Hypothesis-led approach

Mine Pubmed, Google scholar → List of processes/concepts → Mine FlyBase → Gene list for each process → Mine FlyAtlas for expression of each gene → Sort by common enrichment

Hypothesis-free approach

Download FlyAtlas.org dataset → Extract columns (tissues) of interest → Sort by common enrichment → Sort by Gene ontology → Candidate gene clusters with predicted functions → Gene clusters with unexpected (or unknown) functions