Exercice 1

ADN	anti-sens	5’-TTACGTATTTCGAA-3’
	brin sens	3’-AATGCATAAAGCTT-5’
ARN		5’-UUCGAAAUACGUAA-3’

Exercice 2

brin sens

5’-**T**TGCACGCAT **T**AAGCATATA **A**AGCACCAGC **A**TGCCGTACA **C**AATGACGGC

-50 -40 -30 -20 -10

TTACGTCCG**C** CTAGTTCAA**G** CATCGAAGC**A** –3’

+1 +10 +20 +30

5’- UUACGUCCGC CUAGUUCAAG CAUCGAAGCA –3’

ARN

Exercice 3

5’-AUCCGACUGC GAAUGUAUGC ACCAUGGACA GUAGCUUCAC CGUAAUGUUA

N- Met Asp Ser Ser Phe Thr Val Met Leu

CGCAGCUGAA GCCAUAAGCA UCGCCAUCAG–3’

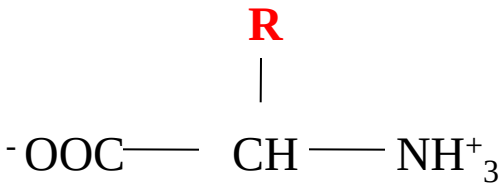
Arg Ser -C

11 aa

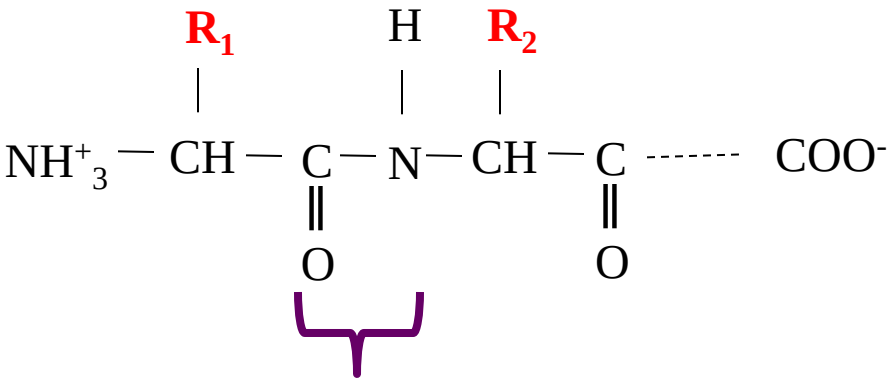
Code génétique (de l’ARN en acides aminés)

Première position (extrémité 5')	Seconde position U	Seconde position C	Seconde position A	Seconde position G	Troisième position (extrémité 3')
U	Phé	Sér	Tyr	Cys	U
	Phé	Sér	Tyr	Cys	C
	Leu	Sér	Stop	Stop	A
	Leu	Sér	Stop	Trp	G
C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Sér	U
	Ile	Thr	Asn	Sér	C
	Ile	Thr	Lys	Arg	A
	Mét	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

un acide aminé :

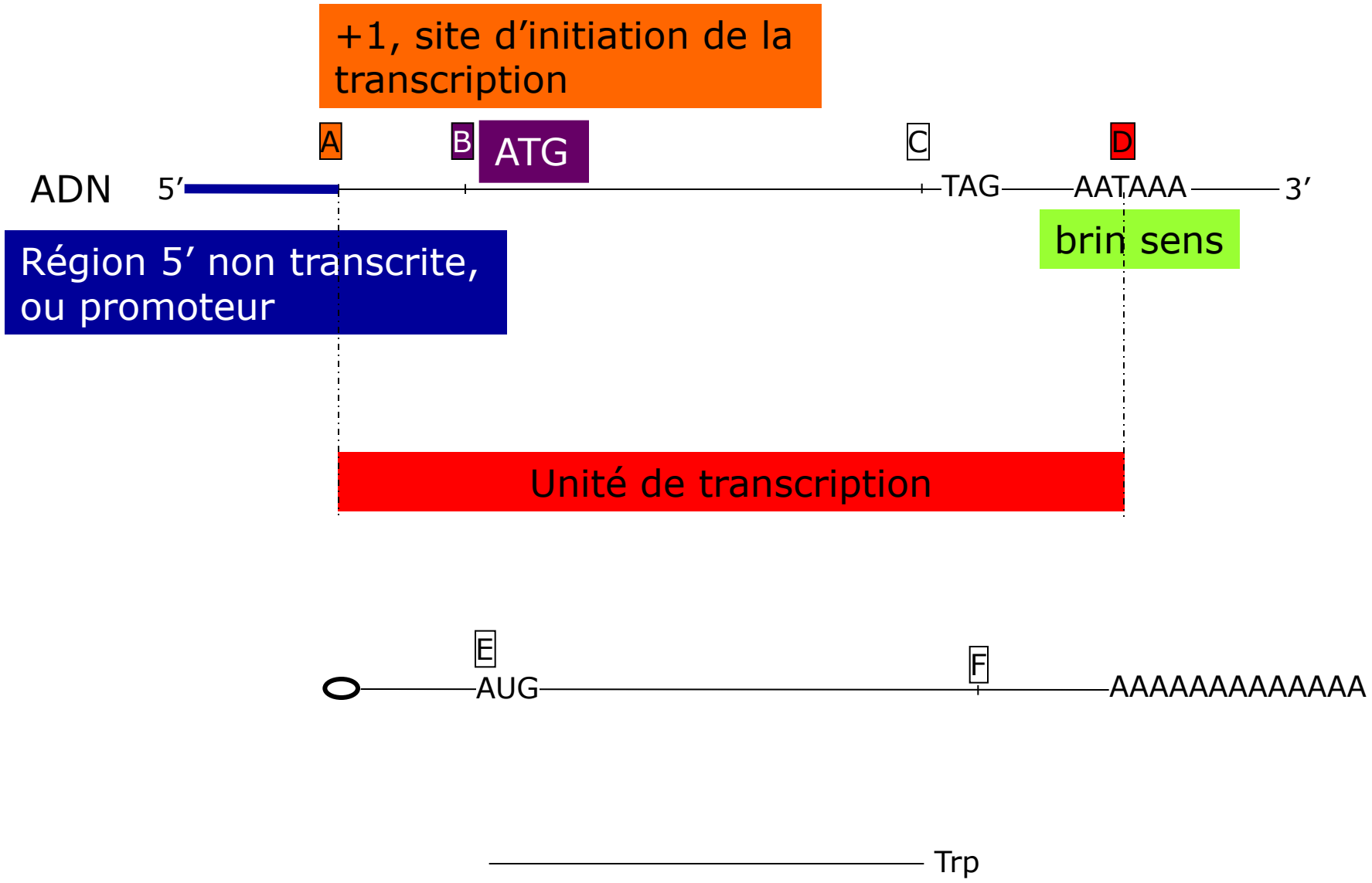


un peptide :



Liaison peptidique

Exercice 4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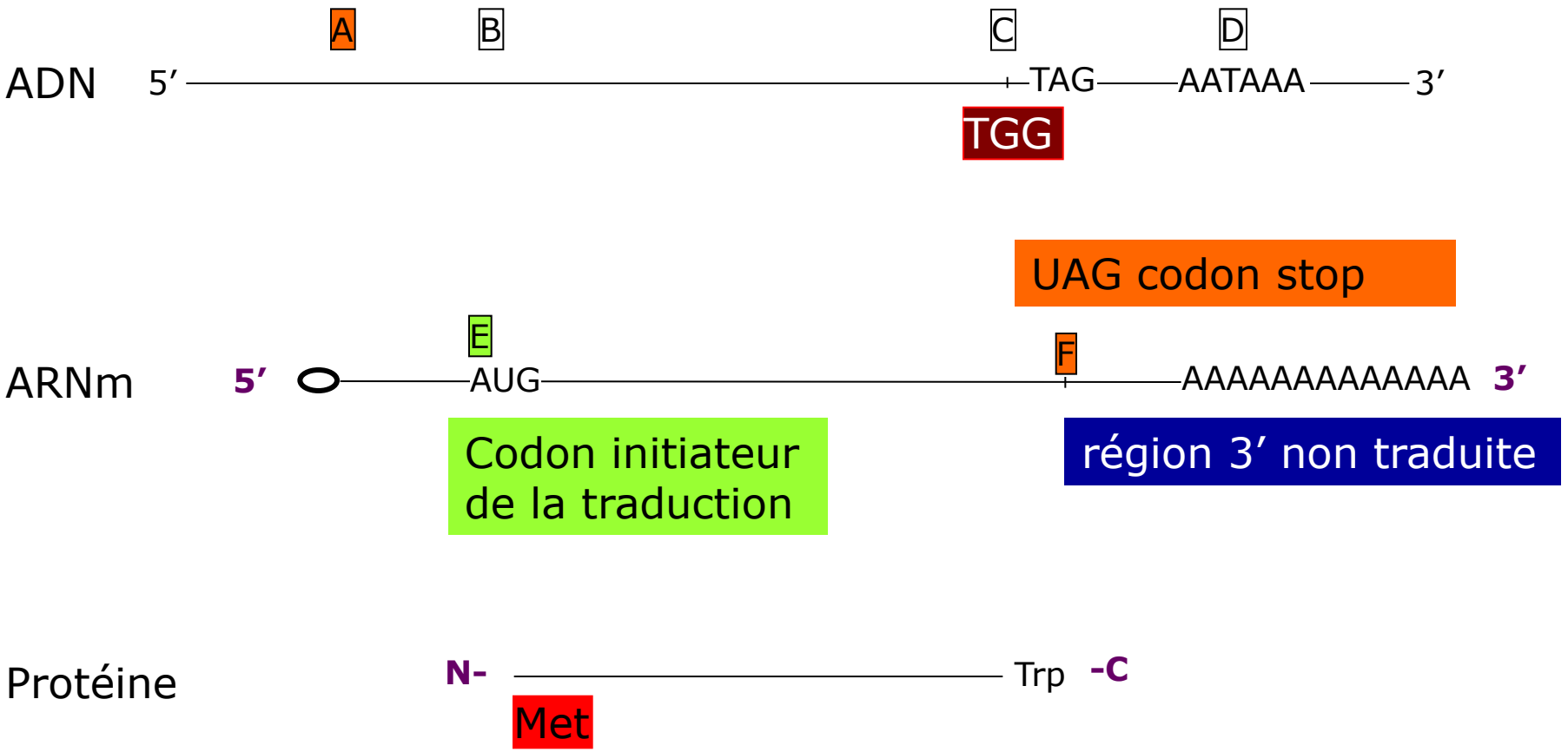
A
B
ATG
C
D
ADN
5'
TAG
AATAAA
3'
brin sens
Région 5' non transcrite, ou promoteur
Unité de transcription
E
F
AUG
AAAAAAAAAAAA
Trp

Exercice 4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B
C
D
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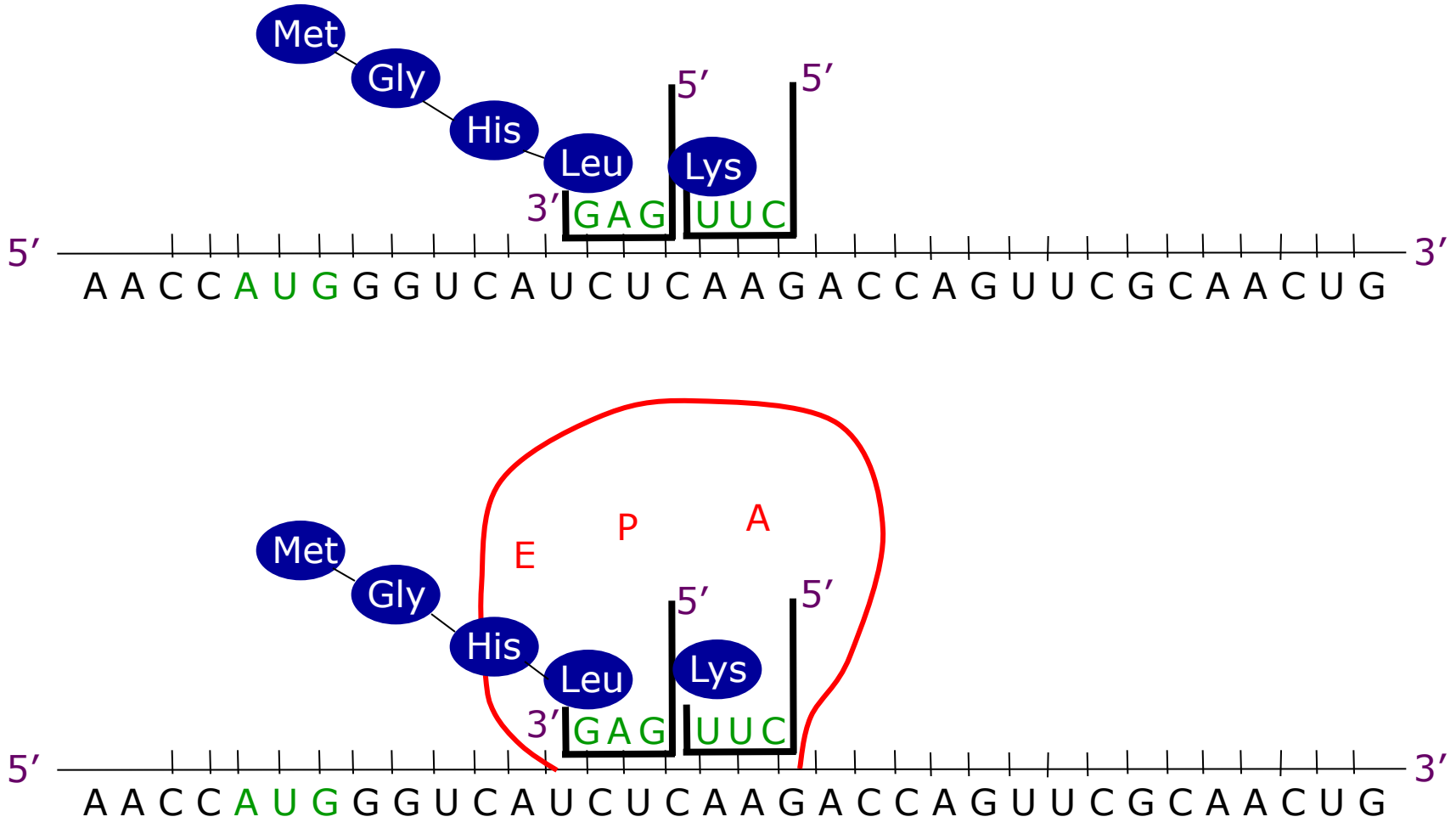
5’
TAG
AATAAA
3’
TGG
UAG codon stop
E
F
ARNm
5’
AUG
AAAAAAAAAAAA
3’
Codon initiateur
de la traduction
région 3’ non traduite
Protéine
N-
Trp
-C
Met

Exercice 5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His
Leu
Lys
5′
5′
3′
G A G
U U C
5′
3′
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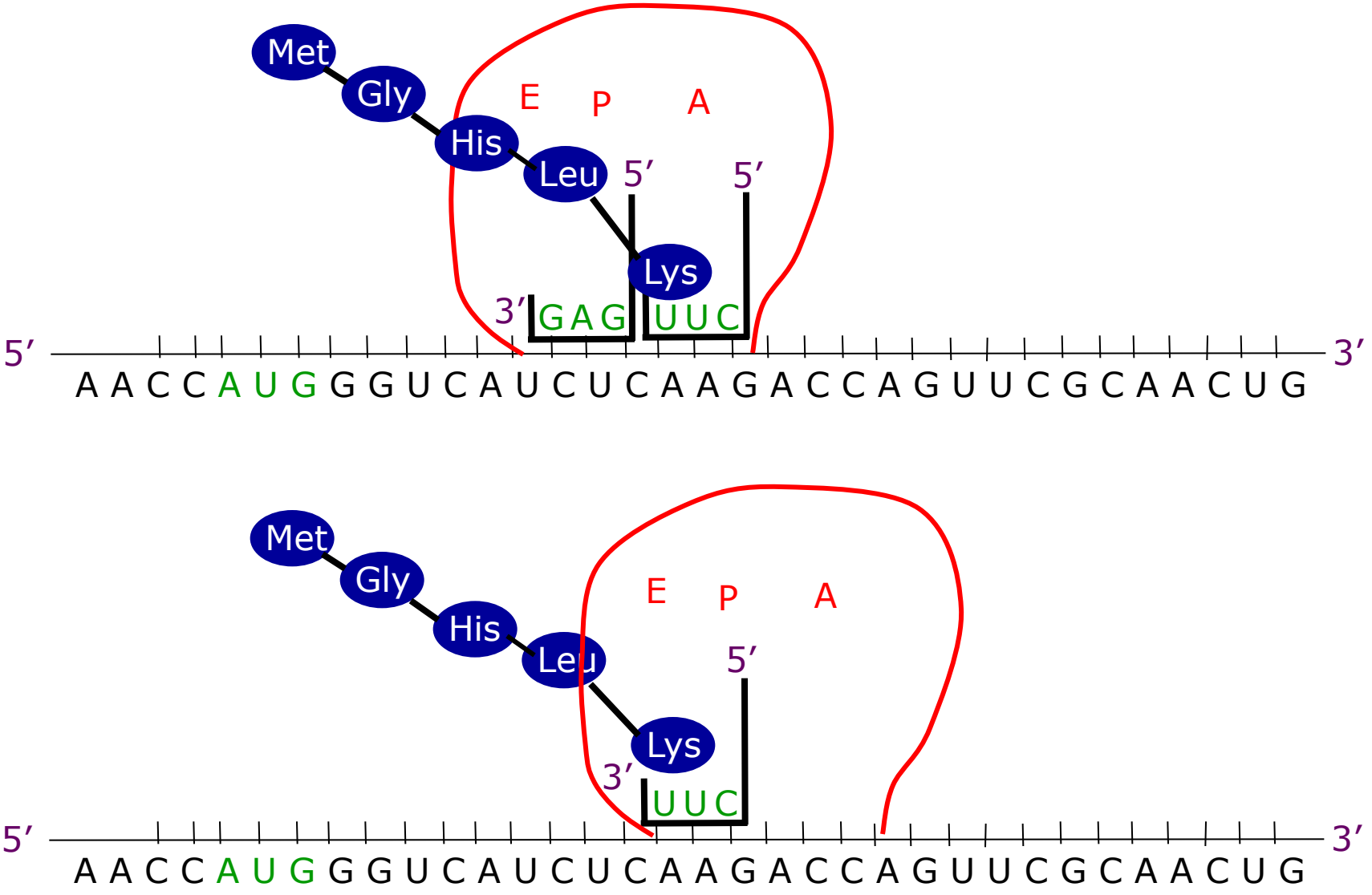
E
P
A
Met
Gly
His
Leu
Lys
5′
5′
3′
G A G
U U C
5′
3′
A A C C A U G G G U C A U C U C A A G A C C A G U U C G C A A C U G

Exercice 5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His
Leu
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E
P
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5′
3′
GAG
UUC
5′
3′
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Met
Gly
His
Leu
Lys
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A
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3′
UUC
5′
3′
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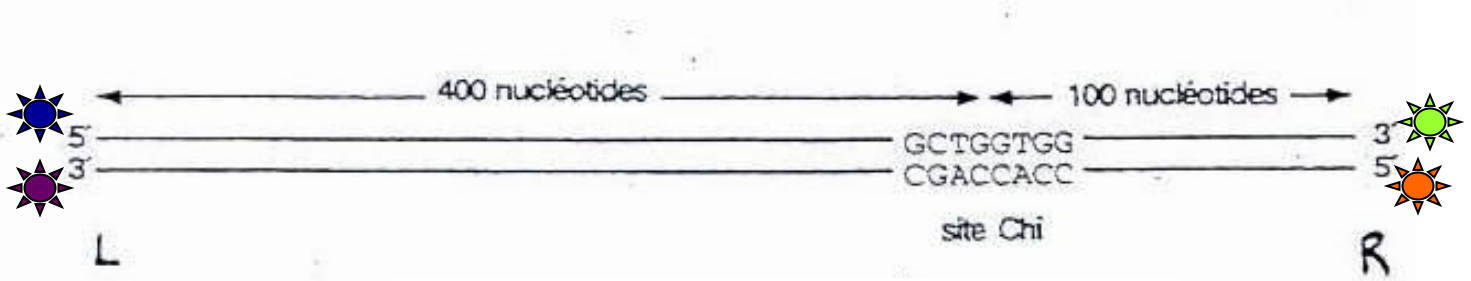
Exercice 6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100 nucléotides
5'
3'
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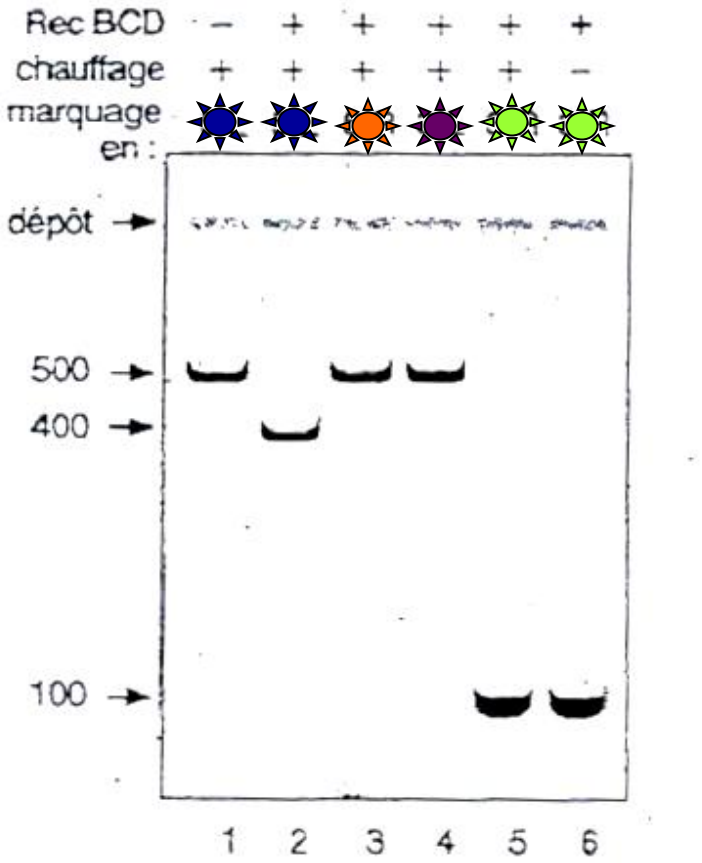
CGACCACC
3'
5'
site Chi
L
R


Rec BCD
chauffage
marquage en :
dépôt
500
400
100
1
2
3
4
5
6

Exercice 7

a ARNm 5’-ACAGUUAAAG-3’ transcription débute au 1ier nucléotide

```
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 61 gattttcatt ctcttgtatt tcttgacttc tttaactaca tatgtatgca taactaagca
121 atatatagca ttgttttaca agttttagag ttgaatgtat atgaattgtc atactattta
181 tttttctaca tctttctctt tttgcctcat cacatttctg agttcagtct tcttttattg
241 gcgtataata ctacatccta acatcccata aggtatttat tctgttattg atggacgttt
```

b

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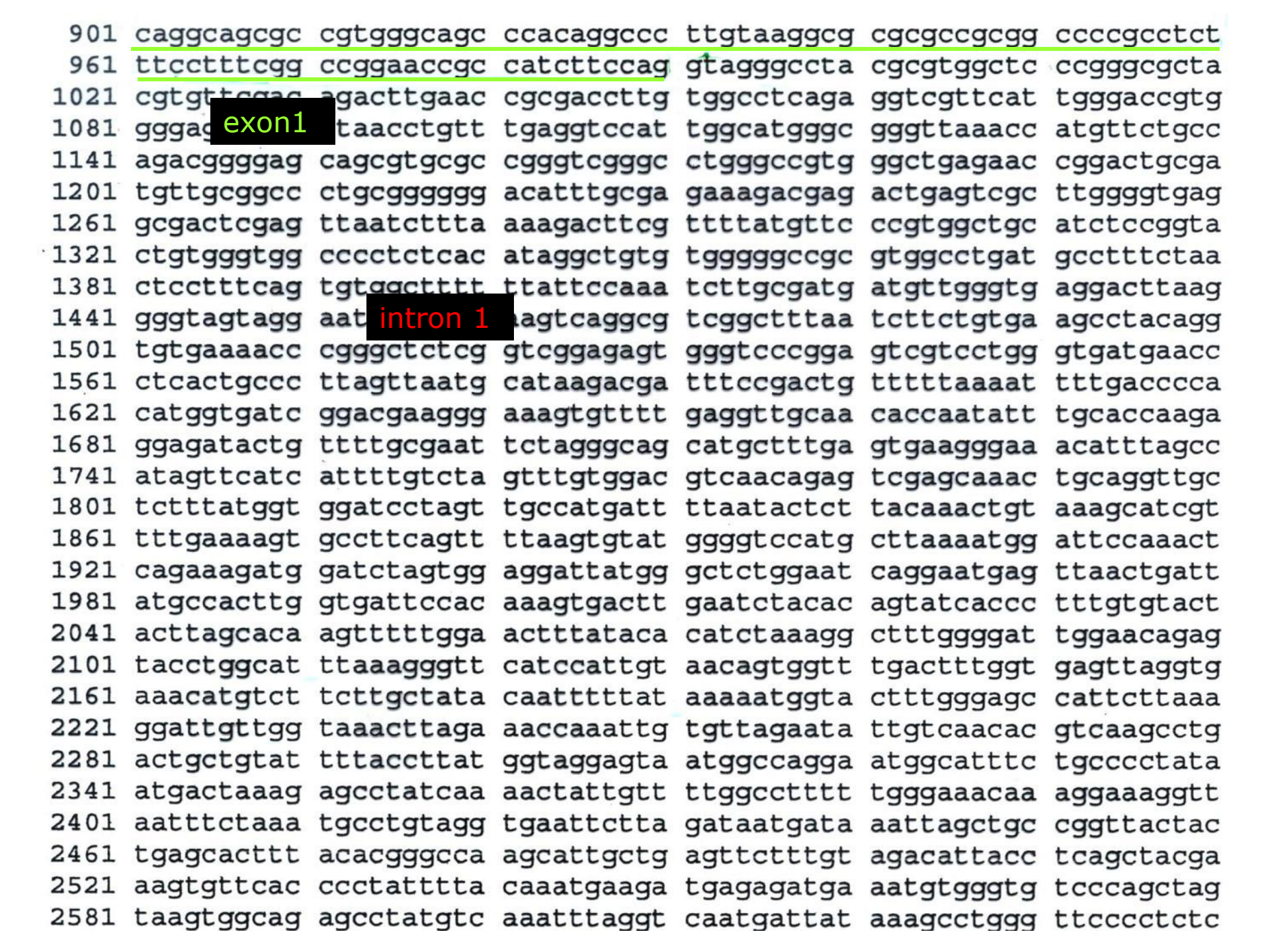


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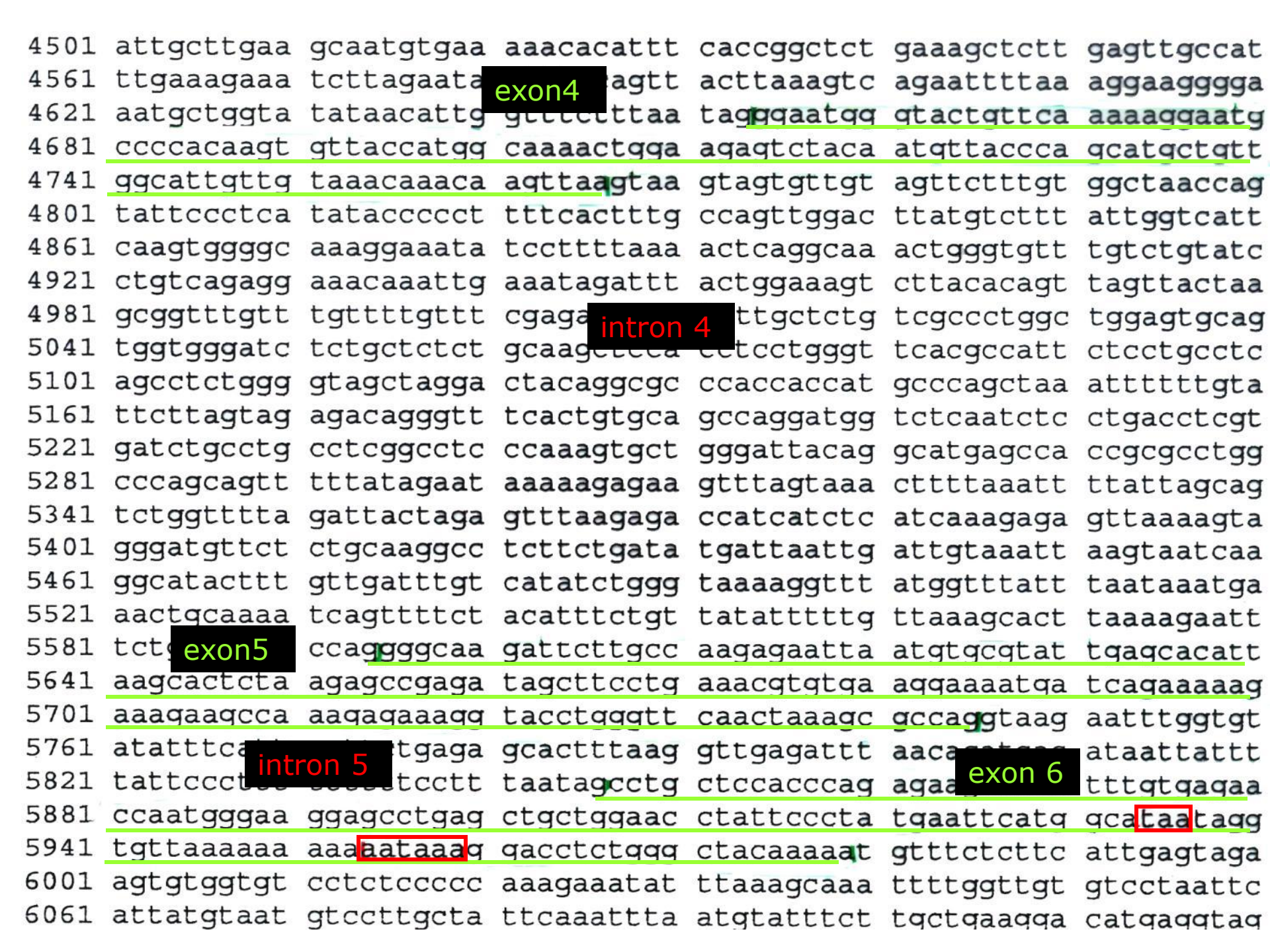
exon2
intron 2
exon3
intron 3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intron 4
exon5
intron 5
exon 6

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d

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en cours	GUA AGU 100 100 60 74 84 50	---- CAG 78 100 100