

BERG/STRYER VI STUDY GUIDE

CHAPTER 28

1. HOMEWORK 1, 2, 5, 6. The central concept of this chapter is the replication of DNA, and the focus of replication is the **Replication Fork** (Fig 28.21 & 28.27). You should understand how **Okazaki fragments** are formed and then changed into DNA on the lagging strand. Know the various proteins mentioned in the chapter and what their functions are in replication, including Helicase (DnaB), Primase, Gyrase (Type II Topoisomerase), DNA Pol I and Pol III, DNA Ligase, SSB Proteins, and DnaA. 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 28.29, p. 764). Replicated strands then are sorted into the 2 halves of the soon-to-divide cell. Understand "**DNA Gyrase math**" as on p. 789: $Lk = Tw + Wr$, the linking number equals twists plus writhes. Right-handed twists are (+) but right-handed supercoils are (-). The mechanism of gyrase (Fig. 28.14) was demonstrated in class with beads. "Cipro," the drug used against anthrax, is **ciprofloxacin**, which like **nalidixic acid** is a specific inhibitor of gyrase (792).

2. Understand the differences between DNA Pol I and DNA Pol III. 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** (805f), **Thymine dimers** (806), repair processes (807ff) and the **Ames Test** (811).

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