* Step1: Upload
  + Crosstab file median signal minus background, example file btn
  + Optional: crosstab file signal saturation, example btn file
  + Optional: kinase-substrate mapping file or use build in file btn
  + Btn = to start
* Step2: Design Option
  + Select groups based on input (ctl vs case)
  + Qc options:
    - Max signal
    - R2
    - Optional; Signal saturation
    - LFC or p value (maybe per chip analysis option), across chip?
    - Iter number, seed num
* Step3: Overview:
  + info about qc peptides number, show lfc ,and download option of LFC, and linar model table
  + Heatmap, norm vs normal
  + Boxplot-violin
  + Curve plots
  + Water fall

Step4: Kinase Analysis

* + Kinase table (down load btn)
  + Histograms
  + Reverse krsa
* Step5: Network
  + Z zscore cutoff
  + Network options