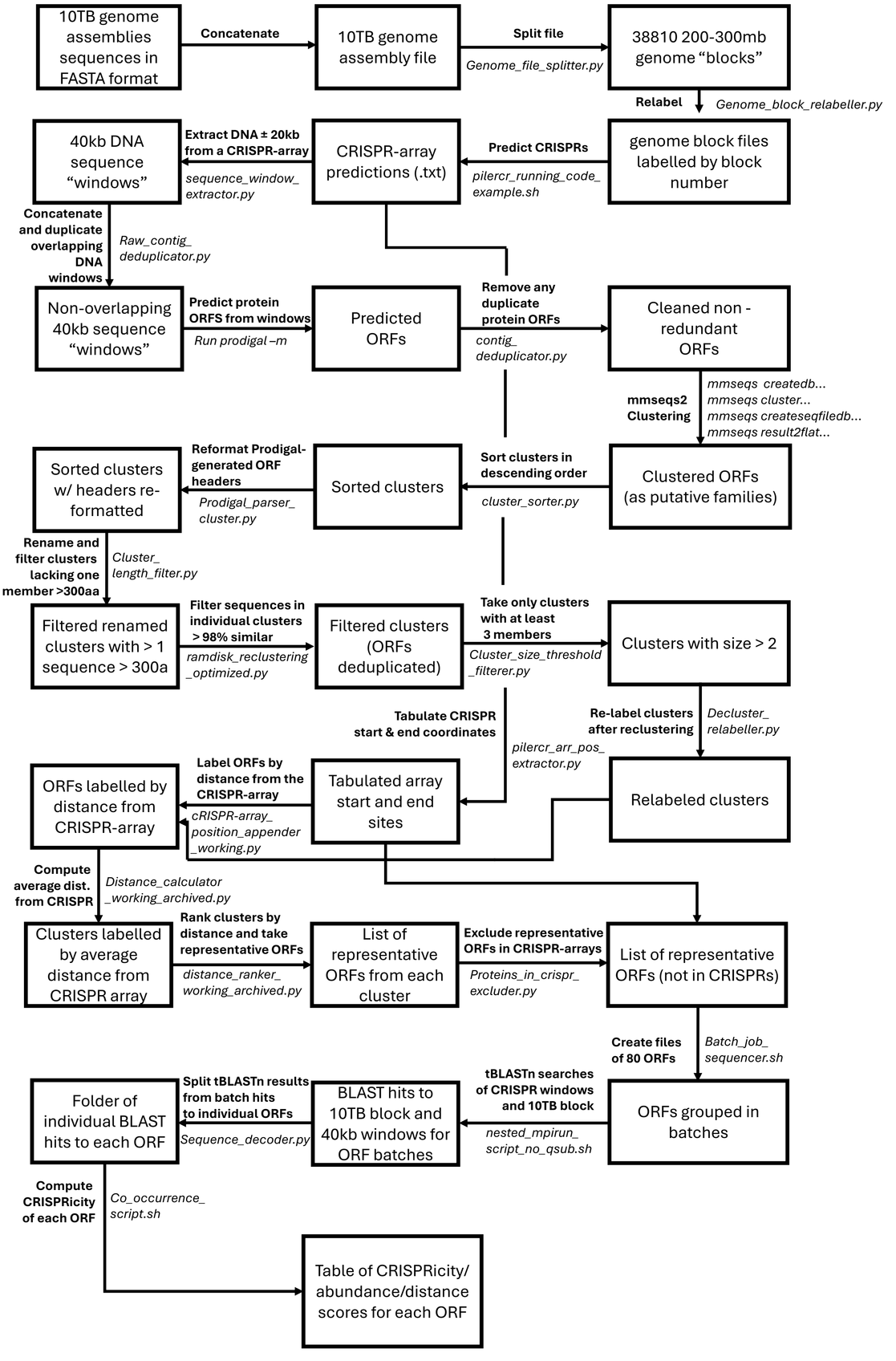
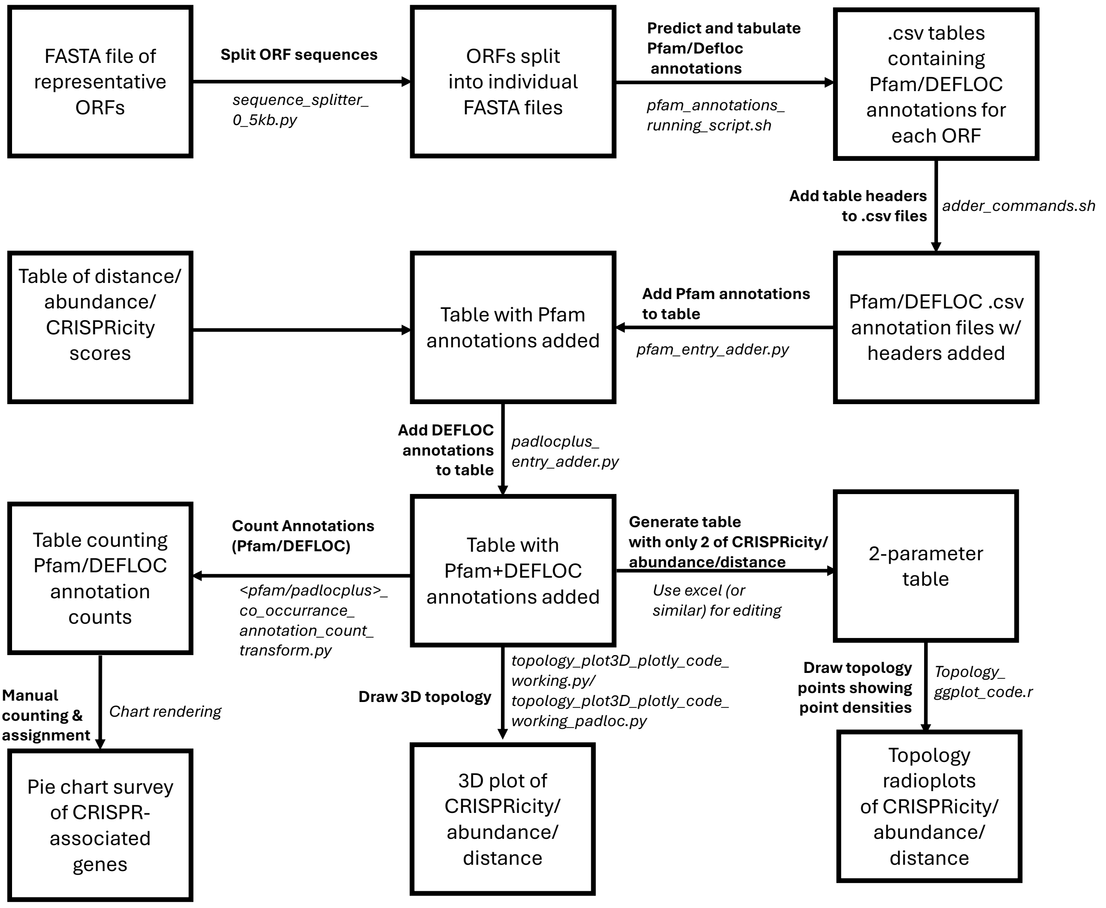
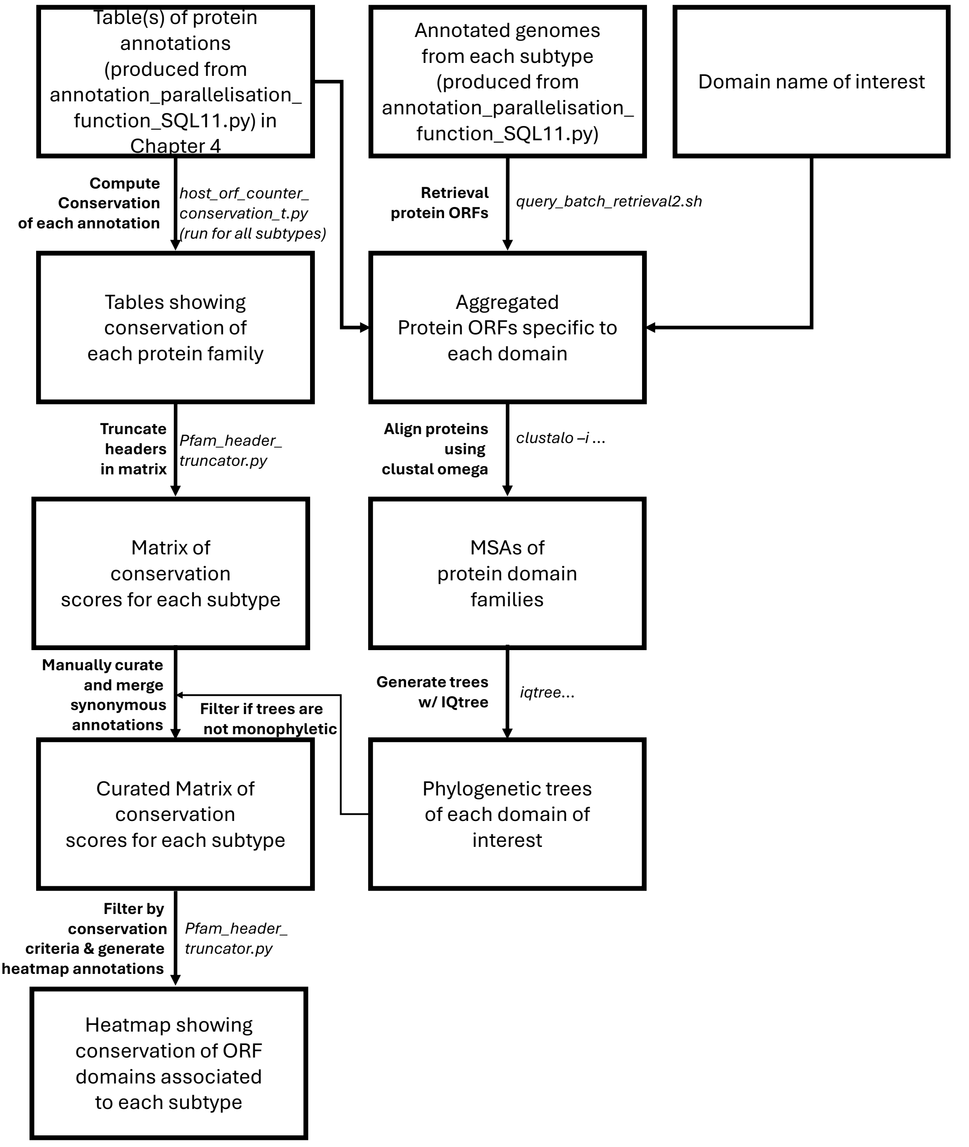
Workflow to mine 10TB data block for CRISPR-associated sequences and compute CRISPRicity



Workflow to annotate ORFs and visualize the abundance, CRISPRicity, distance parameters



Workflow for rendering conservation heatmaps among proteins associated to CRISPR-Cas subtypes