* There have been many recent developments in highly multiplexed FISH experiments, with more and more RNA or DNA molecules being visualized.
  + Methods have evolved that let us visualize hundreds to a thousand RNAs in a tissue.
    - FISSEQ, STARMap, MERFISH, ClampFISH, and osmFISH
  + Poorly designed probes with non-specific affinities could increase background or noise
    - Therefore, proper probe design could improve SNR in complicated microscopy images that involve multiple washing and annealing cycles to readout a probe’s barcode
* To visualize these molecules, FISH probes which hybridize to the molecules of interest in situ must be highly specific to prevent off-target binding
  + - Off-target effects could influence observed levels for low expressed genes that have a high impact on cell type inference
  + Proximity ligation assay designs such as PLAYR and SNAIL have evolved to improve probe specificity
  + However, these designs require the design of additional probes which target the same molecules in close proximity to each other
* Furthermore, with increasing numbers of molecules to visualize and increasing numbers of probes to design to detect those molecules precisely, there is a multiplicative increase in the number of probes to design for each experiment
* Therefore, there is a need to design FISH probes for proximity ligation assays *en masse*, with efficiency and systematic quality assurance.

This is why we developed the SNAIL Probe Designer.