

This is an overhead designed to help you recognize the important sequences in an pre-mRNA transcript. The sites you need to find are listed below the code.

5'ucauaggacuaucgaugacuauuggacaauuagcauuagguaaguacuucagauguauuuggaguagcauucca
ccaggguacuucuccucuacagggucaaggaccauuuuagaugauuacugcgcauuuuuuucaggacuuguaaggg3'

AUG

AGGUAAGU = 5' Splice Site

PNPPyAP = Branch Site

(Py)_nNCAGG = 3' Splice Site

AAUAAA = Poly A Signal

P = A/G

Py = C/T/U

5'ucauaggacuaucgaugacuauuggacaaauuuagcauuagguaaguacuucagauguuuuggaguagcauucca
ccagguacuucuccuacaggucaaggaccauuaauagaugauuacugcgcauuaaaucaggacuguaaggg3'

Differs from what's mentioned in lecture:

C U G/A A C/U