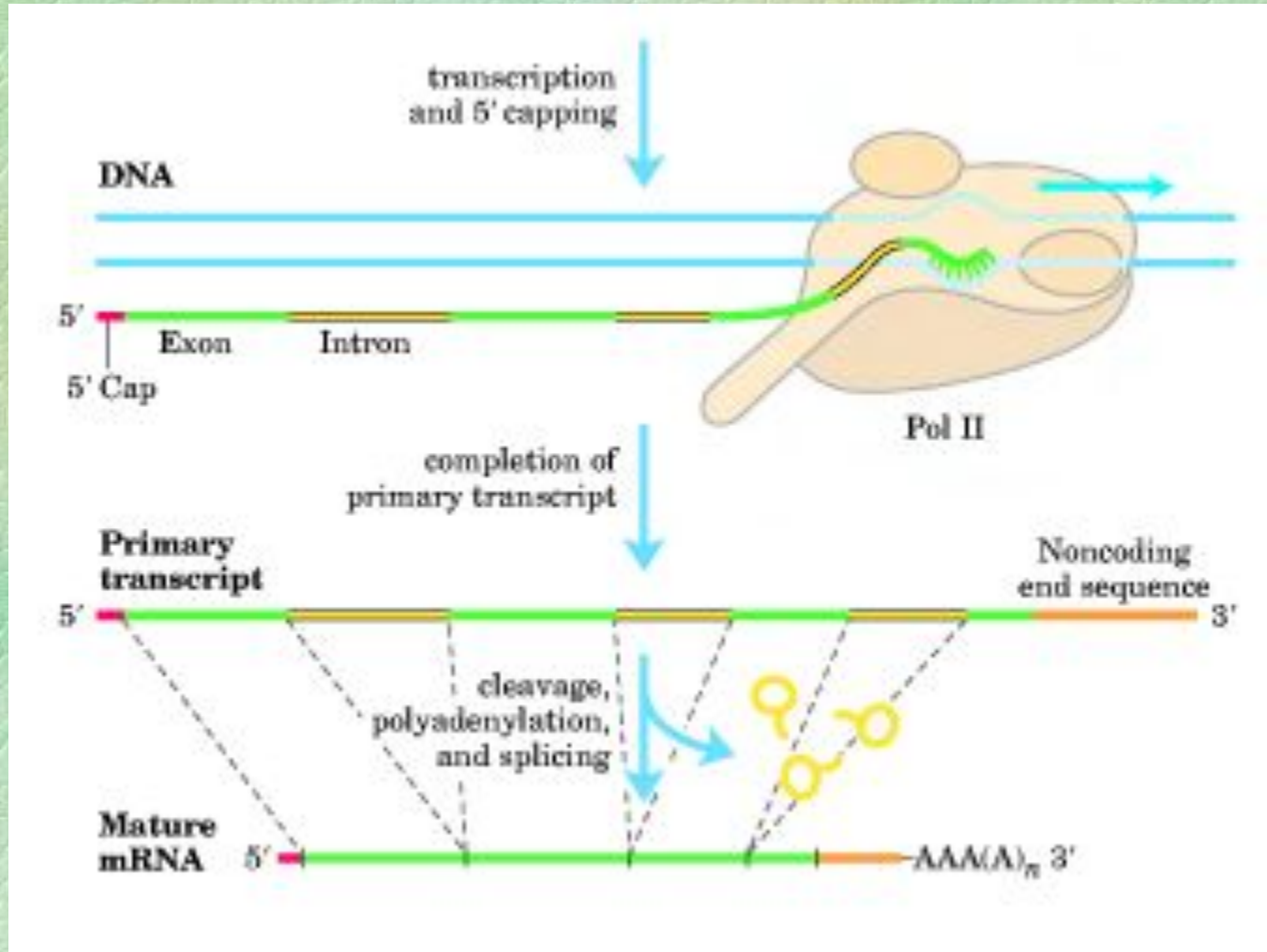
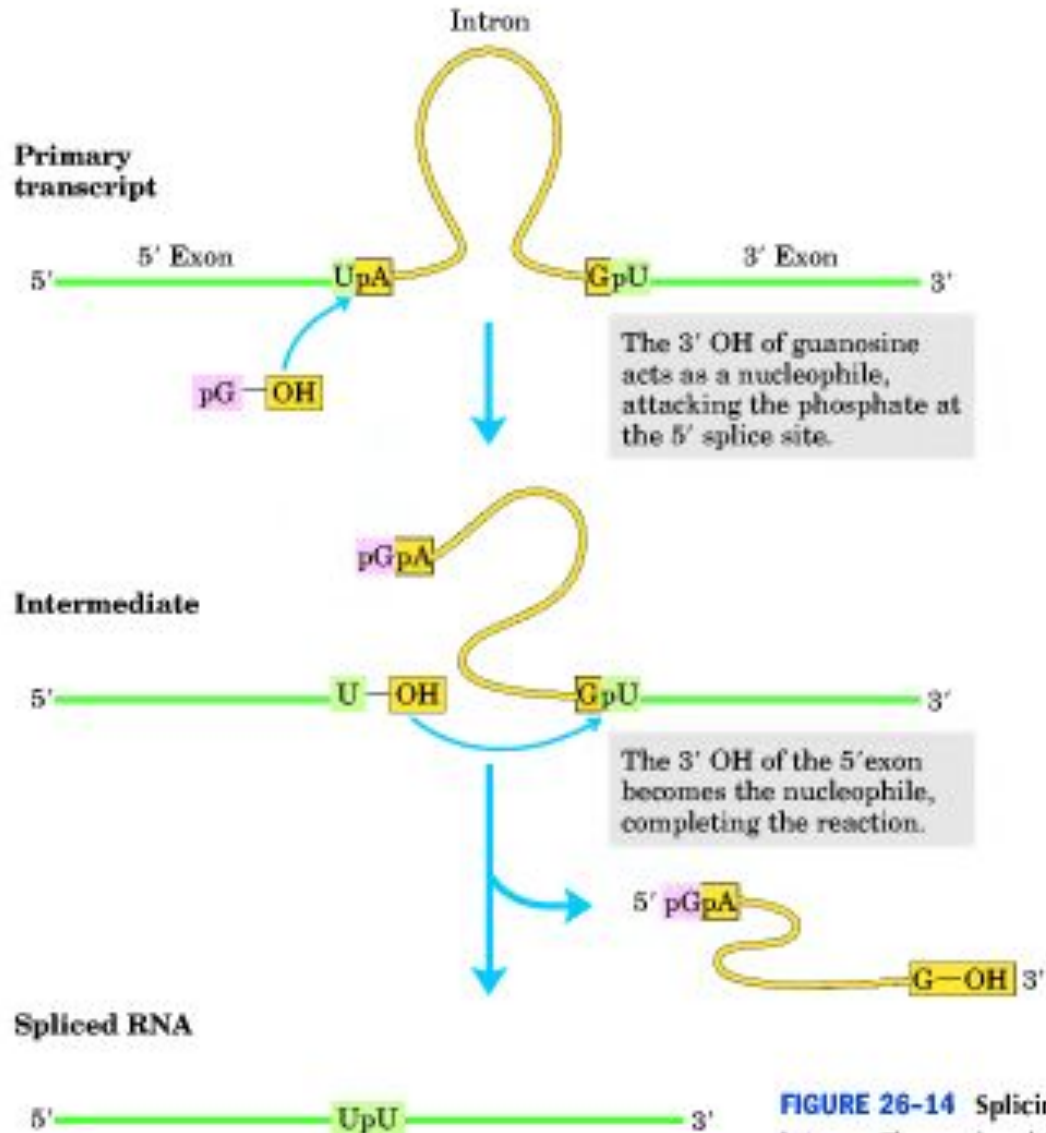


# Процессинг РНК



- Сплайсинг
- Модификация 5' и 3' КОНЦОВ

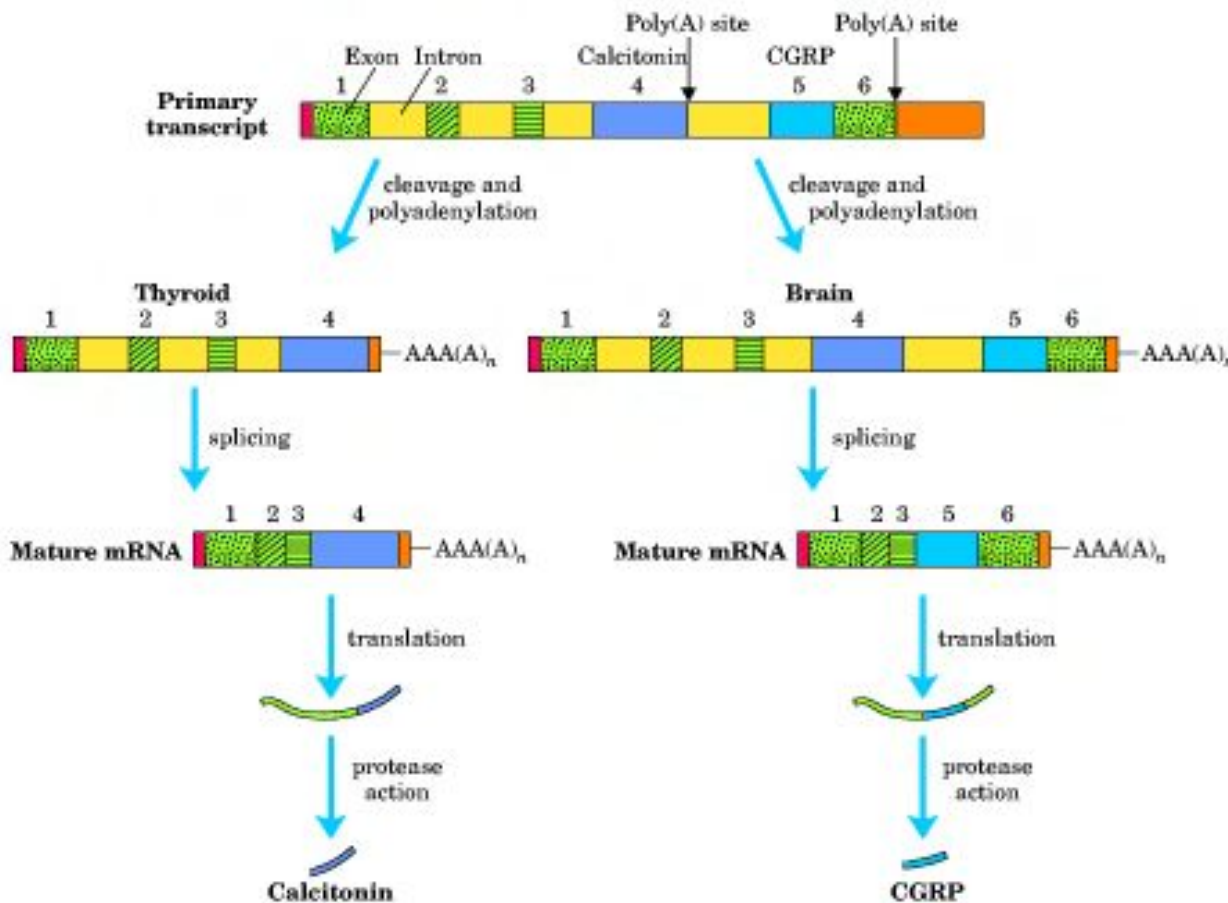
- Сплайсинг – процесс авто-каталитический



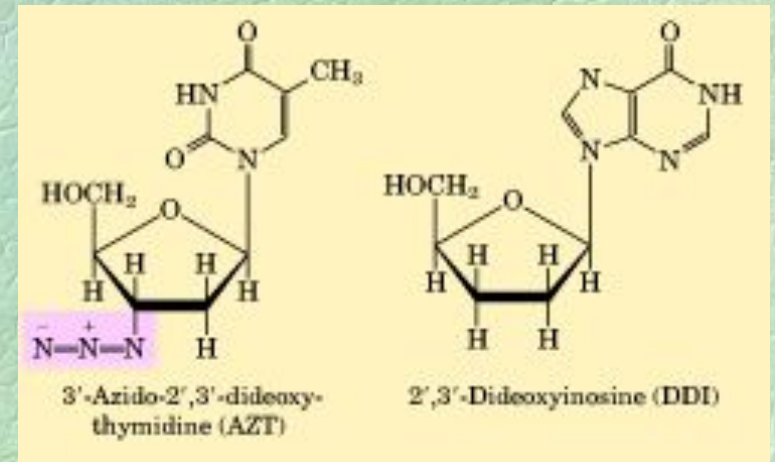
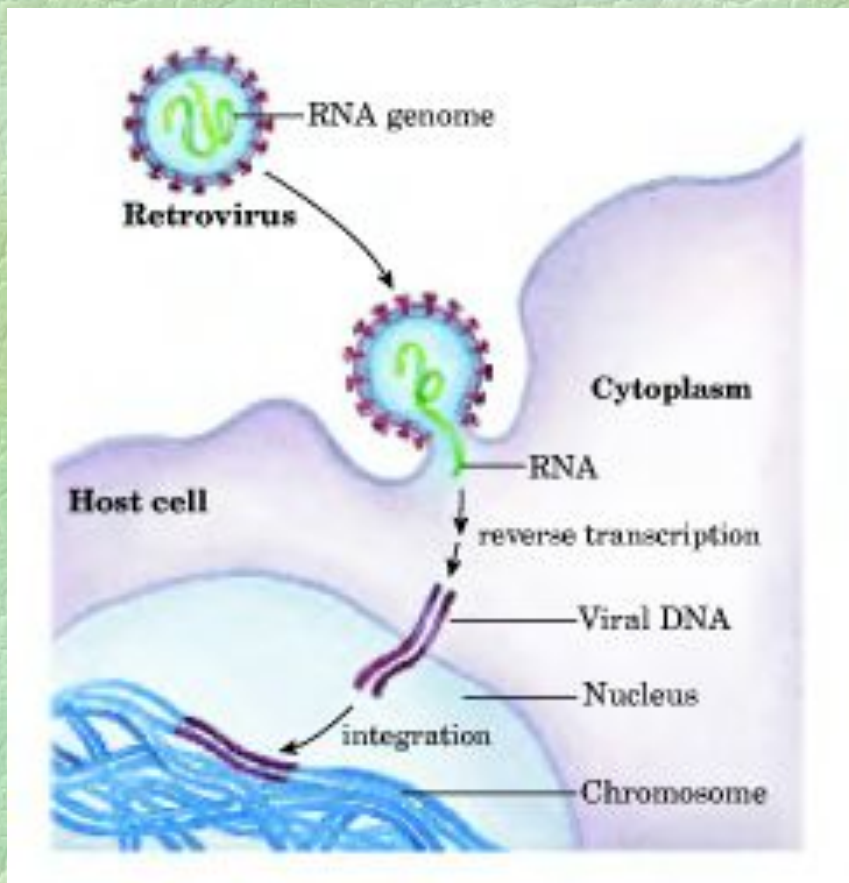
Thomas Cech



# Альтернативный сплайсинг кальцетонина



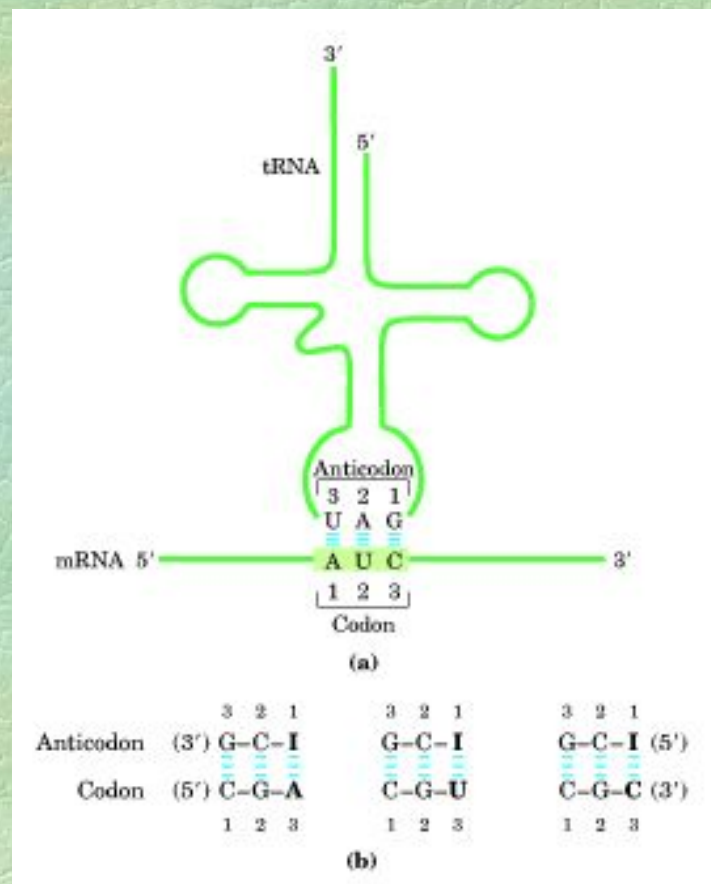
# Обратная транскрипция





# Генетический код

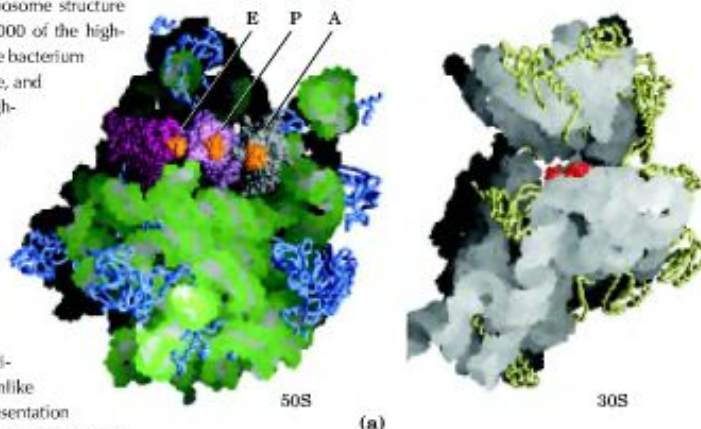
First letter of codon (5' end)		Second letter of codon							
		U		C		A		G	
U		UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys
		UUC	Phe	UCC	Ser	UAC	Tyr	UGC	Cys
		UUA	Leu	UCA	Ser	UAA	Stop	UGA	Stop
		UUG	Leu	UCG	Ser	UAG	Stop	UGG	Trp
C		CUU	Leu	CCU	Pro	CAU	His	CGU	Arg
		CUC	Leu	CCC	Pro	CAC	His	CGC	Arg
		CUA	Leu	CCA	Pro	CAA	Gln	CGA	Arg
		CUG	Leu	CCG	Pro	CAG	Gln	CGG	Arg
A		AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser
		AUC	Ile	ACC	Thr	AAC	Asn	AGC	Ser
		AUA	Ile	ACA	Thr	AAA	Lys	AGA	Arg
		AUG	Met	ACG	Thr	AAG	Lys	AGG	Arg
G		GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly
		GUC	Val	GCC	Ala	GAC	Asp	GGC	Gly
		GUA	Val	GCA	Ala	GAA	Glu	GGA	Gly
		GUG	Val	GCG	Ala	GAG	Glu	GGG	Gly





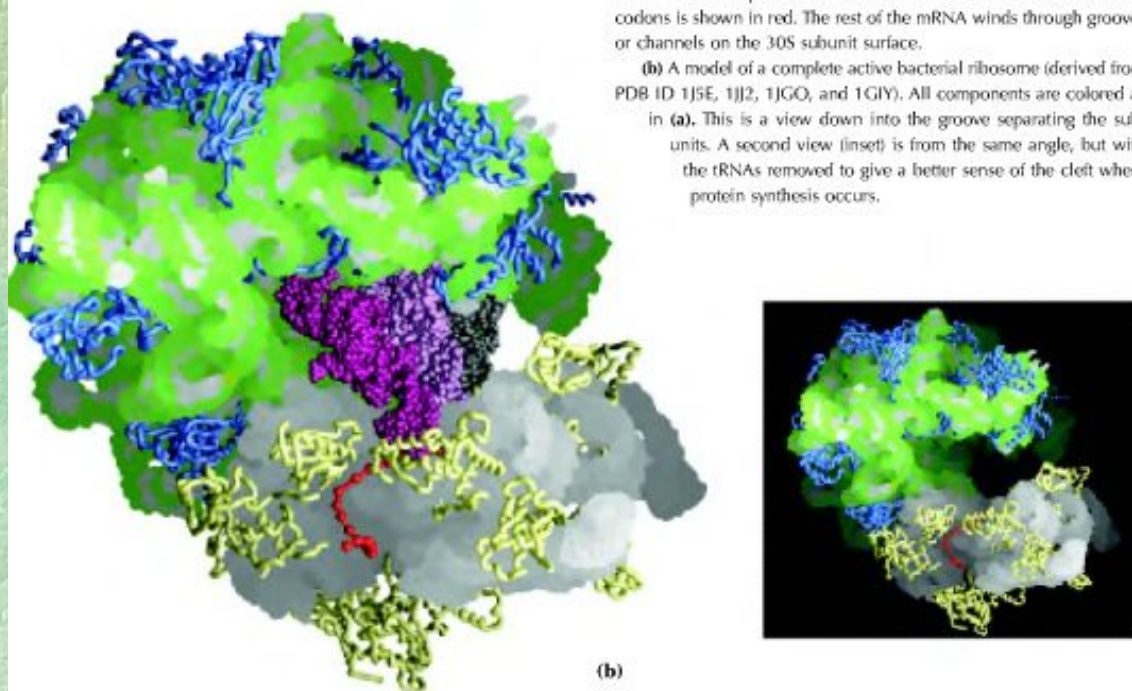
**FIGURE 27-9 Ribosomes.** Our understanding of ribosome structure took a giant step forward with the publication in 2000 of the high-resolution structure of the 50S ribosomal subunit of the bacterium *Haloarcula marismortui* by Thomas Steitz, Peter Moore, and their colleagues. This was followed by additional high-resolution structures of the ribosomal subunits from several different bacterial species, and models of the corresponding complete ribosomes. A sampling of that progress is presented here.

(a) The 50S and 30S bacterial subunits, split apart to visualize the surfaces that interact in the active ribosome. The structure on the left is the 50S subunit (derived from PDB ID 1JJ2 and 1GIY), with tRNAs (purple, mauve, and gray); bound to sites E, P, and A, described later in the text; the tRNA anticodons are in orange. Proteins appear as blue wormlike structures; the rRNA as a blended space-filling representation designed to highlight surface features, with the bases in white and the backbone in green. The structure on the right is the 30S subunit

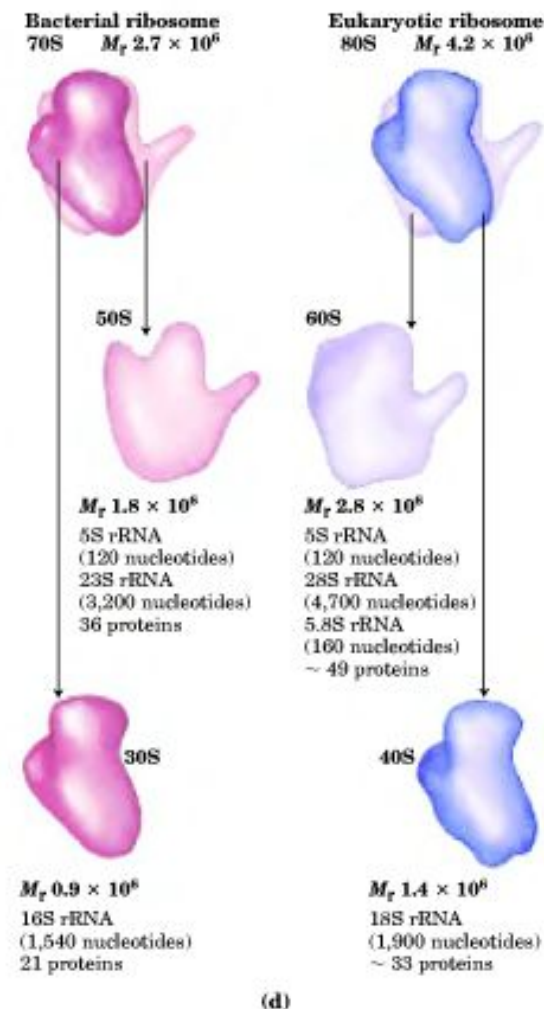


(derived from PDB ID 1J5E and 1JGO). Proteins are yellow and the rRNA white. The part of the mRNA that interacts with the tRNA anticodons is shown in red. The rest of the mRNA winds through grooves or channels on the 30S subunit surface.

(b) A model of a complete active bacterial ribosome (derived from PDB ID 1J5E, 1JJ2, 1JGO, and 1GIY). All components are colored as in (a). This is a view down into the groove separating the subunits. A second view (inset) is from the same angle, but with the tRNAs removed to give a better sense of the cleft where protein synthesis occurs.

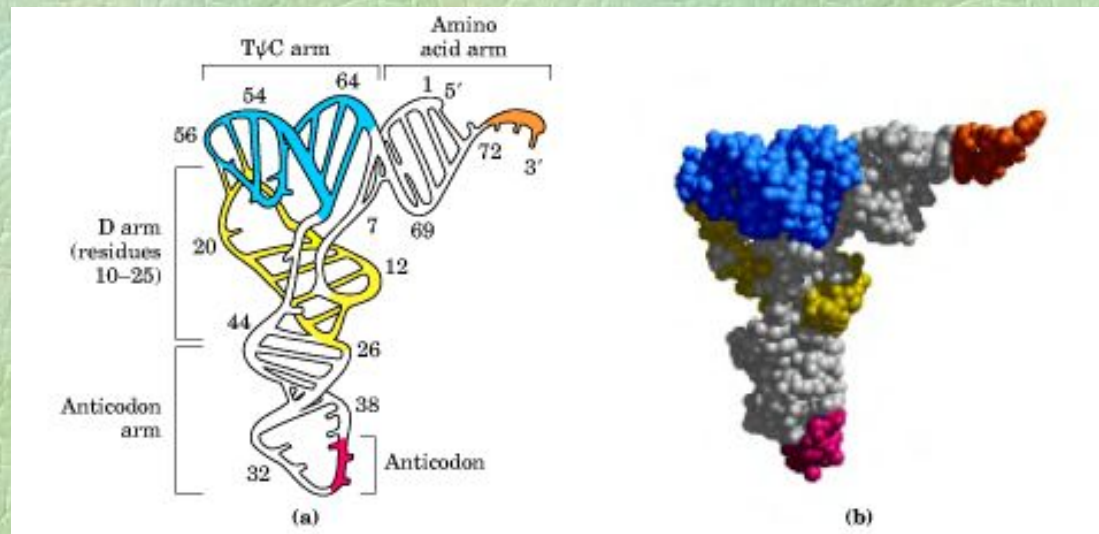
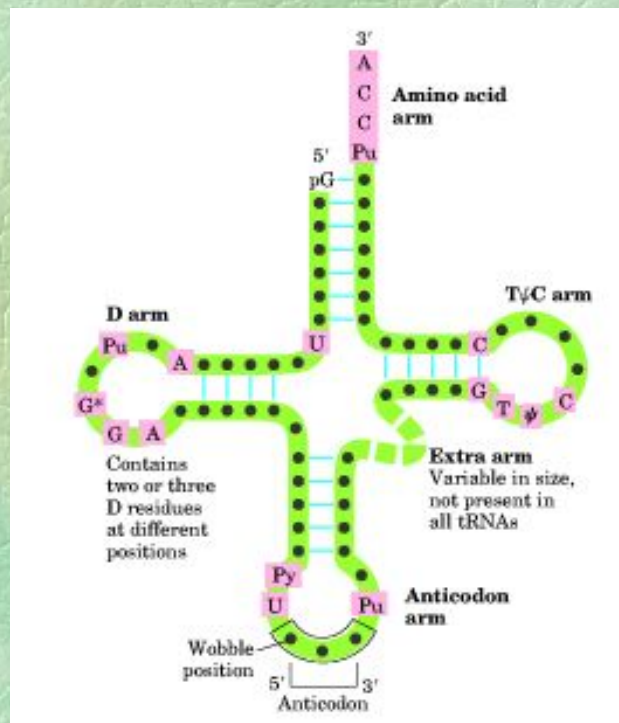


# Рибосомы

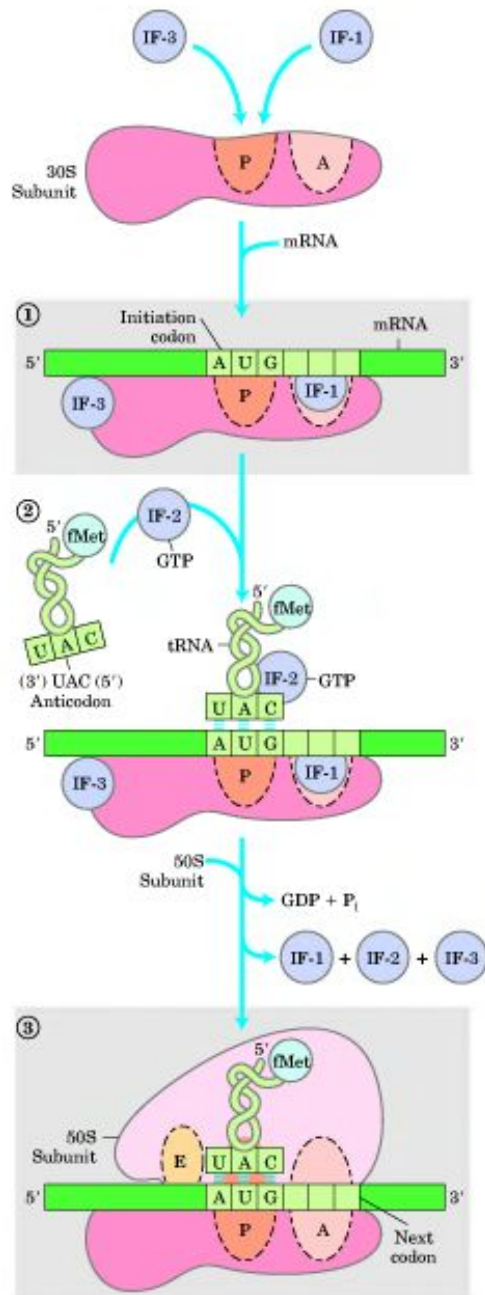




# Инициация трансляции

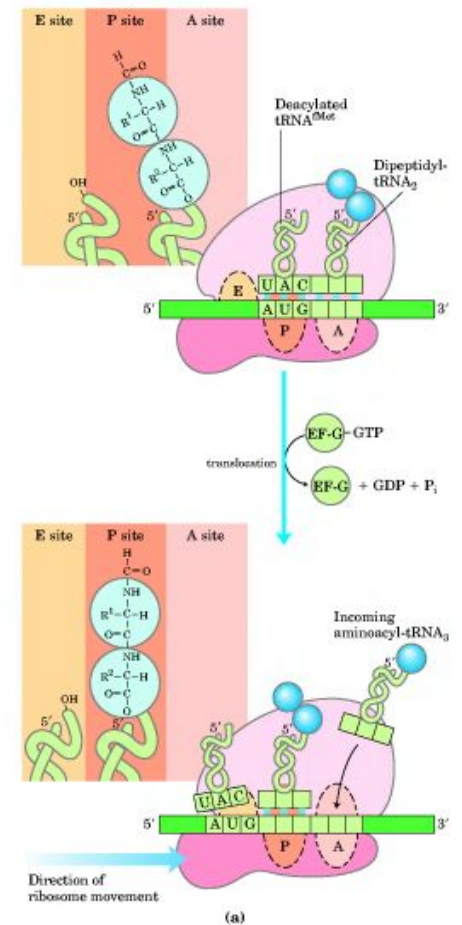
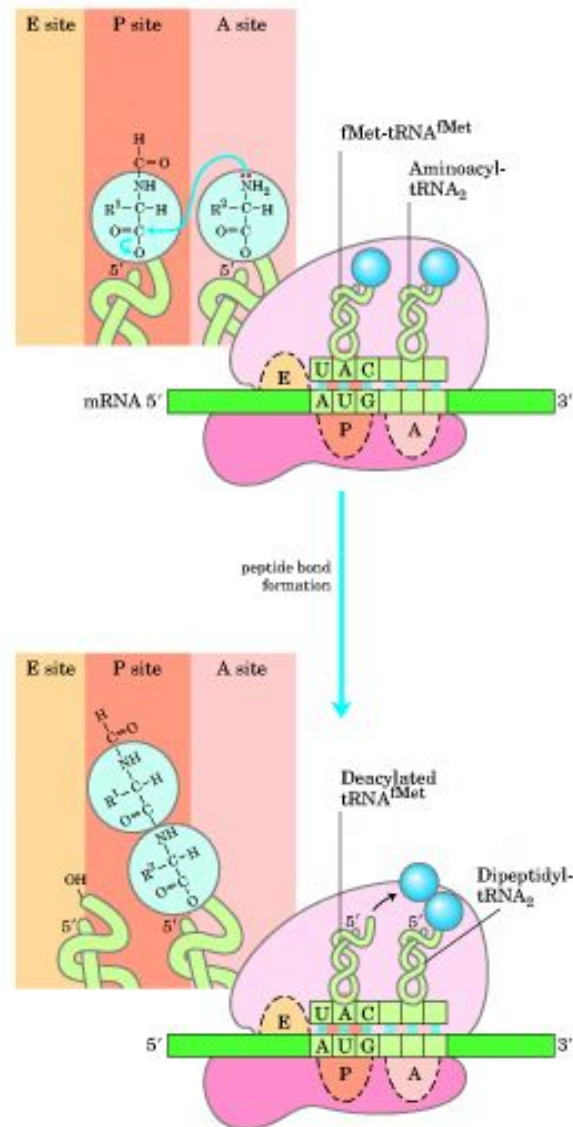
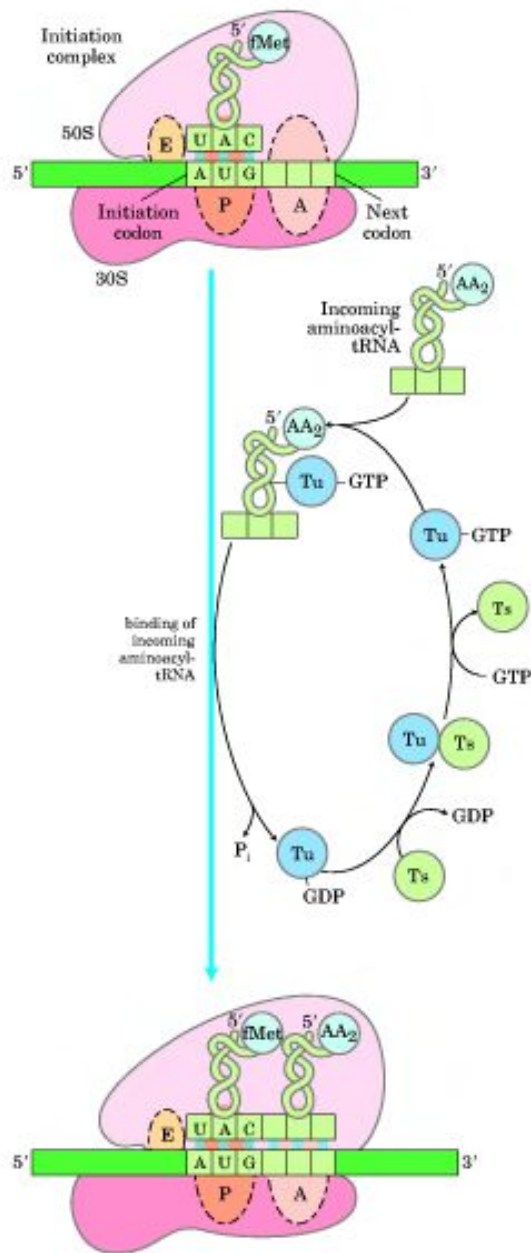


# Инициация трансляции





# Элонгация



# Терминация трансляции

