

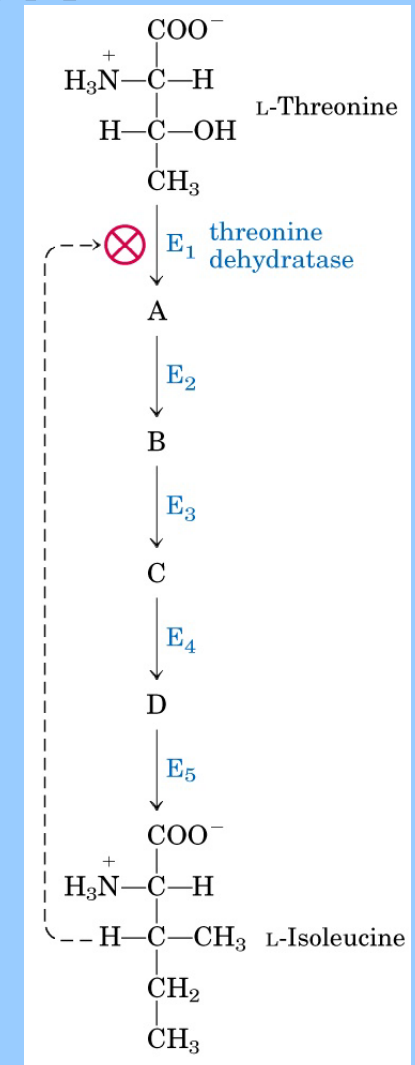
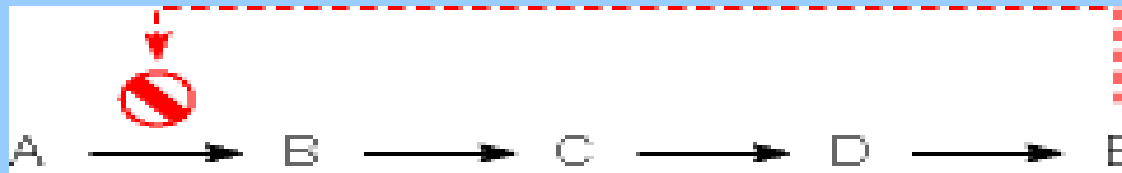
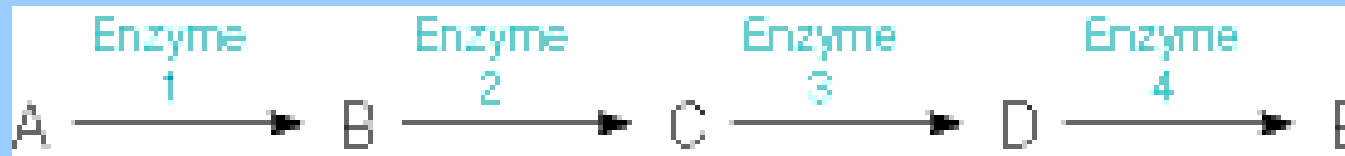
Regolazione dell'attività enzimatica

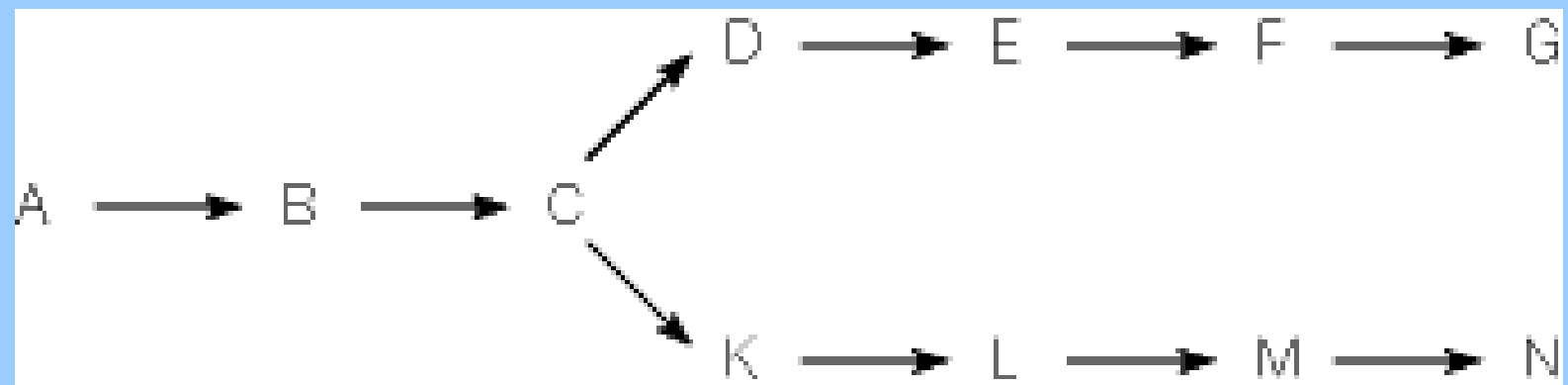
Enzimi regolatori

Enzimi allosterici

Enzimi modificati per modificazioni
covalenti reversibili

Inibizione a feedback

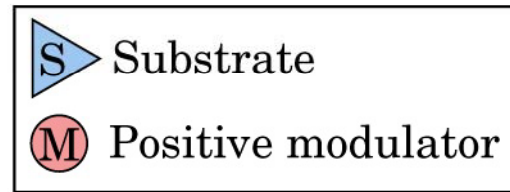
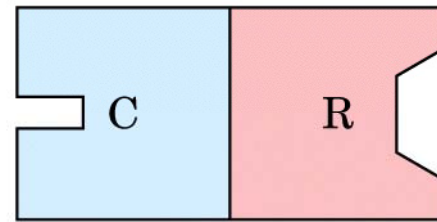




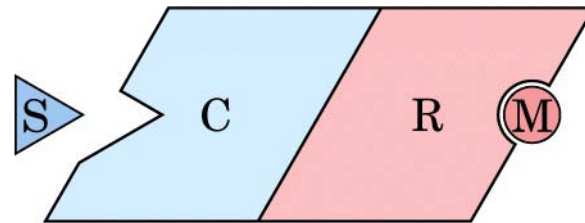
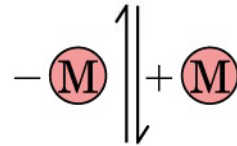
Enzimi allosterici

- L'attività degli enzimi allosterici (altra forma) è regolata mediante il legame non covalente e reversibile di composti regolatori chiamati modulatori allosterici (positivi o negativi –omotropici o eterotropici).

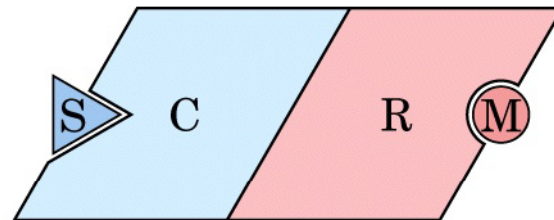




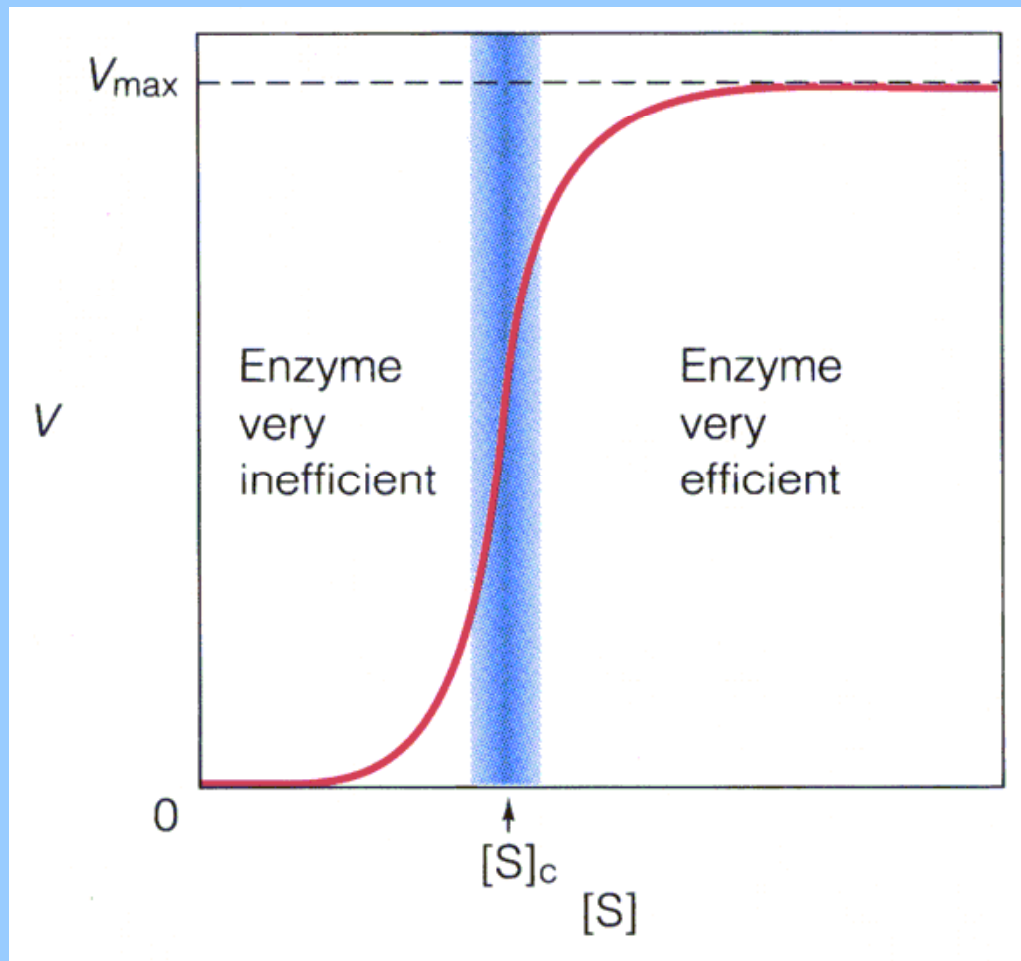
Less-active enzyme

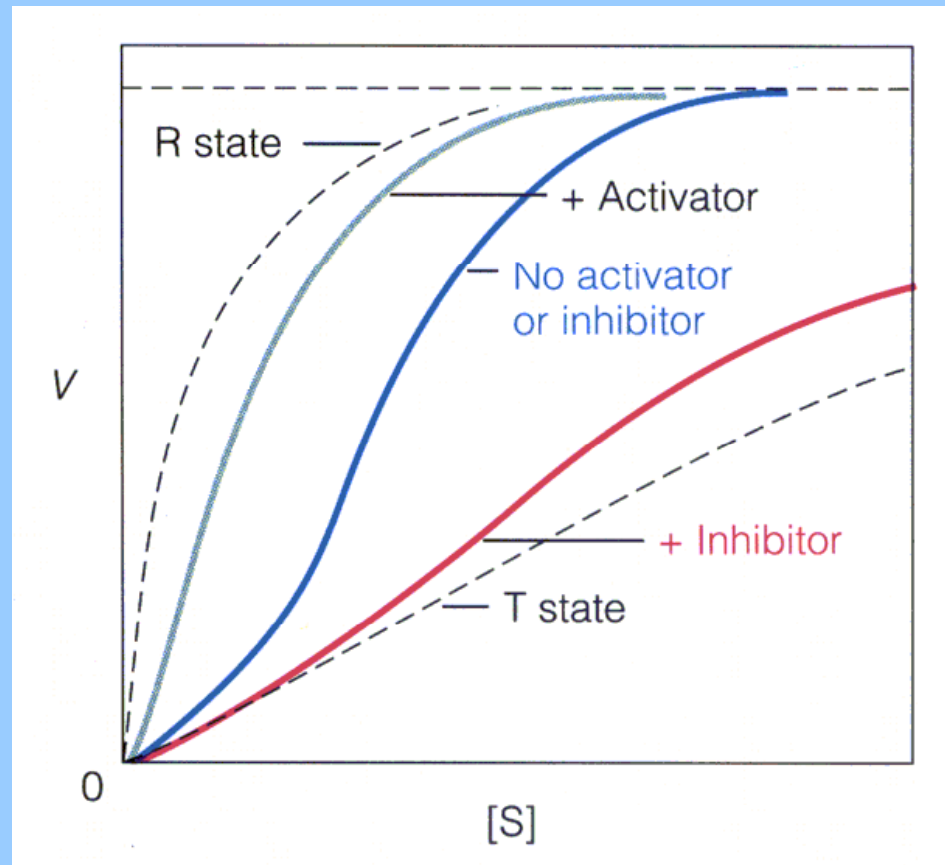


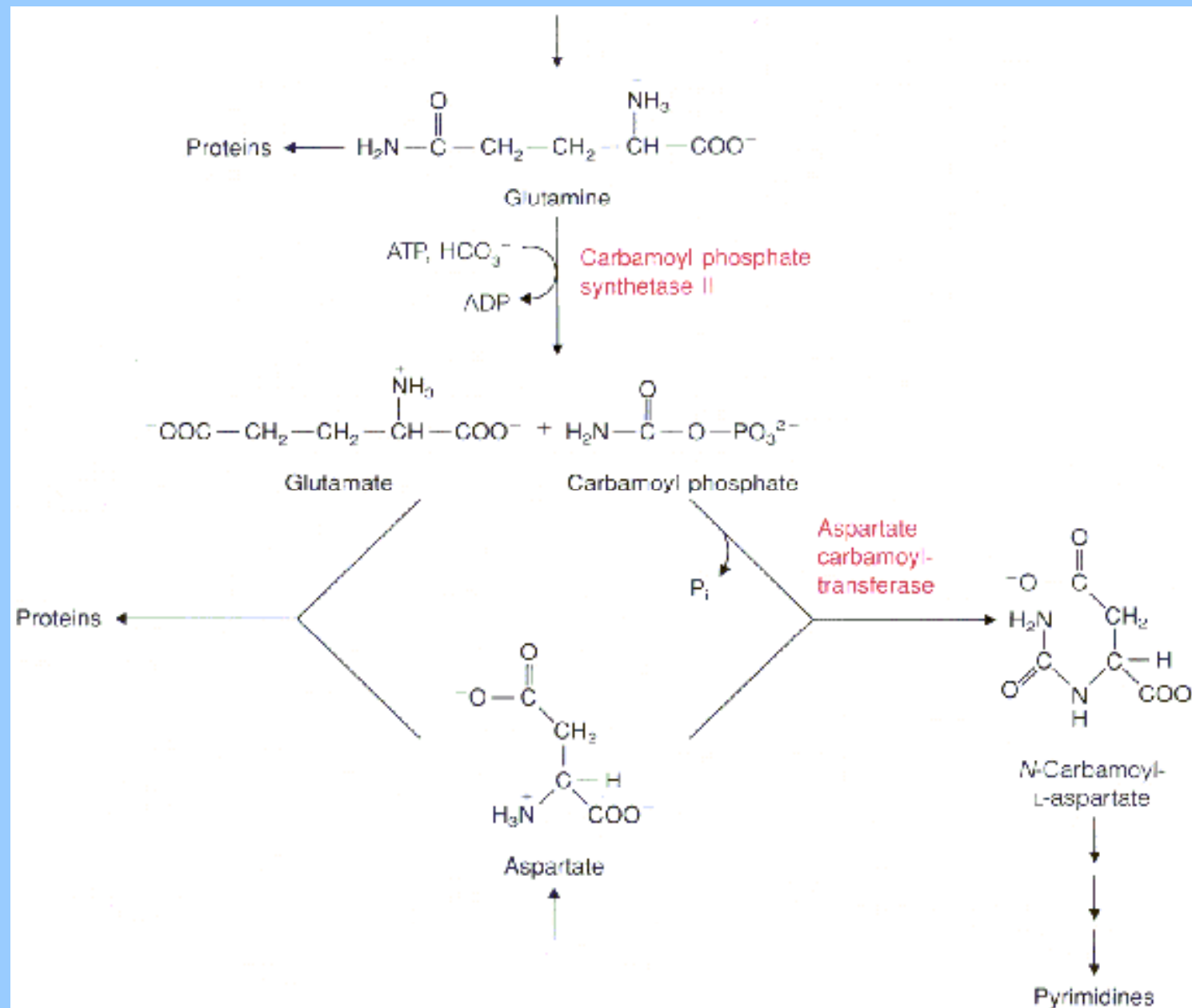
More-active enzyme

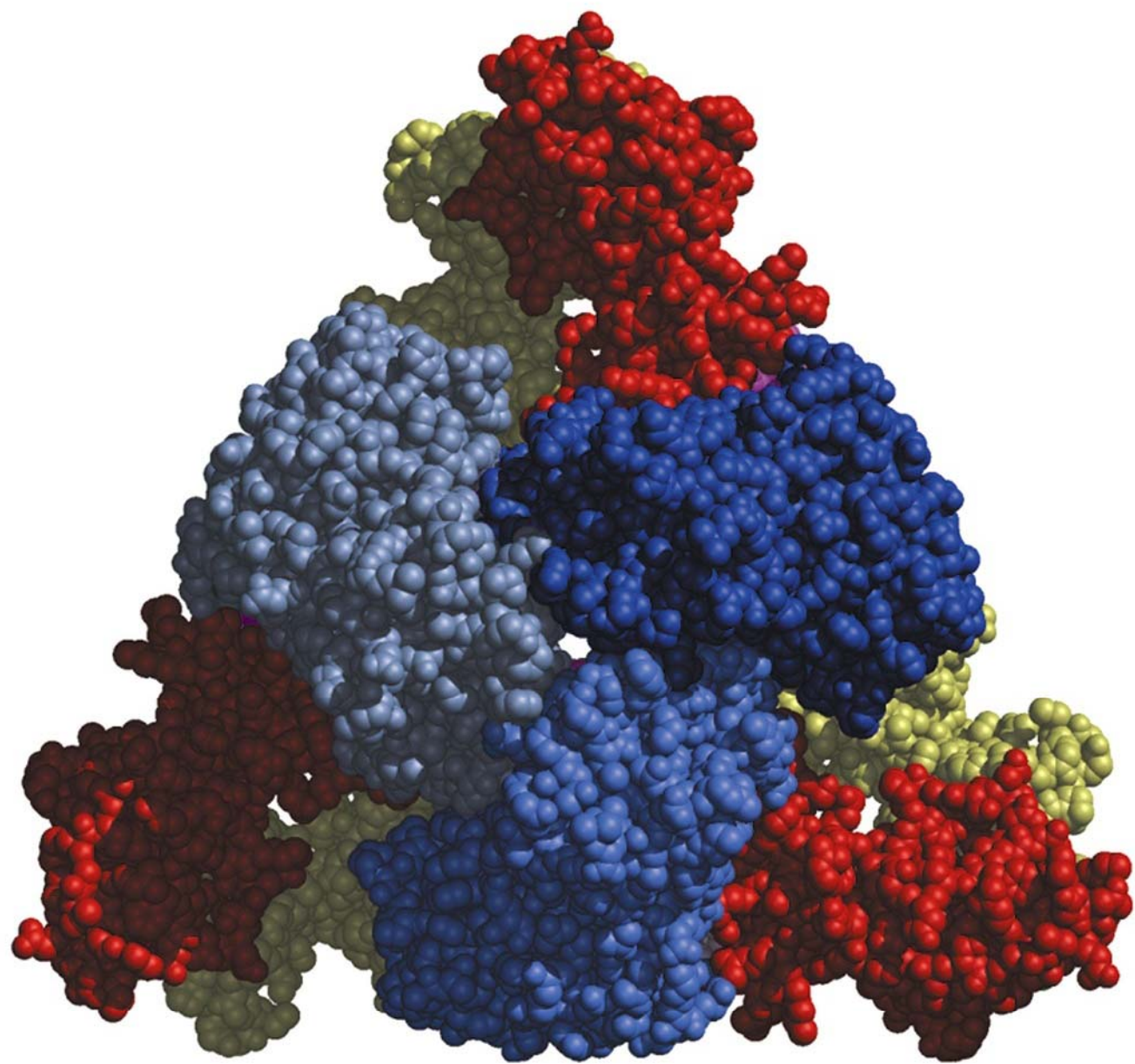


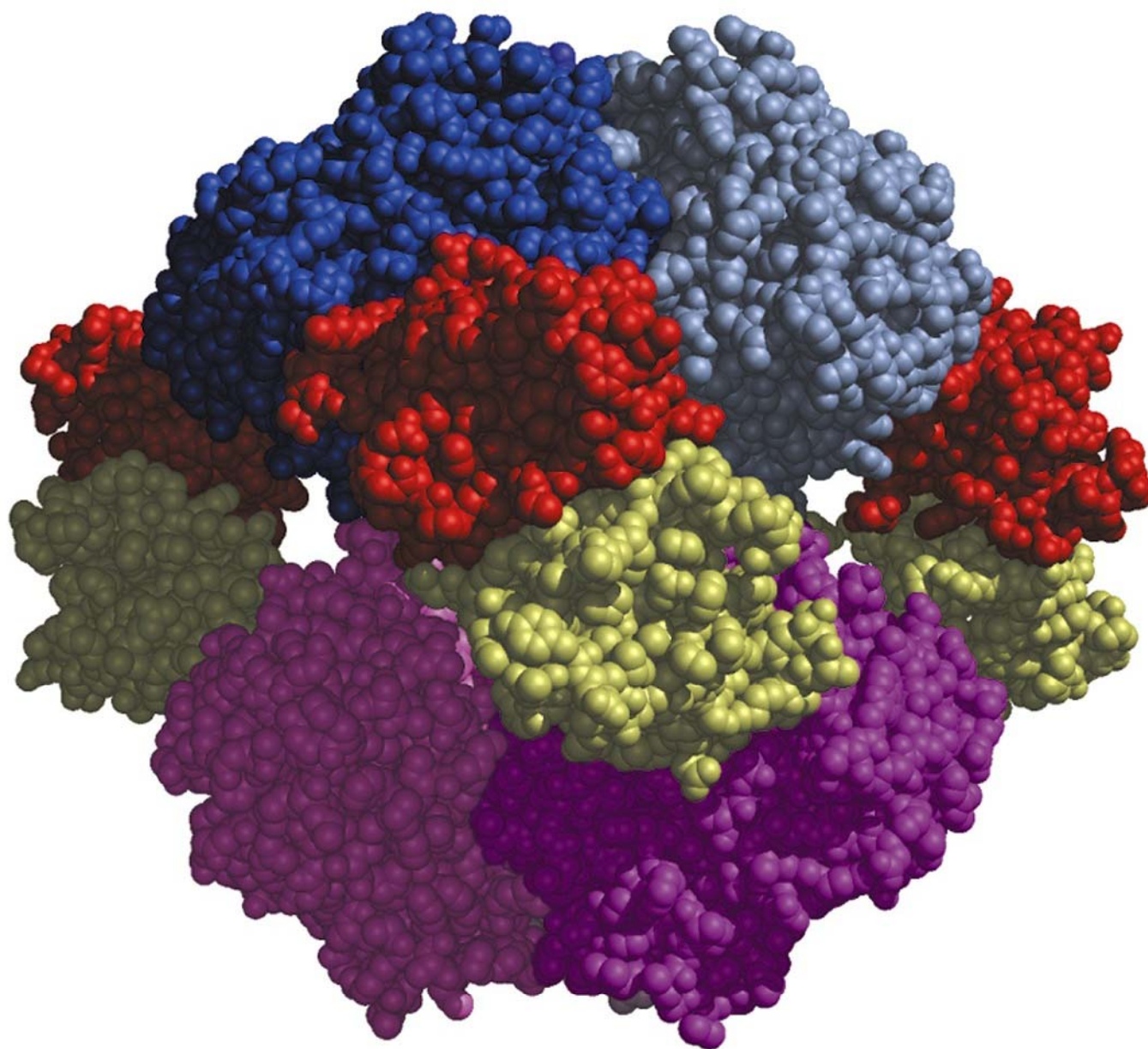
Active
enzyme-substrate
complex

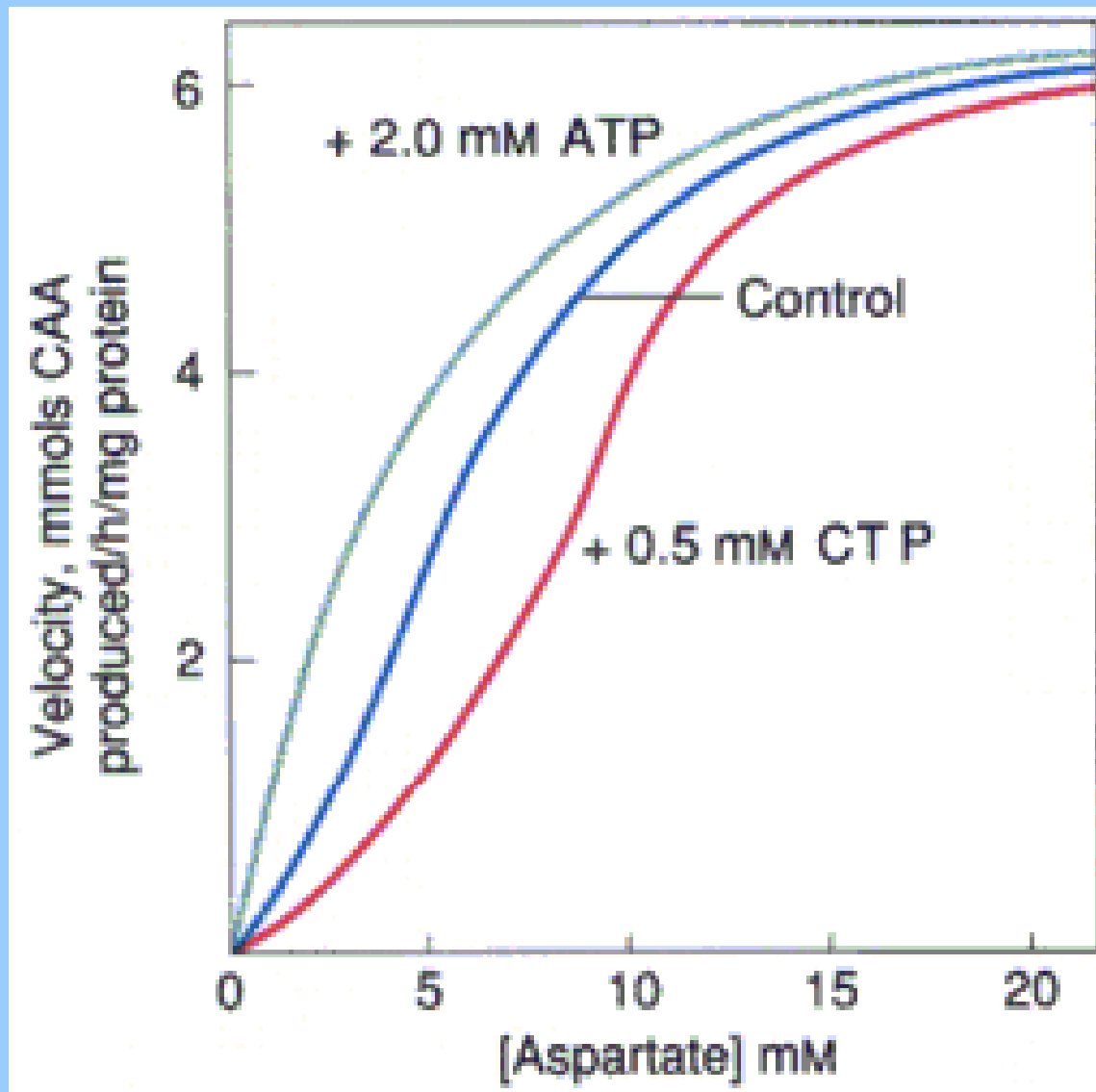


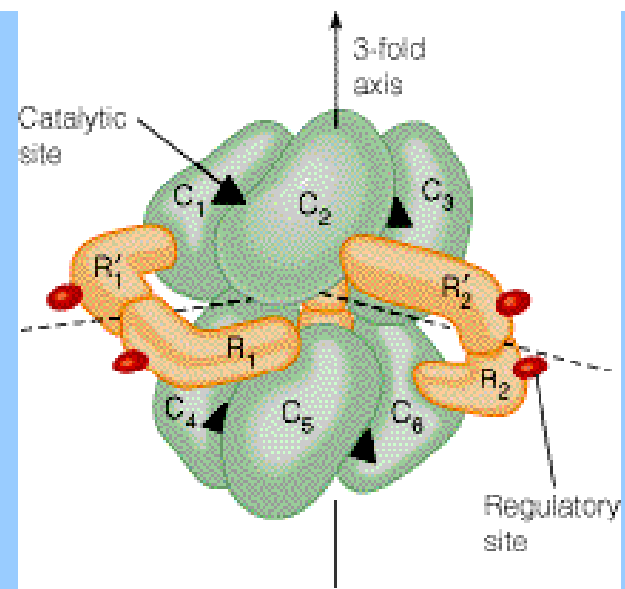




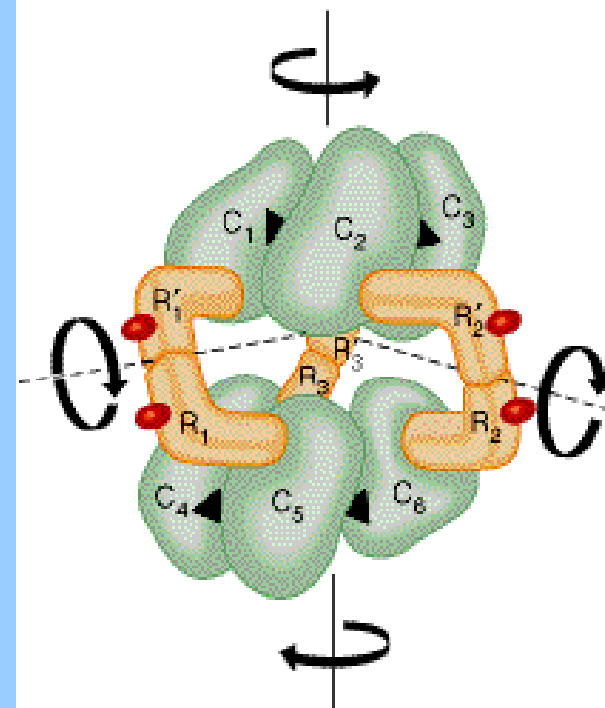




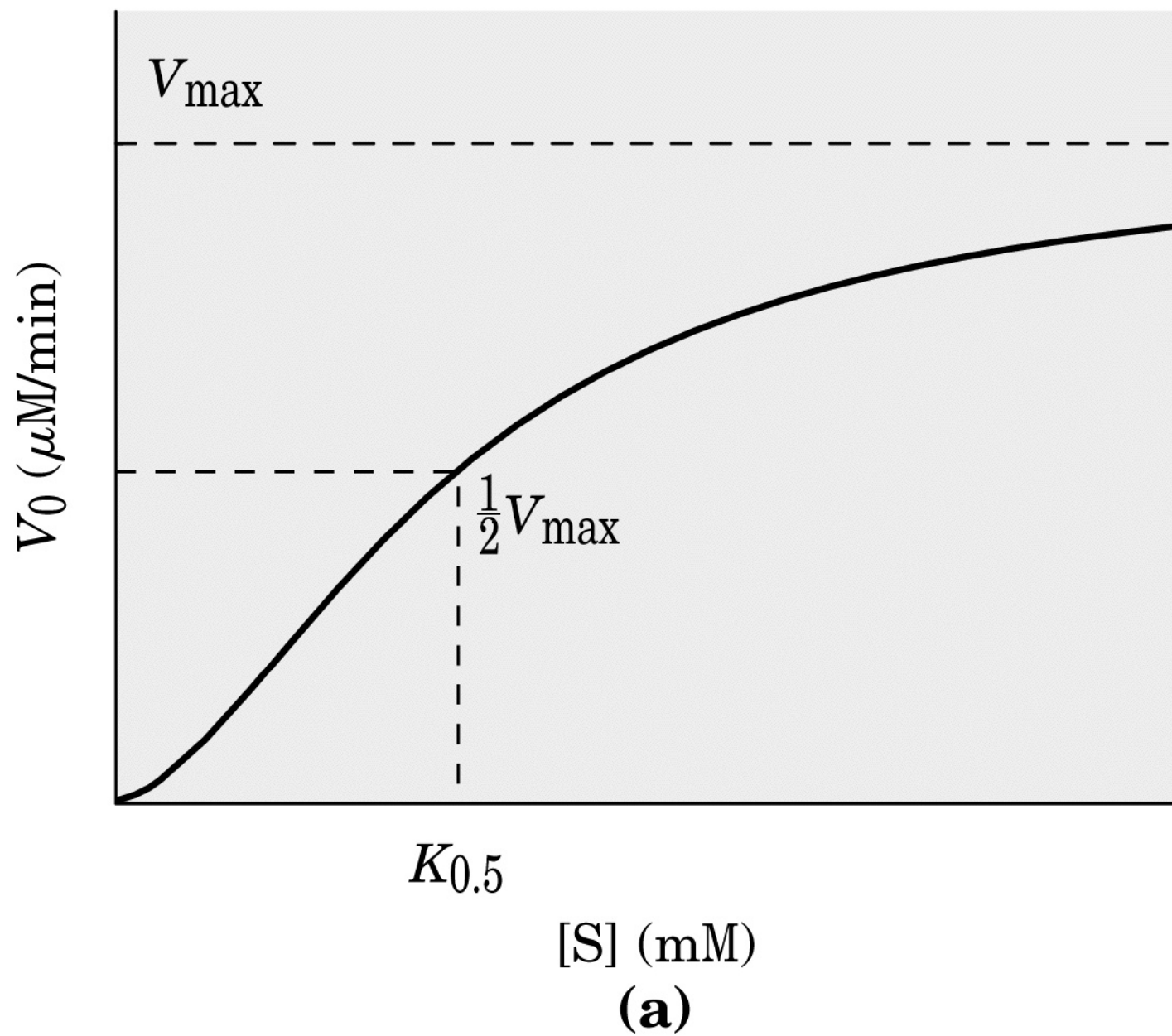


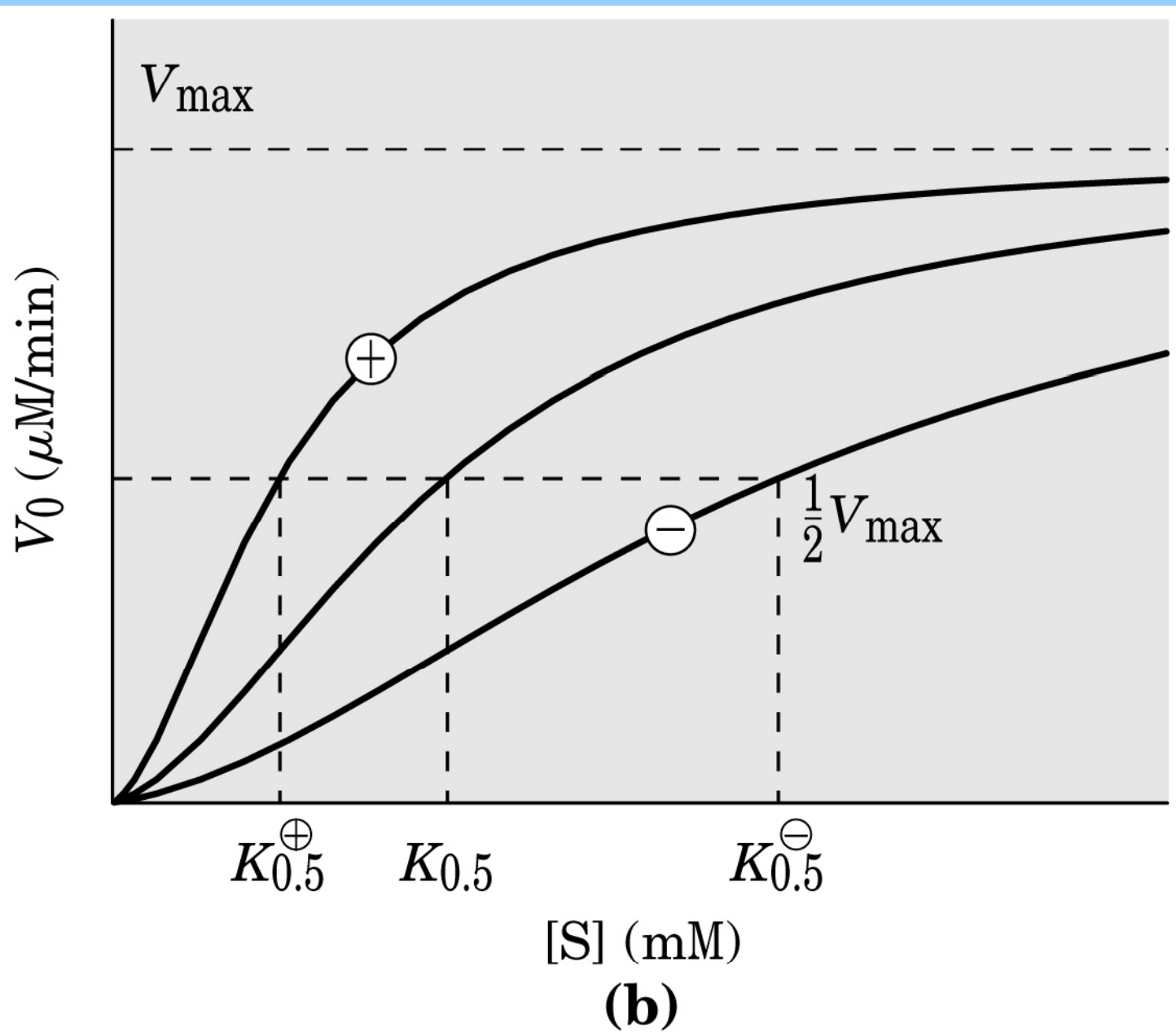


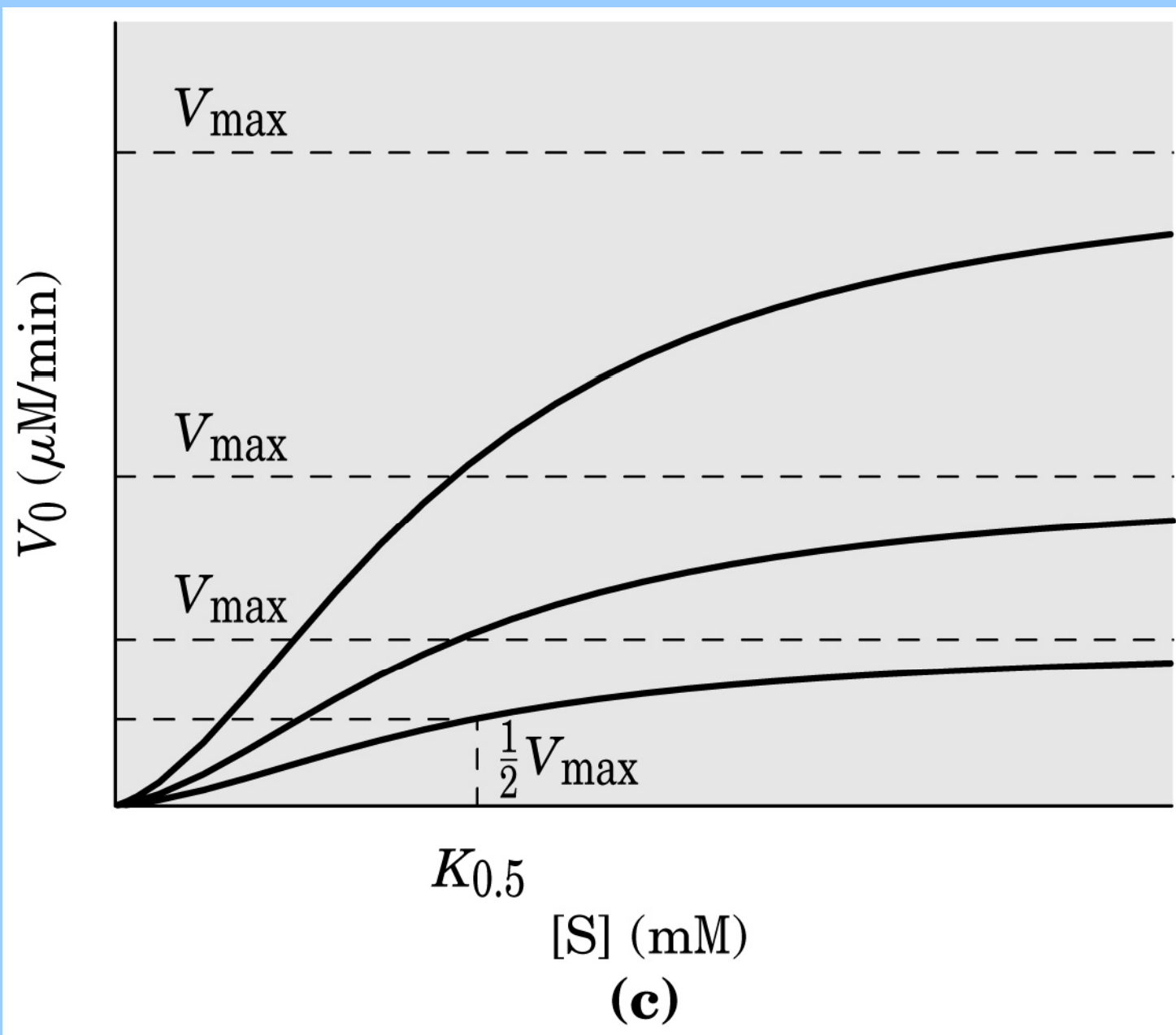
(a) ATCase: T state



(b) ATCase: R state

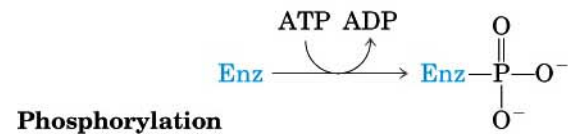




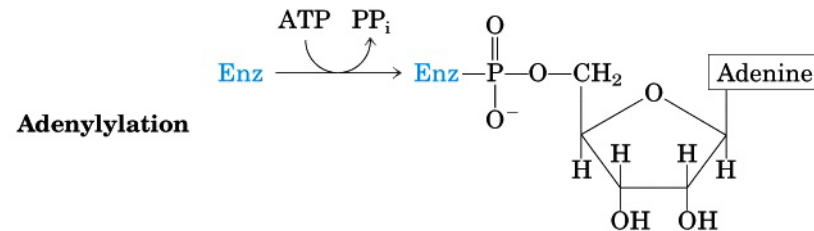


Covalent modification

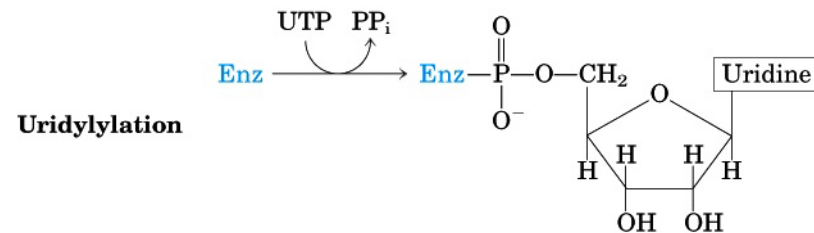
Amino acid residues known to accept covalent modification



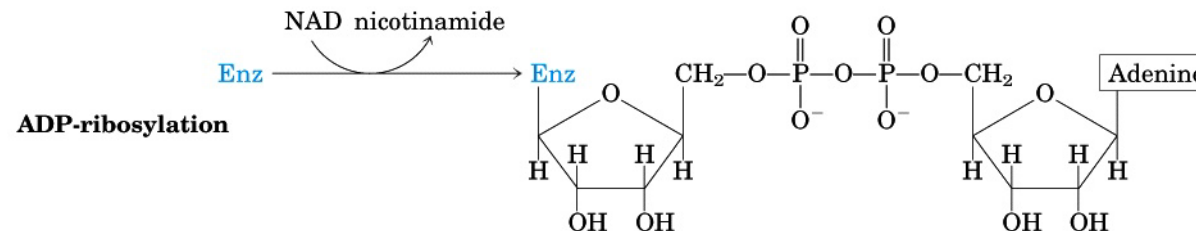
Tyr, Ser, Thr, His



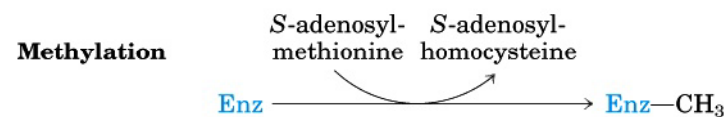
Tyr



Tyr



Arg, Gln, Cys, diphthamide (a modified His)



Glu

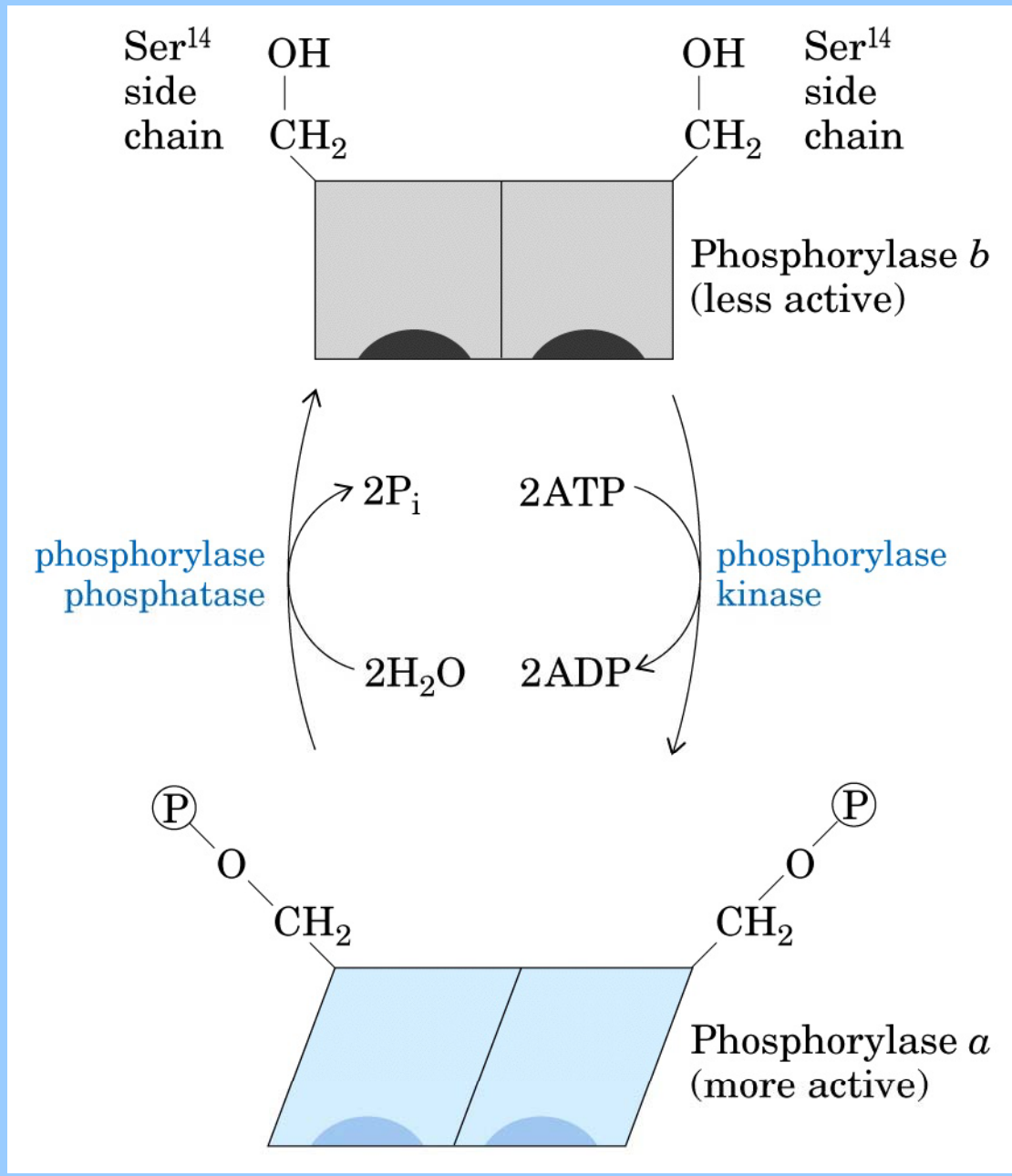


table 8–9

Consensus Sequences for Protein Kinases

Protein kinase	Consensus sequence and phosphorylated residue*
Protein kinase A	–X–R–(R/K)–X–(S/T)–B–
Protein kinase G	–X–R–(R/K)–X–(S/T)–X–
Protein kinase C	–(R/K)–(R/K)–X–(S/T)–B–(R/K)–(R/K)–
Protein kinase B	–X–R–X–(S/T)–X–K–
Ca ²⁺ /calmodulin kinase I	–B–X–R–X–X–(S/T)–X–X–X–B–
Ca ²⁺ /calmodulin kinase II	–B–X–(R/K)–X–X–(S/T)–X–X–
Myosin light chain kinase (smooth muscle)	–K–K–R–X–X–S–X–B–B–
Phosphorylase <i>b</i> kinase	–K–R–K–Q–I–S–V–R–
Extracellular signal–regulated kinase (ERK)	–P–X–(S/T)–P–P–
Cyclin-dependent protein kinase (cdc2)	–X–(S/T)–P–X–(K/R)–
Casein kinase I	–(Sp/Tp)–X–X–(X)–(S/T)–B
Casein kinase II	–X–(S/T)–X–X–(E/D/Sp/Yp)–X–
β-Adrenergic receptor kinase	–(D/E) _n –(S/T)–X–X–X–
Rhodopsin kinase	–X–X–(S/T)–(E) _n –
Insulin receptor kinase	–X–E–E–E–Y–M–M–M–M–K–K–S–R–G– <i>D–Y–M–T–M–Q–I–G–K–K–K–L–P–A–</i> <i>T–G–D–Y–M–N–M–S–P–V–G–D–</i>
Epidermal growth factor (EGF) receptor kinase	–E–E–E–E–Y–F–E–L–V–

Sources: Pinna, L.A. & Ruzzene, M.H. (1996) How do protein kinases recognize their substrates? *Biochim. Biophys. Acta* **1314**, 191–225. Kemp, B.E. & Pearson, R.B. (1990) Protein kinase recognition sequence motifs. *Trends Biochem. Sci.* **15**, 342–346. Kennelly, P.J. & Krebs, E.G. (1991) Consensus sequences as substrate specificity determinants for protein kinases and protein phosphatases. *J. Biol. Chem.* **266**, 15,555–15,558.

*Shown here are deduced consensus sequences (in roman type) and actual sequences from known substrates (italic). The Ser (S), Thr (T), or Tyr (Y) residue to undergo phosphorylation is in red; all amino acid residues are shown as their one-letter abbreviations (see Table 5–1). X represents any amino acid; B, any hydrophobic amino acid; Sp, Tp, and Yp, already phosphorylated Ser, Thr, and Tyr residues.

Chymotrypsinogen (inactive)

1 245

↓ trypsin

π -Chymotrypsin (active)

1 15 16 245
Arg Ile

↓ chymotrypsin
→ Ser¹⁴-Arg¹⁵
+ Thr¹⁴⁷-Asn¹⁴⁸

α -Chymotrypsin (active)

1 13 16 146 149 245
Leu Ile Tyr Ala
A B C

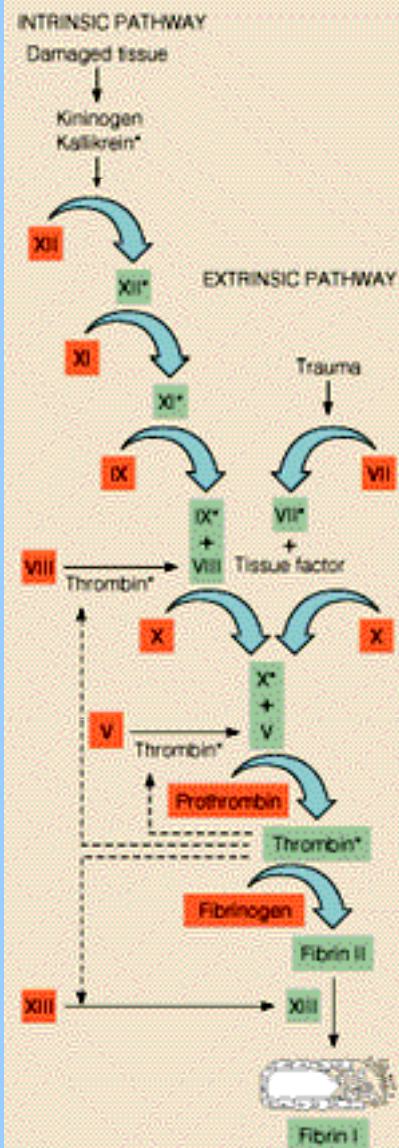
Trypsinogen (inactive)

1 6 7
Val-(Asp)₄-Lys-Ile-

↓ enteropeptidase
→ Val-(Asp)₄-Lys

Trypsin (active)

7 245
Ile



Factor key:

V	Proaccelerin
VIII	Proconvectin
VIII	Antihemophilic factor
IX	Christmas factor
X	Stuart factor
XI	Thromboplastin antecedent
XII	Hageman factor
XIII	Fibrin stabilizing factor