

DON'T NEED TO KNOW BUT DID YOU KNOW. YOU KNOW?...

Explaining restriction enzyme recognition sites

Because you need a recognition site on each strand that are close together, the enzyme usually recognises a code that is a "*repeat inverted palindrome*" (place a **mirror** in the middle of the code and the each half will be complementary) e.g. if recognition site is GTATAC and **cut** is between G and T:

G T T A C G G T A T A C T A T T G C G C
C A A T G C C A T A T G A T A A C G C G

That ensures that the corresponding recognition sequence is close by on the opposite strand. Therefore the sticky ends will be short and most of the fragment will remain double stranded.

In the sequence we just looked at, no other 6 base sequence could work as a recognition site. Try and find one...

G T T A C G G T A T A C T A T T G C G C
C A A T G C C A T A T G A T A A C G C G

REMEMBER: some restriction enzymes don't produce sticky ends. Can you design one with a 4 base recognition sequence?...

e.g. here's one called HaeIII that recognises GGCC and cuts between G and C:

C G T T A C G G G C C T A T T G C G C A
G C A A T G C C C G G A T A A C G C G T