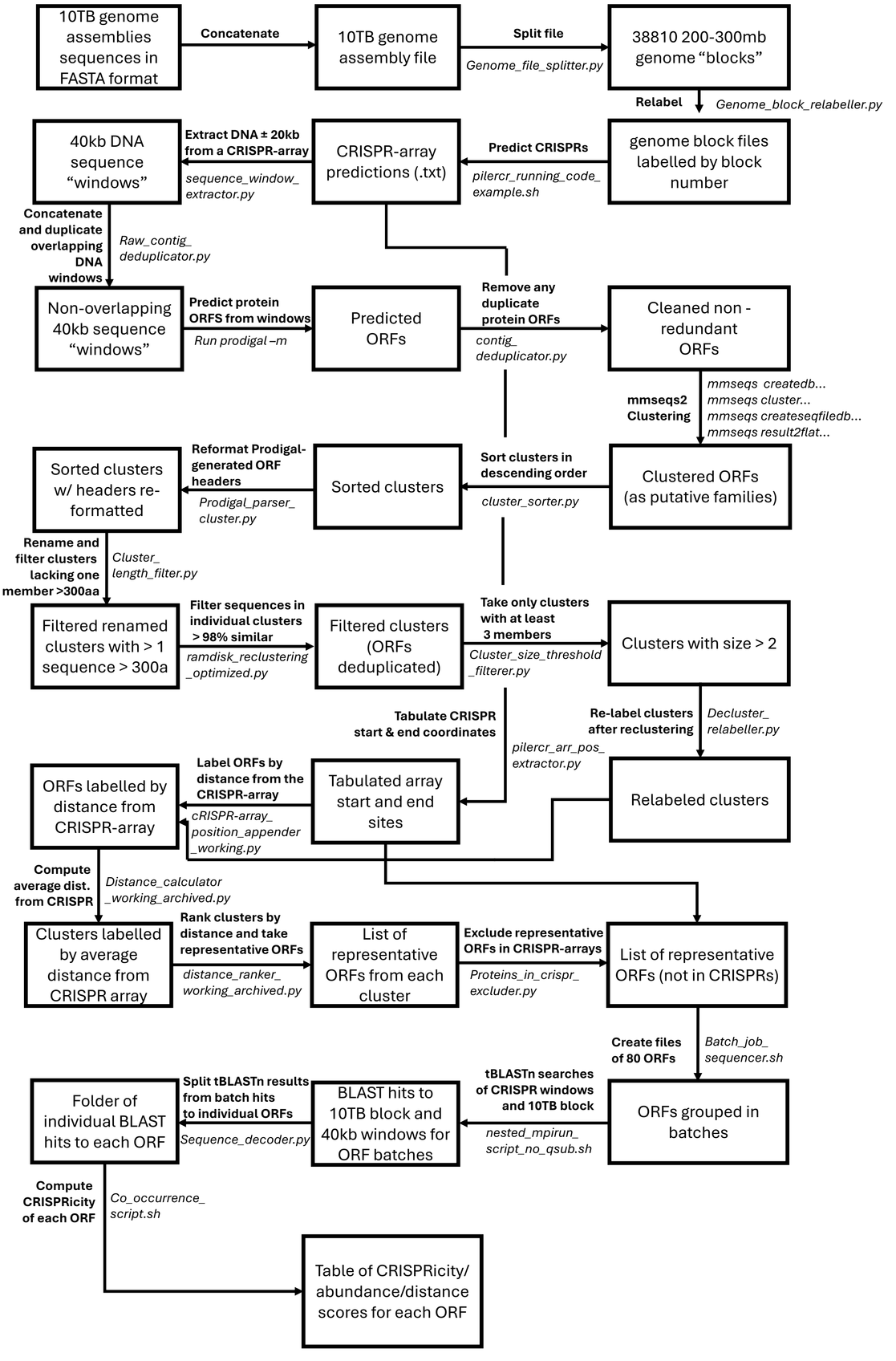
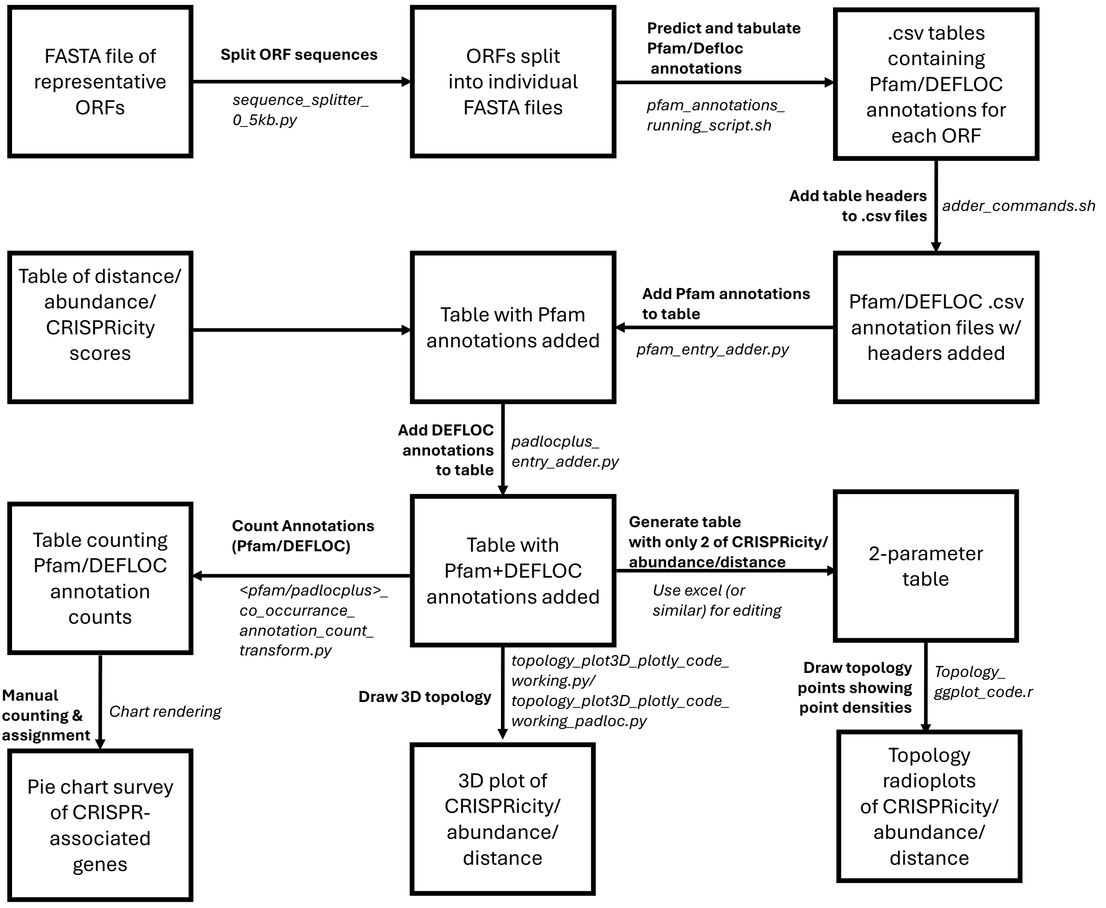
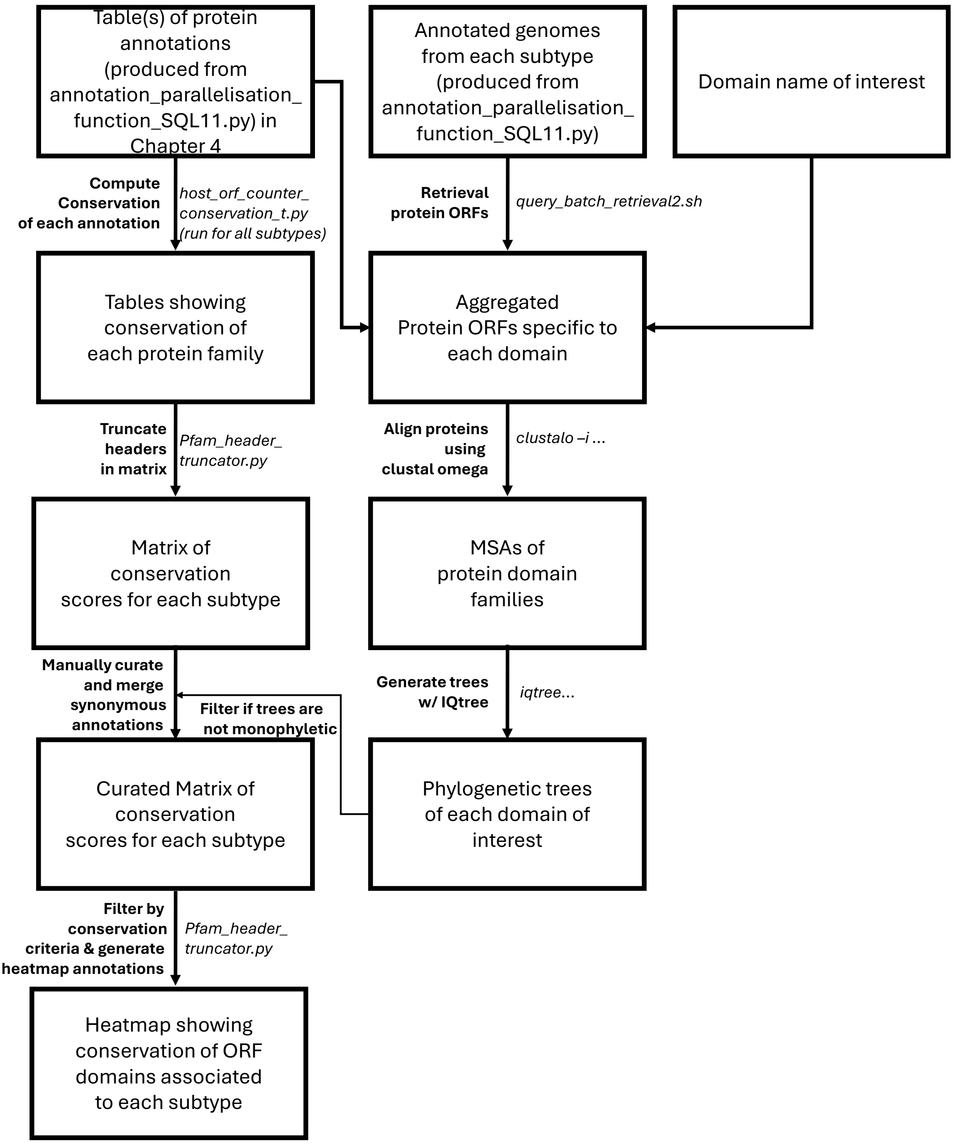
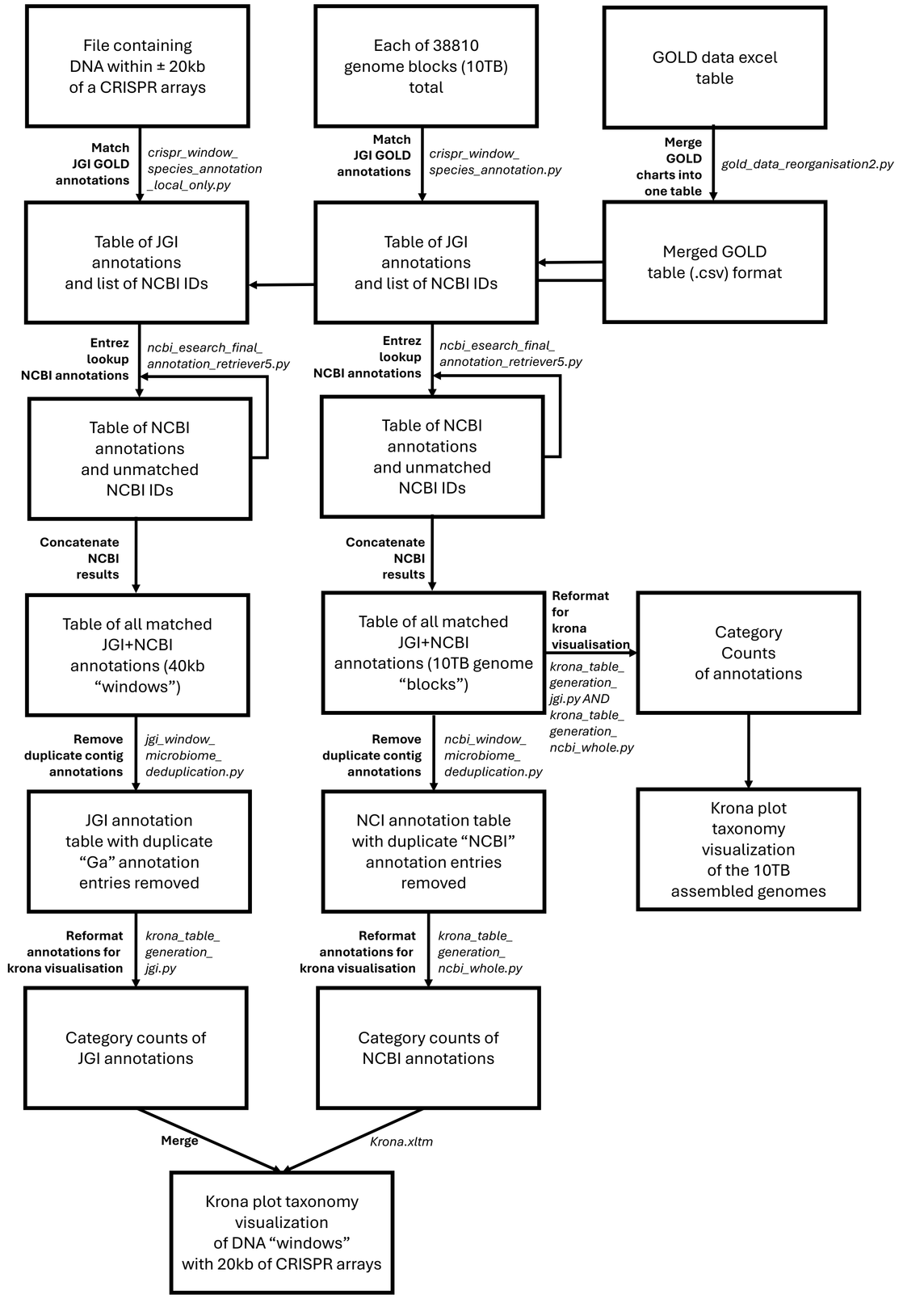
# Workflow to mine 10TB data block for CRISPR-associated sequences and compute CRISPRicity



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



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



# Workflow for sequence metadata retrieval and visualisation