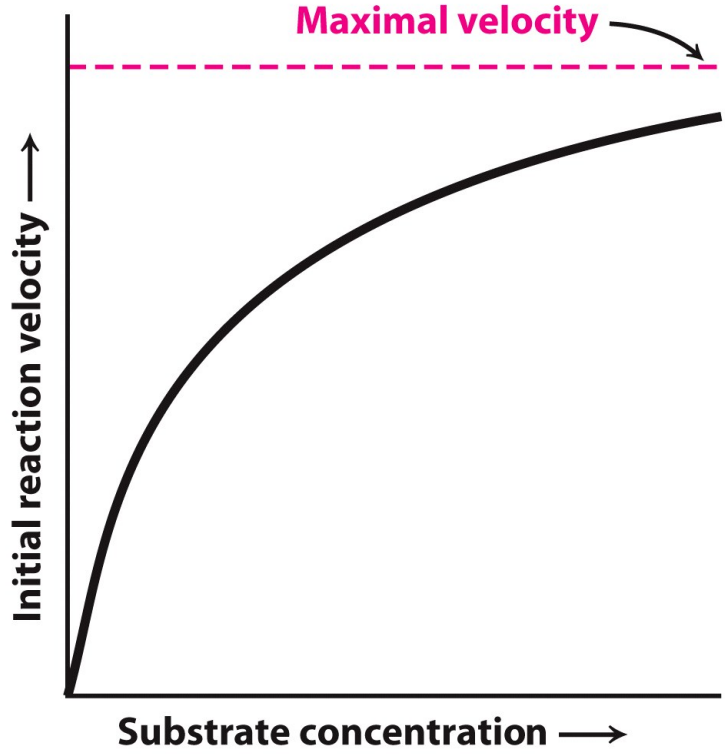

Figure 7.1
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1

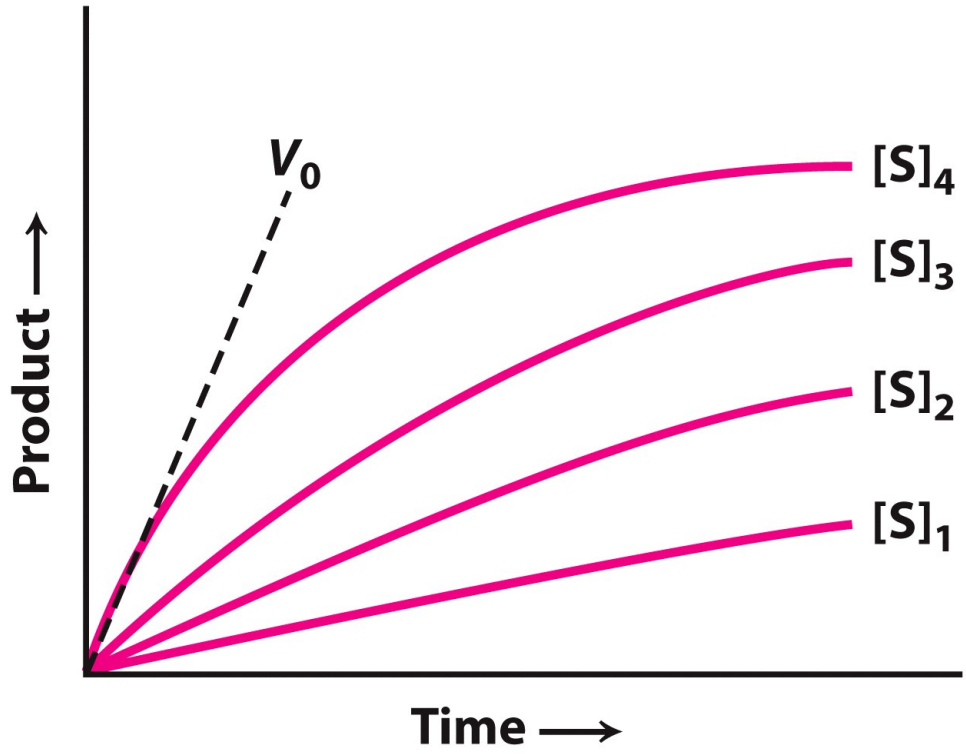

Figure 7.2
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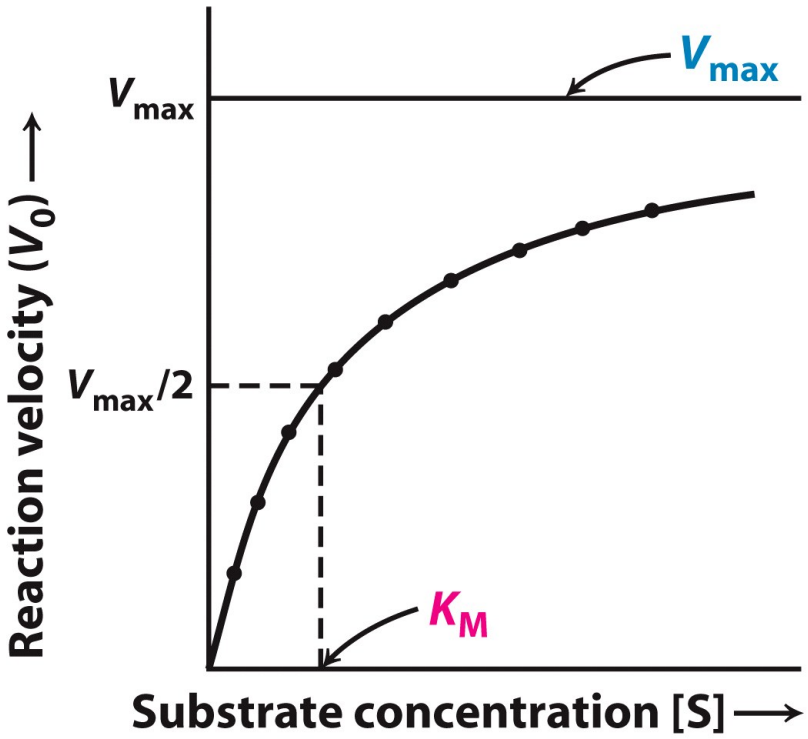
2



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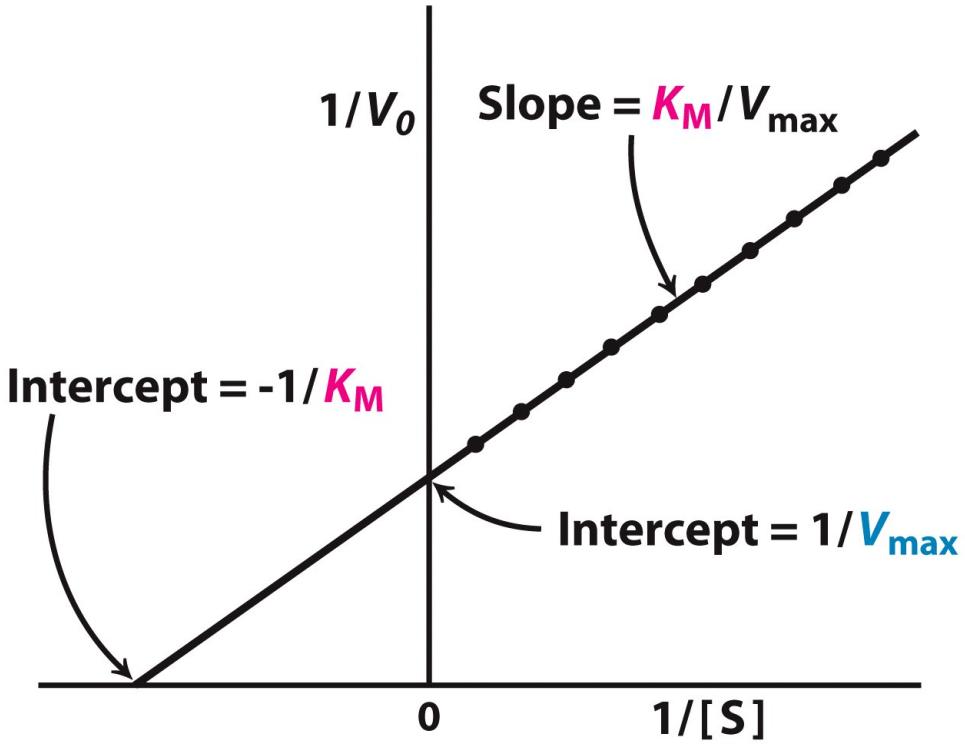

Figure 7.5
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Table 7.1 K_M values of some enzymes

Enzyme	Substrate	K_M (μM)
Chymotrypsin	Acetyl-L-tryptophanamide	5000
Lysozyme	Hexa-*N*-acetylglucosamine	6
β-Galactosidase	Lactose	4000
Carbonic anhydrase	CO_2	8000
Penicillinase	Benzylpenicillin	50

Table 7.1
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Table 7.2 Turnover numbers of some enzymes

Enzyme	Turnover number (per second)
Carbonic anhydrase	600,000
3-Ketosteroid isomerase	280,000
Acetylcholinesterase	25,000
Penicillinase	2,000
Lactate dehydrogenase	1,000
Chymotrypsin	100
DNA polymerase I	15
Tryptophan synthetase	2
Lysozyme	0.5

Table 7.2
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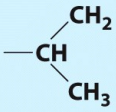
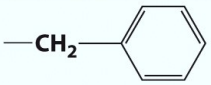
Table 7.3 Substrate preferences of chymotrypsin

Amino acid in ester	Amino acid side chain	k_{cat}/K_M (s^{-1} M^{-1})
Glycine	H	1.3×10^{-1}
Valine		2.0
Norvaline	—$CH_2CH_2CH_3$	3.6×10^{2}
Norleucine	—$CH_2CH_2CH_2CH_3$	3.0×10^{3}
Phenylalanine		1.0×10^{5}

Source: After A. Fersht, *Structure and Mechanism in Protein Science: A Guide to Enzyme Catalysis and Protein Folding* (W. H. Freeman and Company, 1999), Table 6.3.

Table 7.3
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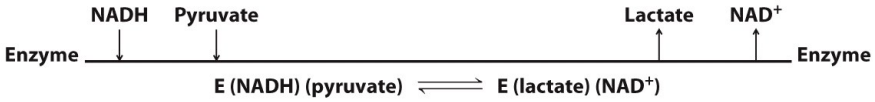
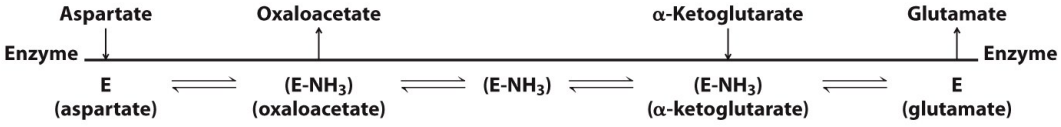


(A) **Sequential reaction**



(B) **Double-displacement reaction**

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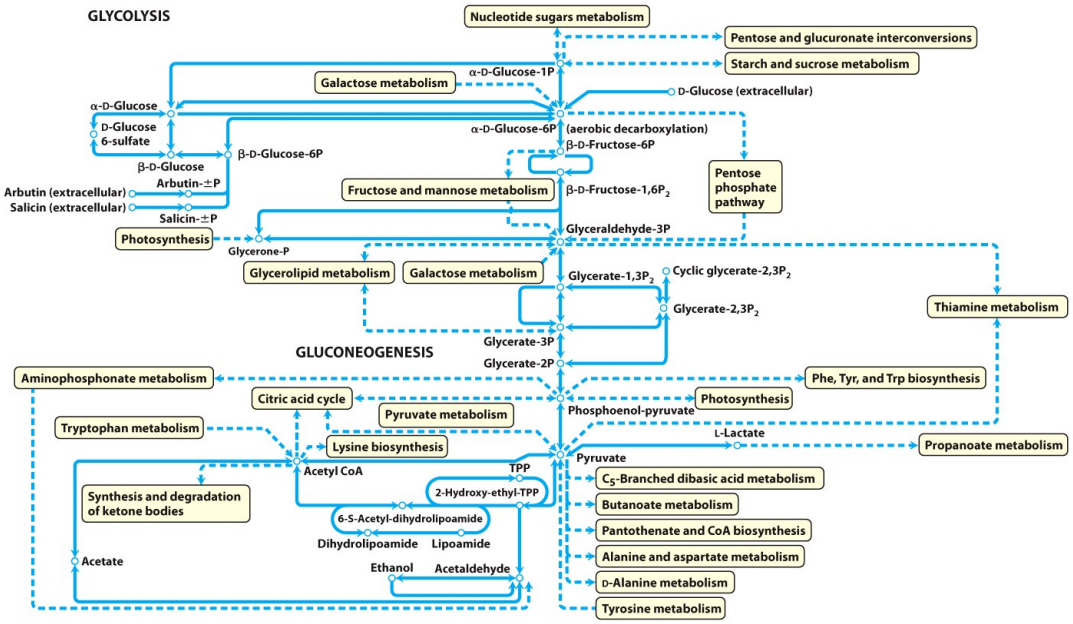

Figure 7.7b
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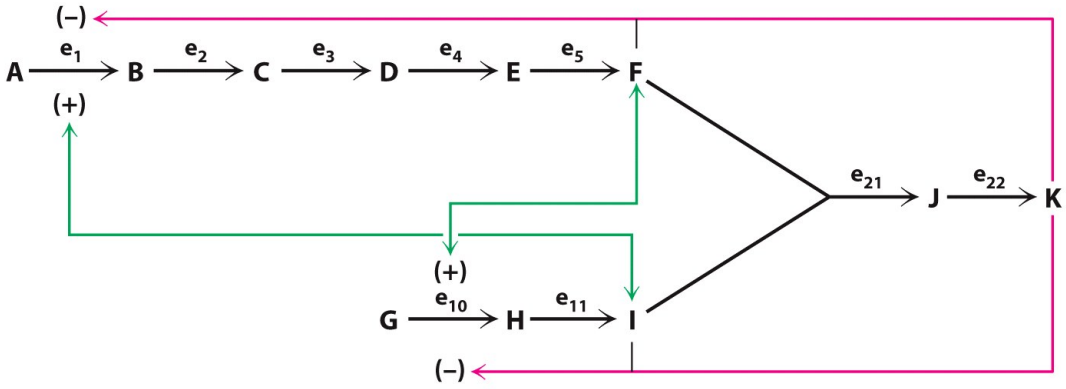

Figure 7.8
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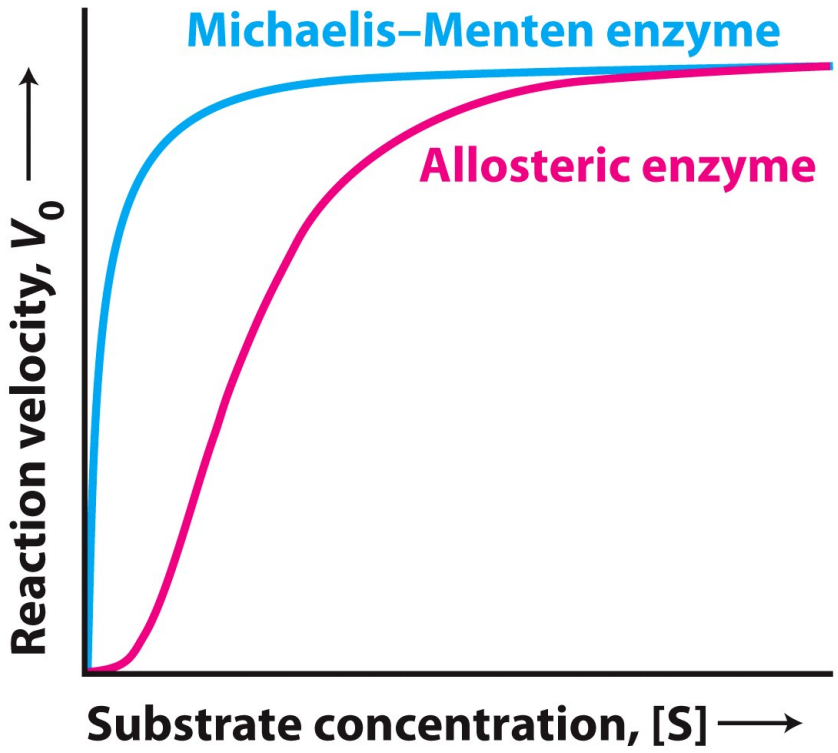

Figure 7.9
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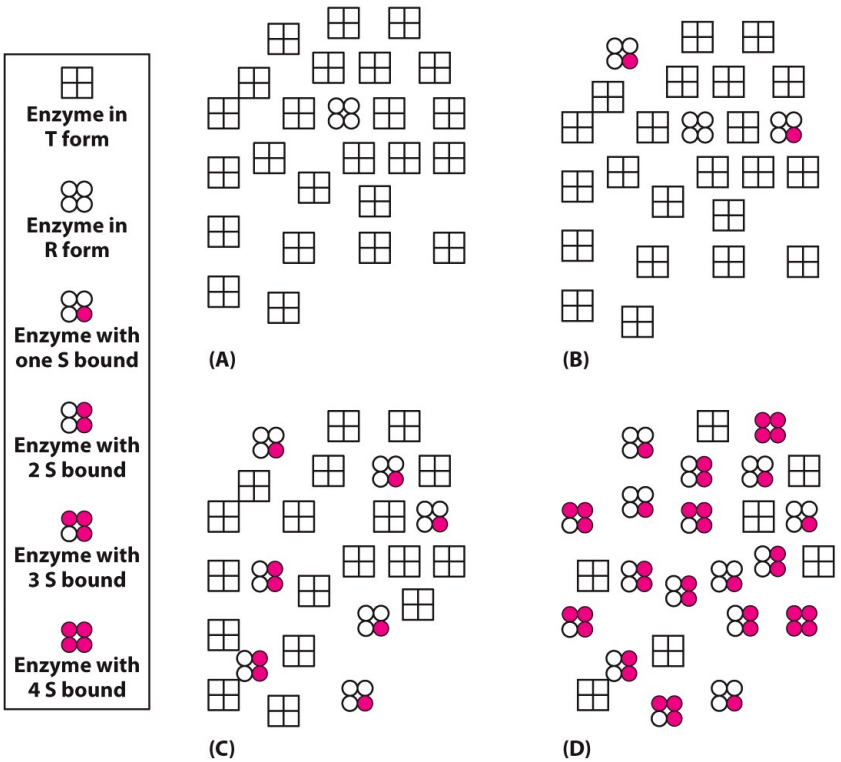

Figure 7.10
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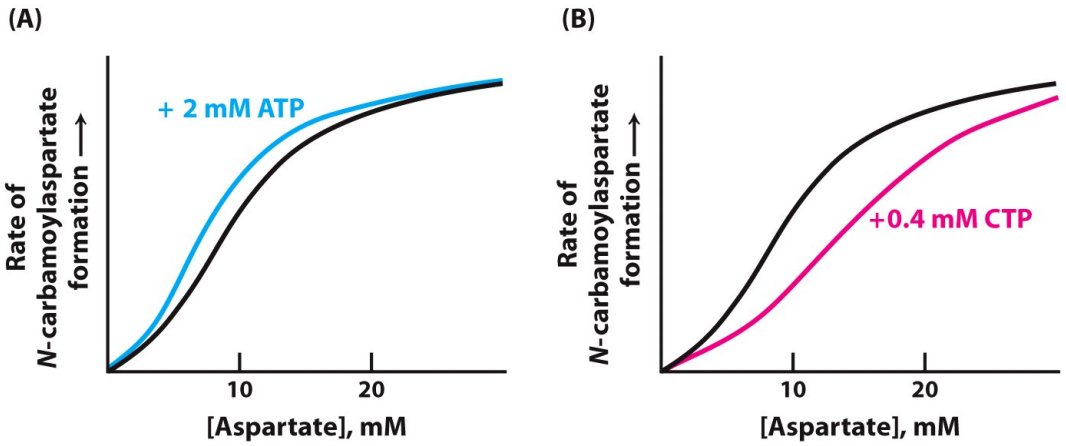

Figure 7.11
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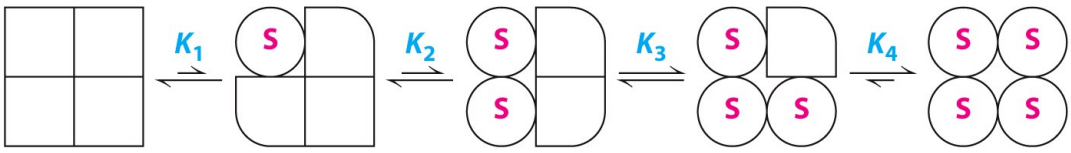

Figure 7.12
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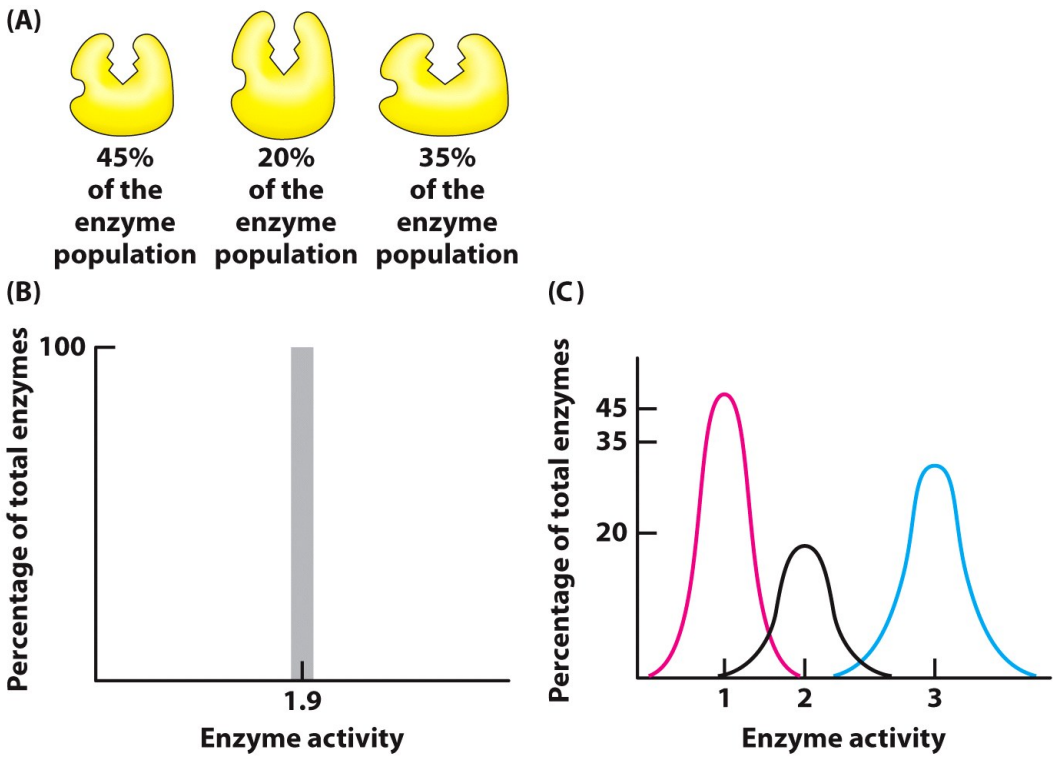

Figure 7.14
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