

Rank of change

U-G rare
 U-C often
 C-U often
 A-C rare
 C-A rare

Arg	<u>CCU</u>	<u>CUU</u>	<u>AAU</u>	<u>ACC</u>	A
AAG	GGA	GAA	UUG	UGG	
AGG	UGA	UAA	UUU	UUG	
CCG	<u>GUA</u>	<u>GCU</u>		<u>UGU</u>	
ACG	GGC	<u>GAC</u>			

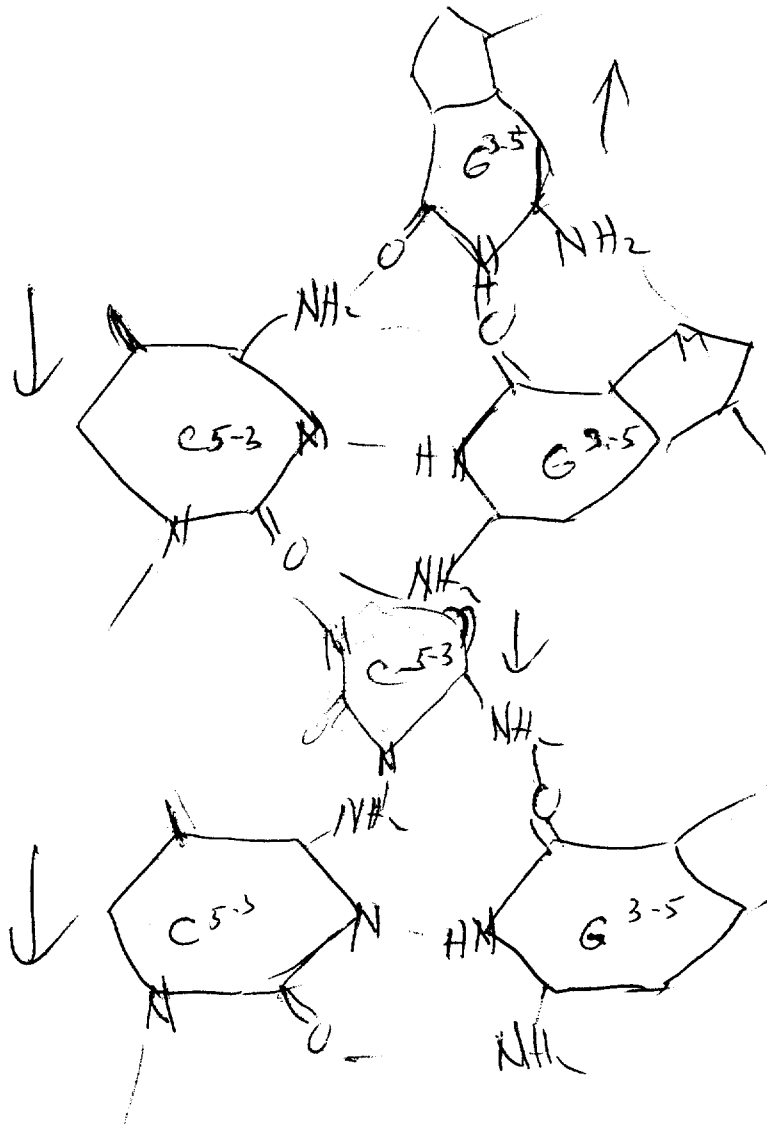
ii

Single Codons

	AAU	AAA
Tyrosine	UUA	UAU
Valine	GUU AAU	UAG?
Hist	CUA	CUA ?
Met	UAG?	
Asp	UAG?	
Glu	AAG?	
Trypt	ACC	UGG

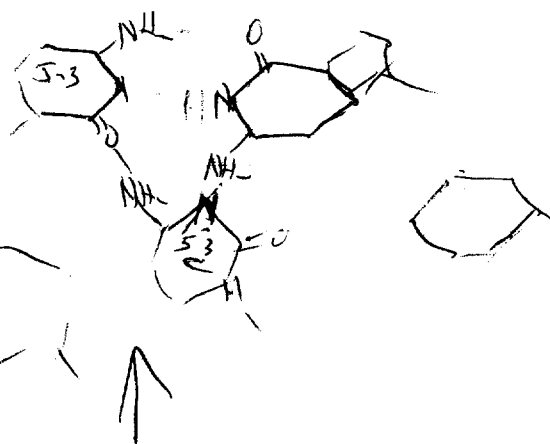
Double Codons

	CCA	CAU	Change
Threonine	CCA	CAU	C→A
Asp-NH ₂	AAC	AAU	C→U
Leu	UUC	UCC	C→U
Ile	CUU	CUU	C→U
Cys?			ψ
Leu	AAU	AAA	A→U
Pro	CCC	CCC	ψ
		CAC	C→U
		CAC	C→U
		CAC	C→U
		CAC	C→U
Arg	AAG	CCG	C→A
Glu-NH ₂	AAC	ACG	C→G
		AAG?	C→G

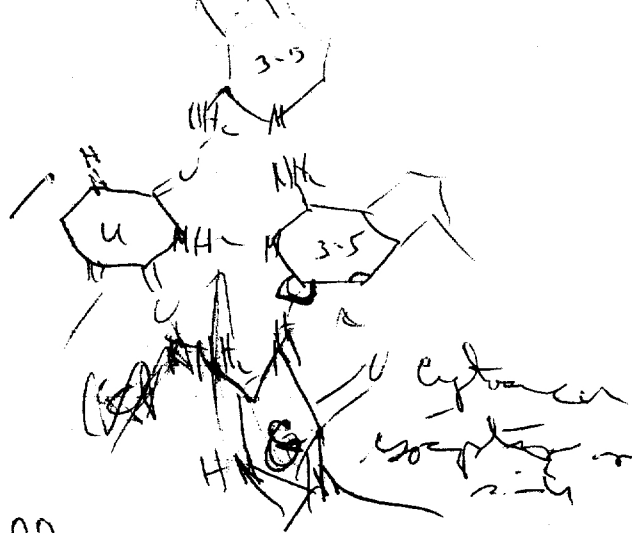


Read up/down the DNA
groove with RNA polymerase.
Strands of DNA do not have
to separate.

would expect to get
high-stranded interaction



If you could see double || RNA on ribbons,
could not double strand 2 way



cytosine
acceptor
side

Both reading is possible

