

## BERG/STRYER V STUDY GUIDE

### CHAPTER 27

- HOMEWORK 1, 3, 6, 7. The central concept of this chapter is the replication of DNA, and the focus of replication is the **Replication Fork** (Fig 27.32 p. 763). You should understand how **Okazaki fragments** are formed and then changed into DNA on the lagging strand (760-761). Know the various proteins mentioned in 27.4.4 and 27.4.5 and what their functions are in replication. The "**primosome**" (760) conceptually would include primase, DNA Pol III, and a translocase (n' and dnaB). Some bacteriophage viruses may use the primosome, but for bacterial replication DNA Pol III exists as a dimer (the "replisome") situated *outside* the plasma membrane. The arriving DNA is replicated using the "**trombone model**" (Fig 27.33, p. 764). Replicated strands then are sorted into the 2 halves of the soon-to-divide cell. Understand "**DNA Gyrase math**" as on p. 755:  $Lk = Tw + Wr$ , the linking number equals twists plus writhes. Right-handed twists are (+) but right-handed supercoils are (-). The mechanism of gyrase (759) was demonstrated in class with beads. "Cipro," the drug used against anthrax, is **ciprofloxacin**, which like **nalidixic acid** is a specific inhibitor of gyrase (759).
- Understand the differences between DNA Pol I and DNA Pol III (762-763). DNA Pol I has one subunit and is not very **processive** – it adds 20 nucleotides and falls off. DNA Pol III is much faster than Pol I (100 times) and much more processive (adding thousands of nucleotides at a stretch). It also has many subunits and "clamps" onto DNA. Understand **mutagens** and **mutations** (768-9), **Thymine dimers** (770), repair processes (771) and the **Ames Test** (774).

### The Genetic Code

	middle base of codon				base at 3' end of codon
	U	C	A	G	
base at 5' end of codon U	phe-UUU	ser-UCU	tyr-UAU	cys-UGU	U
	phe-UUC	ser-UCC	tyr-UAC	cys-UGC	C
	leu-UUA	ser-UCA	end-UAA	end-UGA	A
	leu-UUG	ser-UCG	end-UAG	trp-UGG	G
C	leu-CUU	pro-CCU	his-CAU	arg-CGU	U
	leu-CUC	pro-CCC	his-CAC	arg-CGC	C
	leu-CUA	pro-CCA	gln-CAA	arg-CGA	A
	leu-CUG	pro-CCG	gln-CAG	arg-CGG	G
A	ile-AUU	thr-ACU	asn-AAU	ser-AGU	U
	ile-AUC	thr-ACC	asn-AAC	ser-AGC	C
	ile-AUA	thr-ACA	lys-AAA	arg-AGA	A
	met-AUG or start	thr-ACG	lys-AAG	arg-AGG	G
G	val-GUU	ala-GCU	asp-GAU	gly-GGU	U
	val-GUC	ala-GCC	asp-GAC	gly-GGC	C
	val-GUA	ala-GCA	glu-GAA	gly-GAA	A
	val-GUG	ala-GCG	glu-GAG	gly-GGG	G