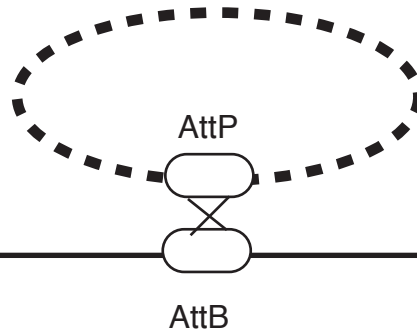


Separate Phage and Bacterial DNA genomes before integration

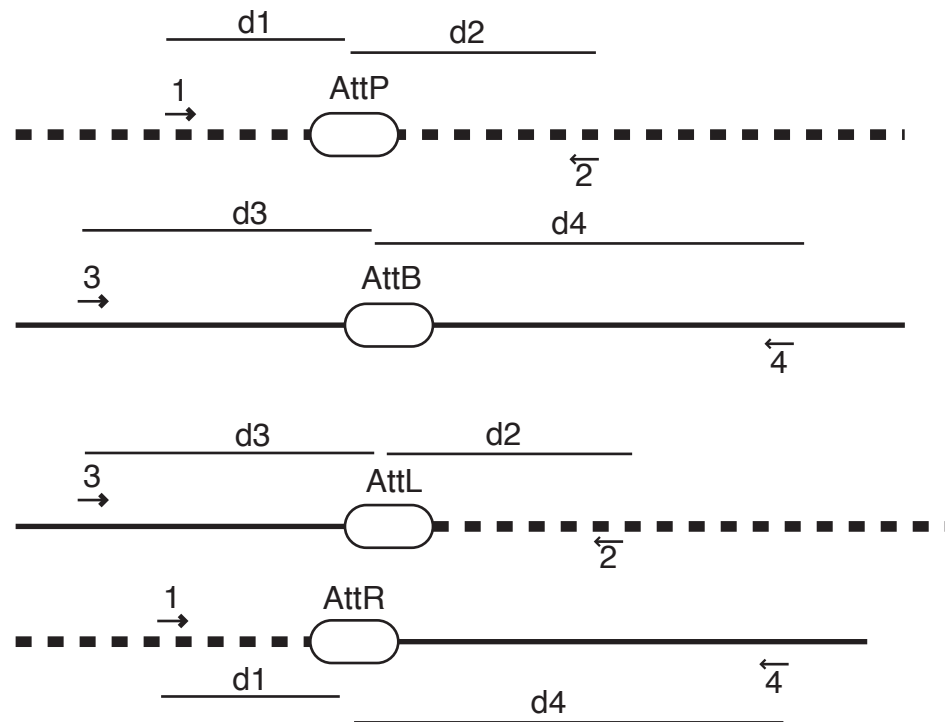


Lysogen structure after recombination



The goals of the web exercise are to use 4 primers and various templates to determine unique PCR product sizes for each template and the optimal conditions for PCR. Product sizes can be determined most easily with Sequence Extractor. PCR conditions, theoretical Tm's can be determined using primer3.

Find new primers using primer3 to compare to those used in the experiment. To begin mark the core sequence in attP with brackets [], to identify it as the "target". Allow the program to pick two new primers and note the distance between the left primer and the target sequence (d1). Determine d2 similarly. Reset the form, paste in AttB and pick 2 new primers, 3 and 4 such that the PCR fragment sizes are distinct.



$$d1 + d2 \neq d3 + d4 \neq d3 + d2 \neq d1 + d4$$

Primer positions can be manipulated by the "included region" and "product size range" parameters.