Library kits

- Your protocol will determine whether you use a kit
  - Whole genome/RNA sequencing mostly use kits
  - ChIP-seq, ATAC-seq, more specialized protocols do many steps outside of kits

- Kit considerations:
  - How much input do you have? (> µg, < 10 ng, single-cell)
  - What quality input do you have?
  - Do you need to worry about fragmentation or amplification biases?
  - RNA: do you want total, poly-A, micro, or ribosomal-depleted RNA?
  - RNA: do you want a strand-specific library? (Yes)