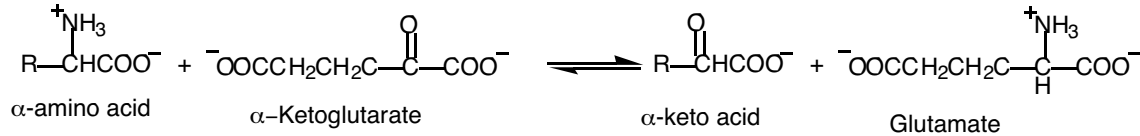


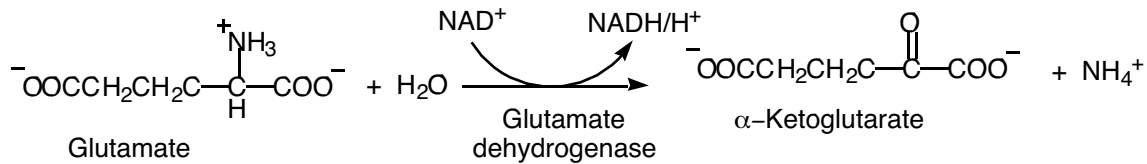
Selected homework answers for chapters 26 and 27

27.8 – Catabolism of an amino acid begins with a transamination reaction that removes the amino acid nitrogen



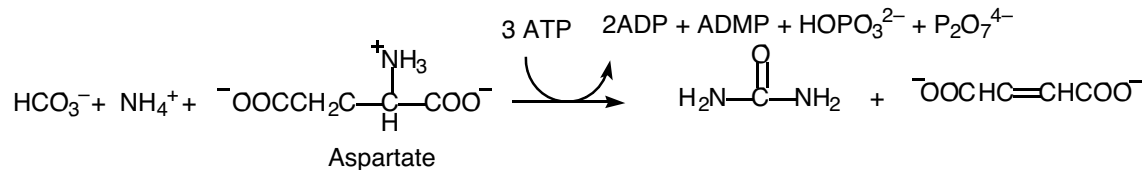
The carbon atoms:

The resulting α -keto acid, which contains the carbons from the original amino acid, undergoes reactions that convert it to a common metabolic intermediate. The intermediate may be a citric acid cycle intermediate, pyruvate, acetyl-SCoA, or acetoacetyl-SCoA.



The nitrogen atoms:

Glutamate, which contains the amino group from the original amino acid, undergoes an oxidative deamination reaction that converts the amino group to ammonium ion and that regenerates, α -ketopglutarate, Either NAD^+ or NADP^+ can be used as the enzyme cofactor



Ammonium ion enters the urea cycle, where it is transformed to urea and is excreted.

27.36 – Ketosis is the major hazard of a high-protein, low carbohydrate diet. Ketosis occurs when the body produces a large amount of acetyl-SCoA that can't enter the citric acid cycle because of a shortage of citric acid cycle intermediates (due to the low level of carbohydrates in the diet. Instead, acetyl-SCoA undergoes ketogenesis, which results in the production of ketone bodies and the lowering of blood pH.

26.22 – Each amino acid has more than one mRNA codon.

Codons for Tyr: UAU, UAC

Codons for Gly: GGU, GGC, GCA, GGC

Codons for Phe: UUU, UUC.

Using the first codon listed:

(a) 5' UAU|GGU|GGU|UUU 3' mRNA

(b) 3' ATA|CCA|CCA|AAA 5' DNA template strand

(c) 5' TAT|GGT|GGT|TTT 3' DNA information strand.

The upper strand of DNA is the template for the synthesis of mRNA, and its sequence of bases is the complement of the sequence of bases that make up the enkephalin gene. The lower strand is the informational strand.

(d) To find the number of DNA sequences multiply the numbers of different codons for each amino acid. $2 \times 4 \times 4 \times 2 = 64$ possible DNA sequences code for the first four amino acids in enkephalins.

26.50 – To say that DNA replication is semiconservative means that each of the two new copies of DNA has a strand of DNA that was the original template and one strand that is newly synthesized.

26.60–62 – The DNA sequence of the template strand is complementary to the DNA sequence of the informational strand. The mRNA sequence is identical to the DNA sequence on the informational strand except that U in mRNA replaces T in DNA.

Informational strand: (5' → 3')	T-A-C-C-G-A
Template strand: (3' → 5')	A-T-G-G-C-T
mRNA: (5' → 3')	U-A-C-C-G-A
Dipeptide:	Tyr — Arg

26.66

	<i>Normal</i>	<i>Mutated</i>
DNA:	A-T-T-G-G-C-C-T-A	A-C-T-G-G-C-C-T-A
mRNA	A-U-U-G-G-C-C-U-A	A-C-U-G-G-C-C-U-A
Amino acids:	Ile---Gly---Leu	Thr---Gly---Leu

The mutation would substitute a Thr for an Ile in the protein

26.70 – Metenkephalin:	Tyr-Gly-Gly-Phe-Met Stop
mRNA (5' → 3'):	UAU-GGU-GGU-UUU-AUG-UUA
	UAC GGC GGC UUU UAG
	GGG GGG UGA
	GGA GGA