

Special Grant - \$70,000 for Two Years



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LAM Cell Atlas (LCA): An Intuitive Web Portal for Integrative Analysis and Visualization of LAM Single Cell Multiomics Data

Lymphangiomyomatosis (LAM) is a rare lung disease of women, with unclear cell origin, tumor microenvironment, and cellular interactions in the LAM lesion. The recent application of single-cell transcriptomics in LAM has shed light on LAM cell identity and likely origin, brought new insights into pathways and gene networks related to LAM disease pathogenesis; but the technical challenges of handling and analyzing a large amount of single-cell multi-omics datasets; and the lack of intuitive and easy-to-use tools for data analysis and visualization, have limited experimental biologists and LAM research experts from directly exploring and utilizing the rich single-cell data resources. We propose to integrate a compendium of LAM single-cell multi-omics datasets and construct an intuitive, interactive, multidimensional LAM cell atlas of LAM lesions and their surrounding microenvironment to expedite data sharing, data reanalyzing, and to facilitate hypothesis generation and collaborative LAM research. Considering the rarity of LAM disease and the limited availability of fresh tissue samples, our long-term goal is to establish a LAM Cell Atlas as a living resource that will iteratively expand to include new single-cell omics data from LAM researchers around the world.

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