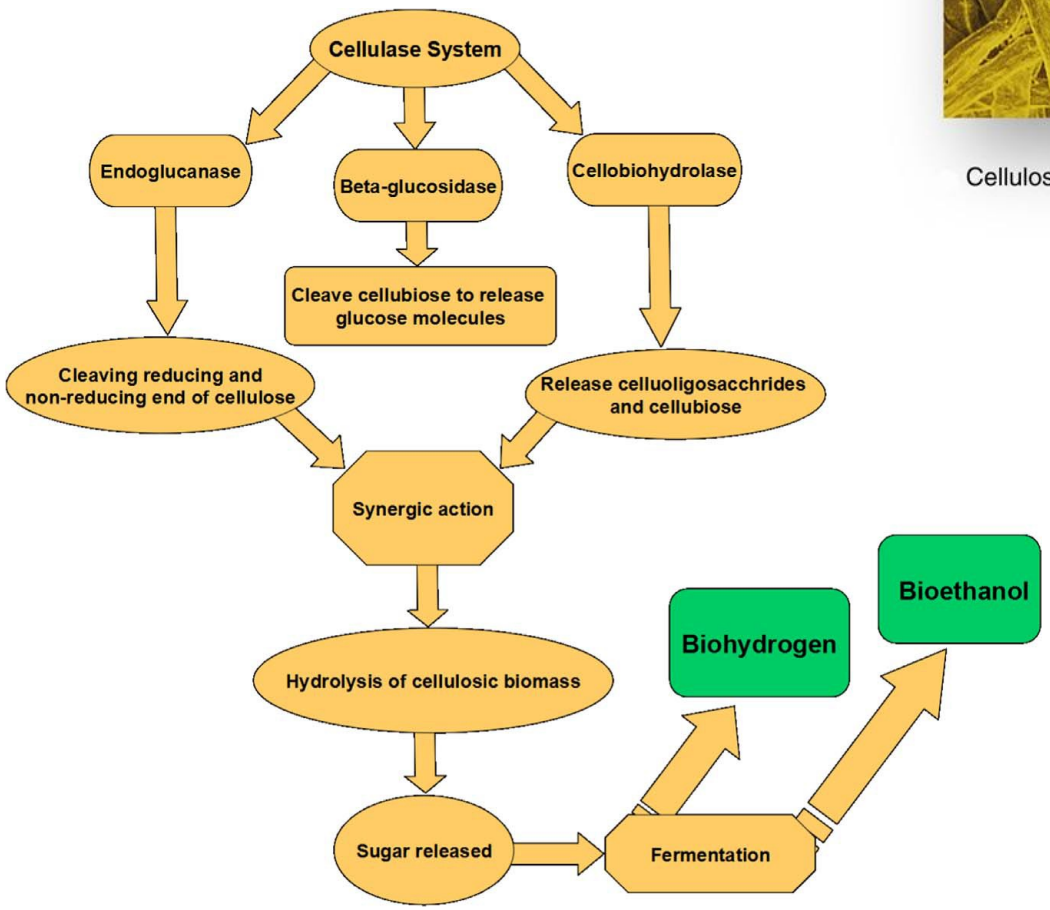


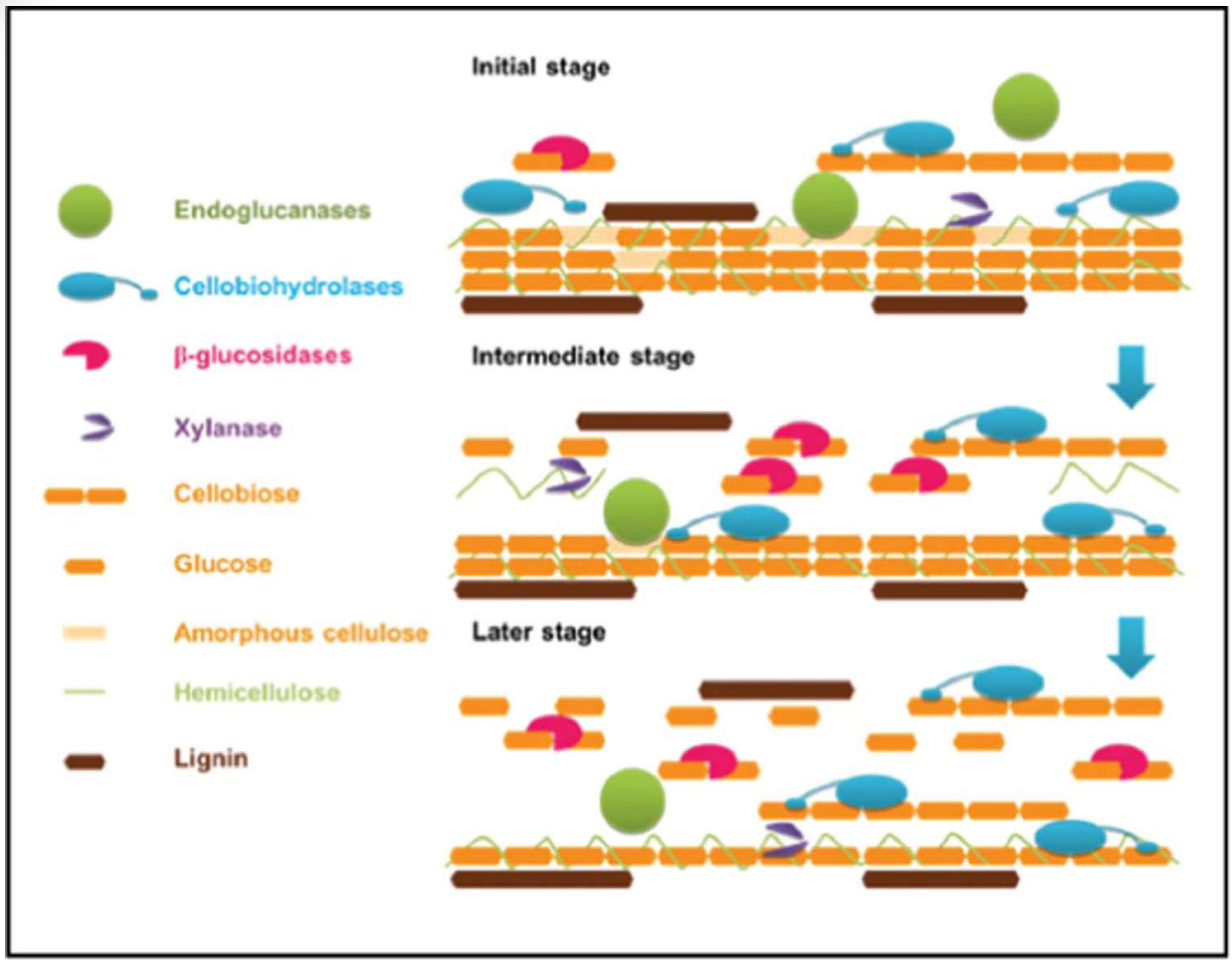
Lytatzakis et al., BBA - General Subjects 1868 (2024) 130718

cellulose



Cellulose structure





cellulase

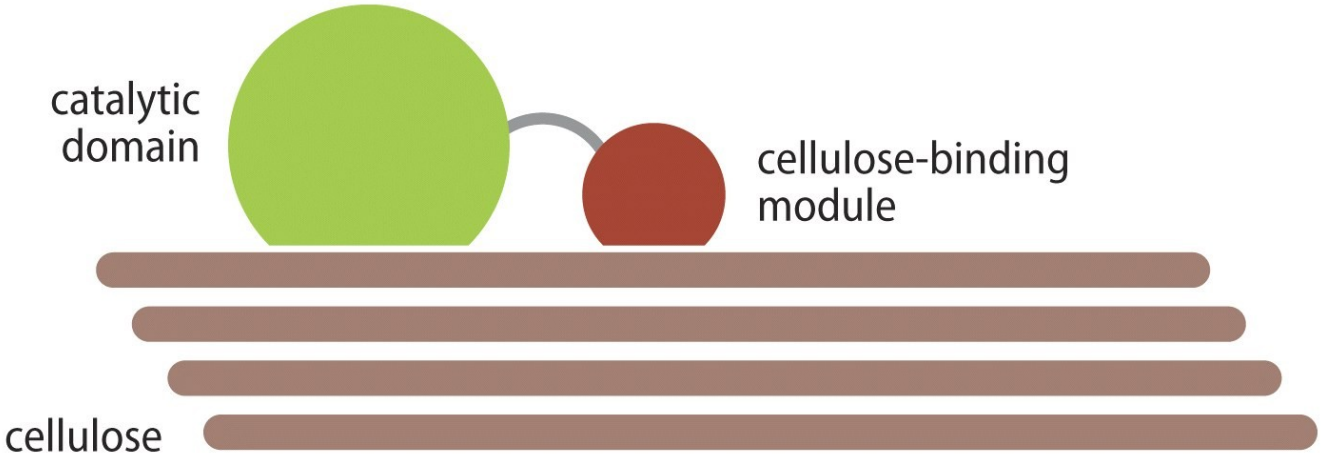
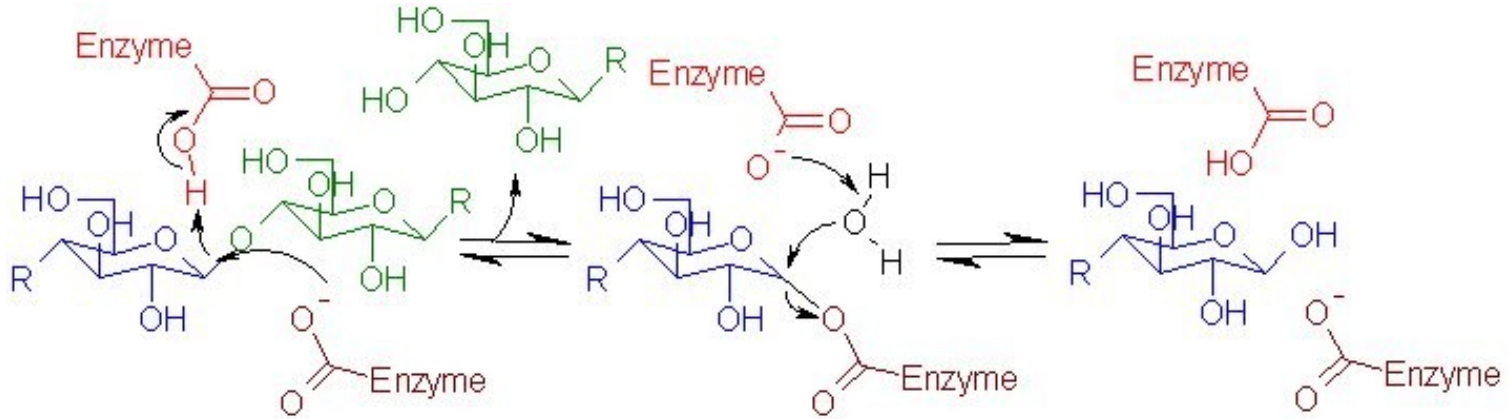
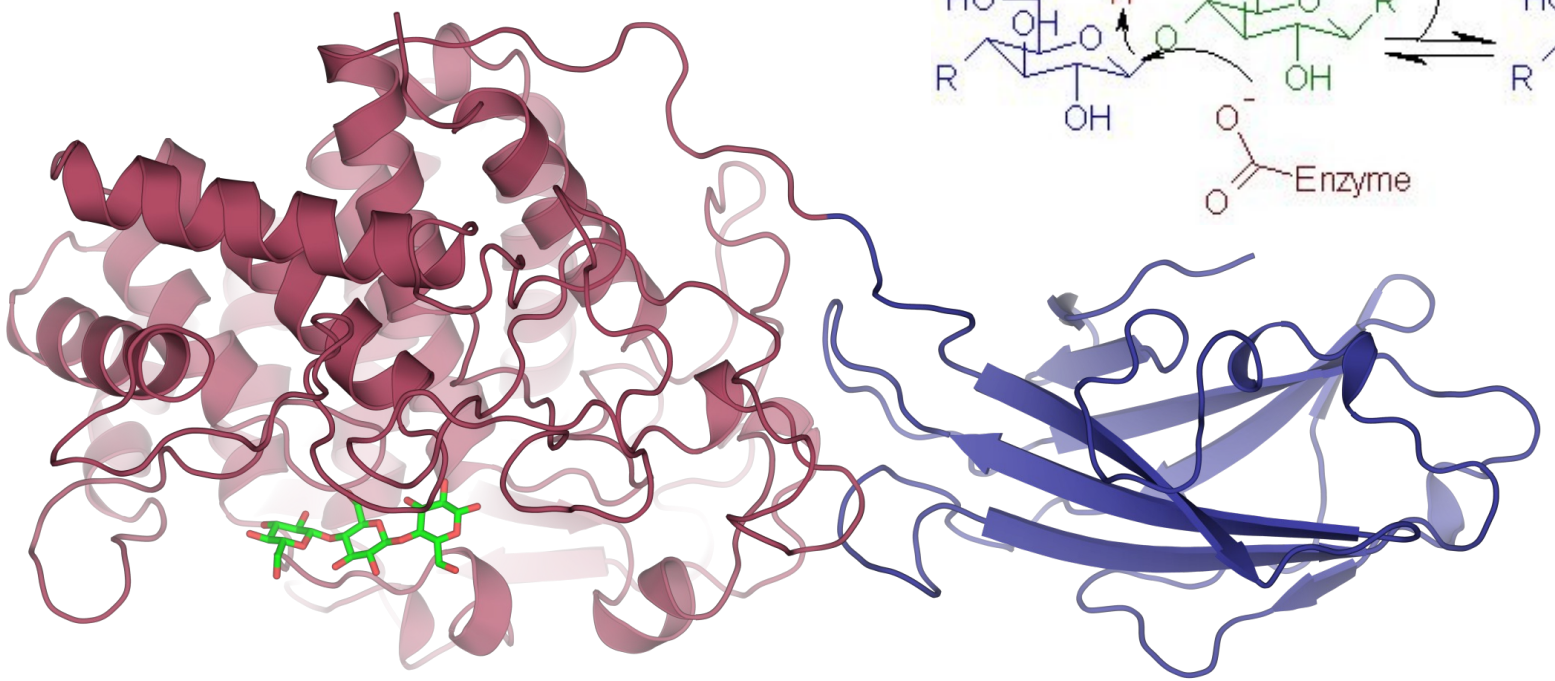


Figure 4.17 How Proteins Work (©2012 Garland Science)





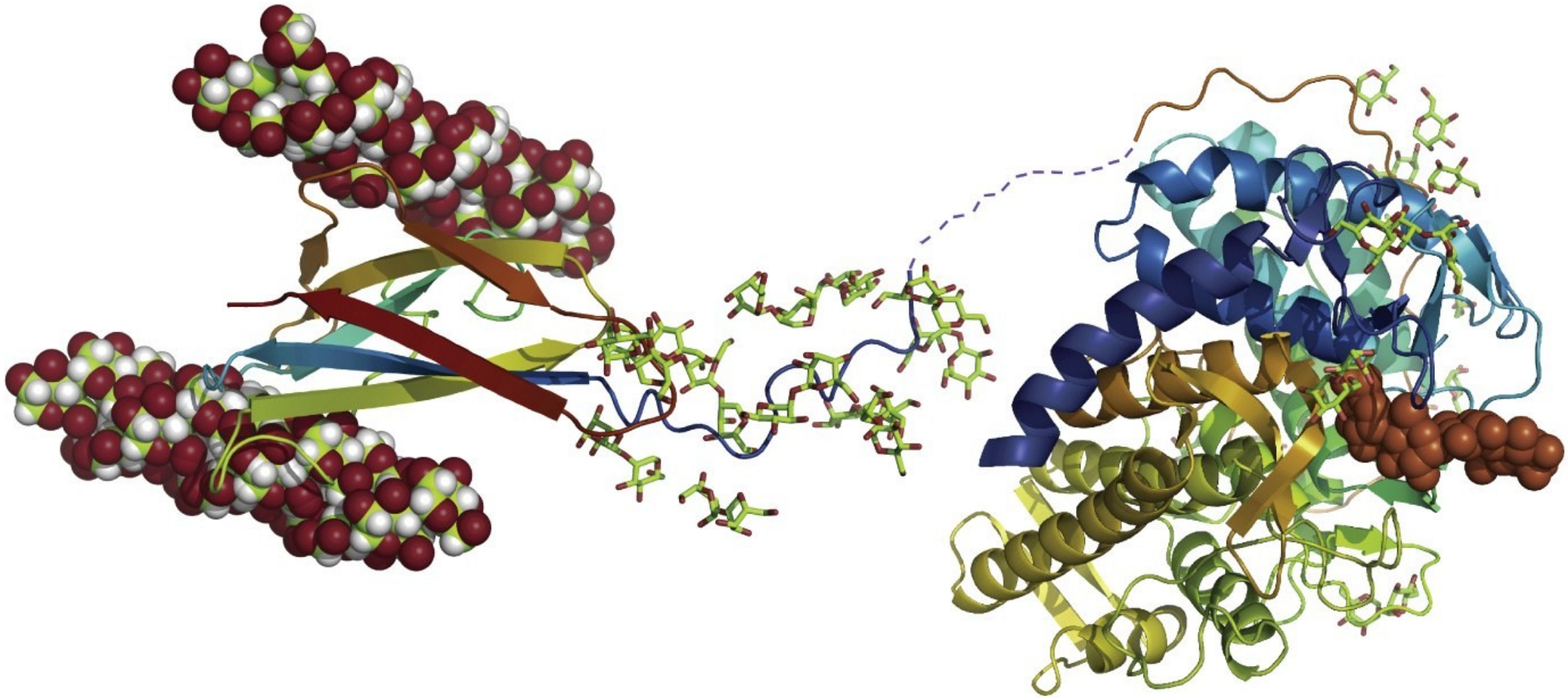
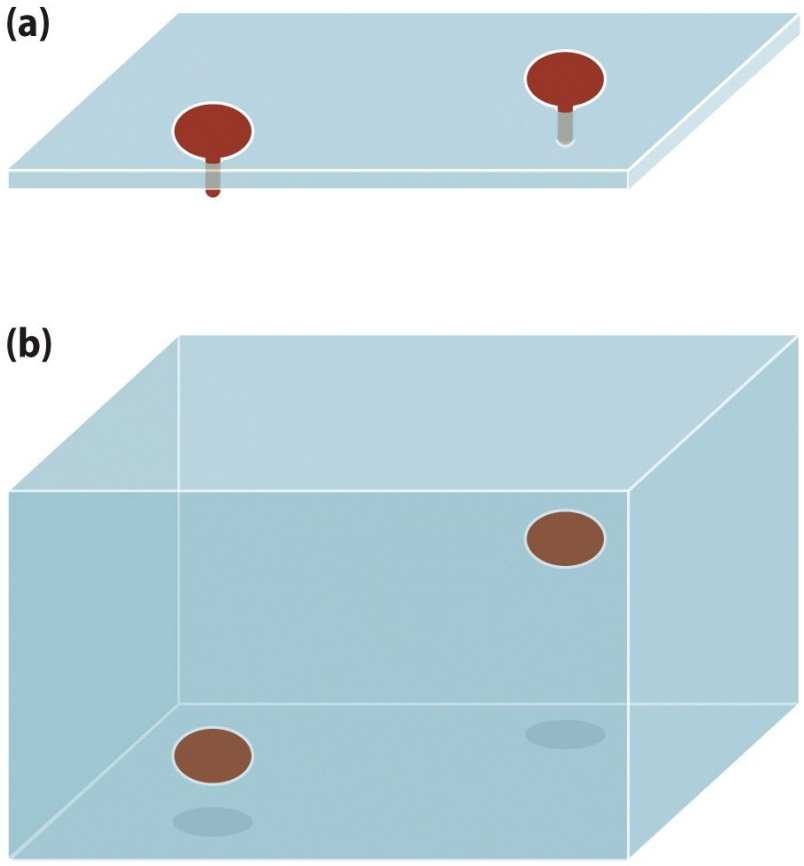


Figure 4.18 How Proteins Work (©2012 Garland Science)

Searching is faster in two dimensions



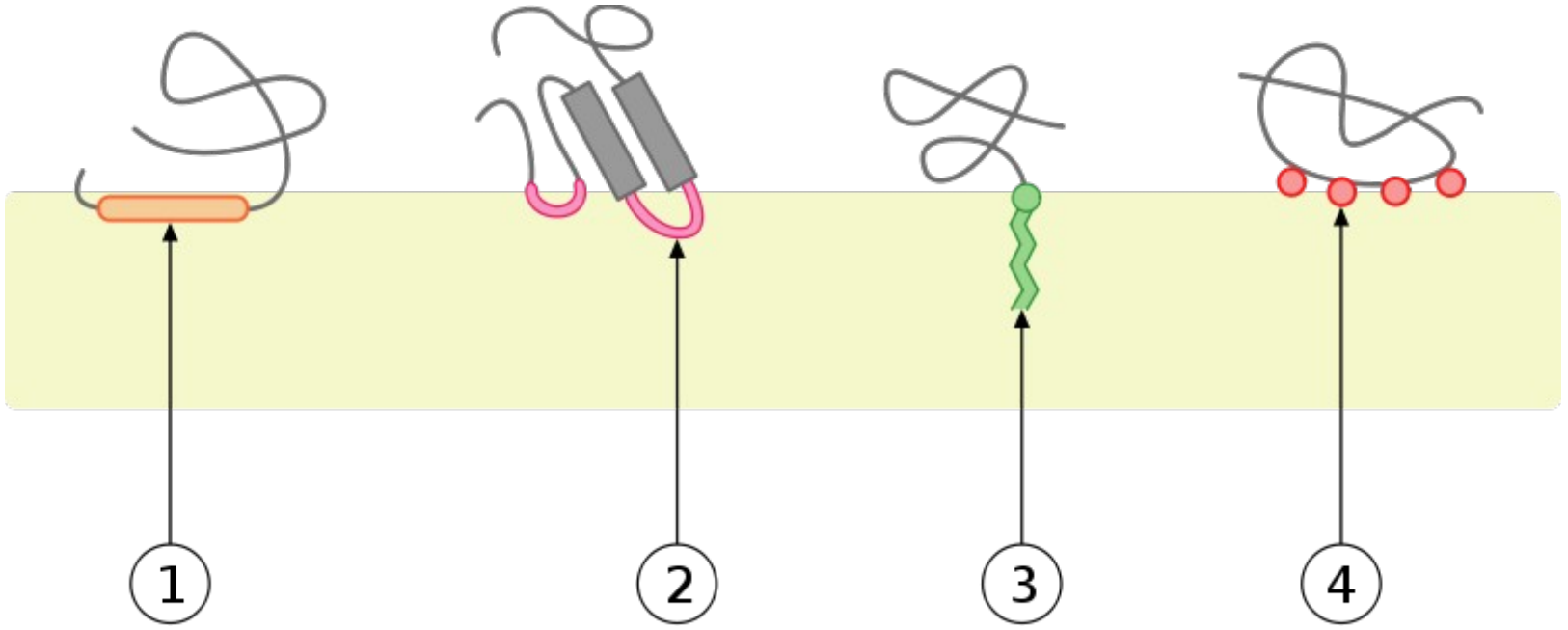
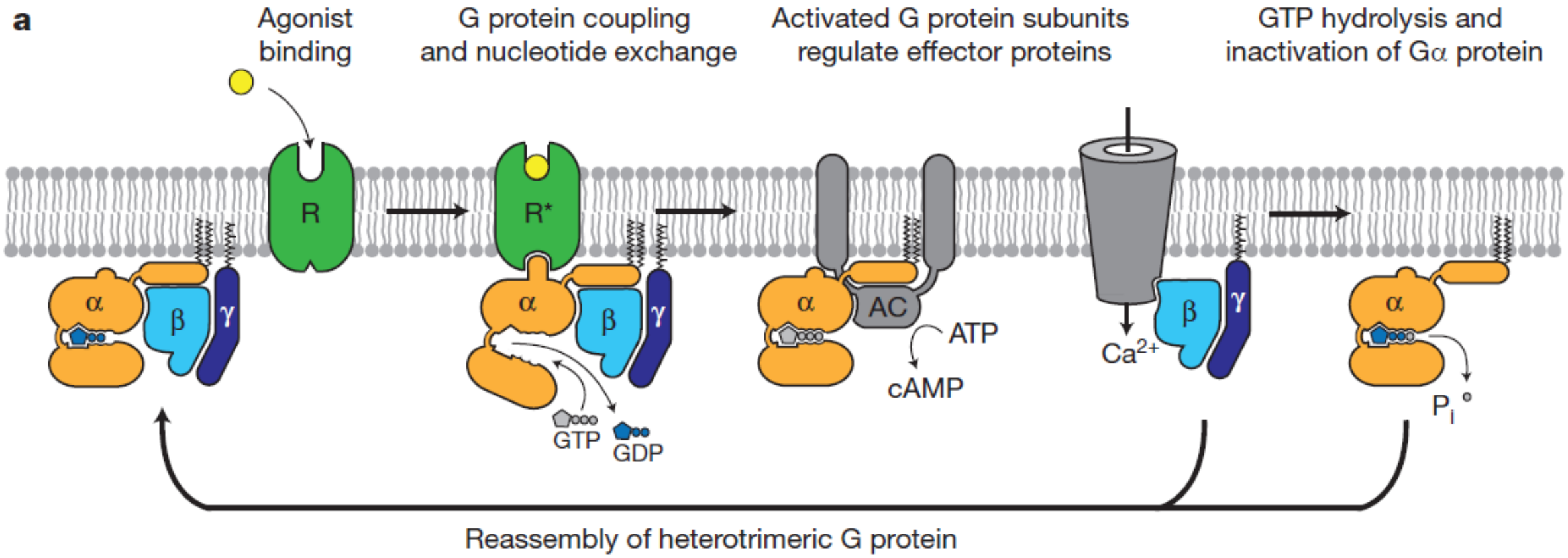
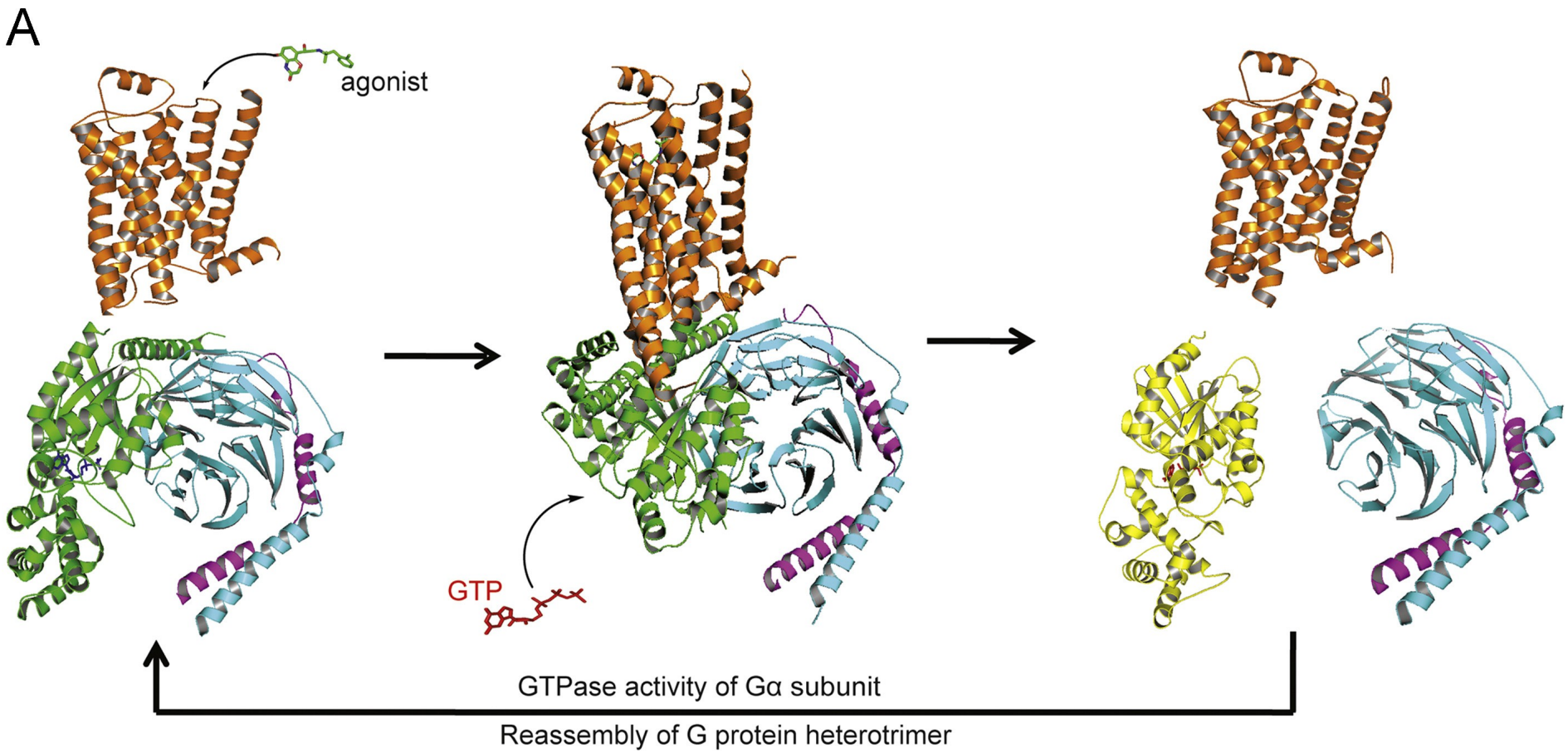


Figure 4.20 How Proteins Work (©2012 Garland Science)

Searching is faster in two dimensions



GPCR-mediated G protein activation process



Searching is slightly faster again in one dimension

Oct-1 has two DNA-binding domains

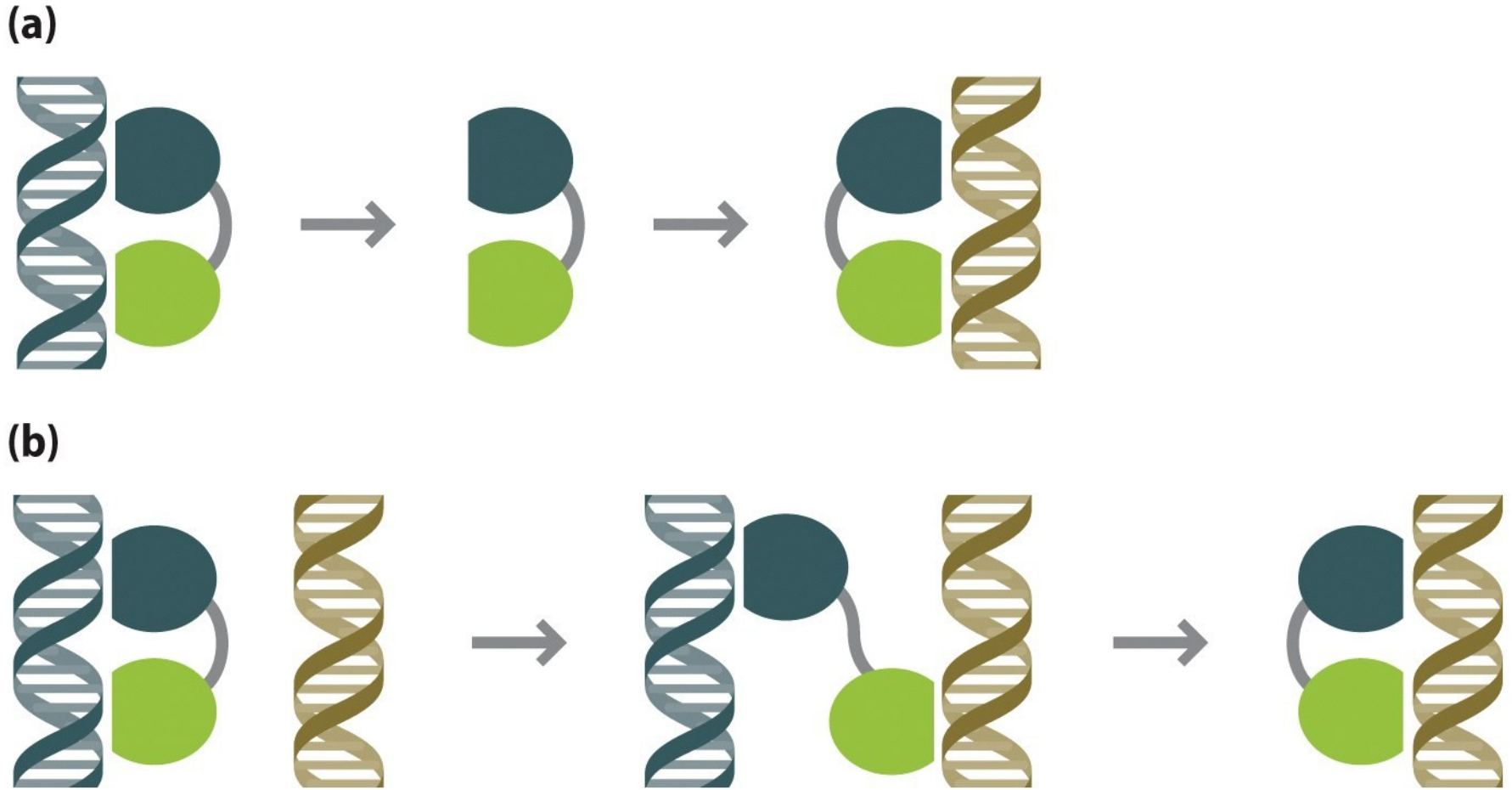
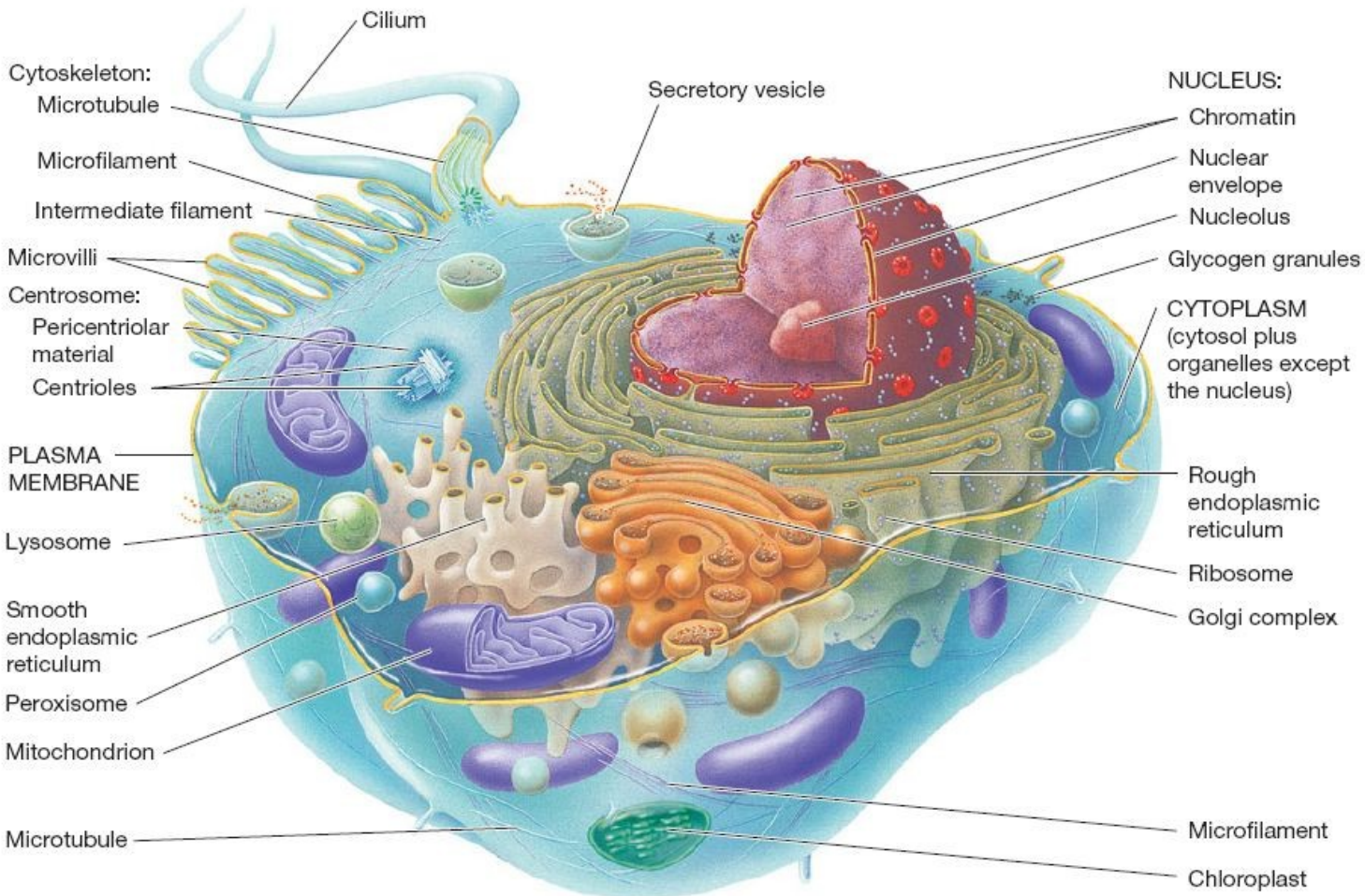


Figure 4.22 How Proteins Work (©2012 Garland Science)

Searching is faster in smaller compartments



Searching is faster in smaller compartments

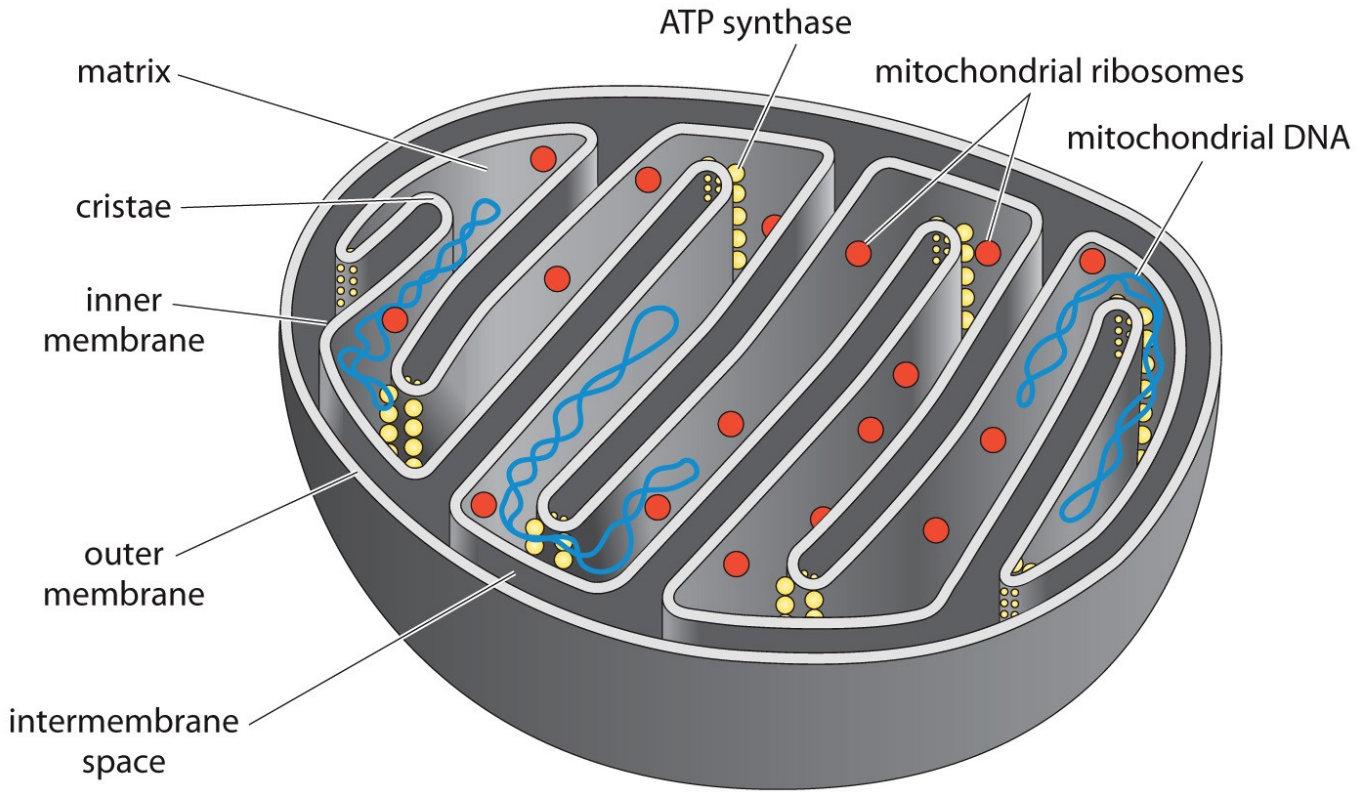
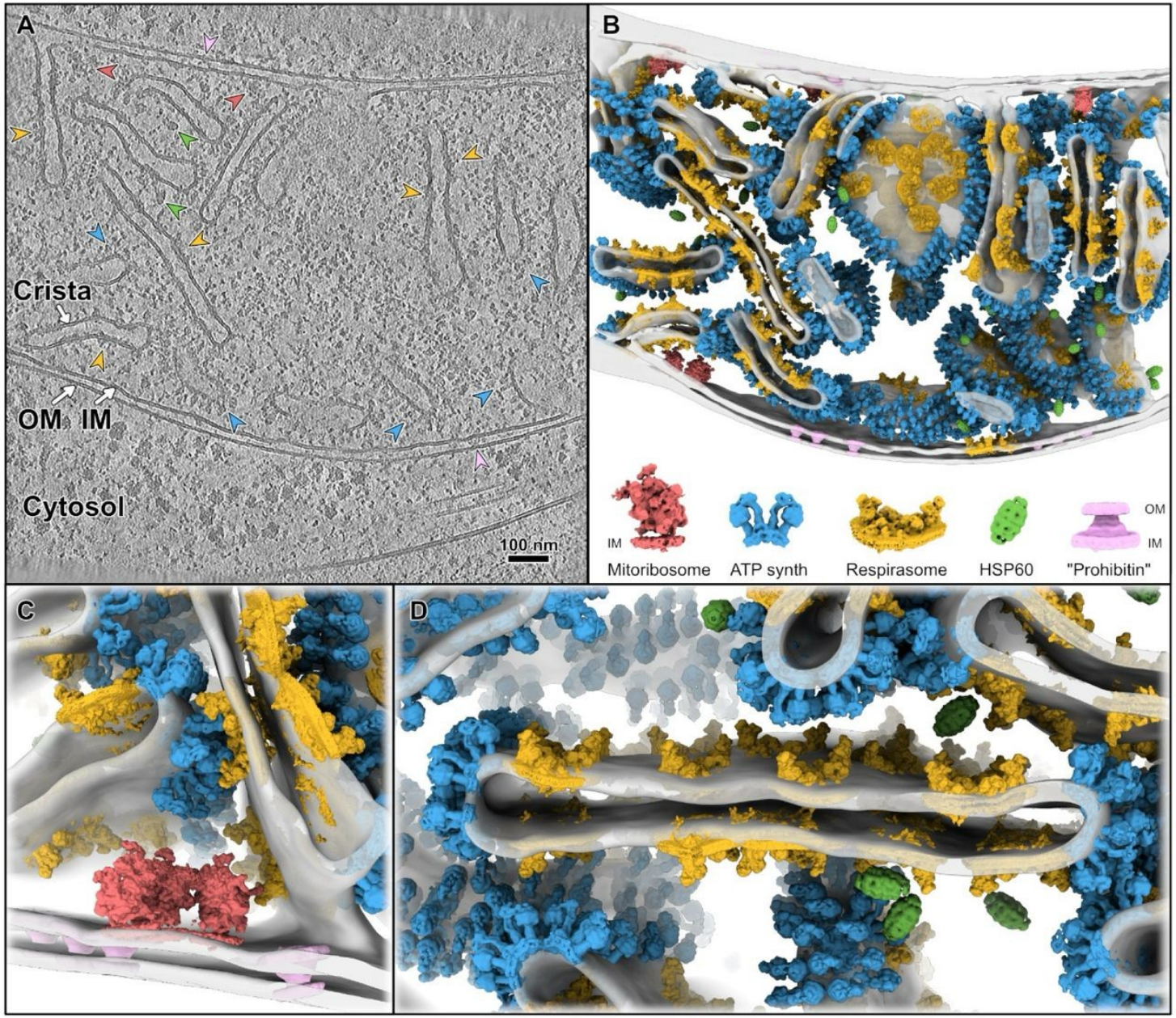


Figure 1.5.1b Molecular Biology of Assemblies and Machines (© Garland Science 2016)

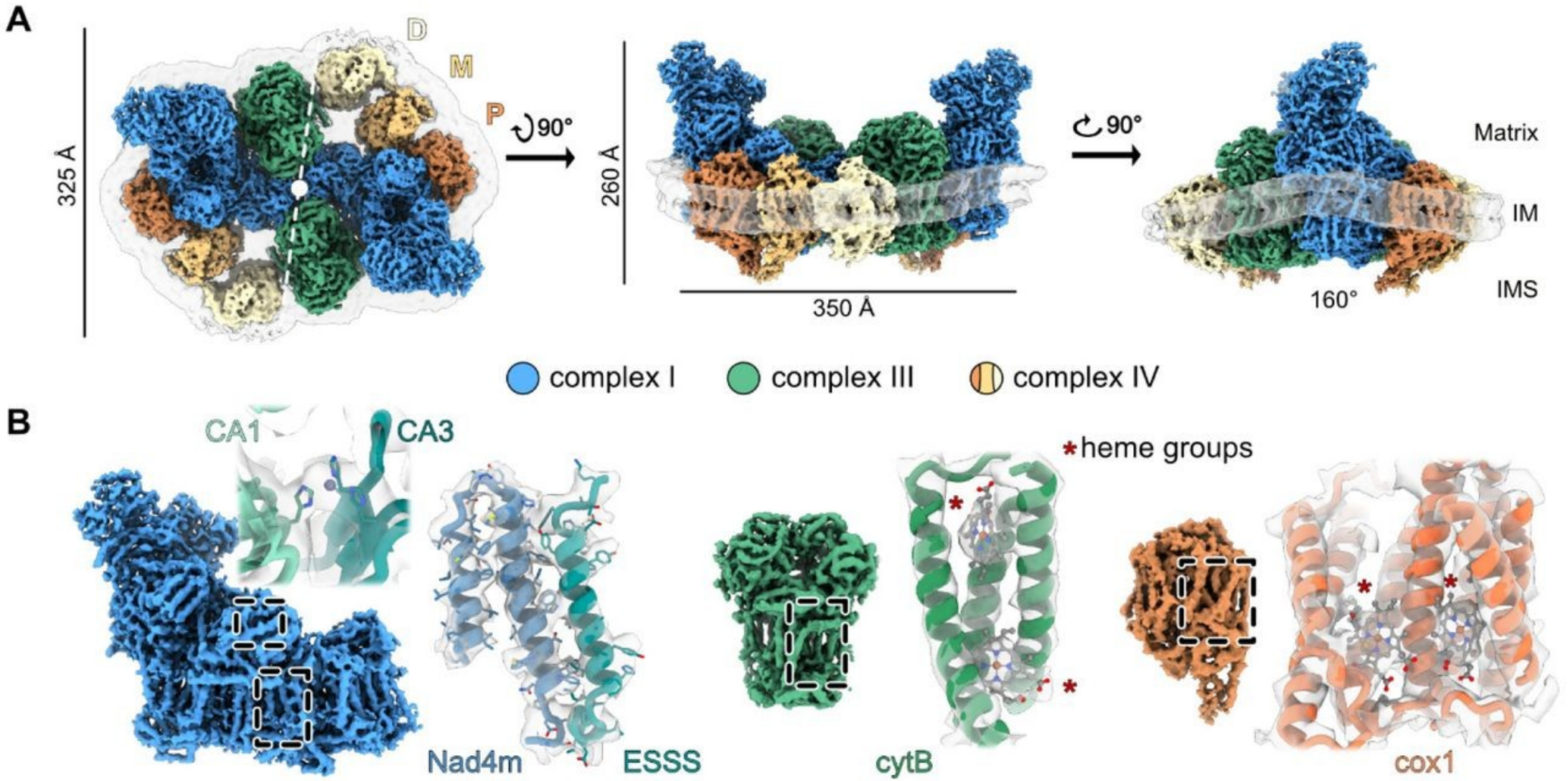
Molecular landscape of Chlamydomonas mitochondria



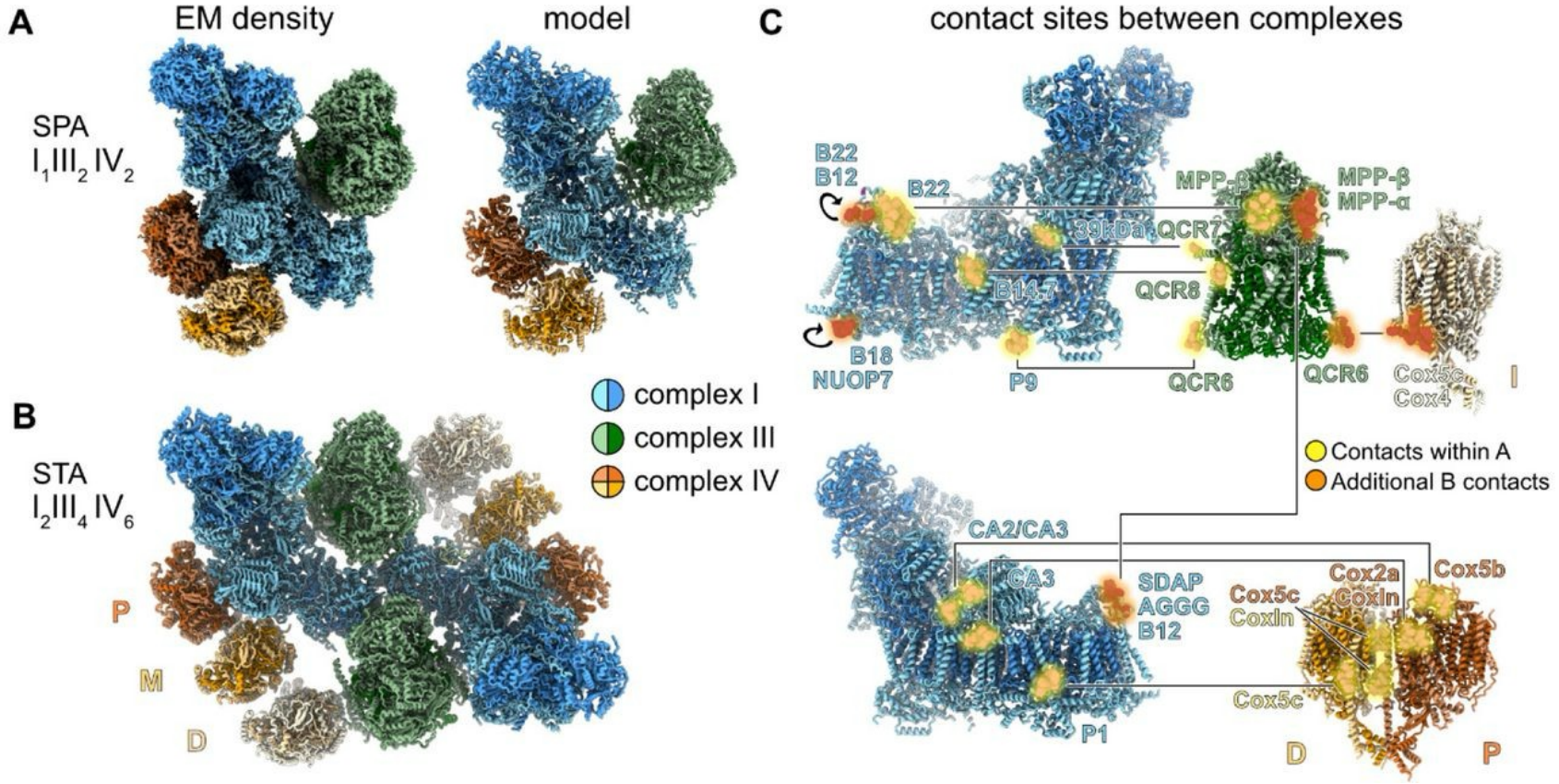
doi: https://doi.org/10.1101/2024.09.03.610704

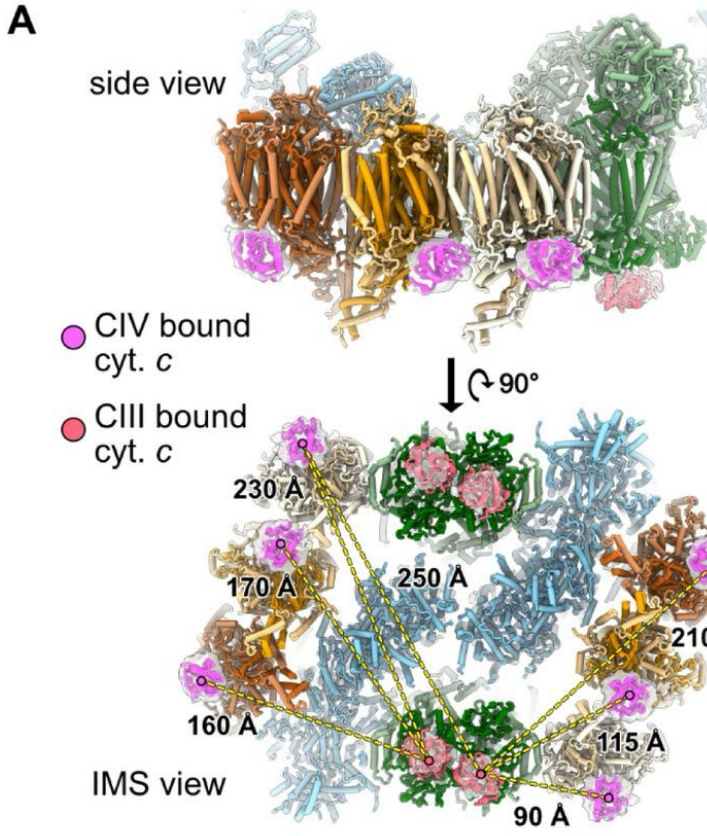
Subtomogram average of the native Chlamydomonas respirasome

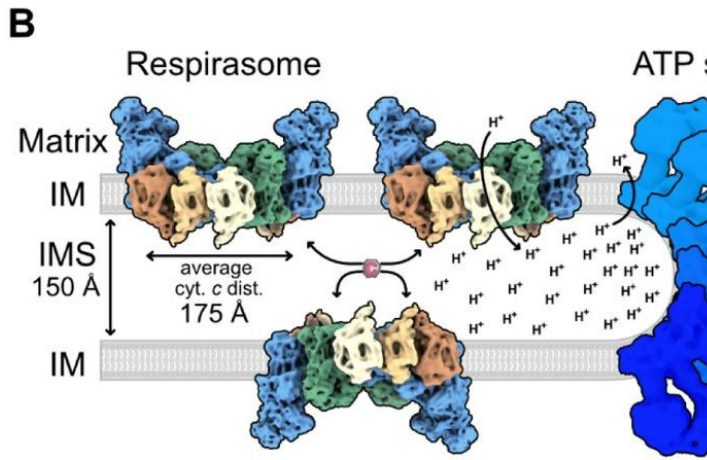
The I_2 III_4 IV_6 respirasome



Models of the isolated and native respirasomes







Sticky arms

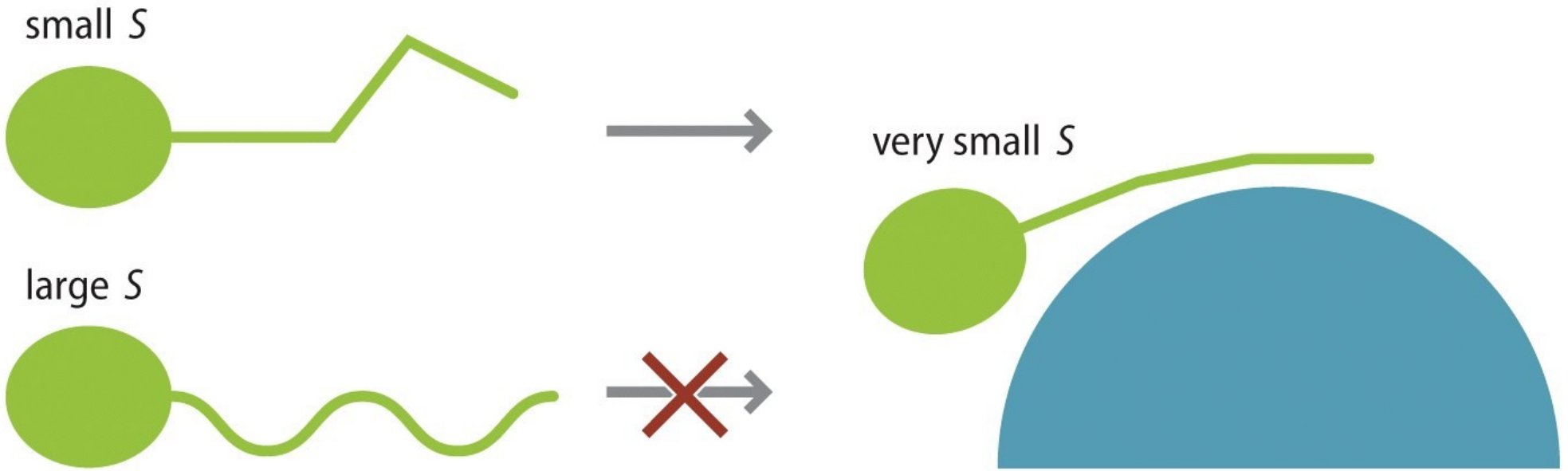
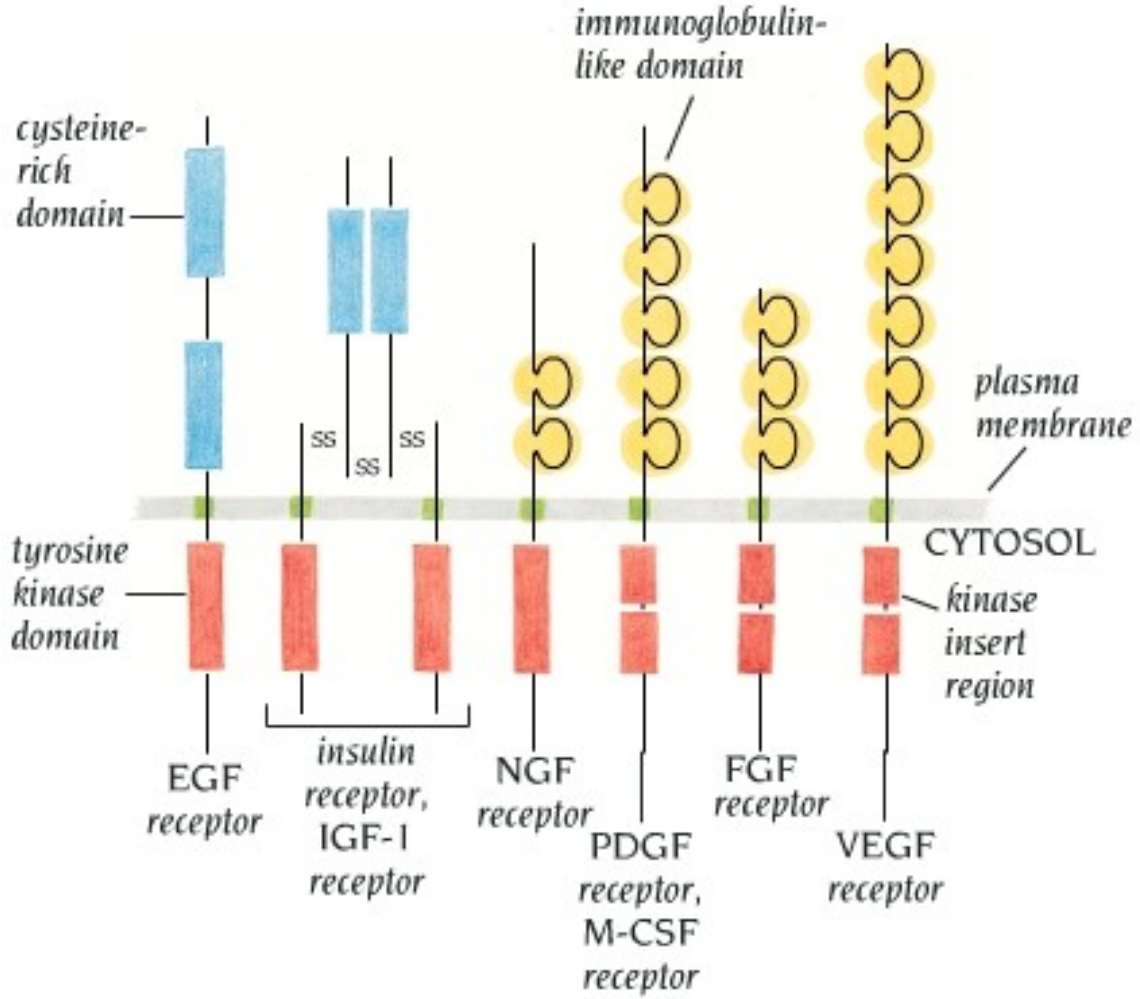
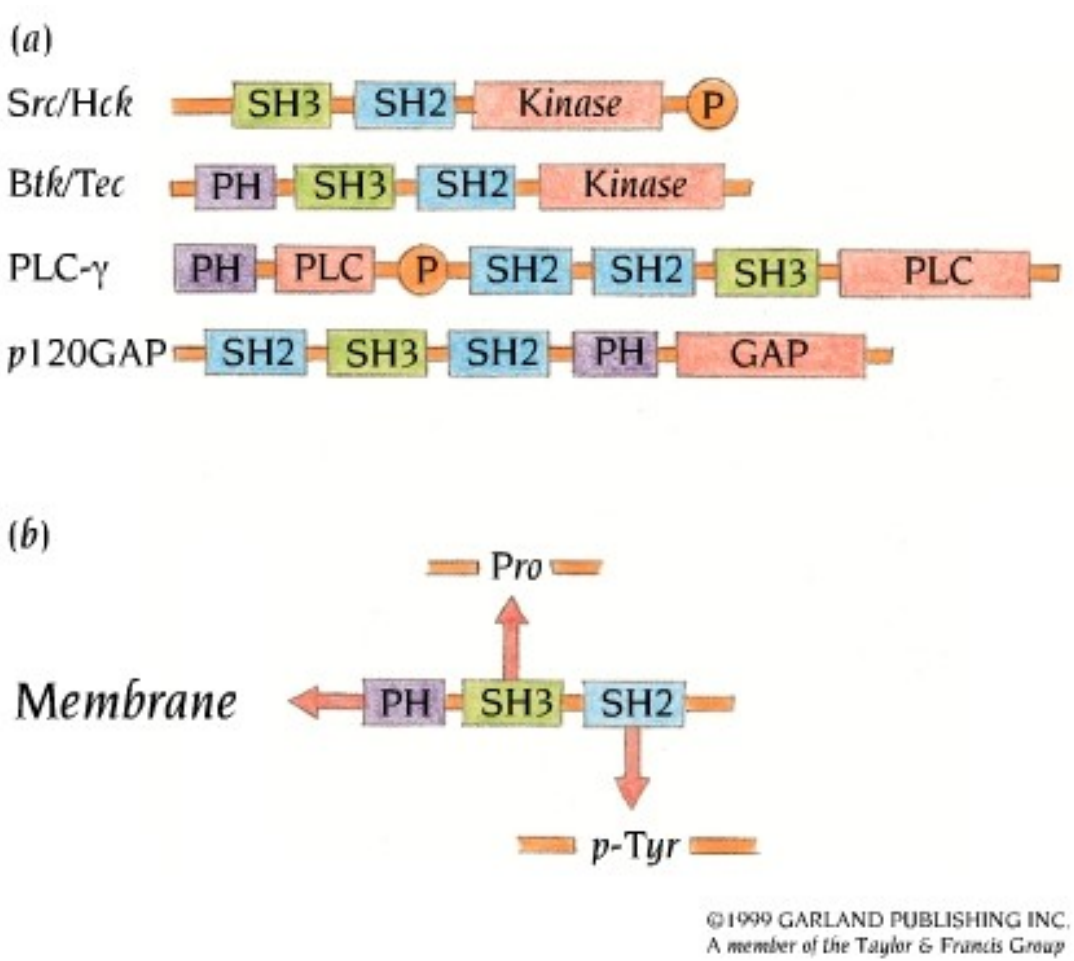


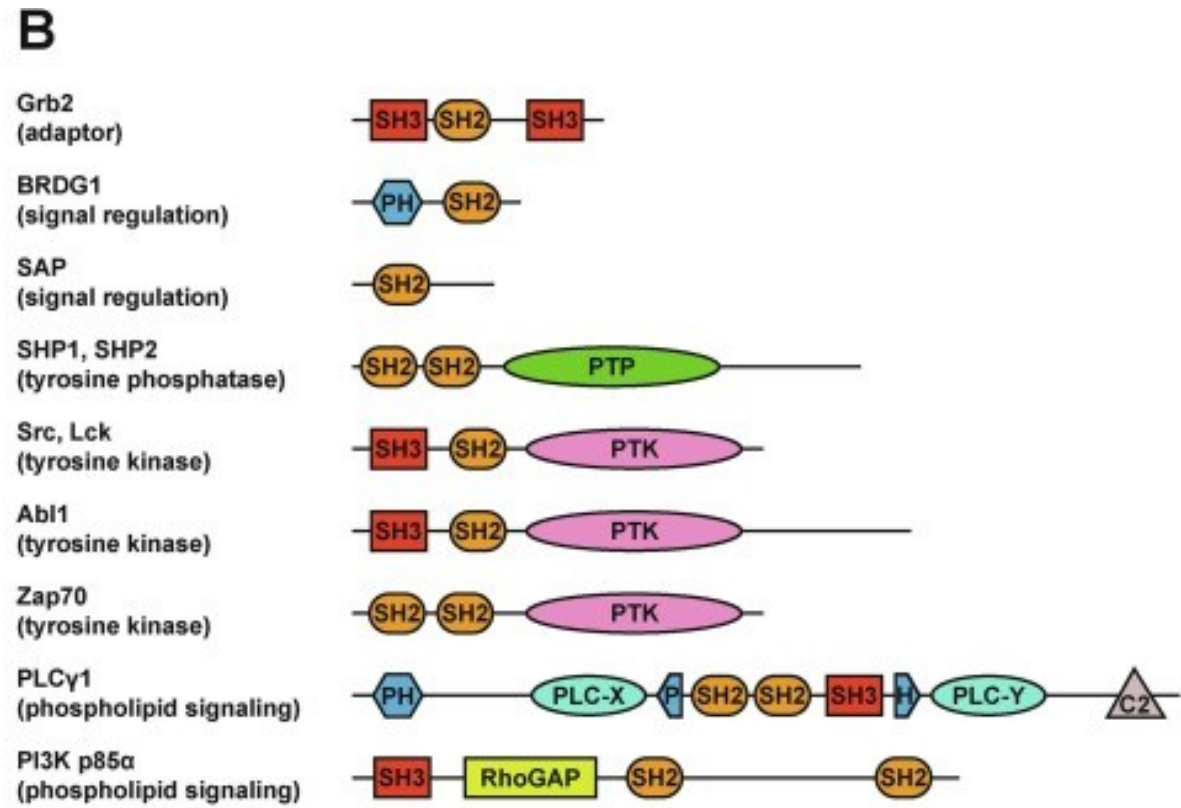
Figure 4.23 How Proteins Work (©2012 Garland Science)

tyrosine kinases receptor

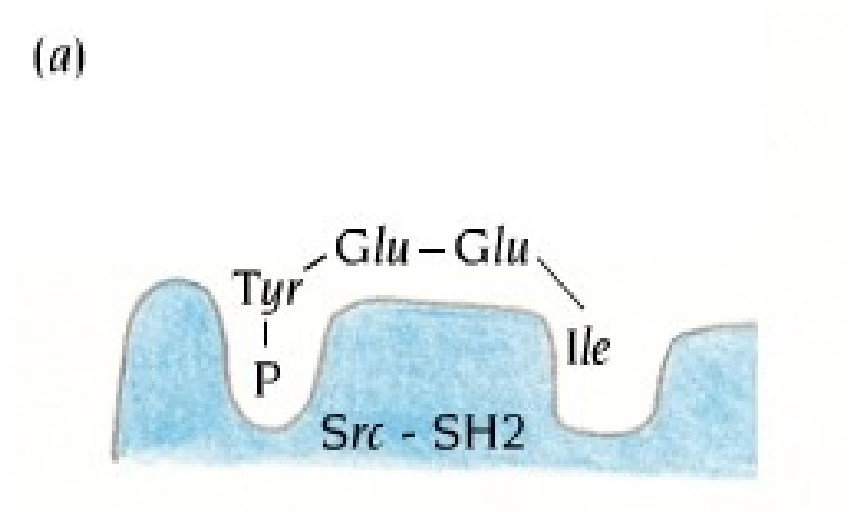


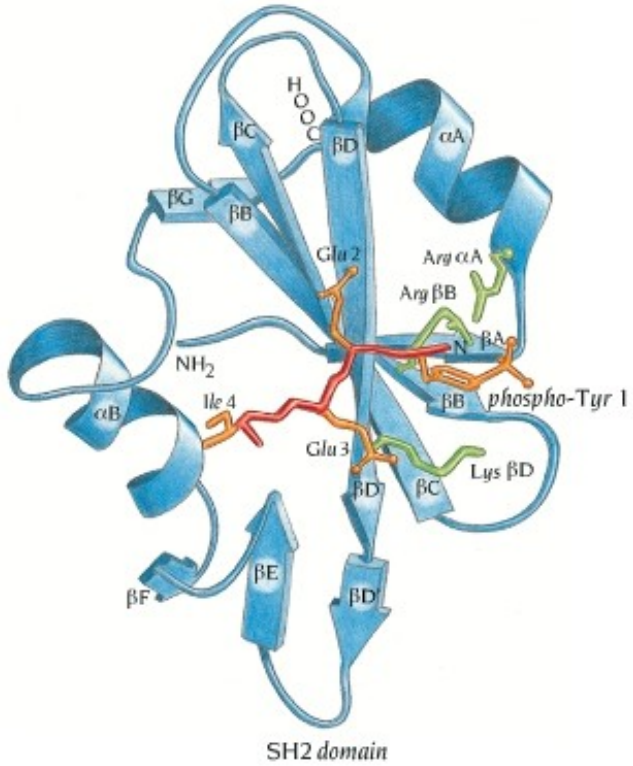
tyrosine kinases receptor





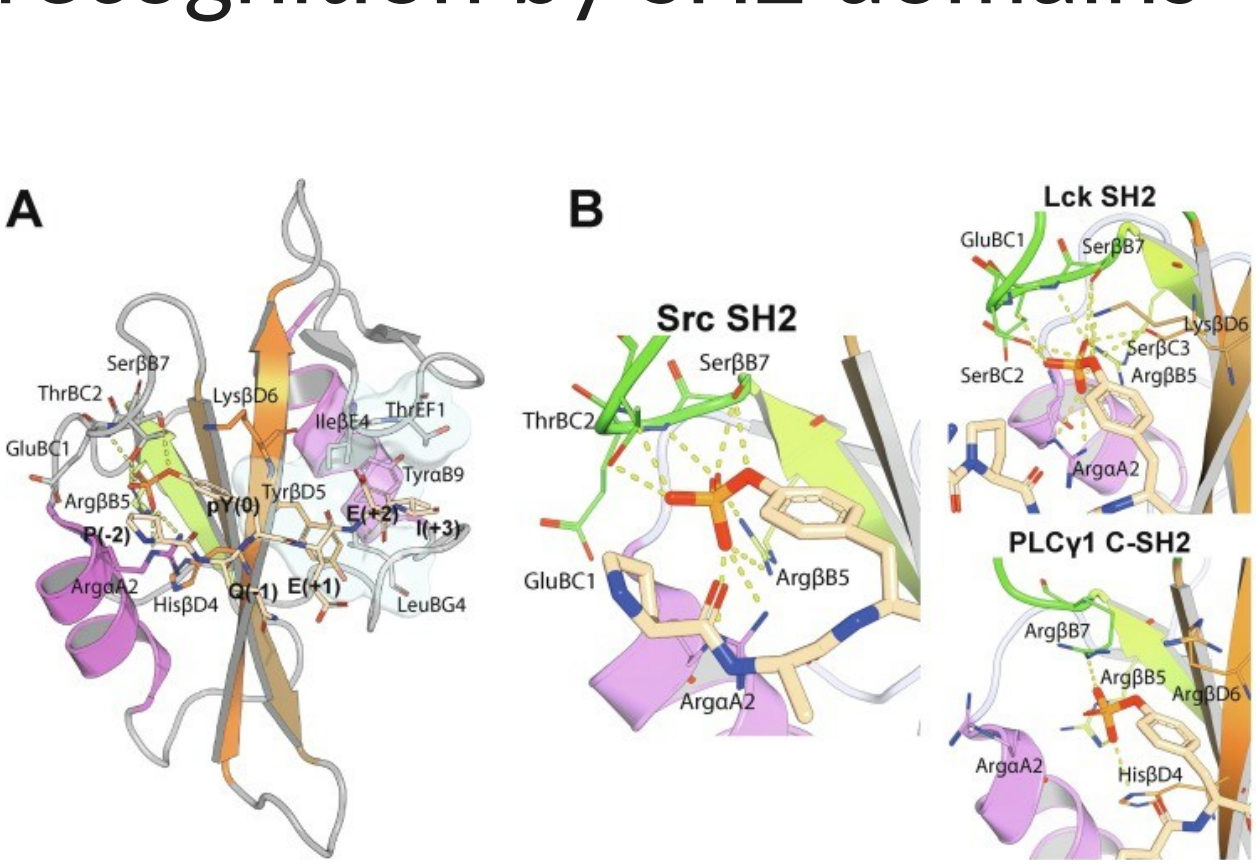
SH2 domains

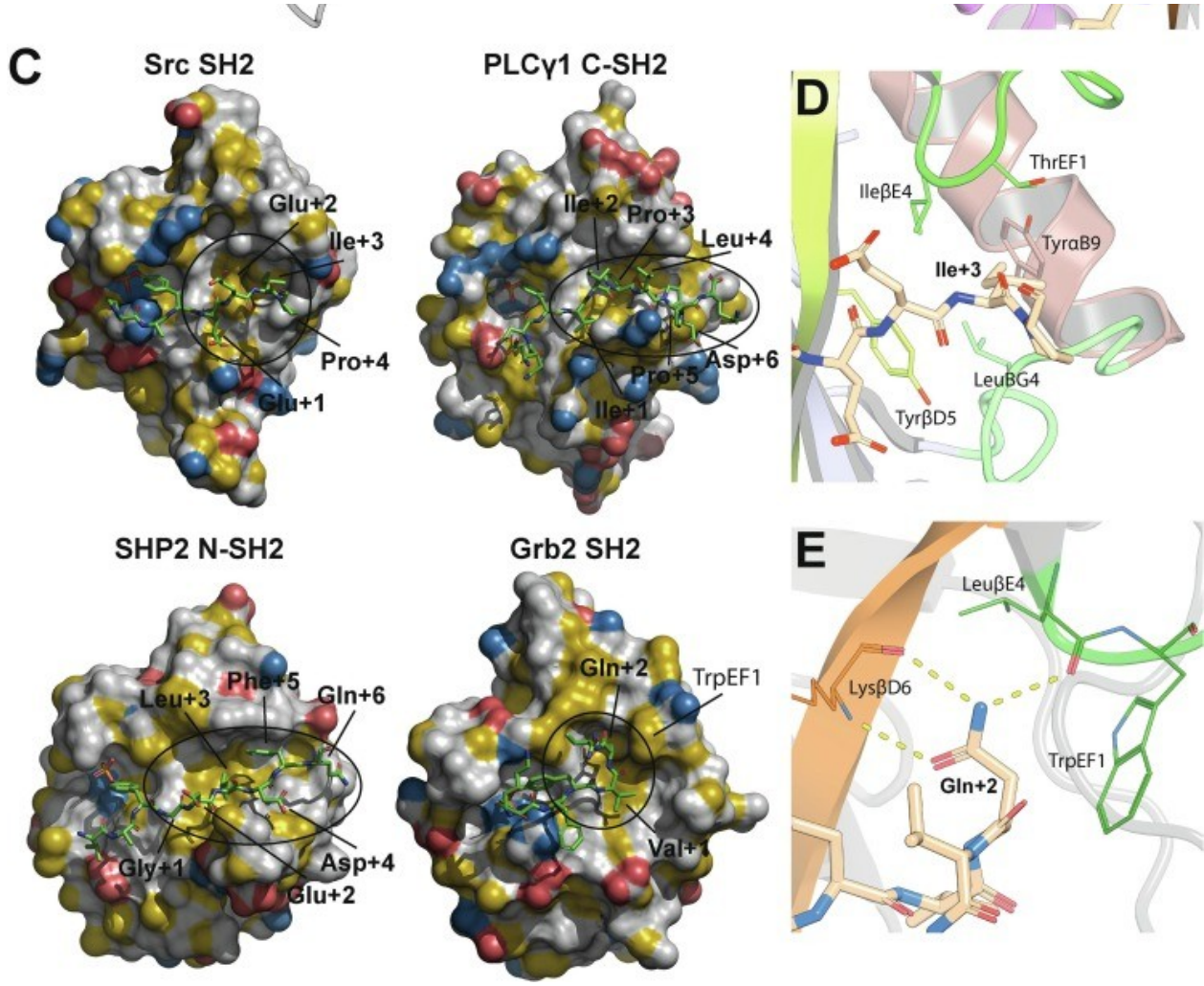




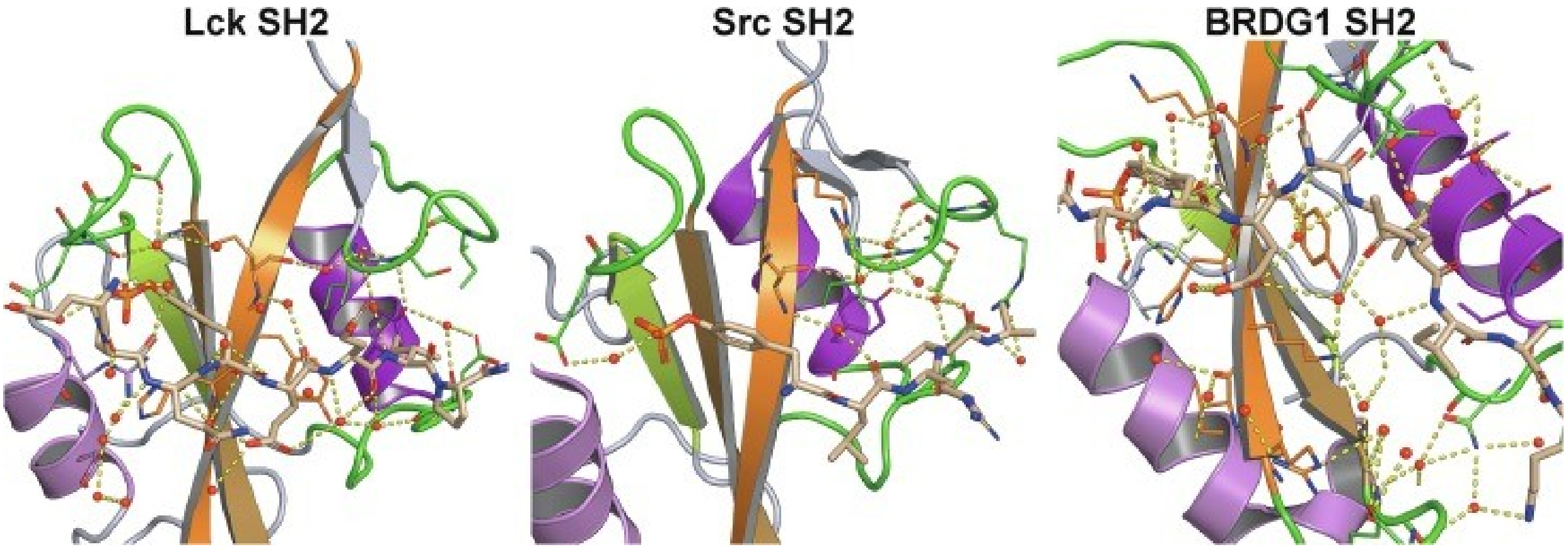
SH2 *domain*

Structural features of recognition by SH2 domains





Structural water molecules mediating protein–peptide interactions



SH3 domains

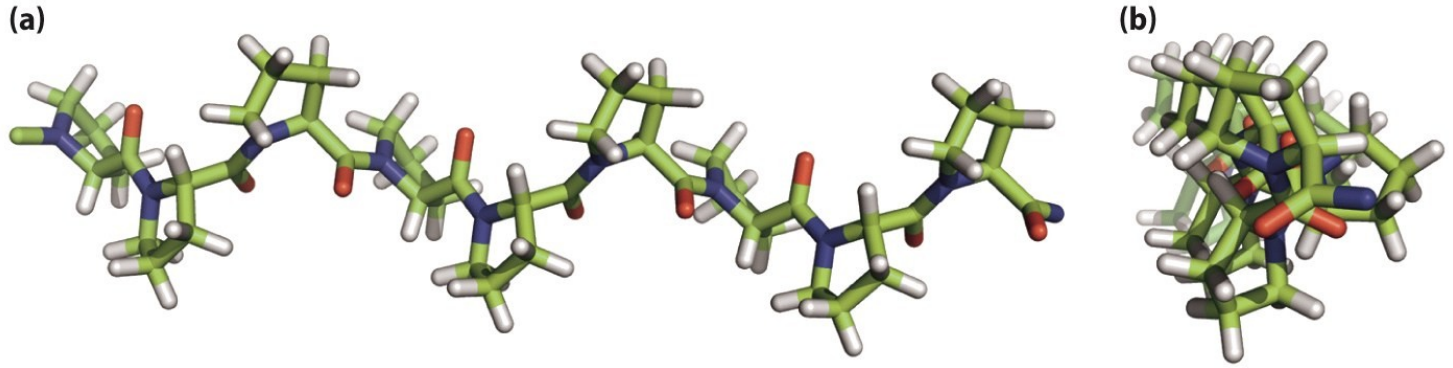
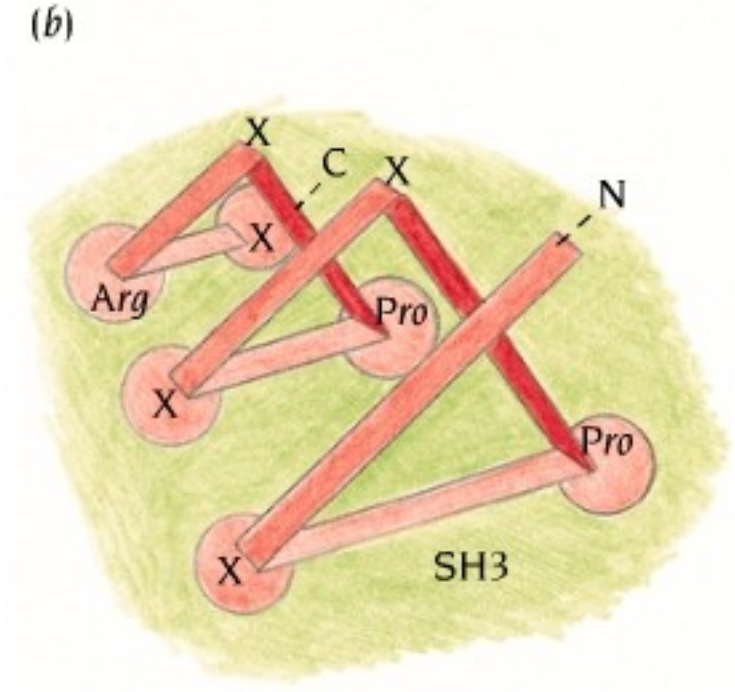


Figure 4.24 How Proteins Work (©2012 Garland Science)



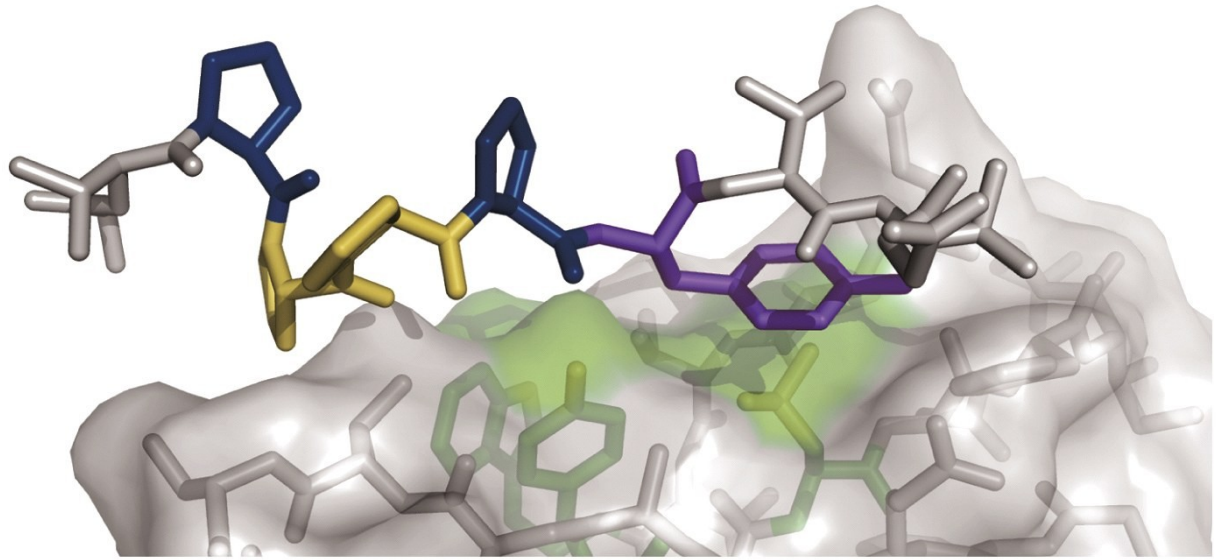


Figure 4.26 How Proteins Work (©2012 Garland Science)

SH3 domain

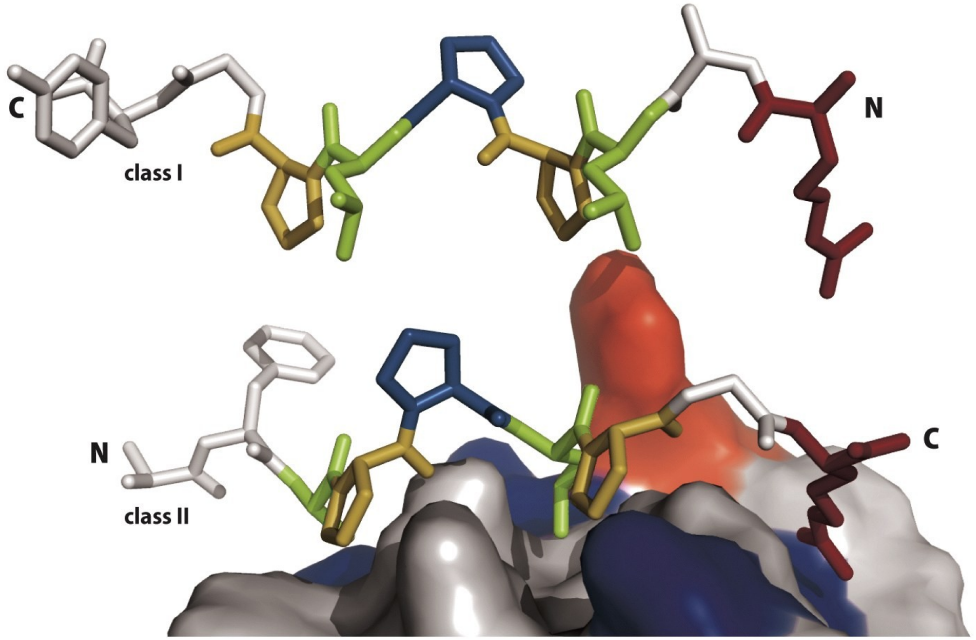
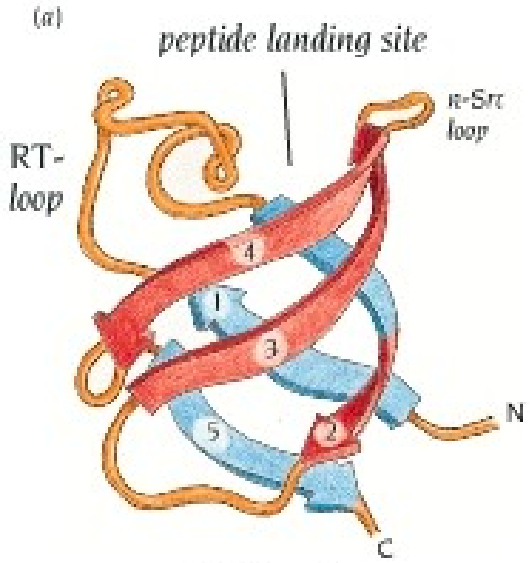
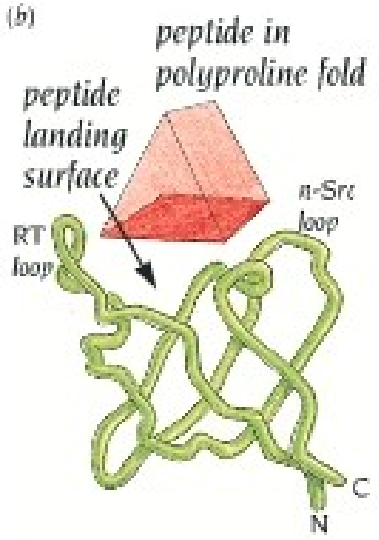


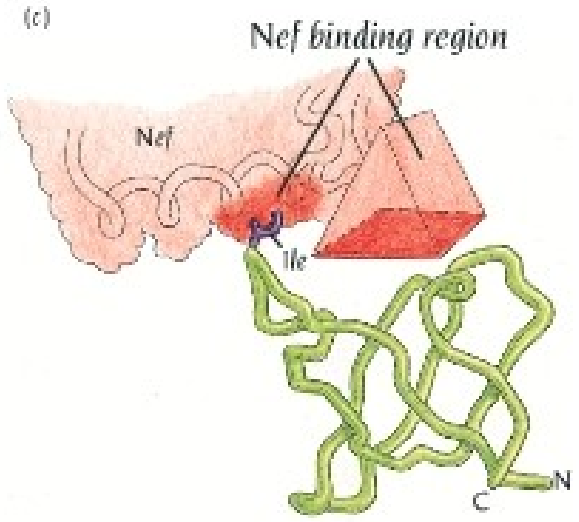
Figure 4.27 How Proteins Work (©2012 Garland Science)



SH3 domain



SH3



SH3

deactivation and activation of kinases

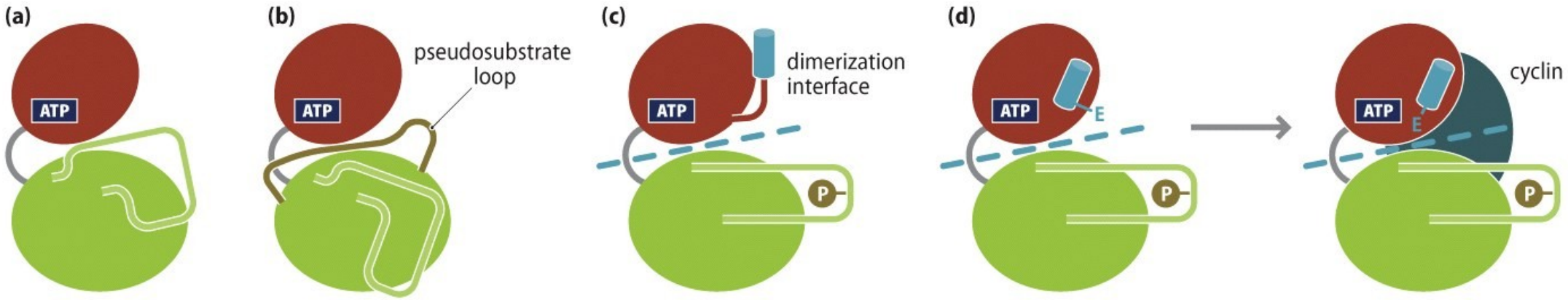
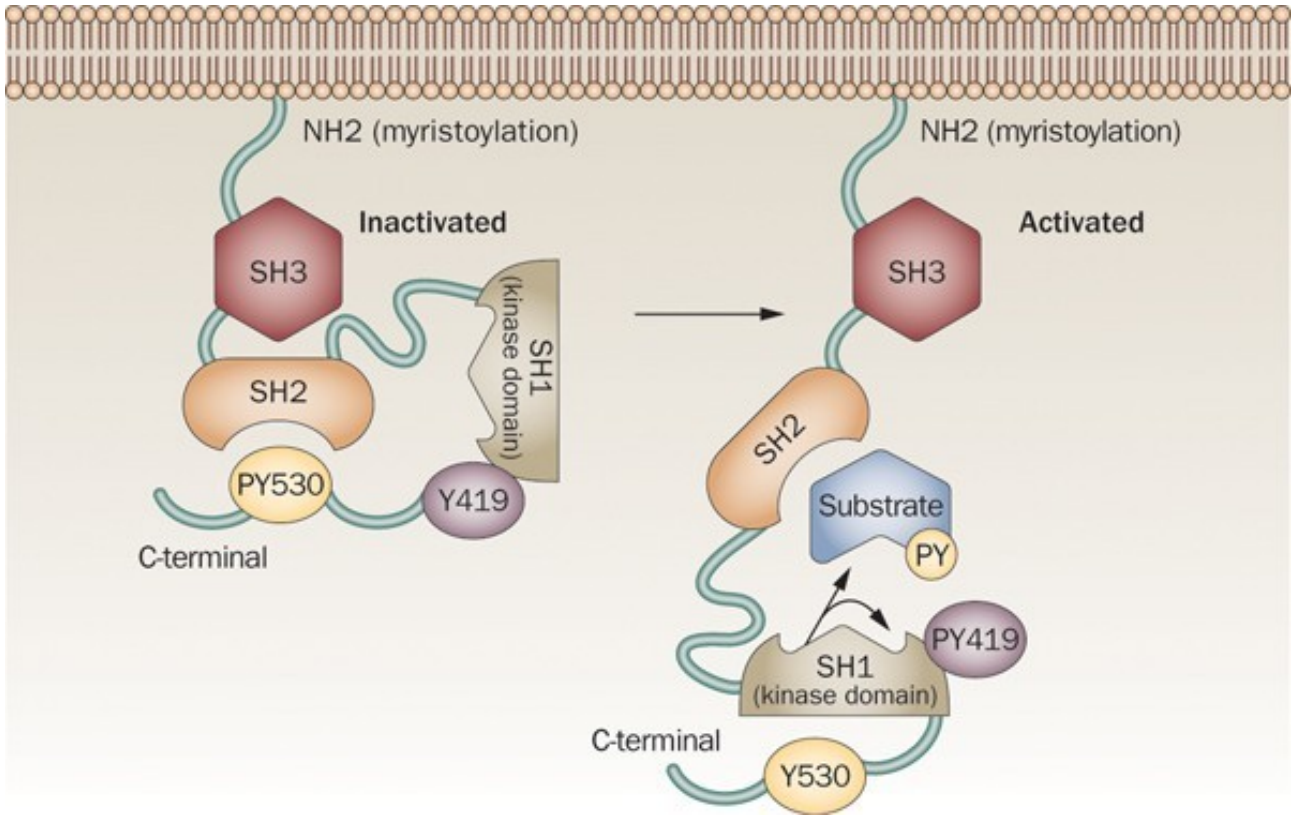
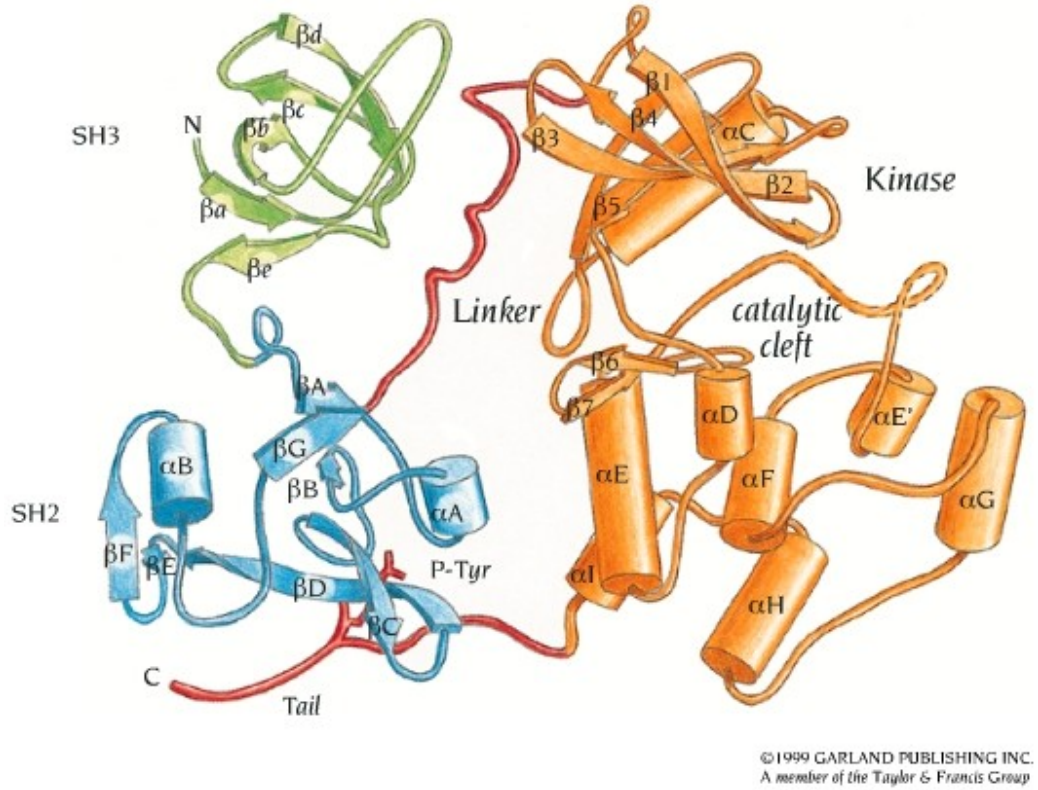


Figure 4.35 How Proteins Work (©2012 Garland Science)

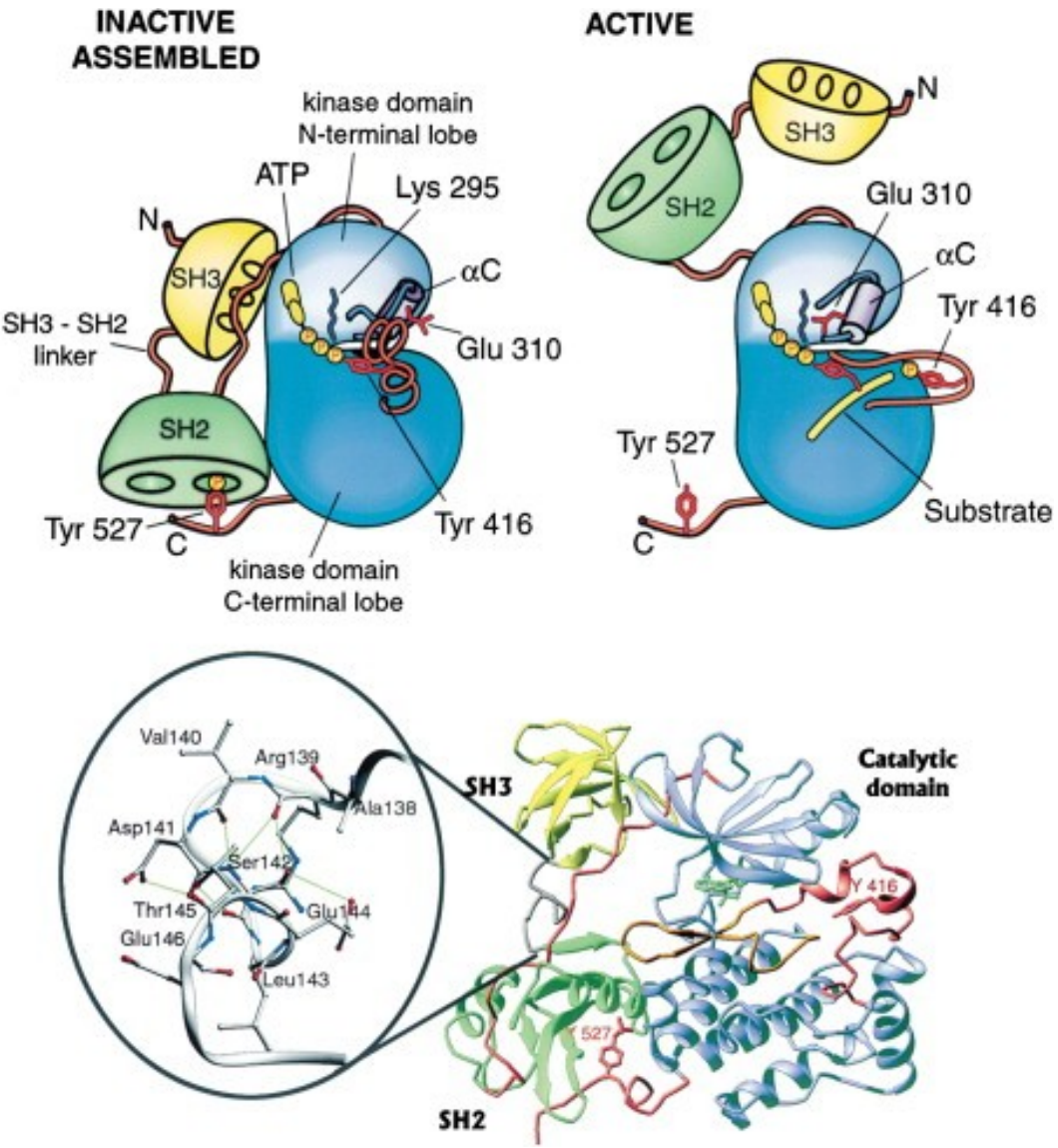
proline-serine-threonine-alanine-isoleucine-arginine-glutamate (PSTAIRE)

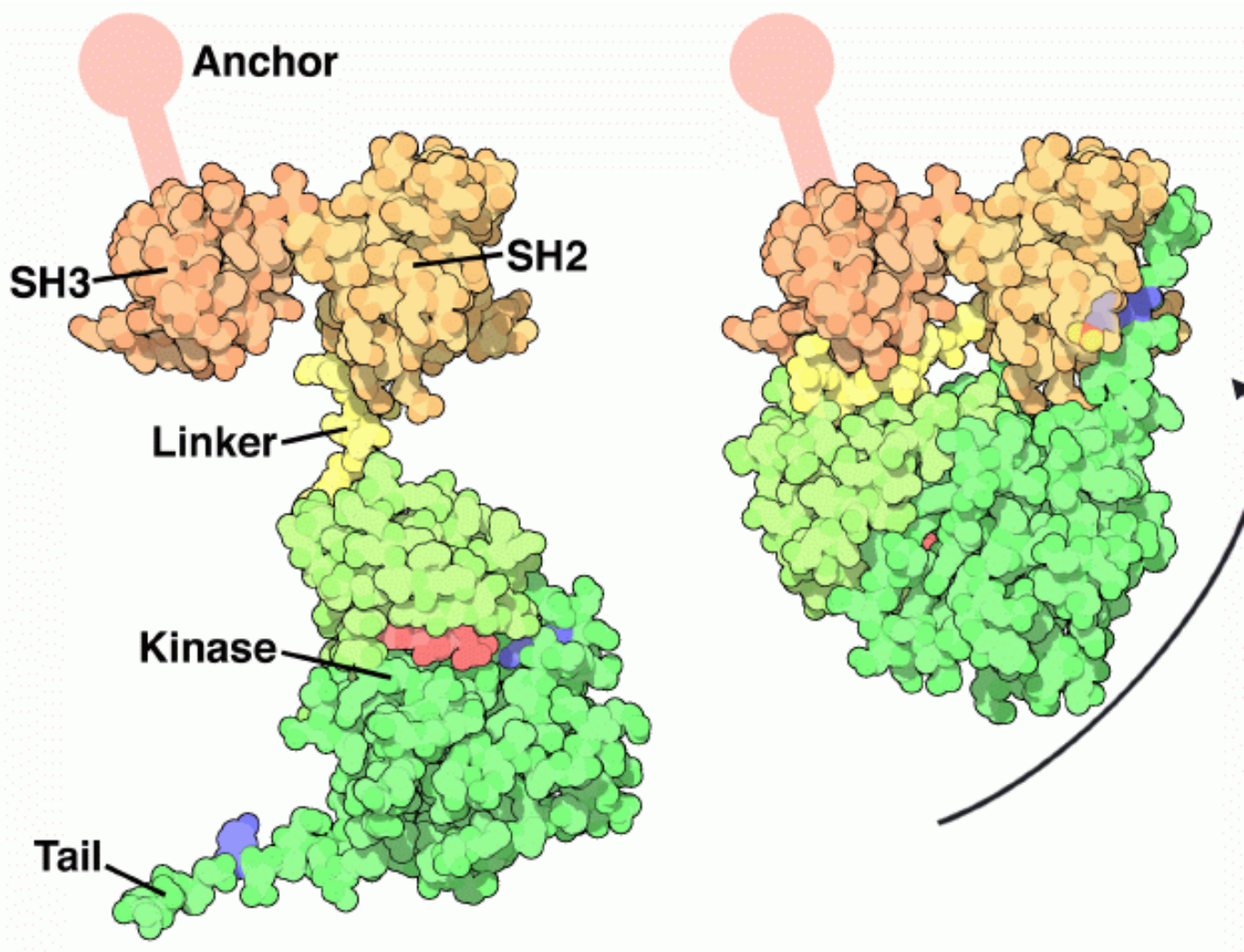
Src tyrosine kinase



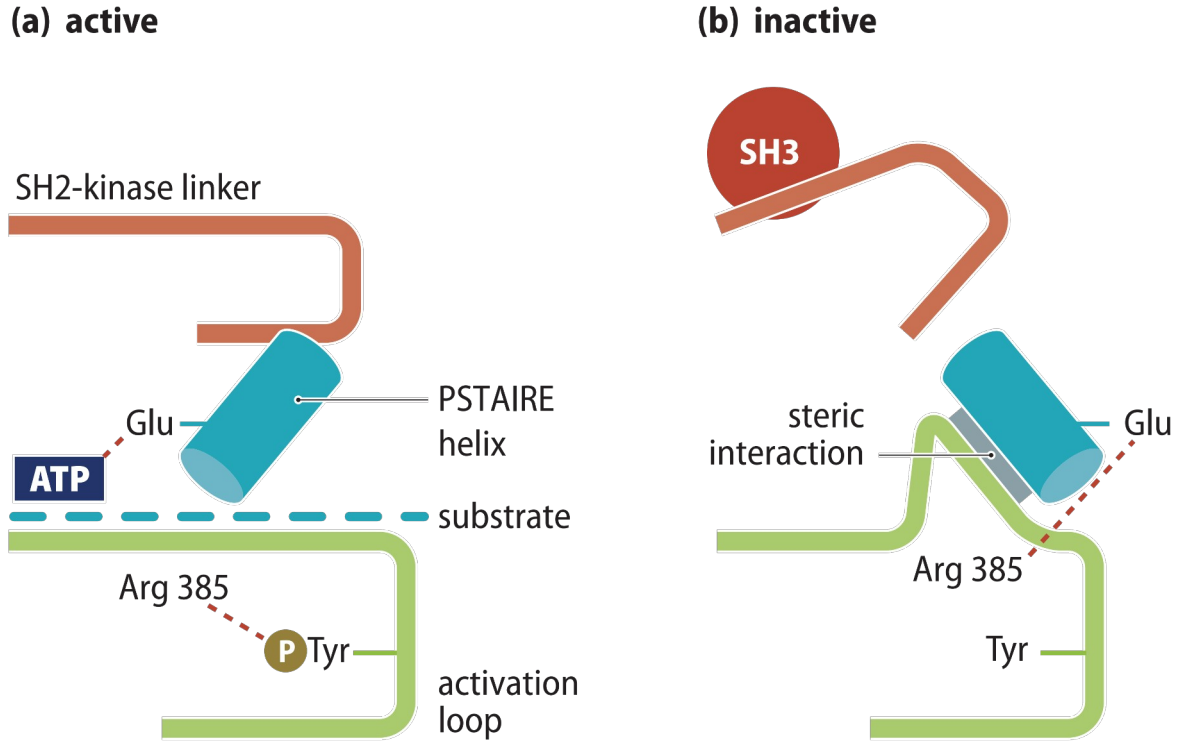


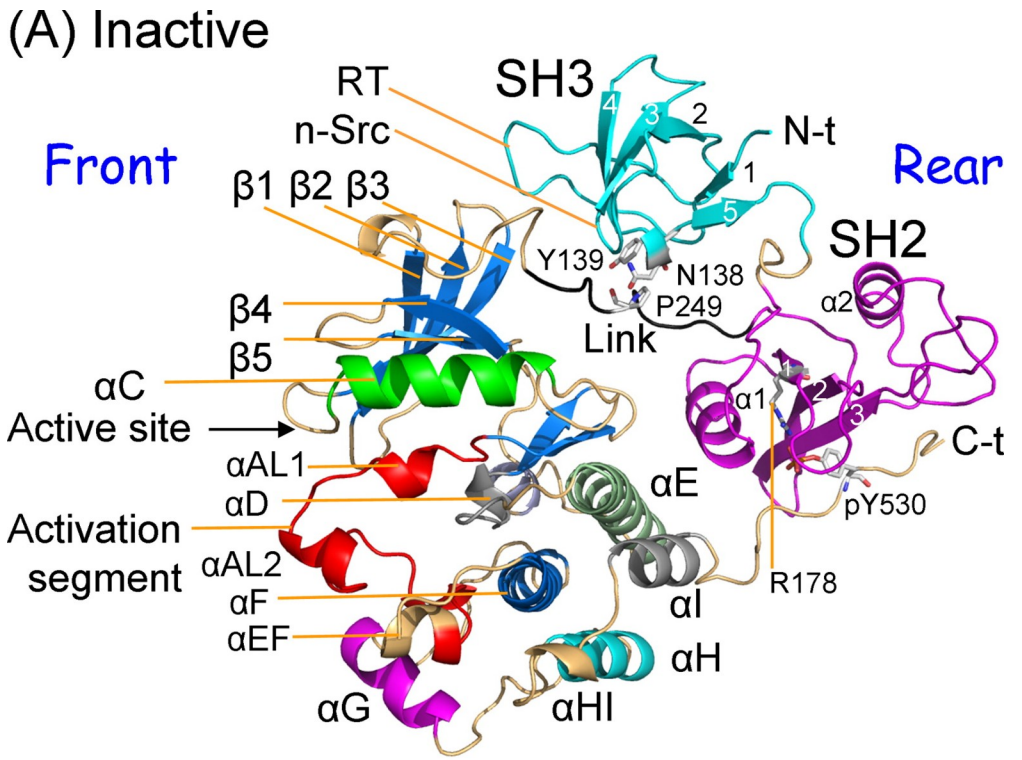
Src tyrosine kinase

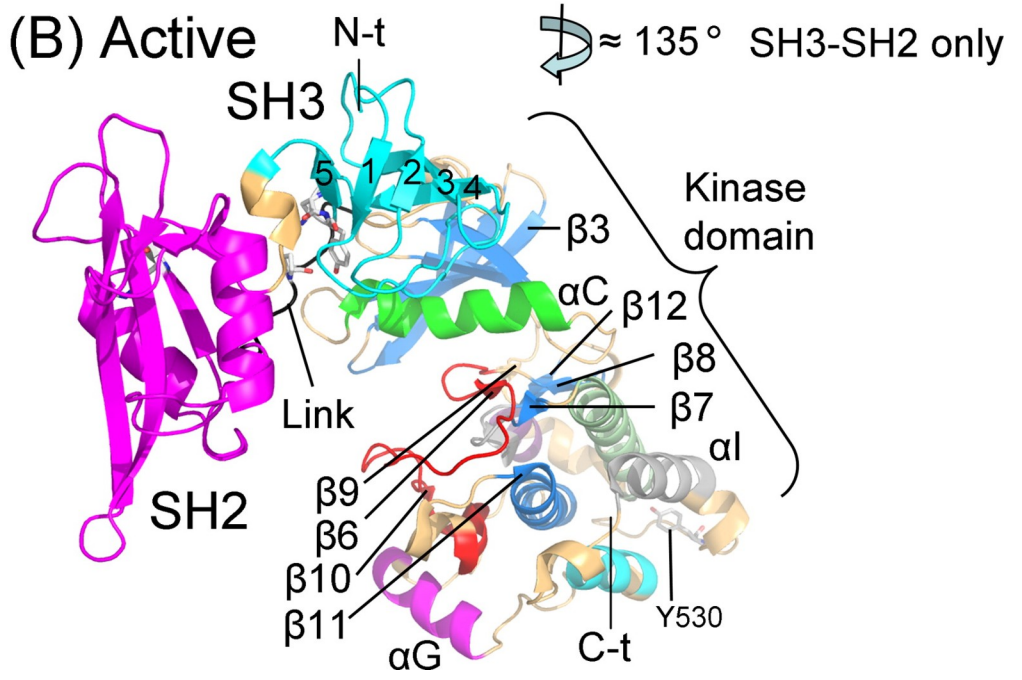




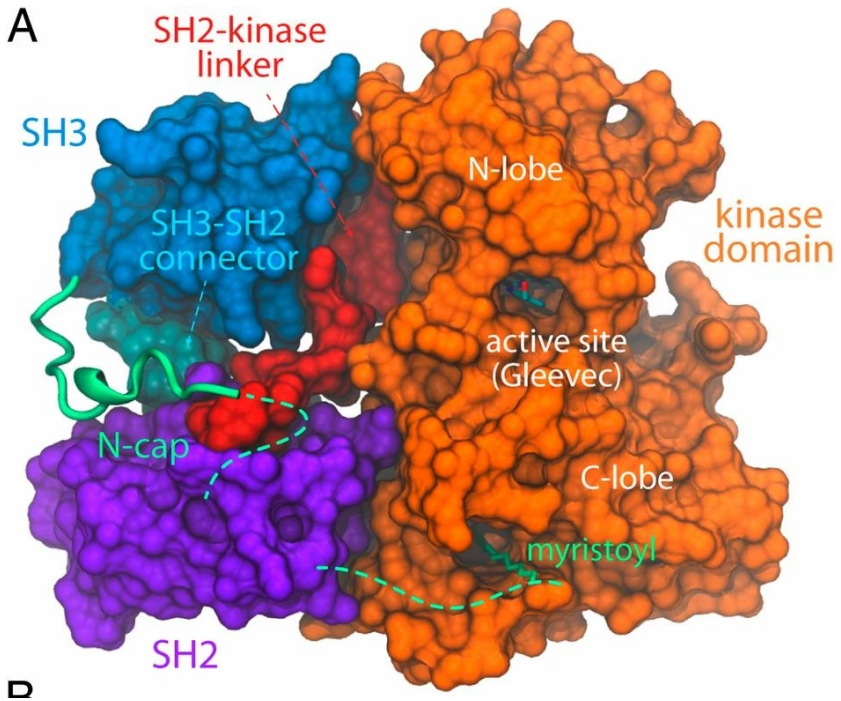
Active vs inactive

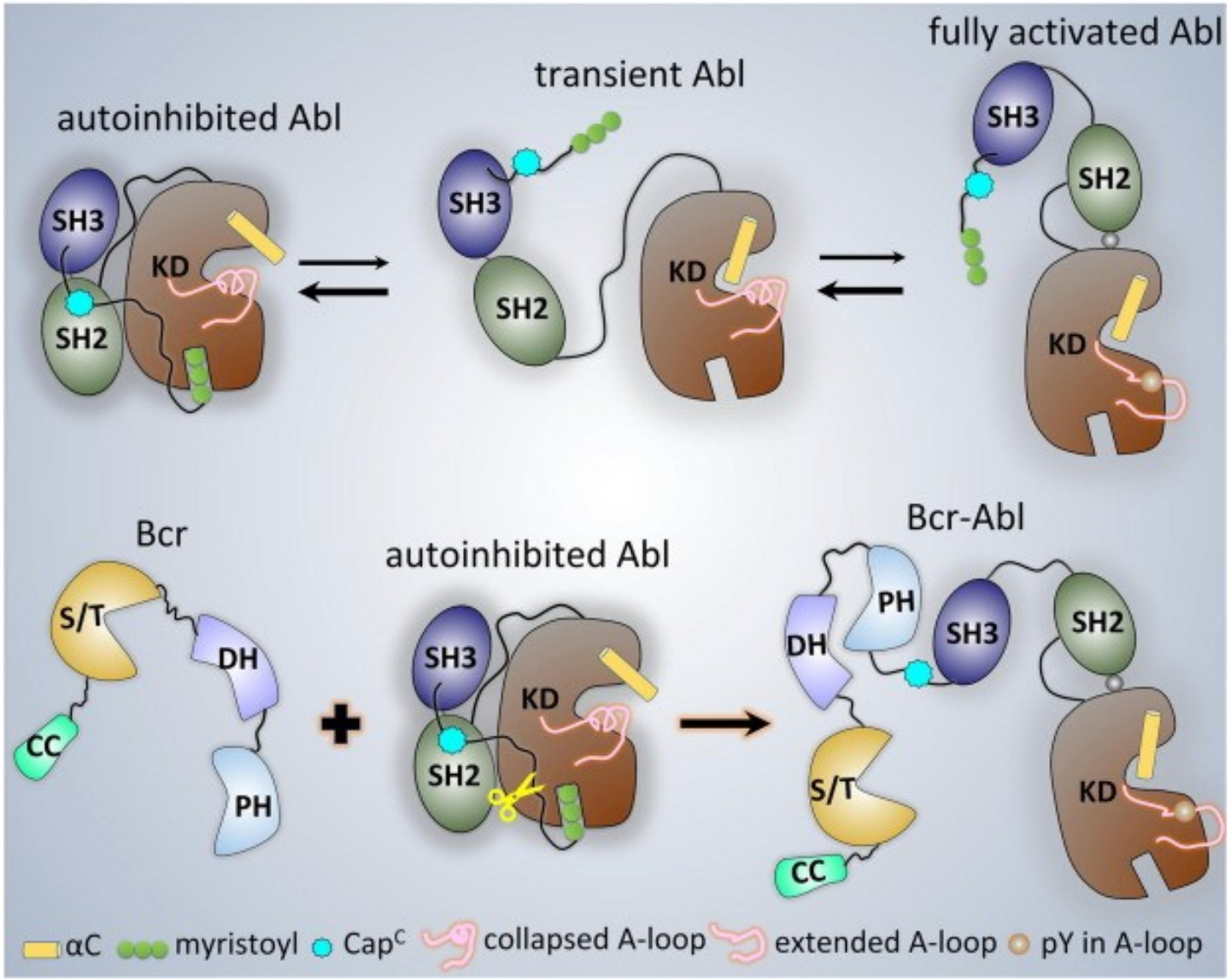






Abl kinase


A
SH2-kinase linker
SH3
N-lobe
SH3-SH2 connector
kinase domain
active site (Gleevec)
N-cap
C-lobe
myristoyl
SH2


autoinhibited Abl
transient Abl
fully activated Abl
SH3
SH2
KD
Bcr
S/T
DH
CC
PH
Bcr-Abl
αC
myristoyl
Cap^C
collapsed A-loop
extended A-loop
pY in A-loop

Post-translational modifications of proteins

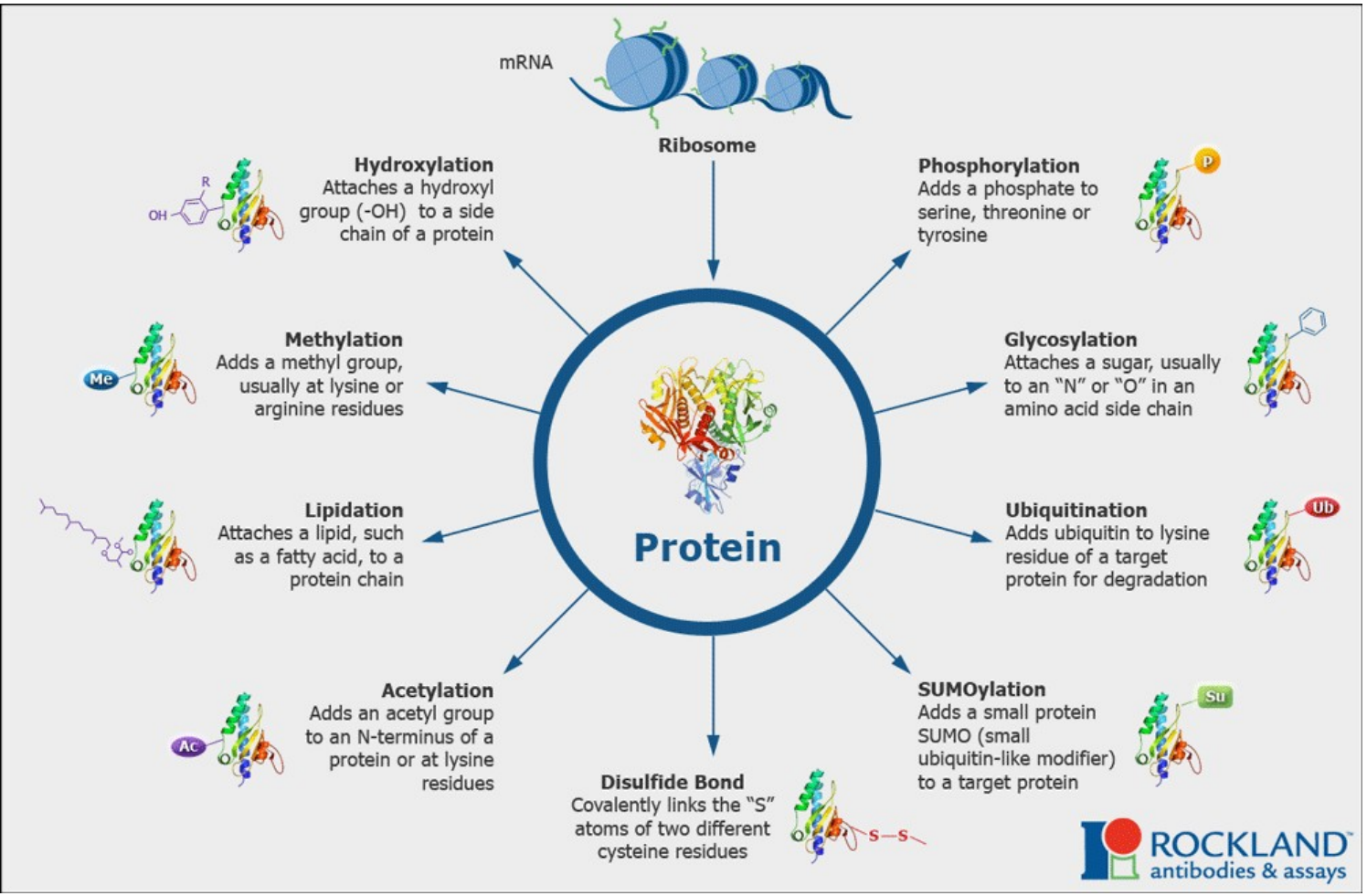


TABLE 4.3 A few covalent modifications of proteins

Modification	Site	Comments
Phosphorylation	Ser, Thr, Tyr	Regulates activity. Regulates assembly
Acetylation	Lys	Creates part of histone code in chromatin
Methylation	Lys	Creates part of histone code in chromatin
Methylation	Arg	
Lipid attachment	Cys, C terminus	Attaches protein to membrane
SUMOylation	Lys	Role in transport, transcriptional regulation, apoptosis
Ubiquitylation	Lys	Regulates transport and degradation, plus histone readout
Limited proteolysis		Activates proteases (zymogens) in extracellular location (e.g. chymotrypsin); activates hormones (e.g. insulin)
Attachment of *N*-acetylglucosamine	Ser, Thr	Regulates activity in enzymes involved in glucose metabolism
Glycosylation	Asn, Ser/Thr	Eukaryotes. Recognition, membrane protein folding
Hydroxylation	Pro	Collagen: to facilitate triple helix formation. Irreversible
ADP ribosylation	Arg, Glu, Asp	As part of signaling, DNA repair and apoptosis
Sulfation	Tyr	Irreversible and probably required for activity
Carboxylation	Glu	Creates γ-carboxyglutamate (Gla), a calcium ligand

Table 4.3 How Proteins Work (©2012 Garland Science)

Phosphorylation

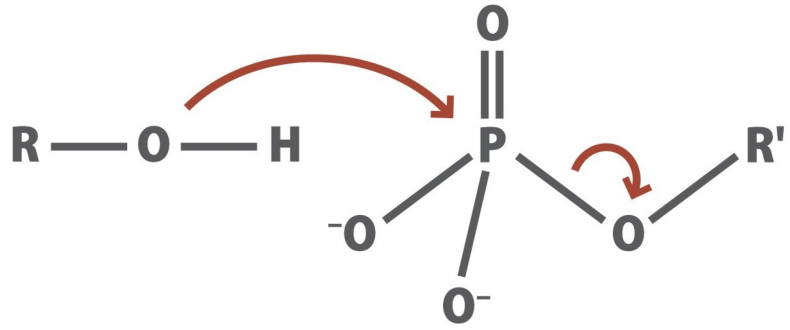


Figure 4.33 How Proteins Work (©2012 Garland Science)

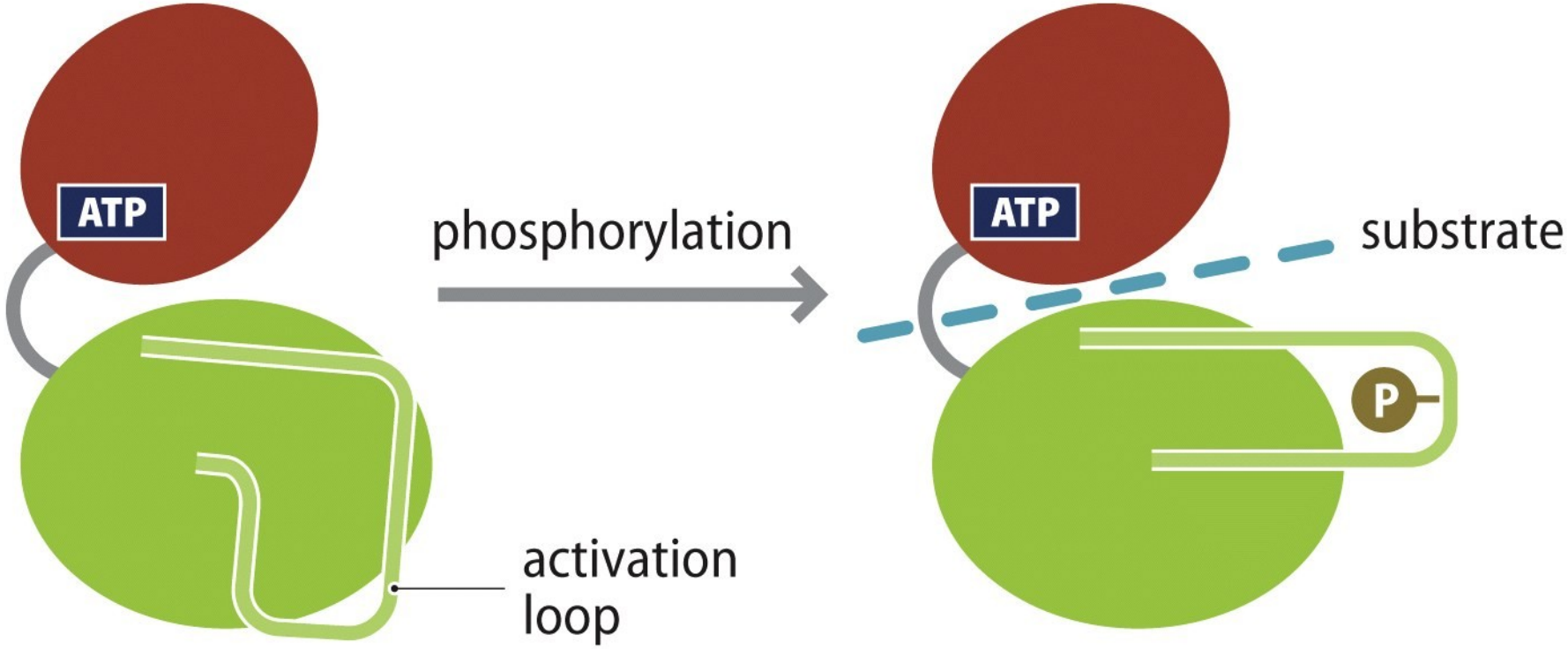
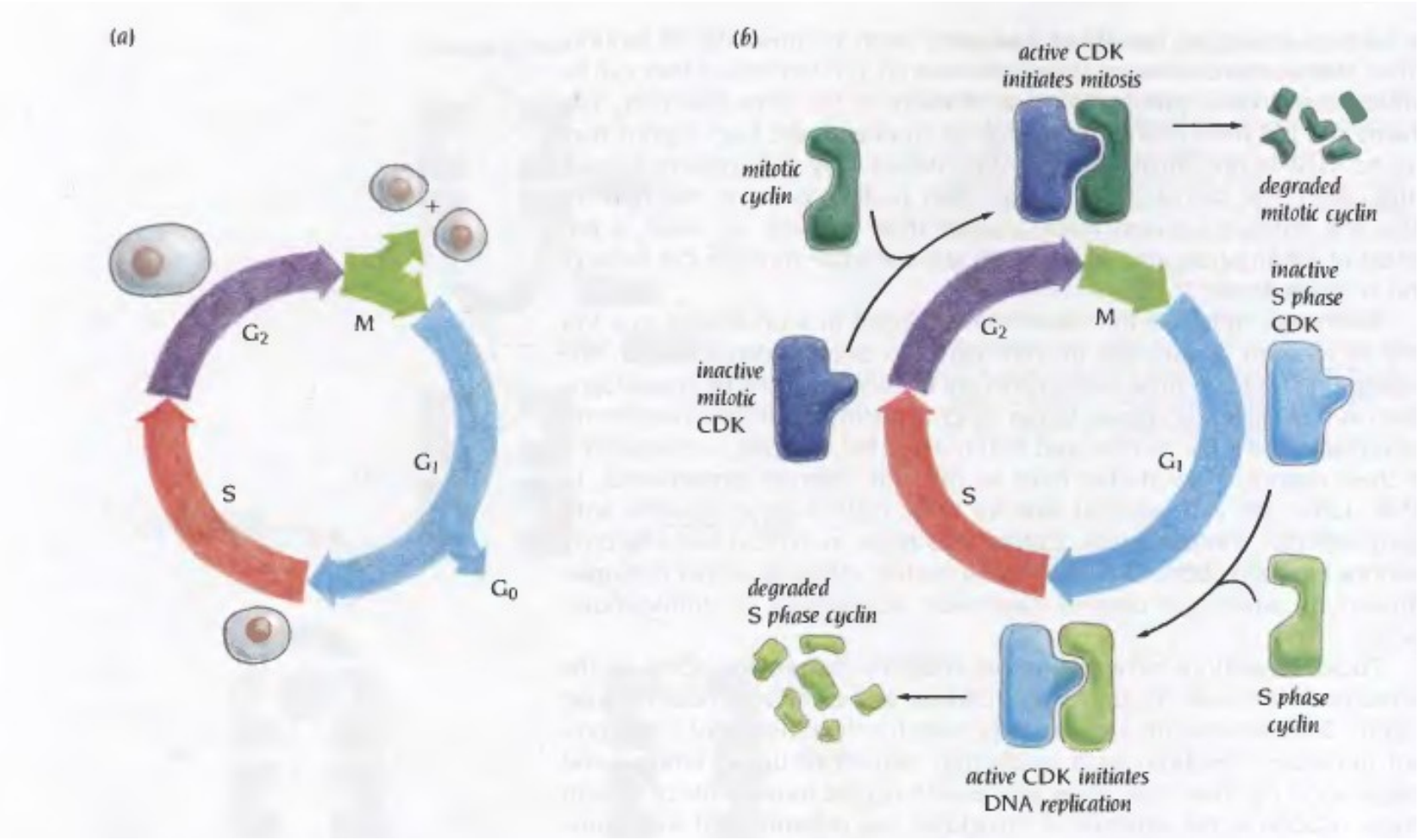


Figure 4.34 How Proteins Work (©2012 Garland Science)

cell cycle



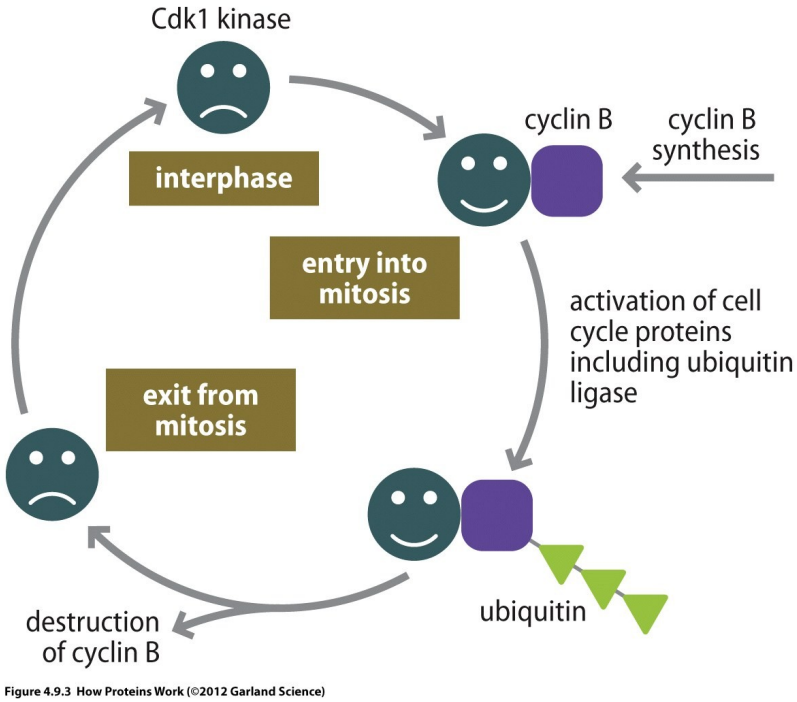
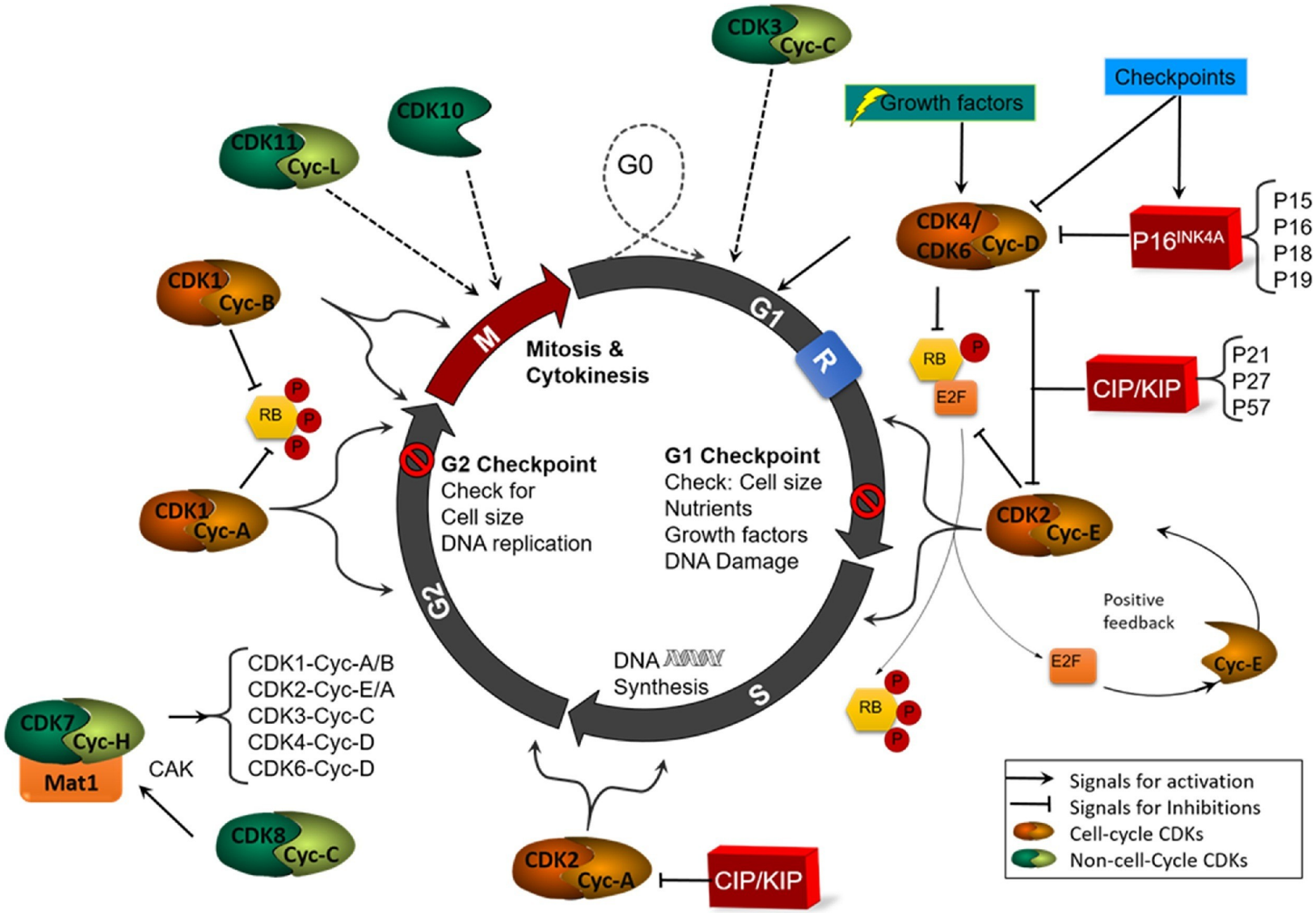


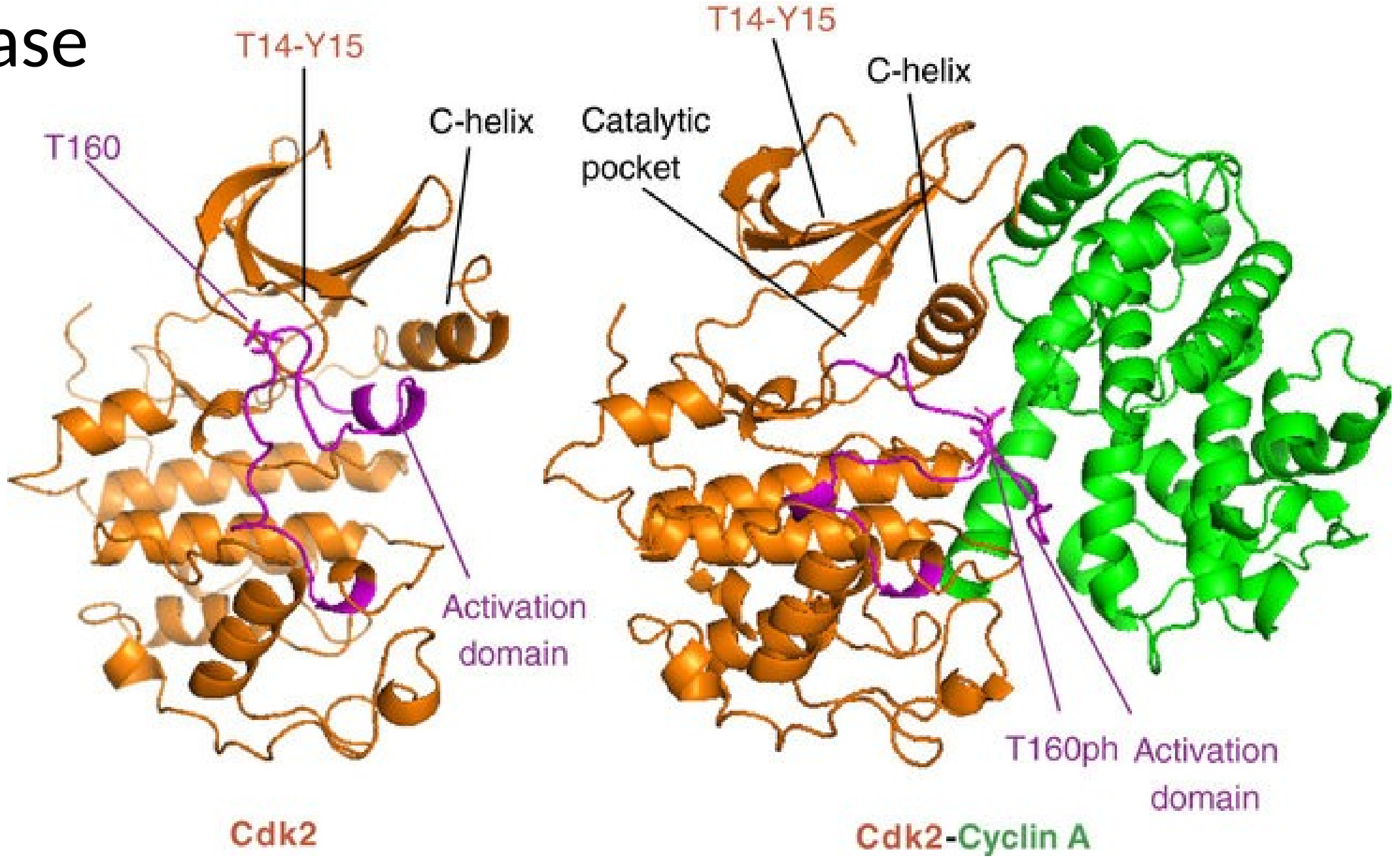
Figure 4.9.3 How Proteins Work (©2012 Garland Science)

cell cycle

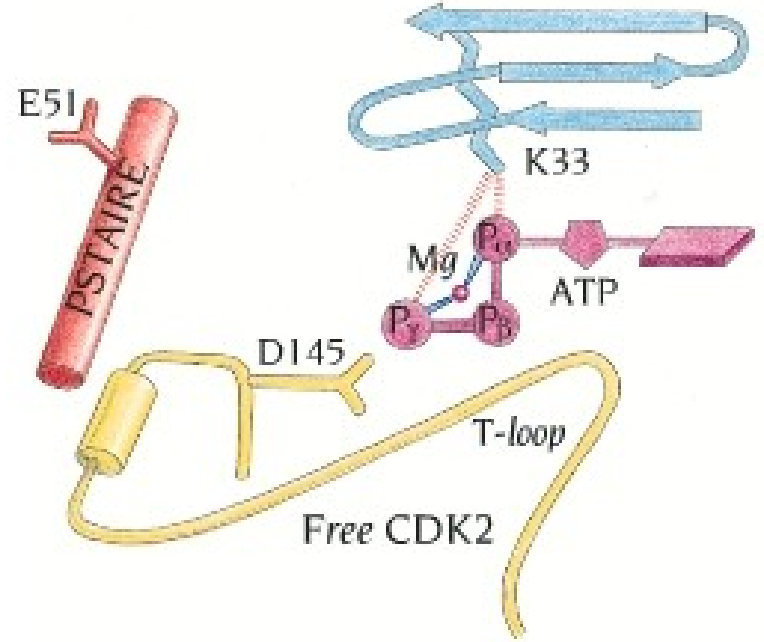


Biomedicine & Pharmacotherapy 107 (2018) 1326–1341

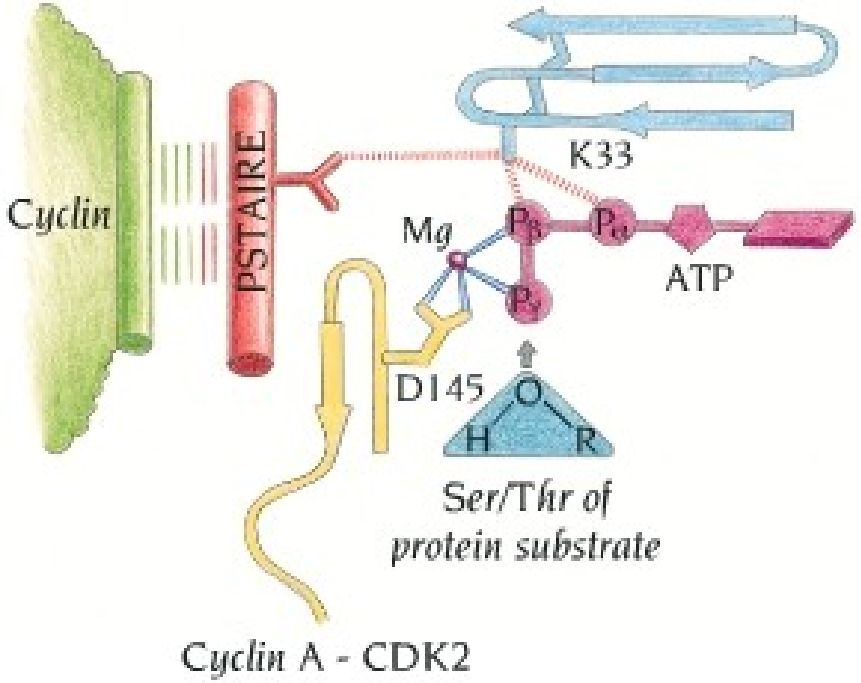
CD kinase


T14-Y15
C-helix
T160
Activation
domain
Cdk2
T14-Y15
C-helix
Catalytic
pocket
T160ph
Activation
domain
Cdk2-Cyclin A

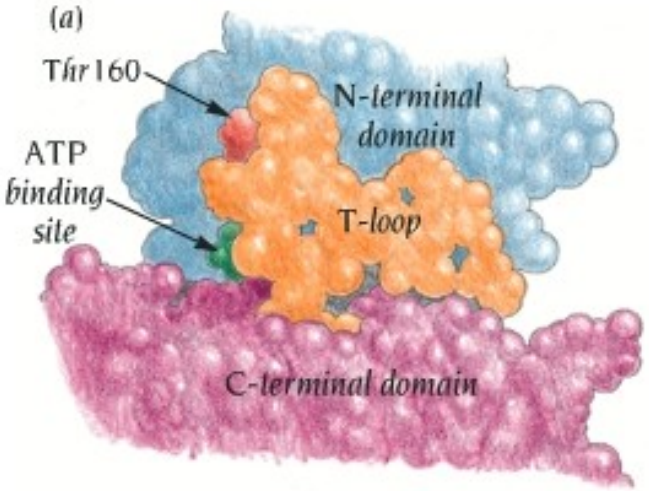
CD kinase

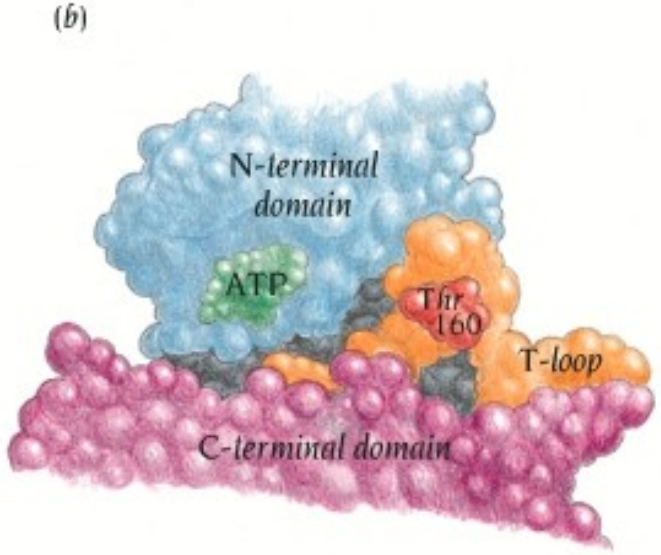


(a)



(b)





ubiquitylation

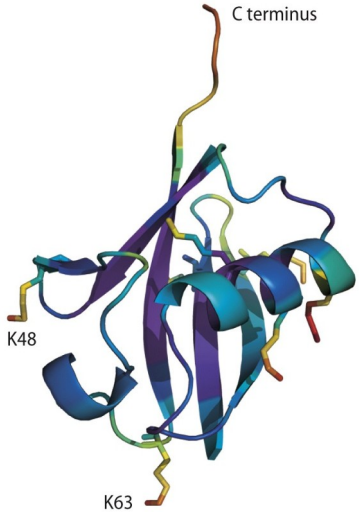


TABLE 4.4 Dependence of half-life of cytoplasmic proteins on their N-terminal residue

N-terminal residue	Half-life
Met, Gly, Ala, Ser, Thr, Val	> 20 h
Ile, Glu	30 min
Tyr, Gln	10 min
Pro	7 min
Leu, Phe, Asp, Lys	3 min
Arg	2 min

Table 4.4 How Proteins Work (©2012 Garland Science)

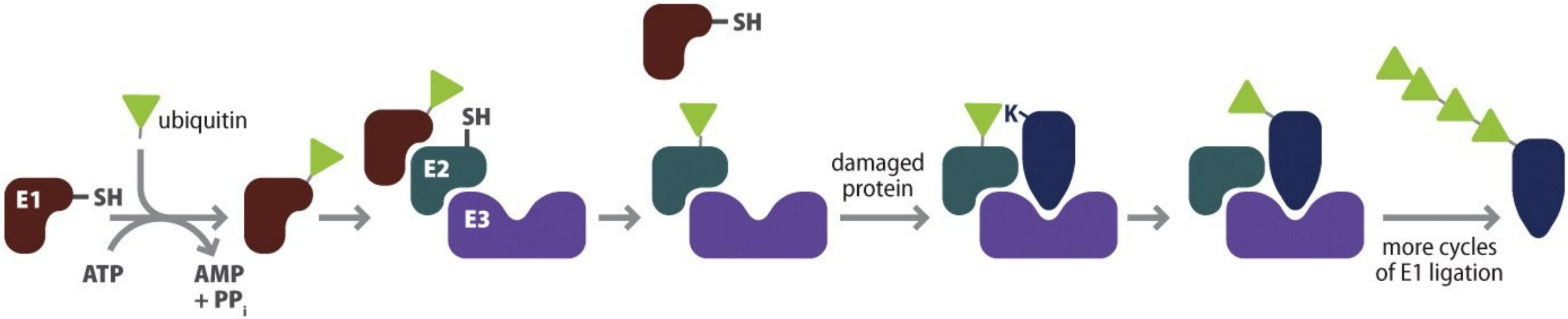
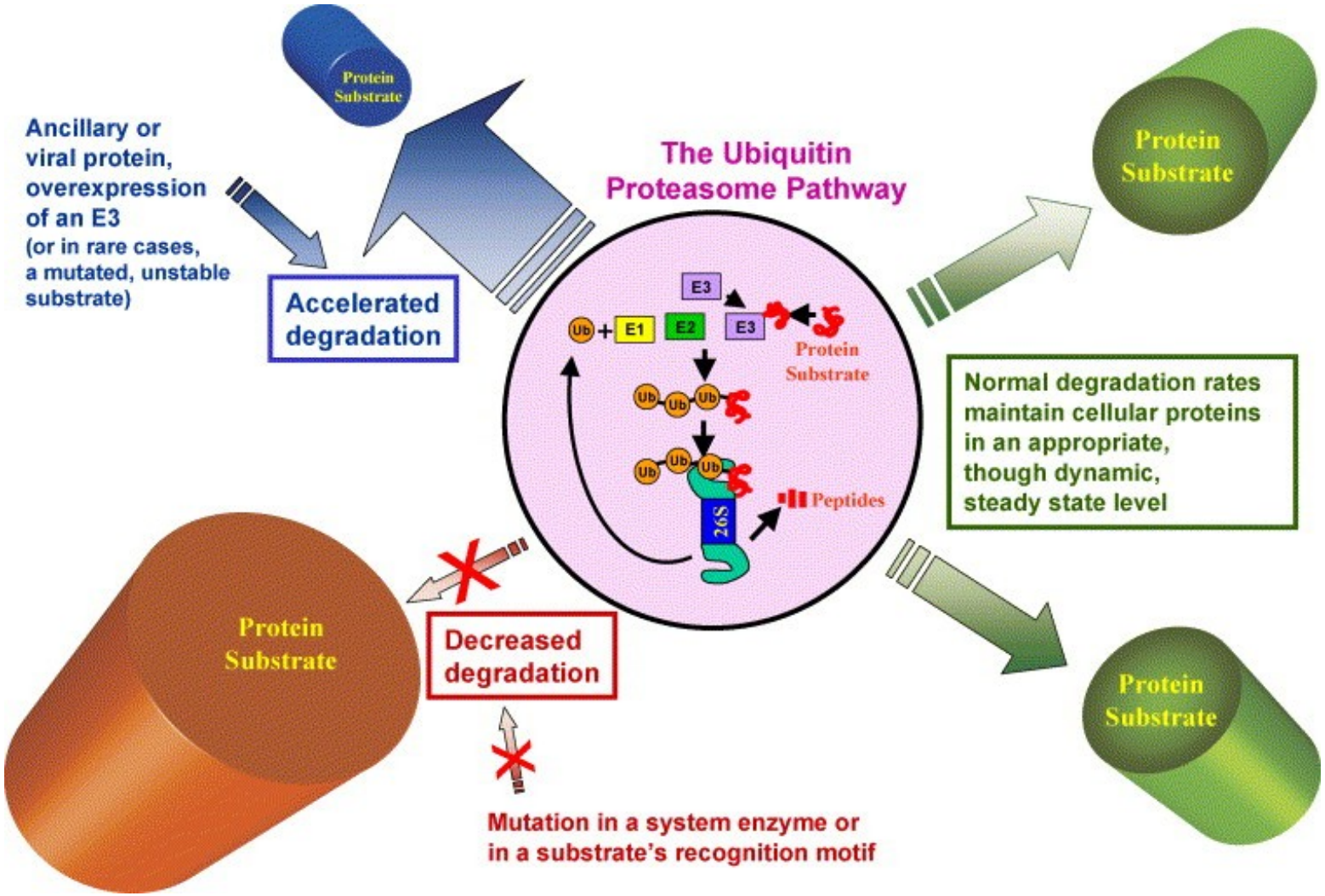
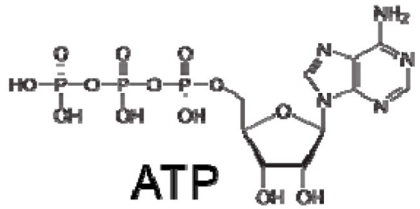


Figure 4.9.2 How Proteins Work (©2012 Garland Science)

ubiquitylation



Phosphatases



ATP

ADP

Kinases

Phosphorylation

- Inducing conformational change
- Providing platform for phospho-binding proteins

Dephosphorylation

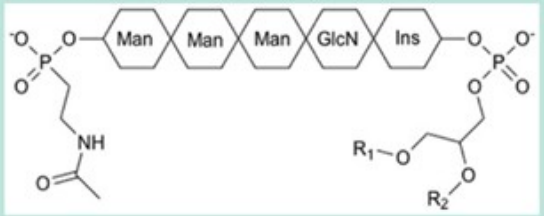
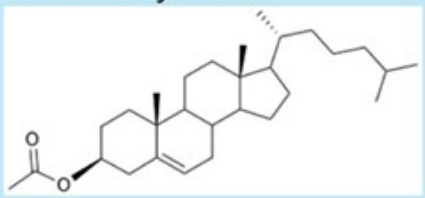
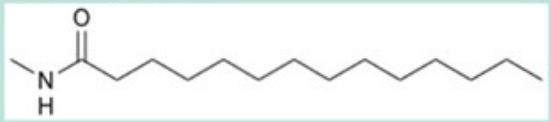
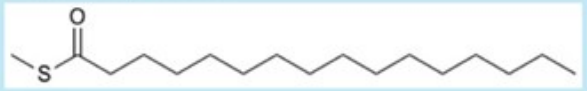
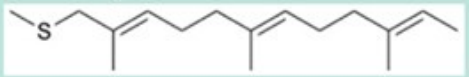
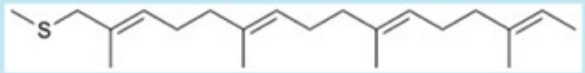
Phosphatases

p

Changes in Protein

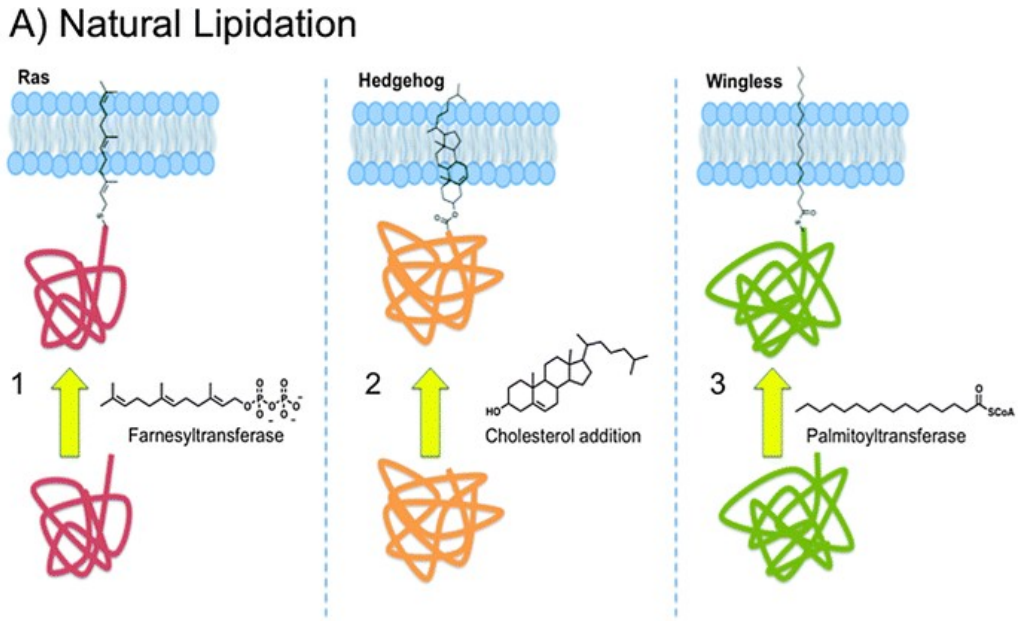
- Stability
- Activity
- Interaction
- Subcellular localization

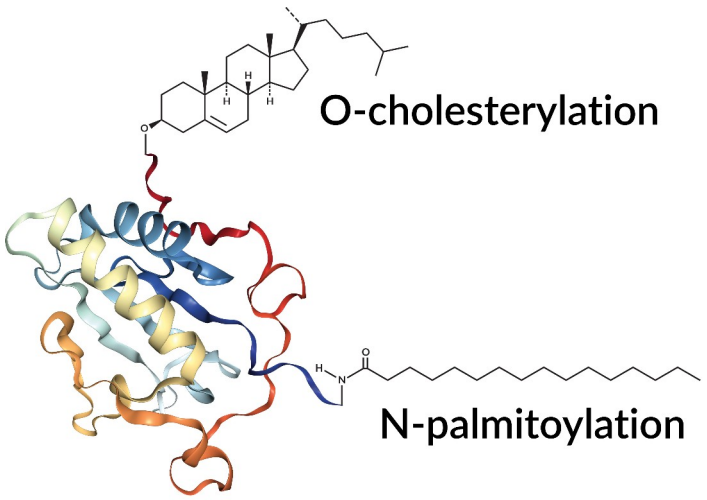
Lipidation

Lipid Structure	Effects on proteins	Effects on downstream signaling in cancer
GPI anchor 	Plasma membrane tethering Incorporation into specific membrane domains Protein-protein interaction	Increase cell division in bladder[197], breast[198], colon[199], and other cancers
Cholesterylation 	Hedgehog signaling activation	Facilitate tumorigenesis and cancer growth in prostate[200], breast[201], bladder[202], and other cancers
Myristoylation 	Membrane localization Autoinhibition	Carcinogenesis in breast [203], lung[204], and other cancers
Palmitoylation 	Plasma membrane localization Partitioning into lipid rafts Protein maturation/quality control	Promote proliferation and invasion in melanoma[170], intestinal[205], and other cancers
Farnesylation 	Membrane localization Conformational change Protein-protein interaction	Promote cell growth, survival and metastasis in lung[206], myeloid leukemia[207], pancreatic[208], and other cancers
Geranylgeranylation 	Membrane localization Protein-protein interaction	Facilitate cell proliferation and migration in lymphoma[177], leukemia[209], and other cancers

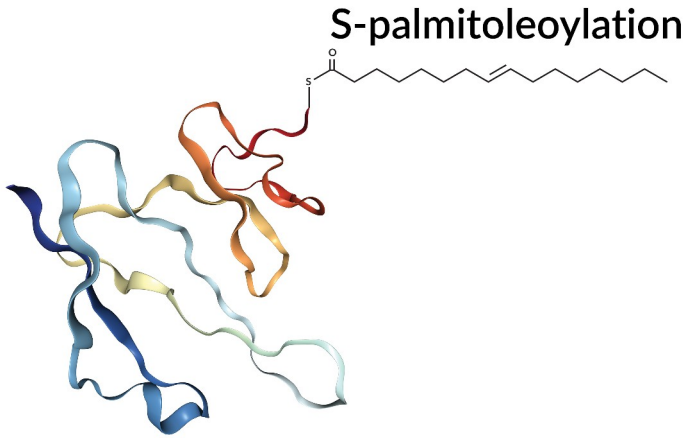
Front. Oncol., 29 June 2017

Lipidation

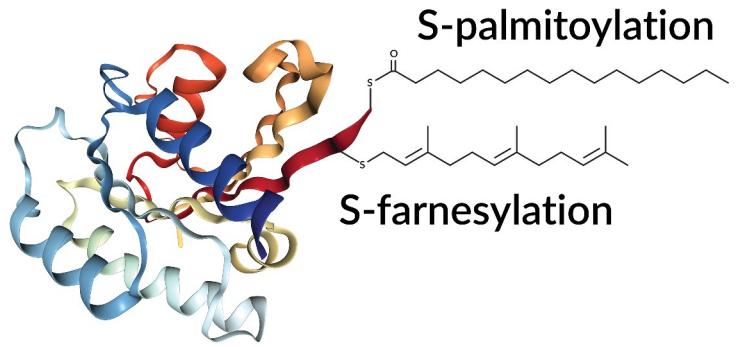




Shh

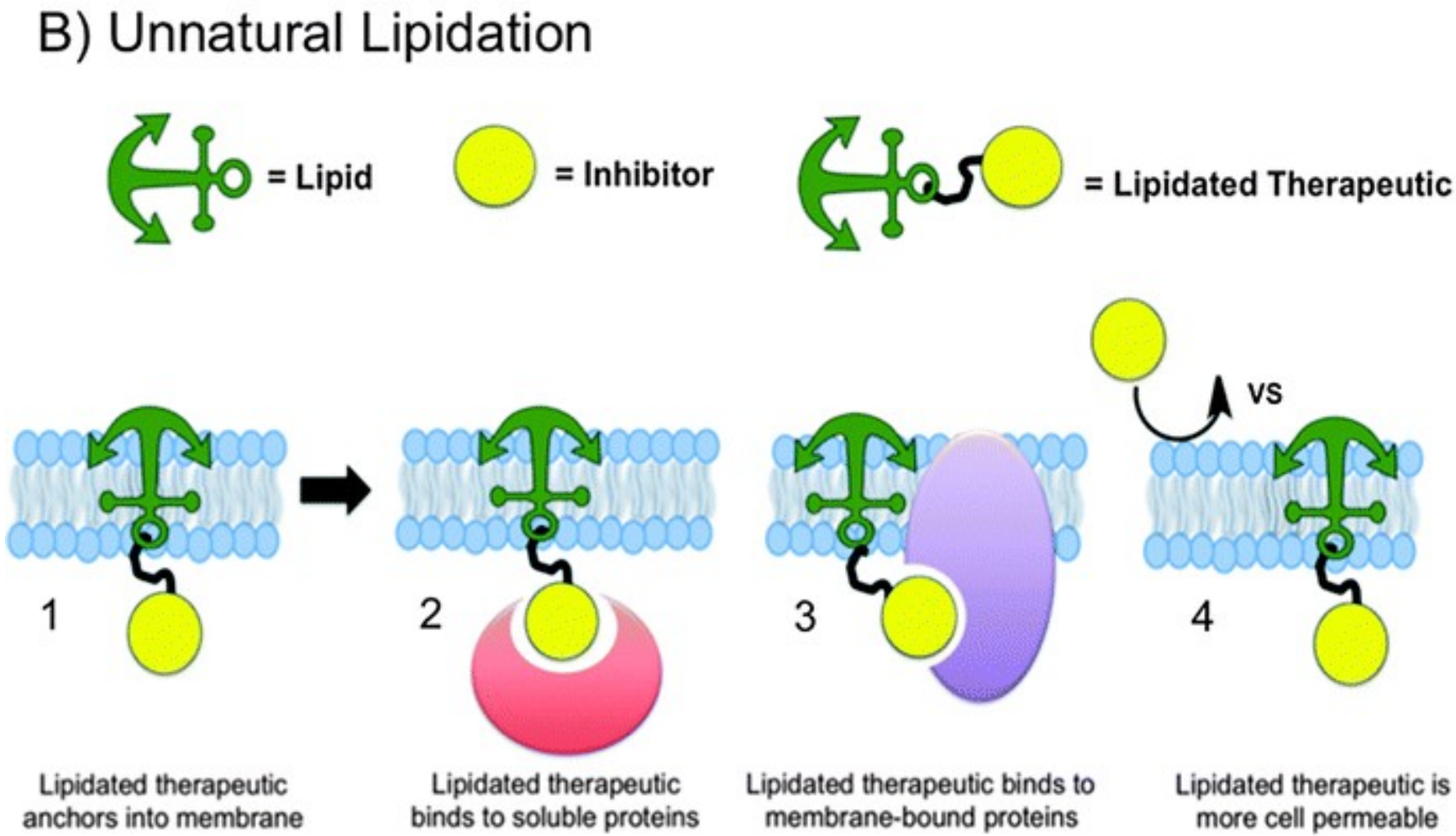


Wnt



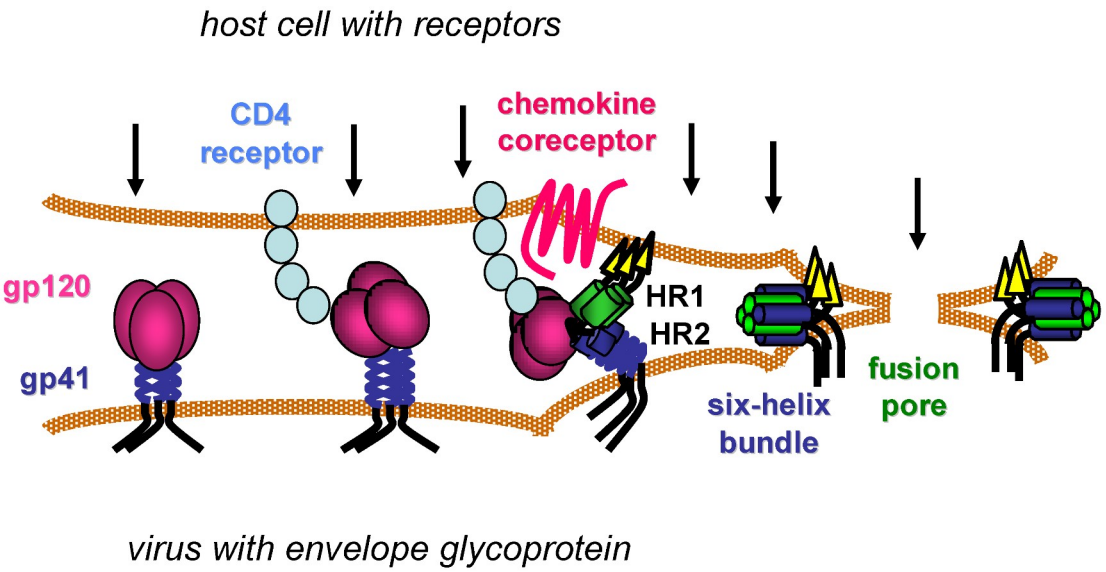
H-Ras

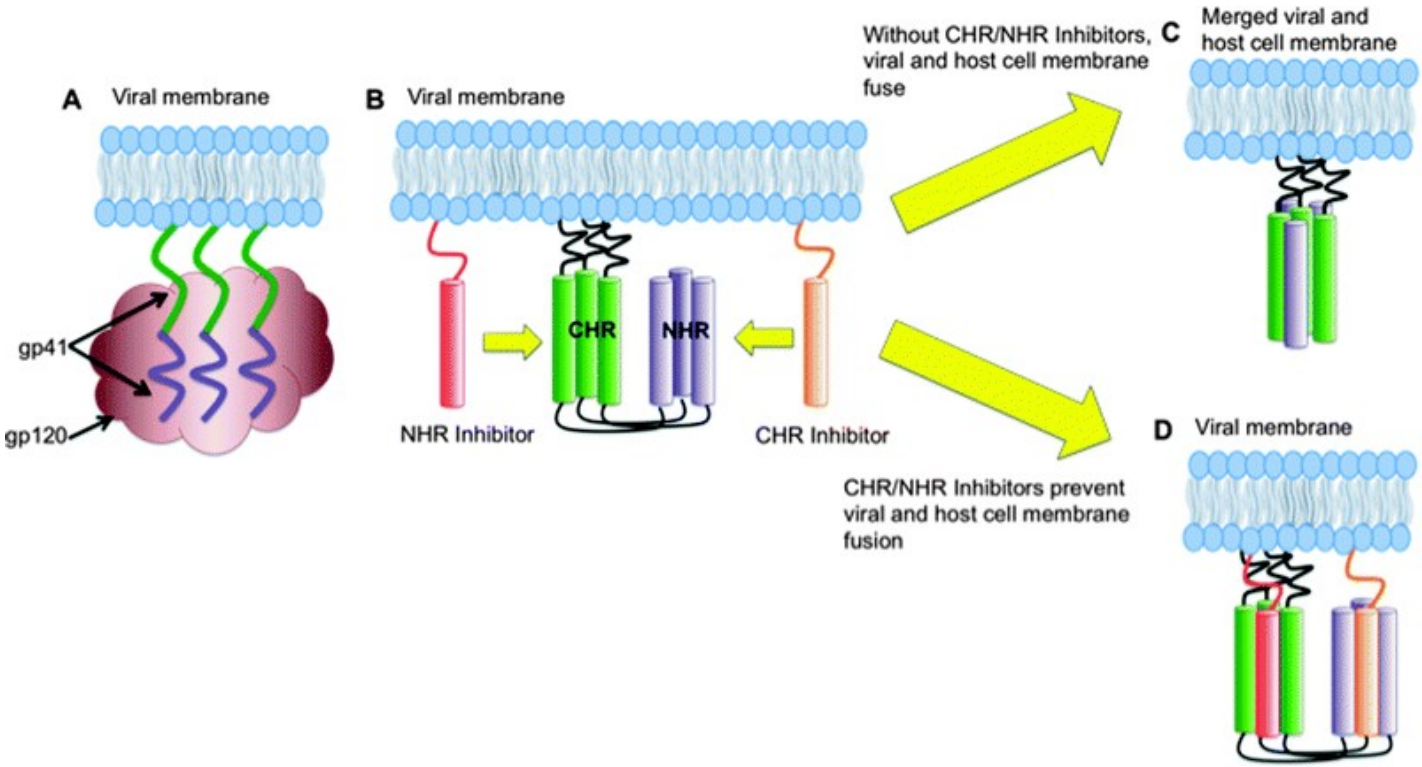
Lipidated therapeutics



Lipidated therapeutics

Escape from Human Immunodeficiency Virus Type 1 (HIV-1)





Viruses **2012**, *4*(12), 3859-3911

chromosome

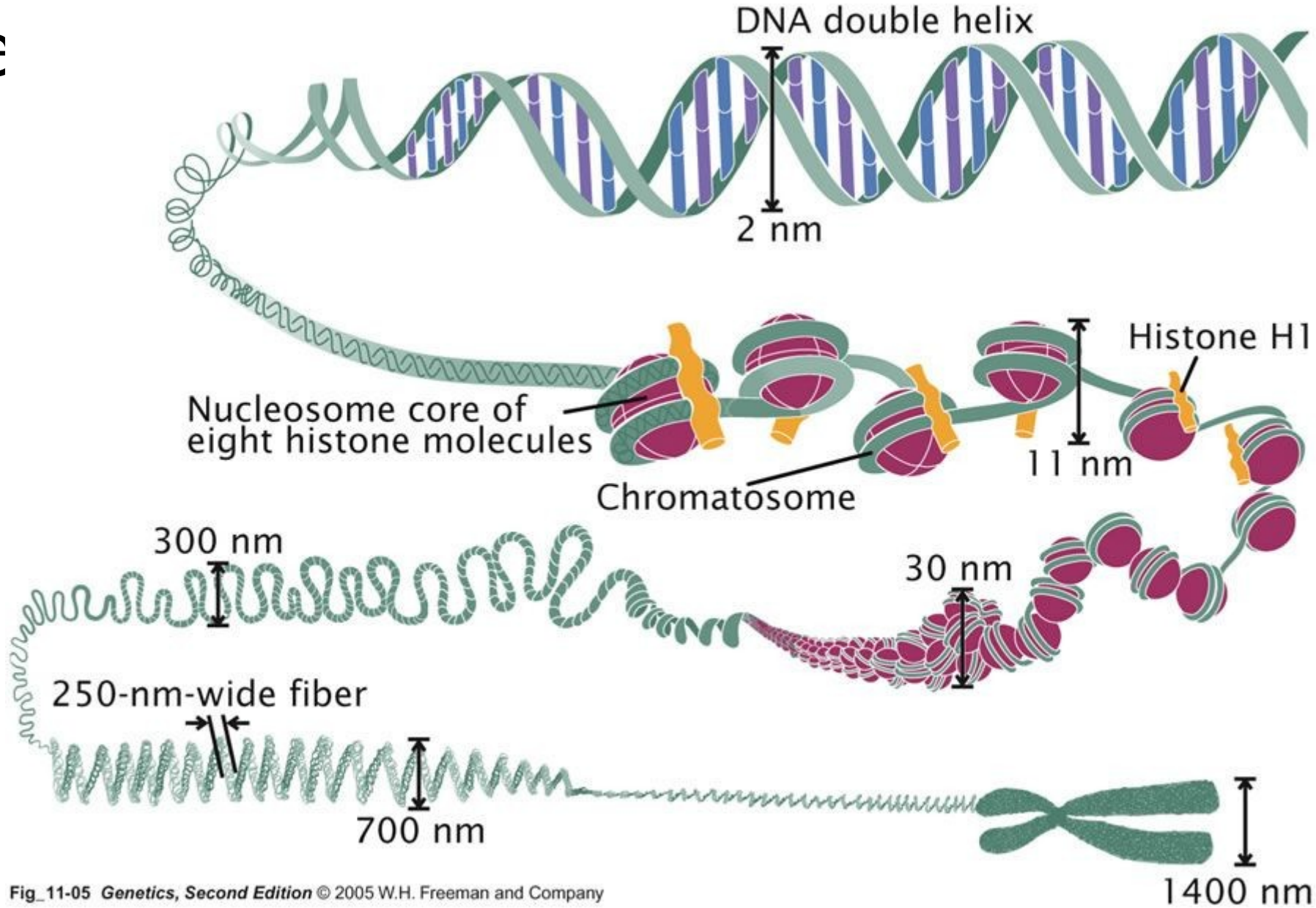


Fig_11-05 *Genetics, Second Edition* © 2005 W.H. Freeman and Company

Drosophila nucleosome core

H2A, H2B, H3, and H4

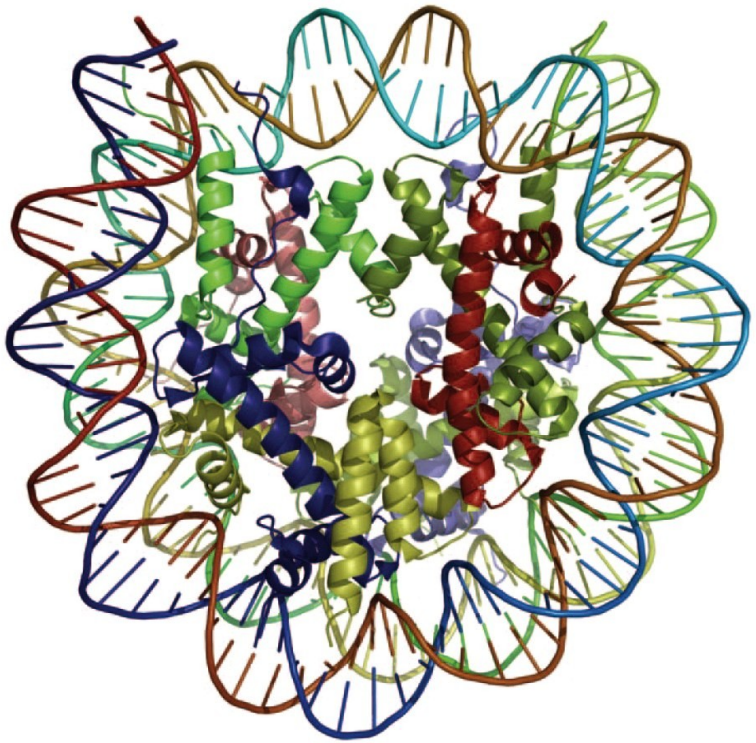
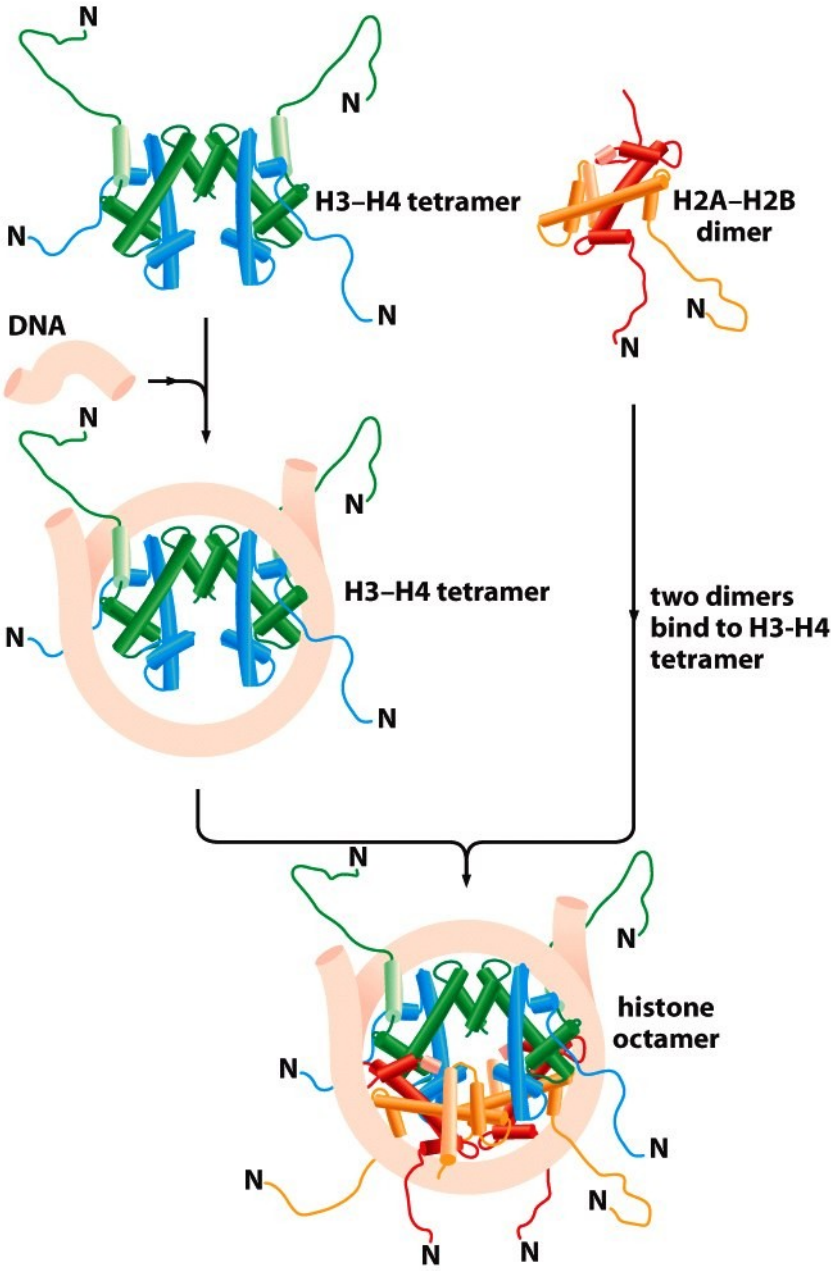
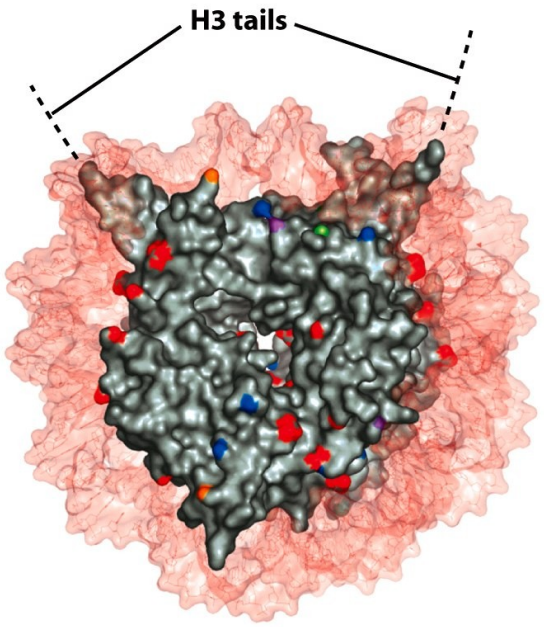
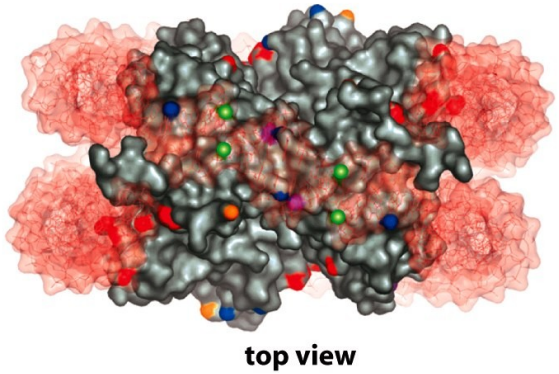


Figure 4.38 How Proteins Work (©2012 Garland Science)

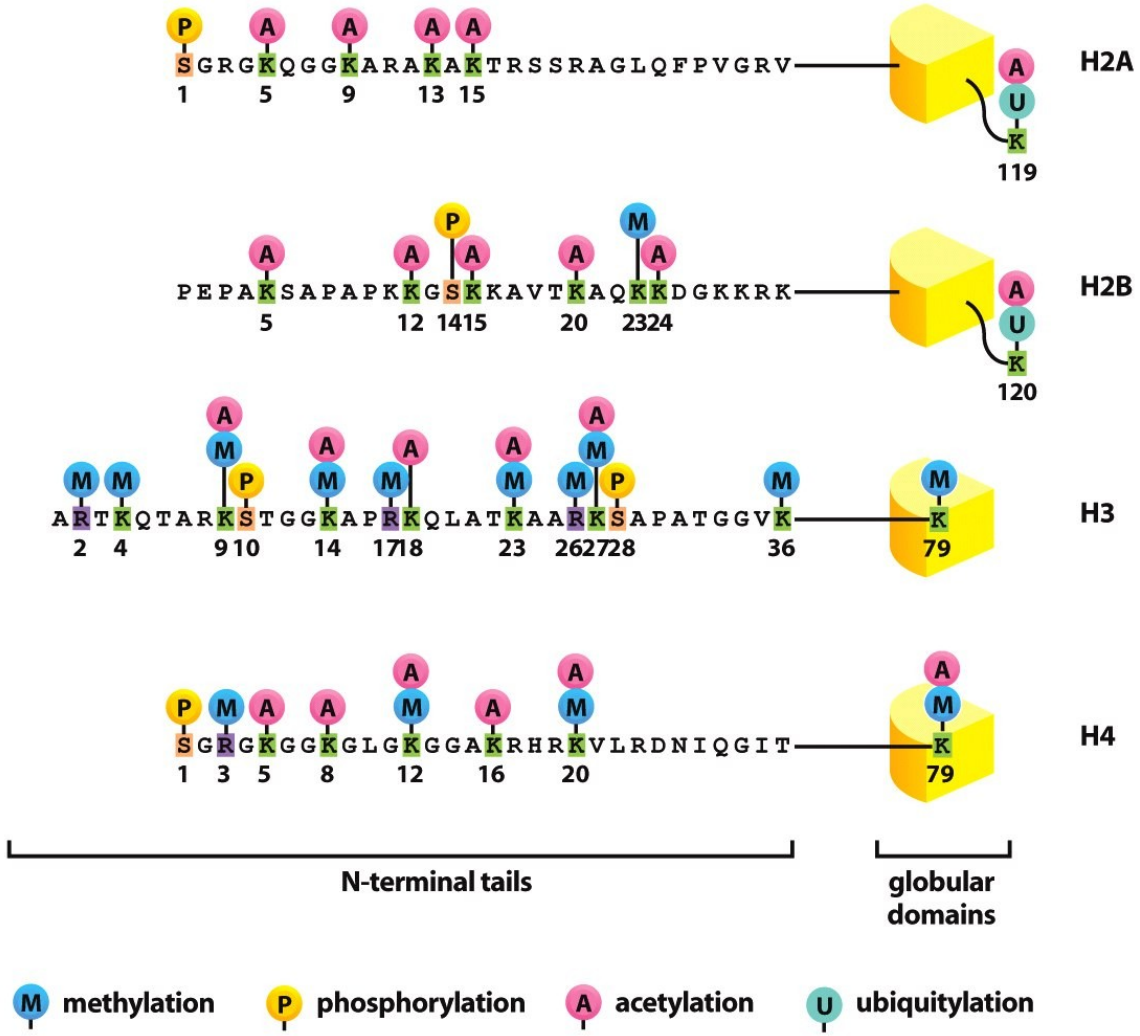


Modification

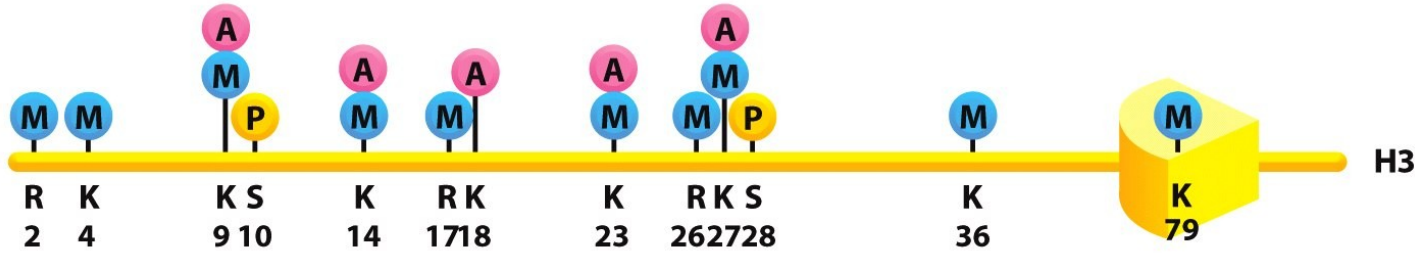


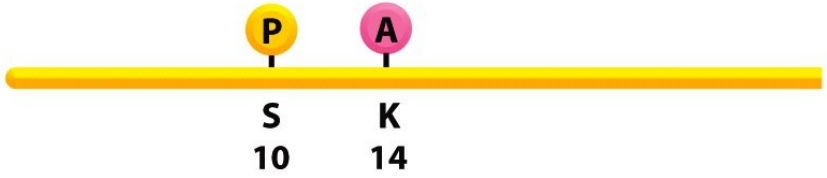


- acetylation
- methylation
- phosphorylation
- ubiquitylation
- acetylation or methylation



Effects



modification state	"meaning"
	heterochromatin formation, gene silencing
	gene expression
	gene expression
	silencing of Hox genes, X chromosome inactivation

effects

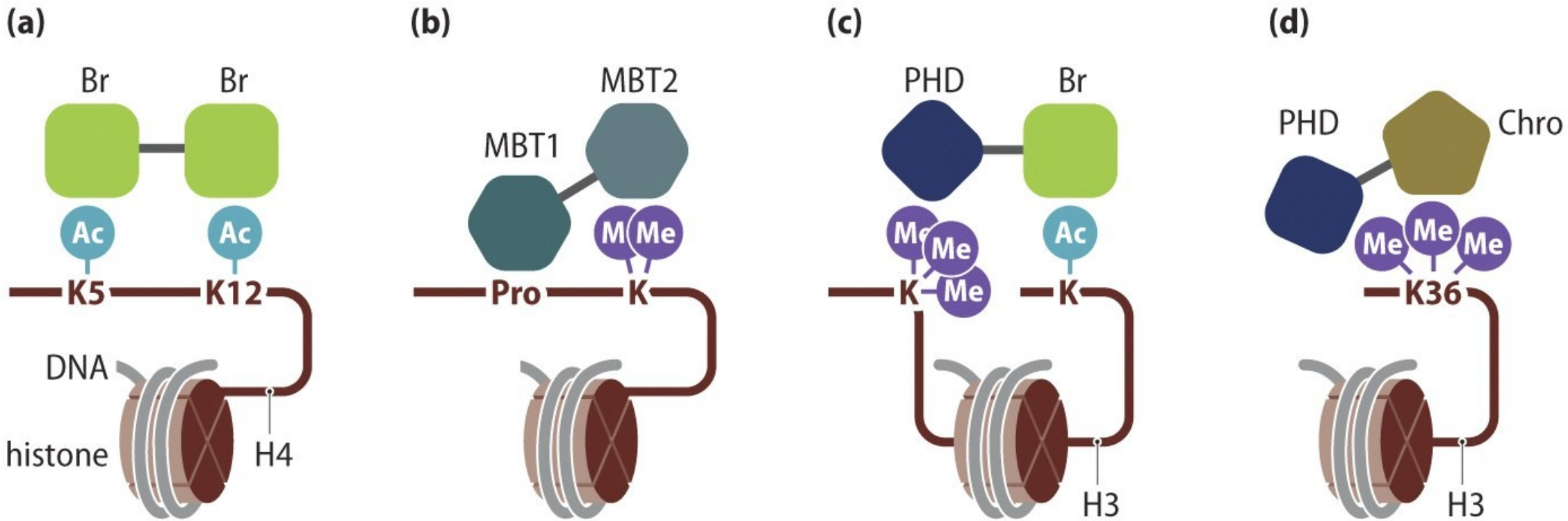


Figure 4.39 How Proteins Work (©2012 Garland Science)

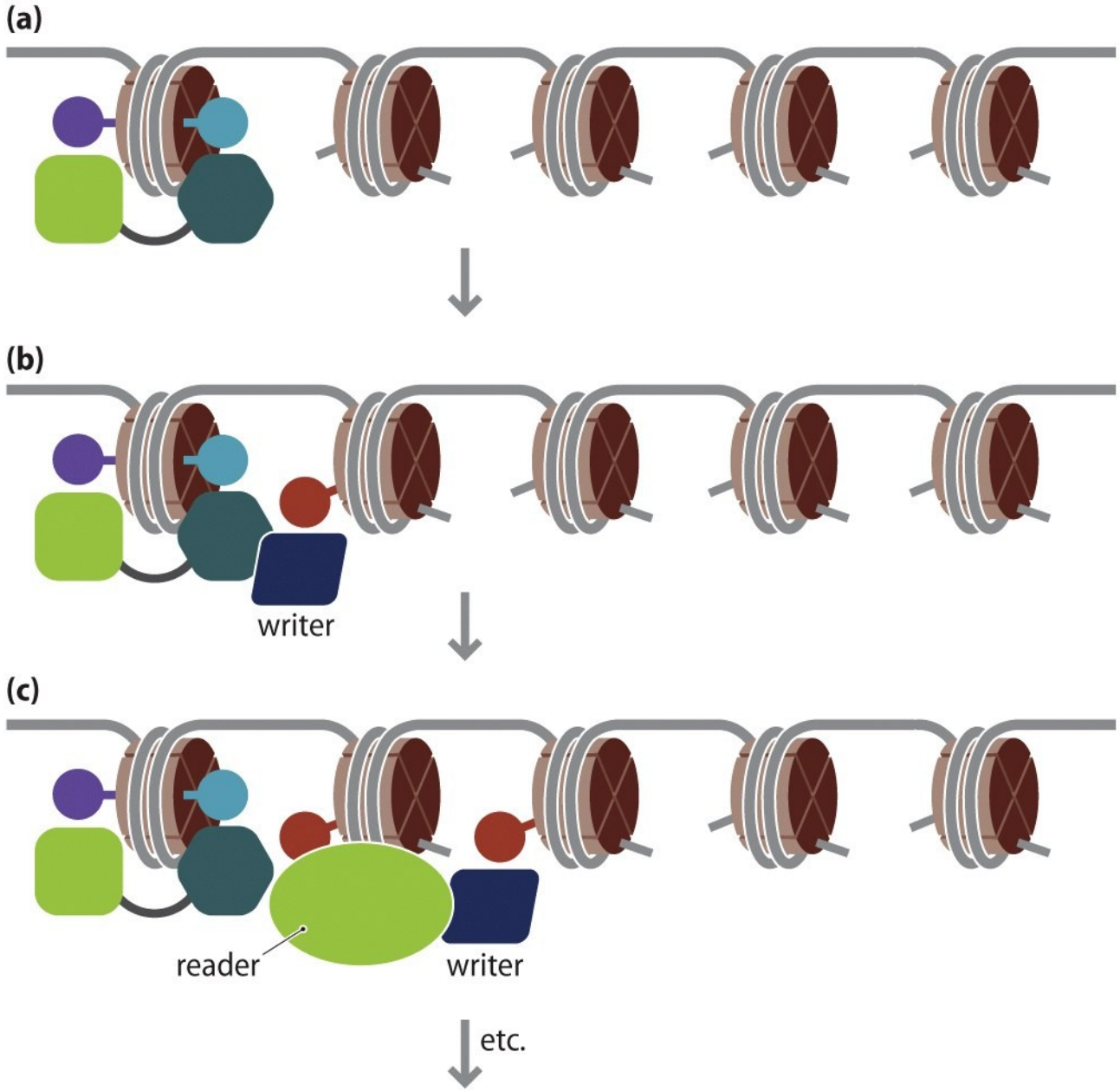
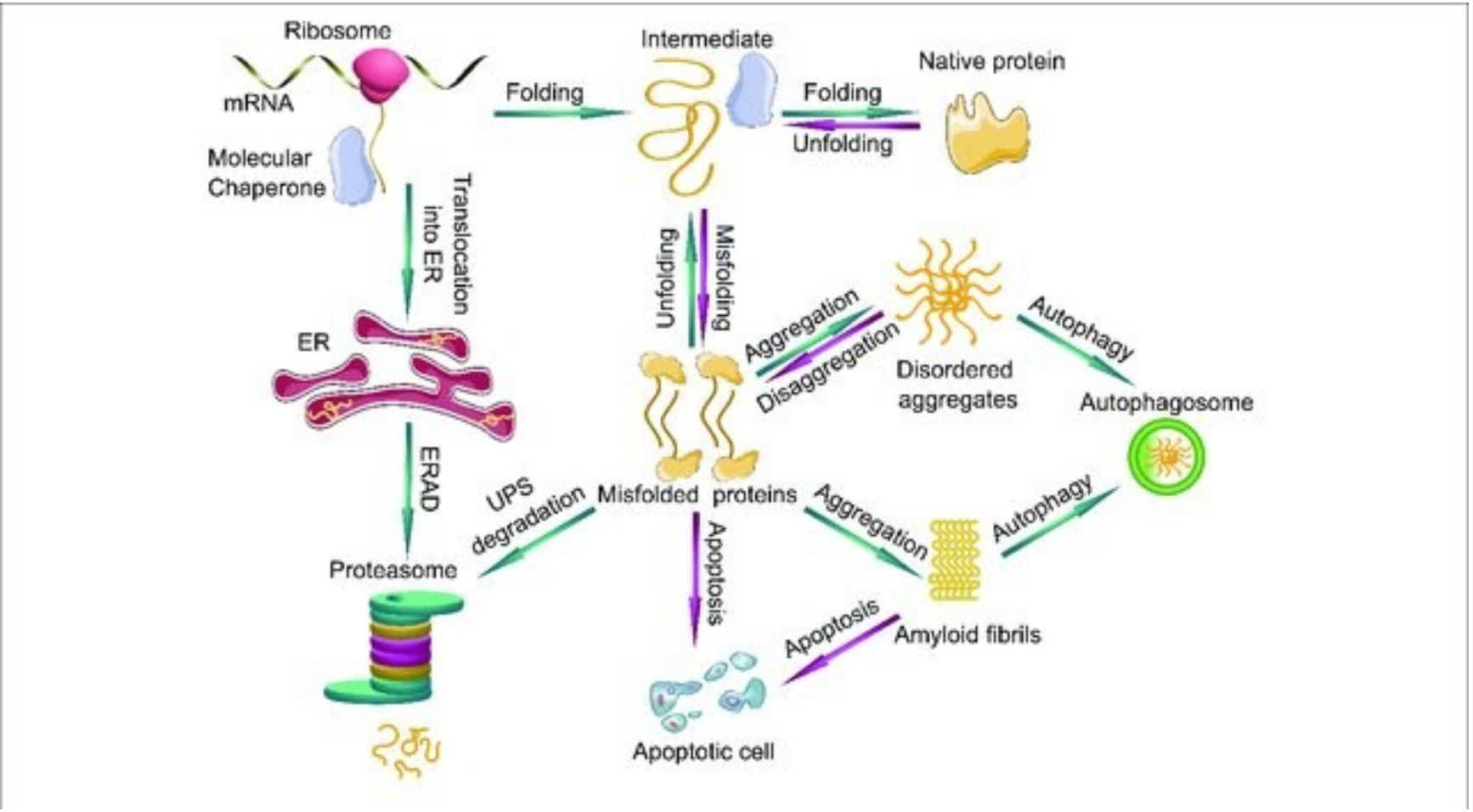


Figure 4.40 How Proteins Work (©2012 Garland Science)

Protein quality control



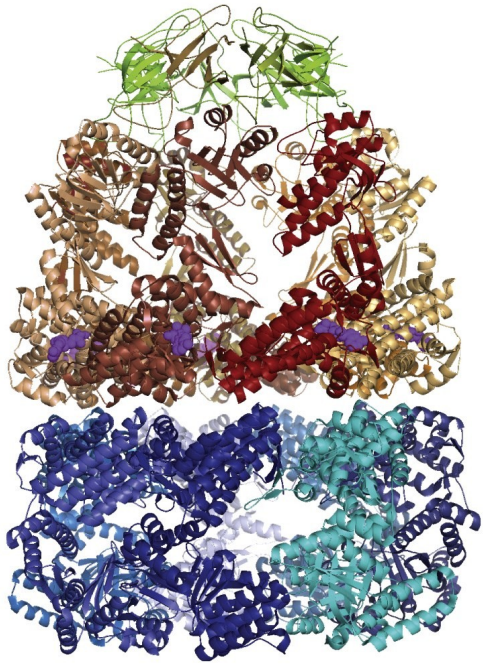


Figure 4.12.1 How Proteins Work (©2012 Garland Science)

Frontiers in Cell and Developmental Biology 8:425

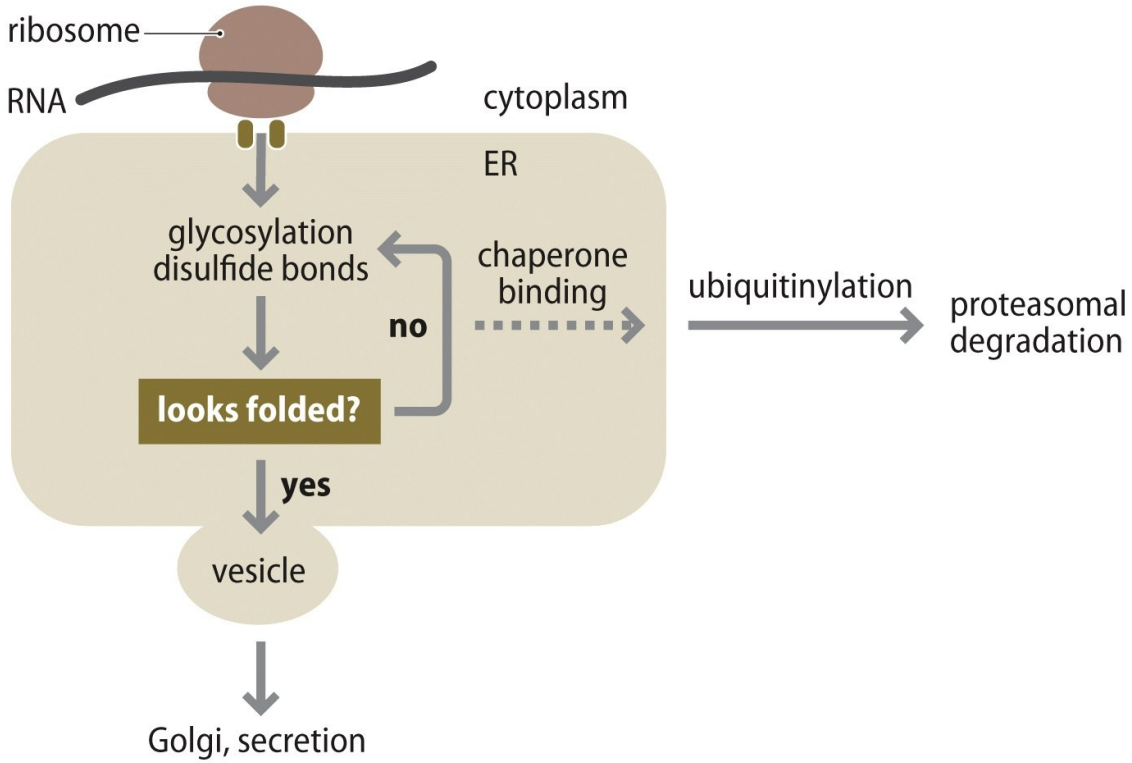


Figure 4.41 How Proteins Work (©2012 Garland Science)

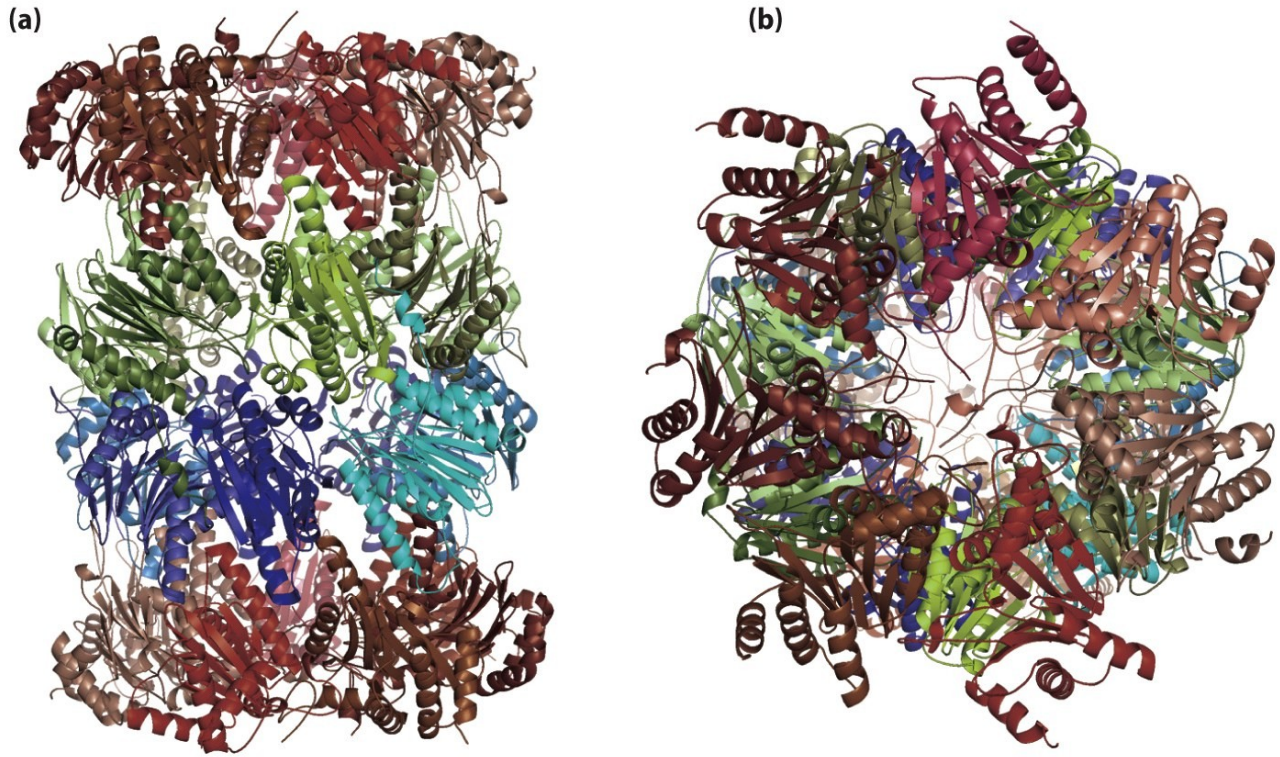
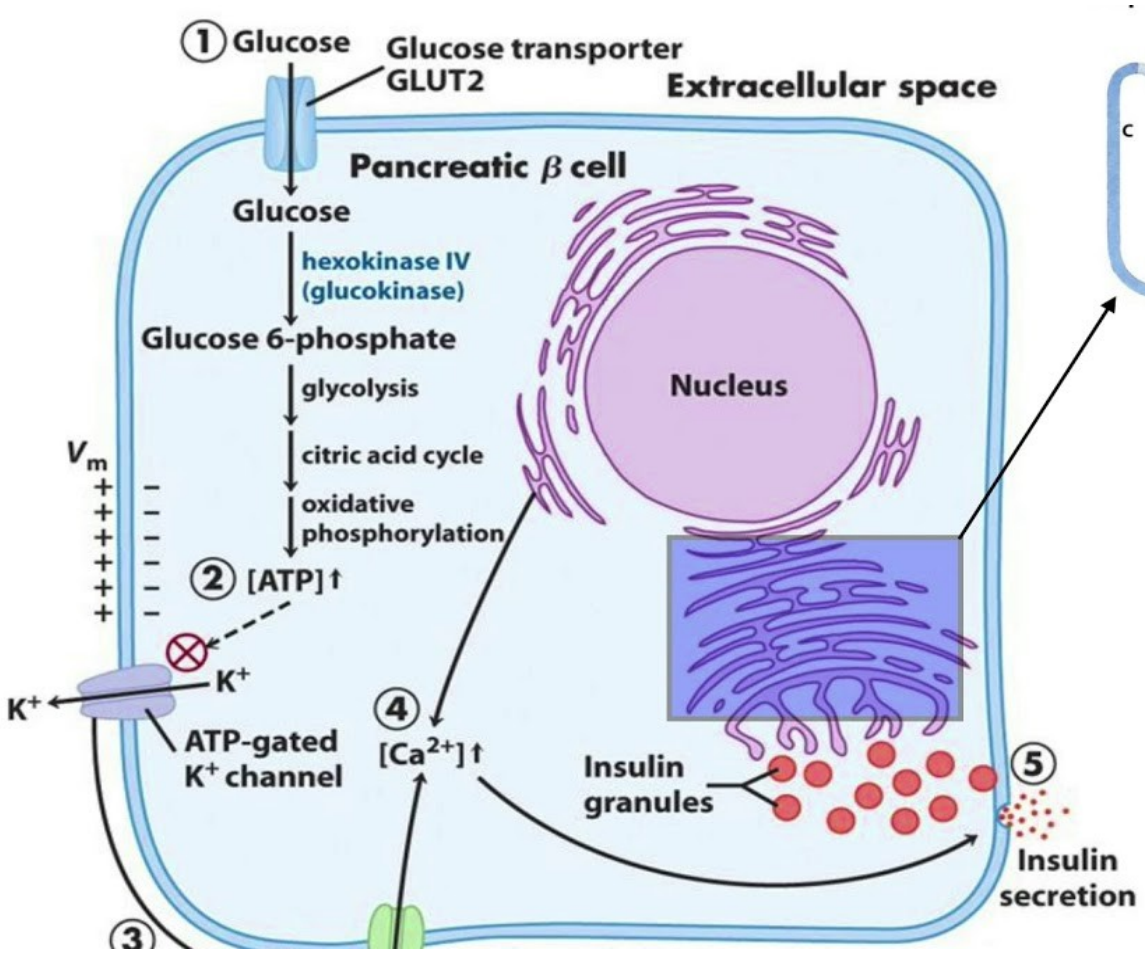
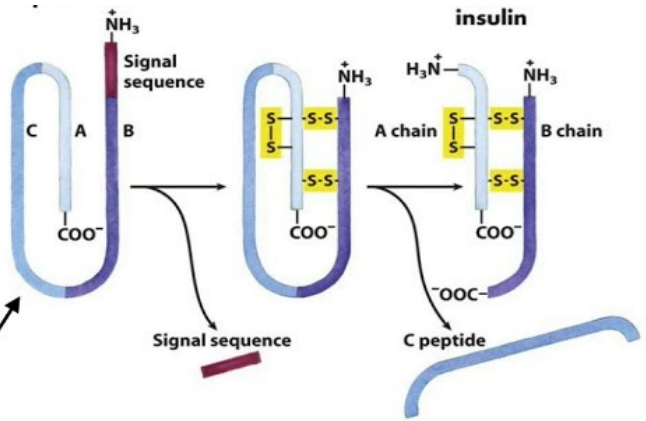


Figure 4.13.1 How Proteins Work (©2012 Garland Science)

Pancreatic β cells





- In pancreatic **β-cells**, glucose release requires **Ca^{2+} influx**.
- **Low** blood glucose:
  - ↓ATP → ↑K^+ efflux → ↑hyperpolarization → ↓Ca^{2+} influx → ↓insulin secretion
- **Elevated** blood glucose
  - ↑ATP → ↓K^+ efflux →

self-splicing polypeptides

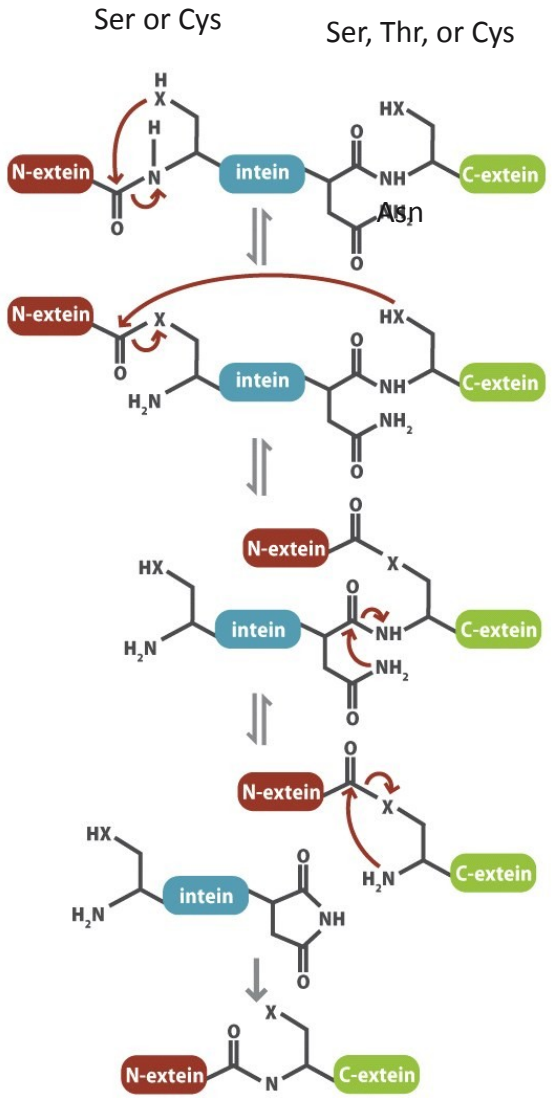


Figure 4.10.1 How Proteins Work (©2012 Garland Science)

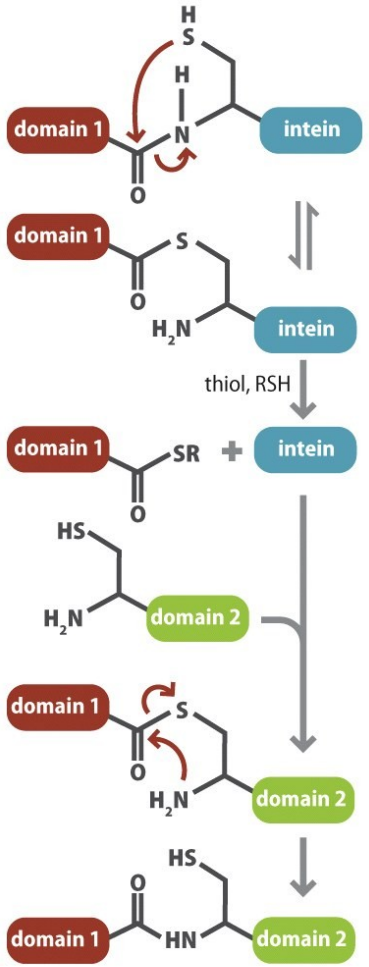
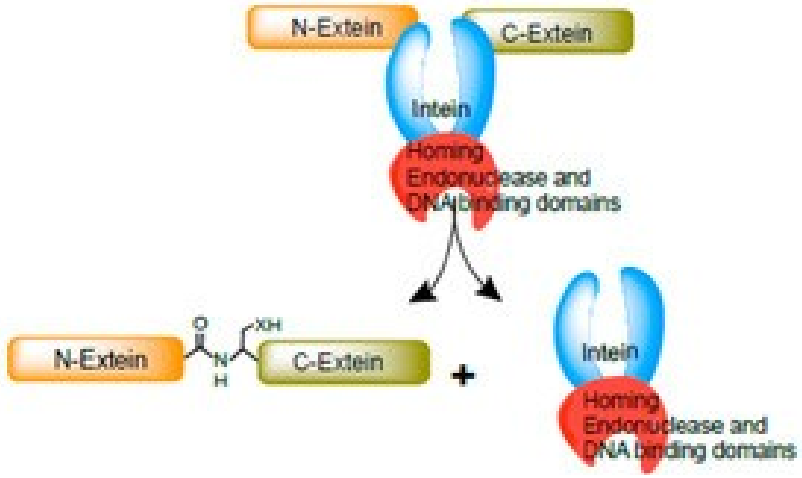


Figure 4.10.2 How Proteins Work (©2012 Garland Science)

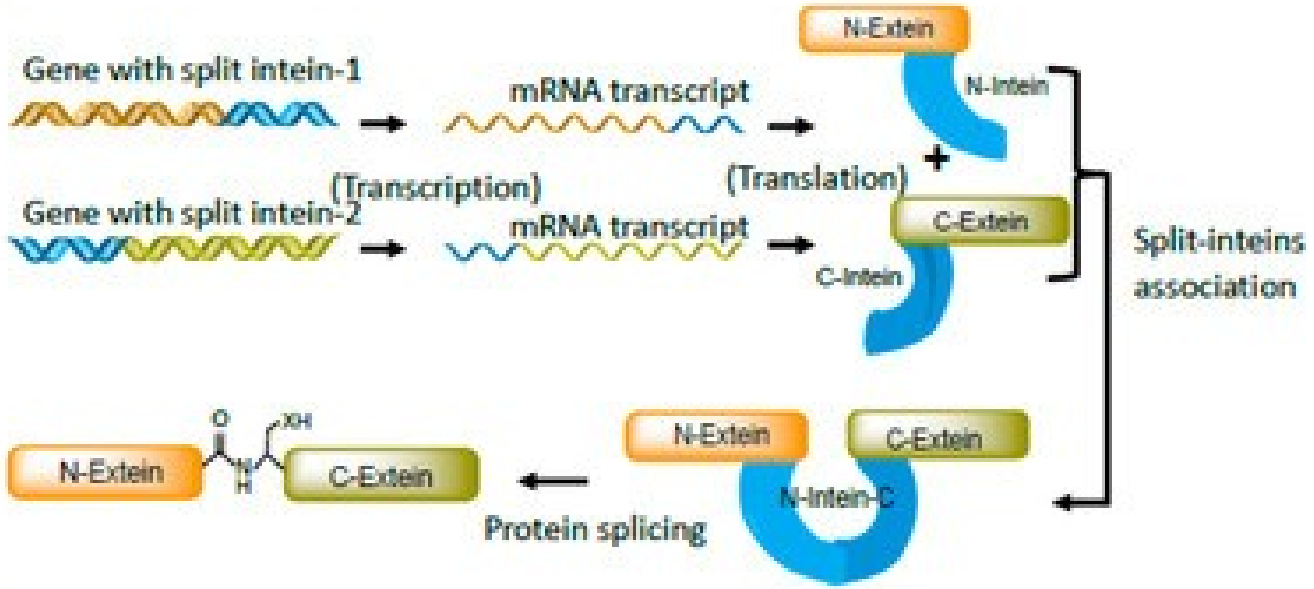
A biotechnological application of inteins. the fusion of domain 1 with an intein (created genetically by fusing the genes) is induced to self-cleave by addition of an external thiol, RSH.

The thioester thus formed is subsequently cleaved by a second domain starting in a cysteine, to give a two-domain protein.

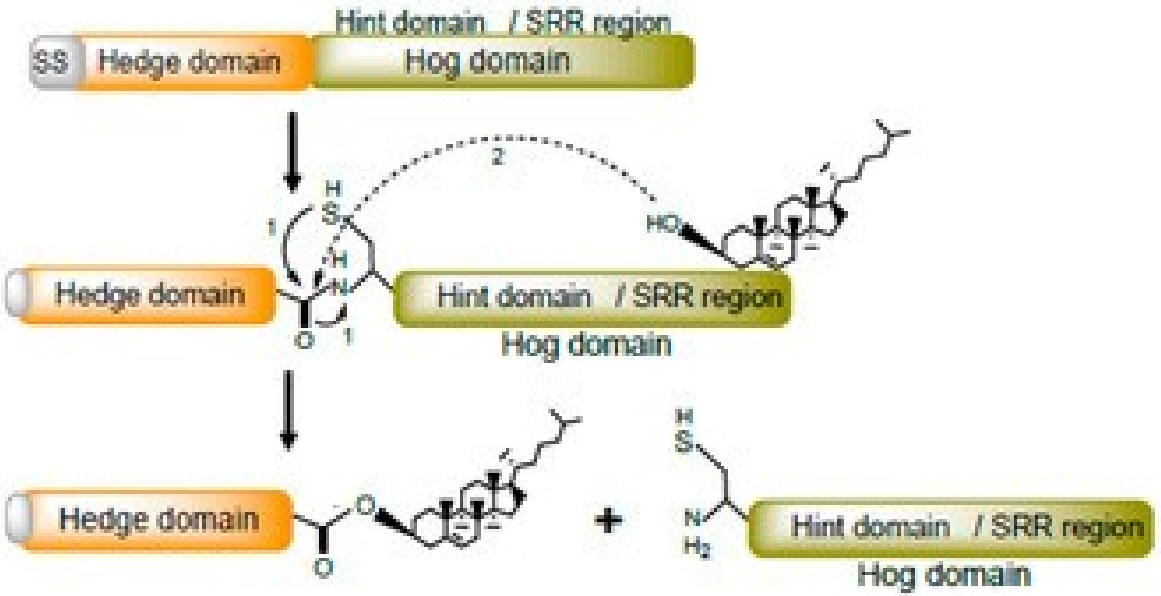
A)


N-Extein
C-Extein
Intein
Homing Endonuclease and DNA binding domains
N-Extein
C-Extein
+
Intein
Homing Endonuclease and DNA binding domains

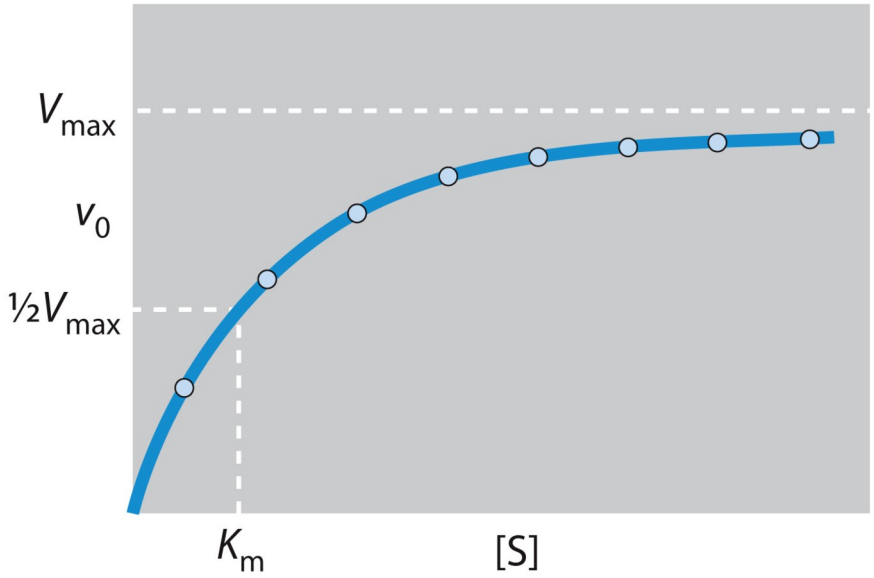
B)


Gene with split intein-1
mRNA transcript
N-Extein
N-Intein
(Transcription)
(Translation)
+
Gene with split intein-2
mRNA transcript
C-Extein
C-Intein
Split-inteins association
N-Extein
C-Extein
N-Extein
C-Extein
N-Intein-C
Protein splicing

C)


Hint domain / SRR region
SS
Hedge domain
Hog domain
Hedge domain
Hint domain / SRR region
Hog domain
Hedge domain
+
Hint domain / SRR region
Hog domain

Catalysis



free energy profiles of uncatalyzed and enzyme-catalyzed reactions

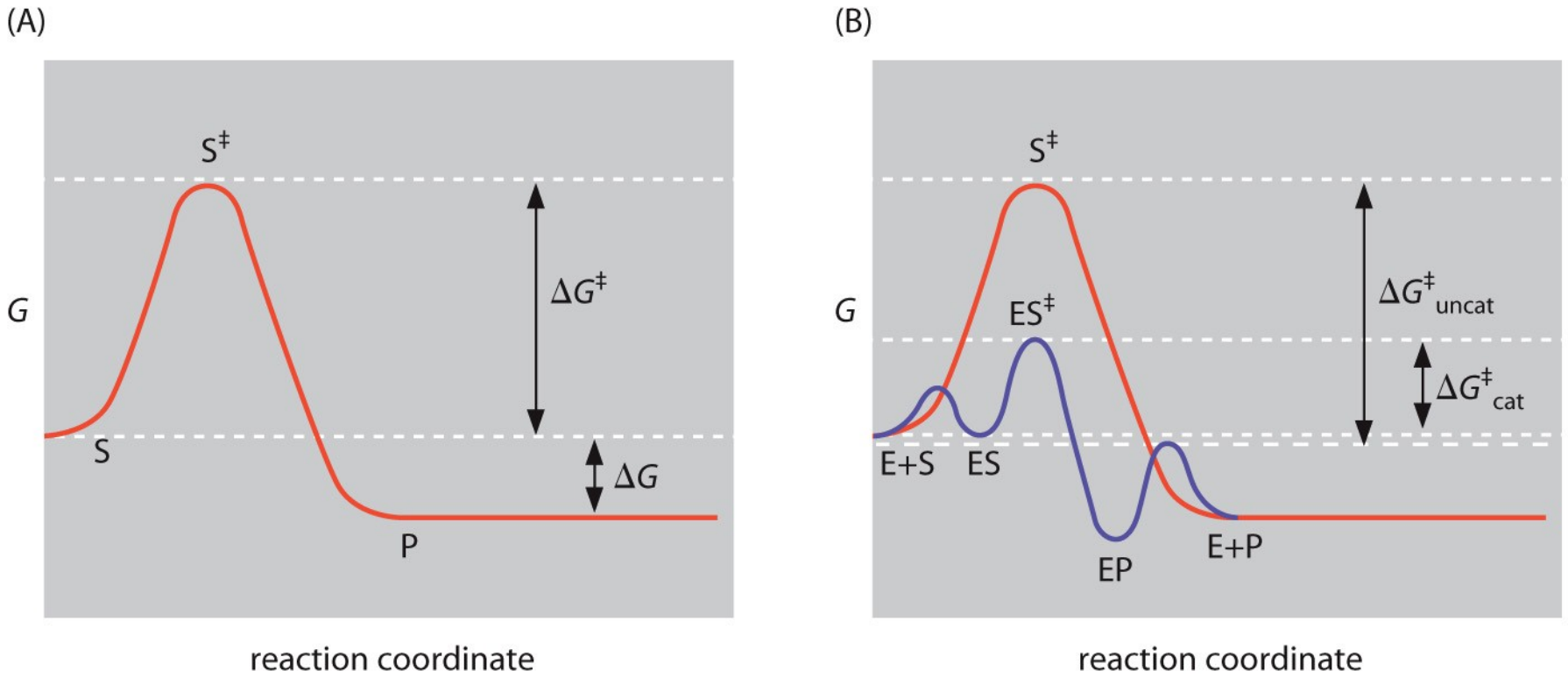
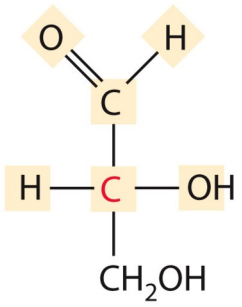
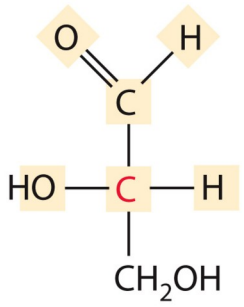


Figure 1.28 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

isomer



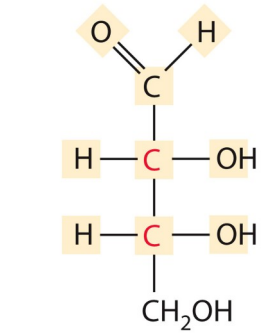
D-(+)-glyceraldehyde



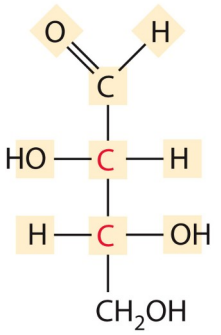
L-(–)-glyceraldehyde

Figure 1.1.1 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

enantiomer



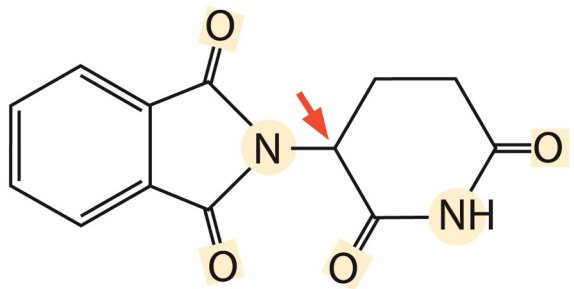
D-erythrose



D-threose

Figure 1.1.2 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

diastereoisomer



thalidomide

Figure 1.1.3 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

catalytic mechanism of the pancreatic protease chymotrypsin

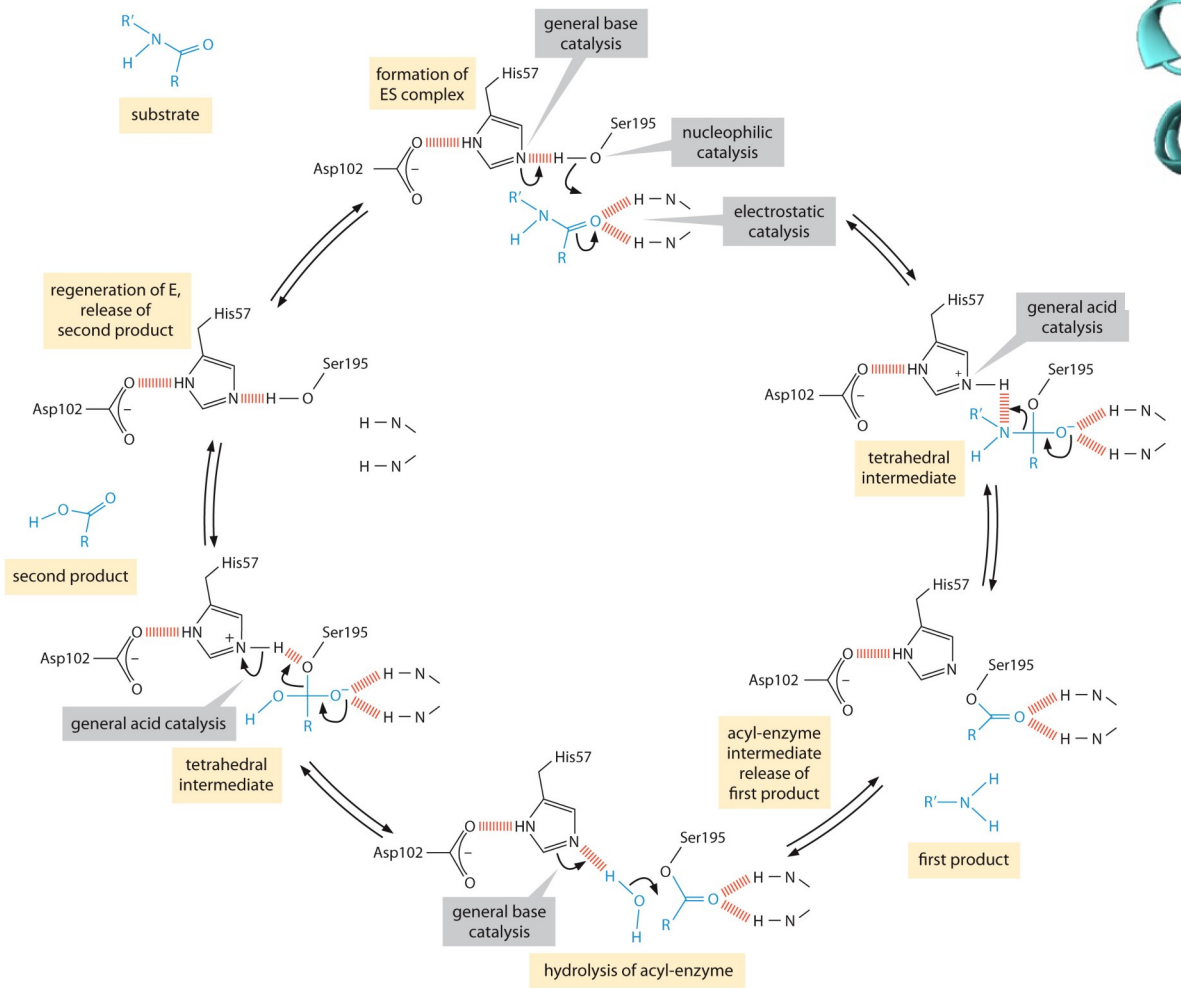
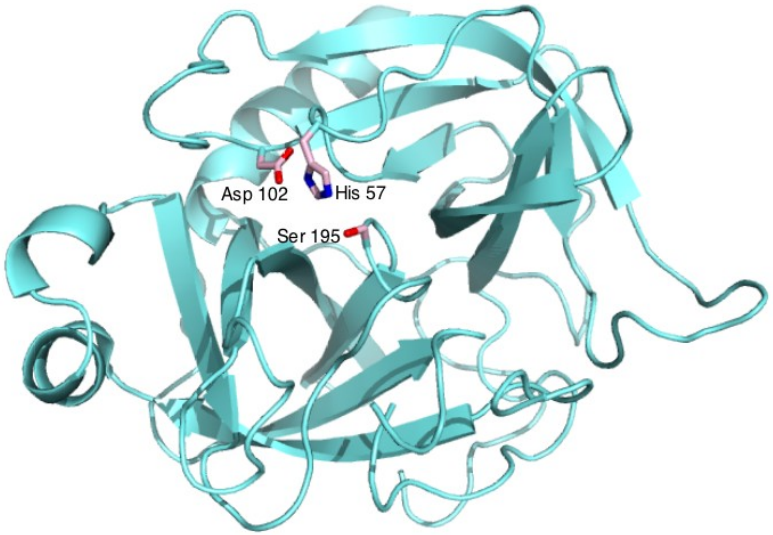


Figure 1.29 Molecular Biology of Assemblies and Machines (© Garland Science 2016)



Substrate specificity

selectivity

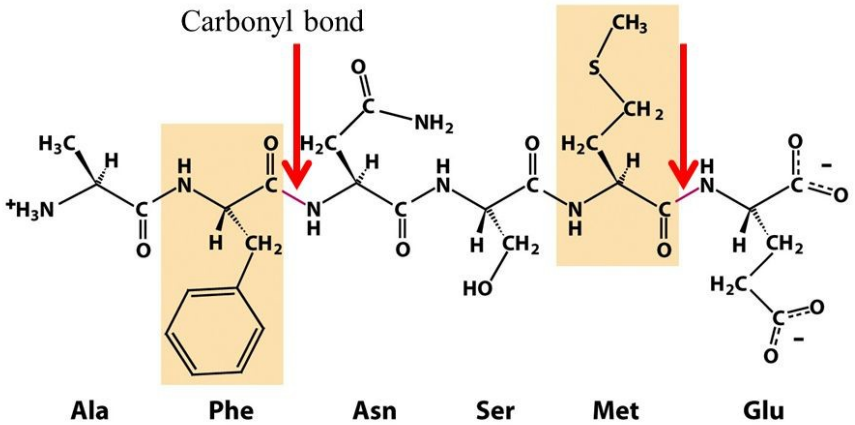
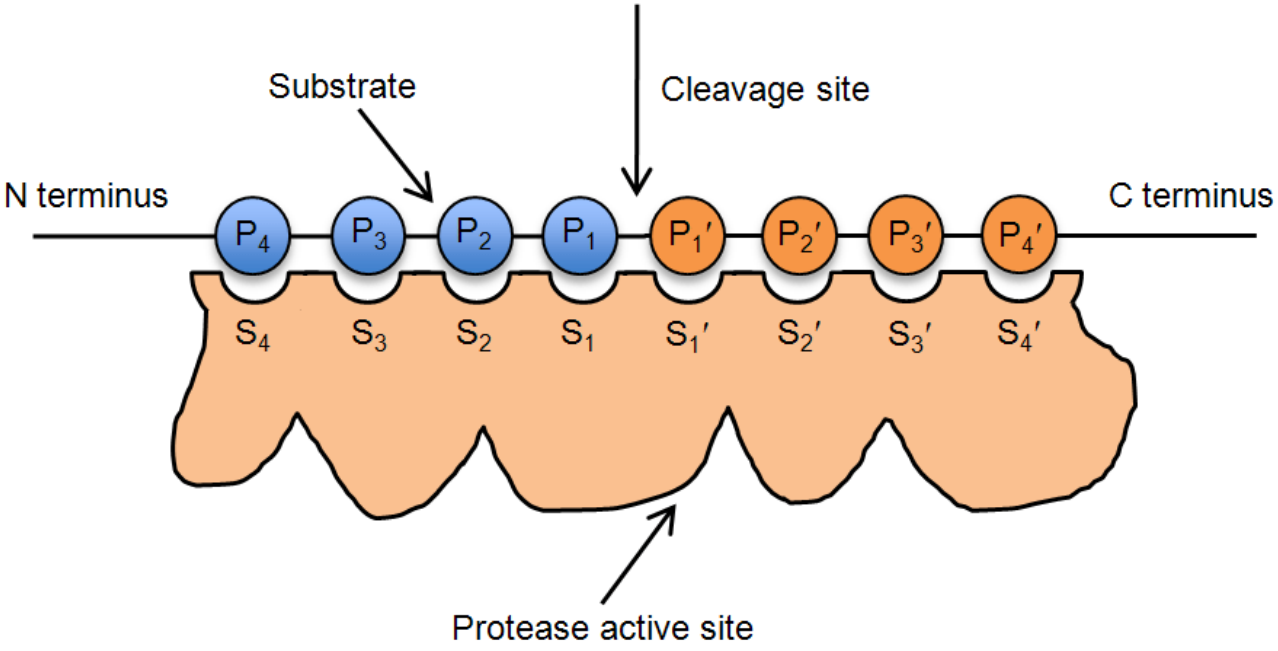
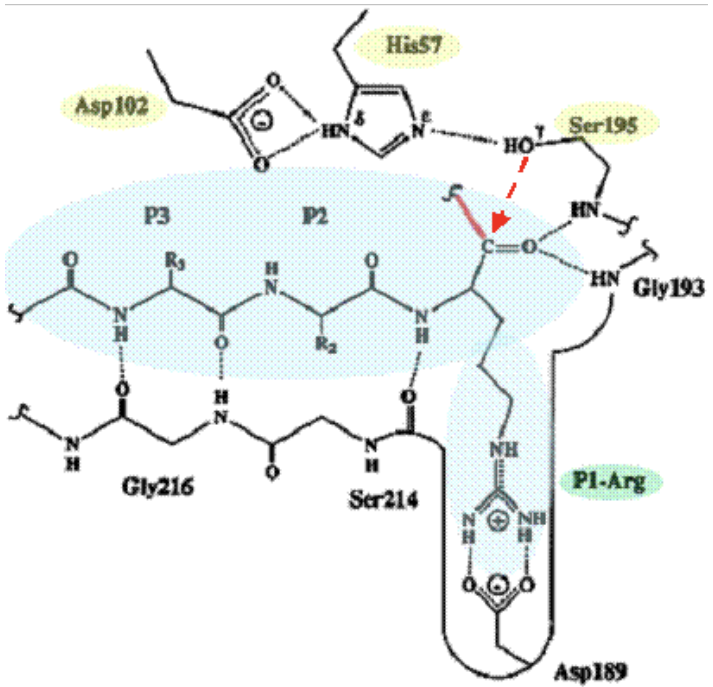


Figure 9-1
Biochemistry, Sixth Edition

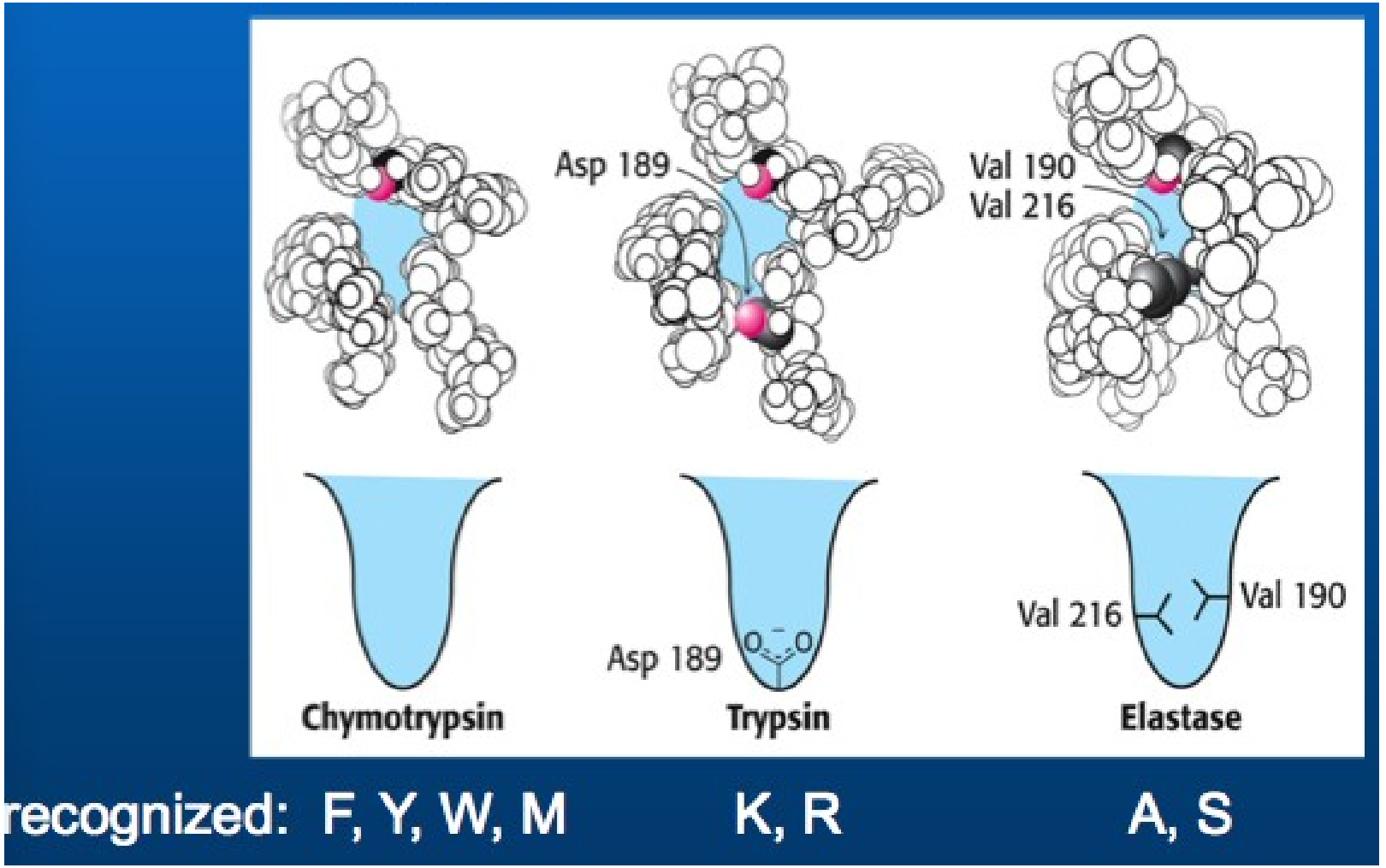
Hydrophobic amino acids





Pocket

F Phenylalanin, Y Tyrosin, W Tryptophan, M Methionine
K Lysine, R Arginine
A Alanine, S Serine



related serine peptidases

Specificity pocket mutations leading to acquisition of tryptic activity