

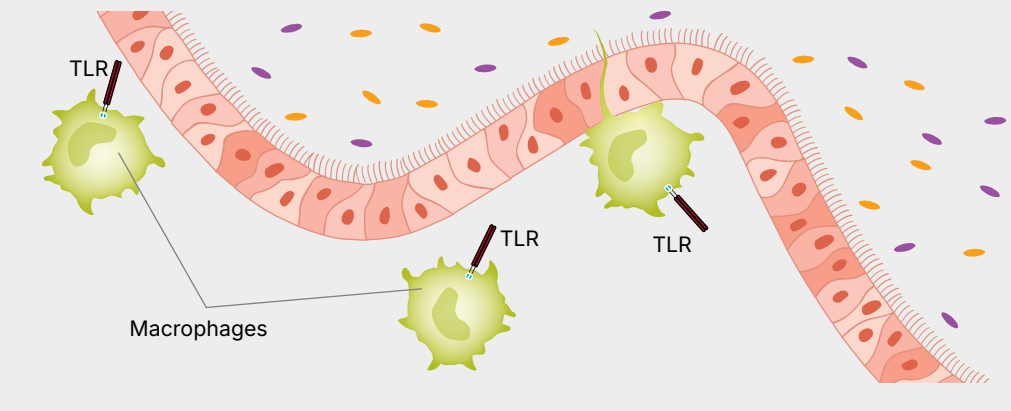
The Complex Biology of Macrophages: Origins, Functions, & Activation States

Common Macrophage Markers

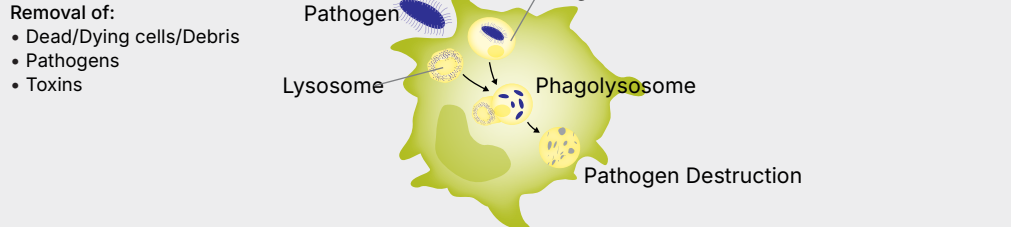
B7-1/CD80 B7-2/CD86 CCR5 CD11b/Integrin αM CD11c CD14 CD15 (SSA-1)/Lewis X CD68/CD11b CD163	EMR1 (Human) F4/80 (Mouse) FcγRI/CD64 FcγRII/CD32 FcγRIII/CD16 Galectin-3/Mac-2 GITR Ligand HLA-DR Integrin αL/CD11a	LAMP2/CD107b LILRB4/CD85k/ILT3 M-CSF R/CD115 MHC Class II Siglec-3/CD33 TLR2 TLR4
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Common Macrophage Functions

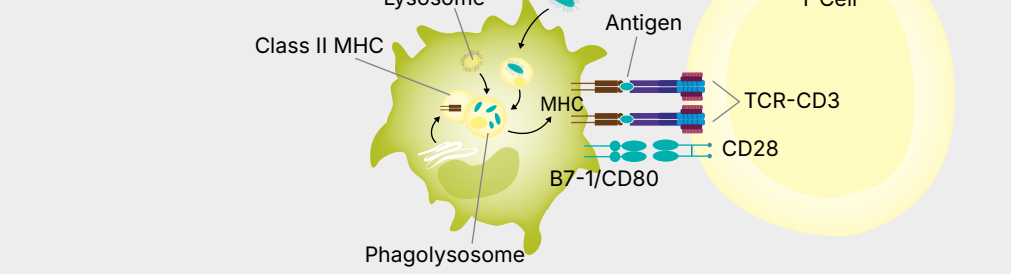
Immune Surveillance



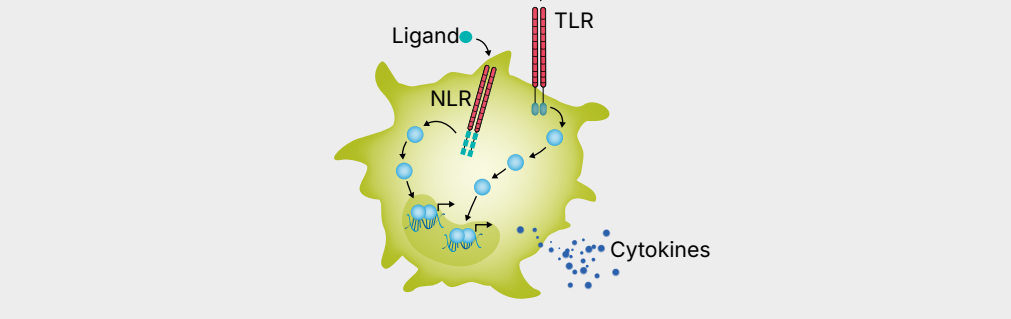
Phagocytosis



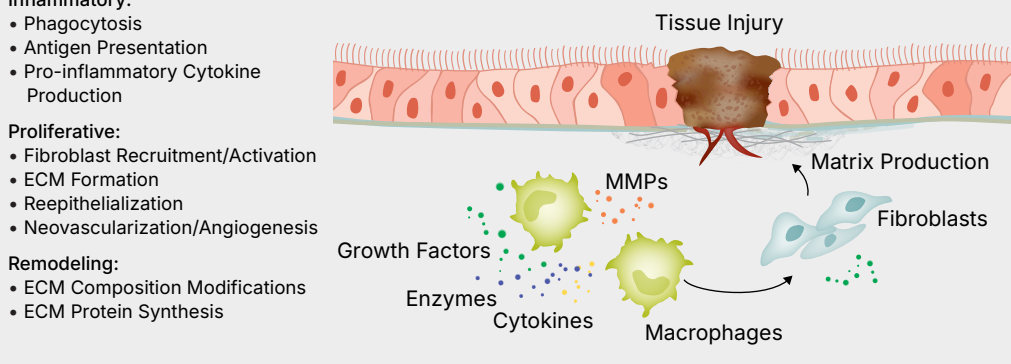
Antigen Presentation



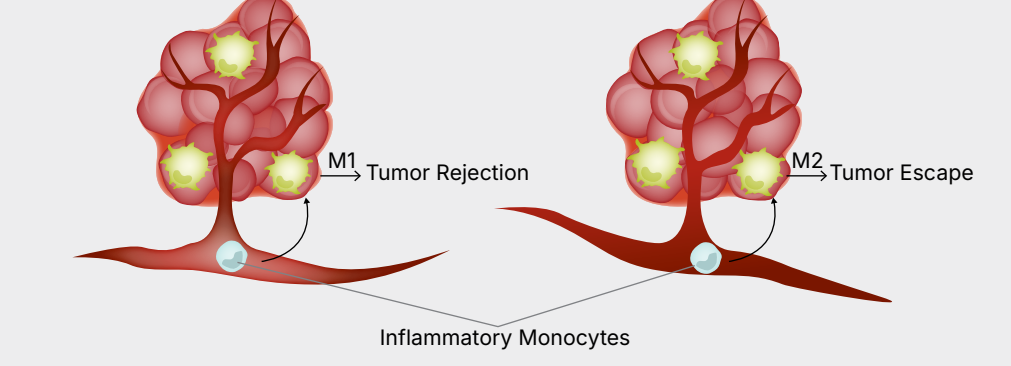
Cytokine Production



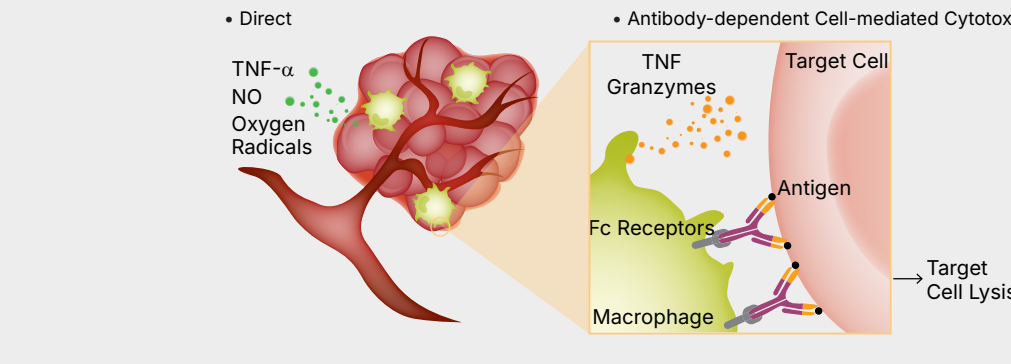
Wound Healing and Tissue Remodeling



Tumor Infiltration



Cytotoxicity



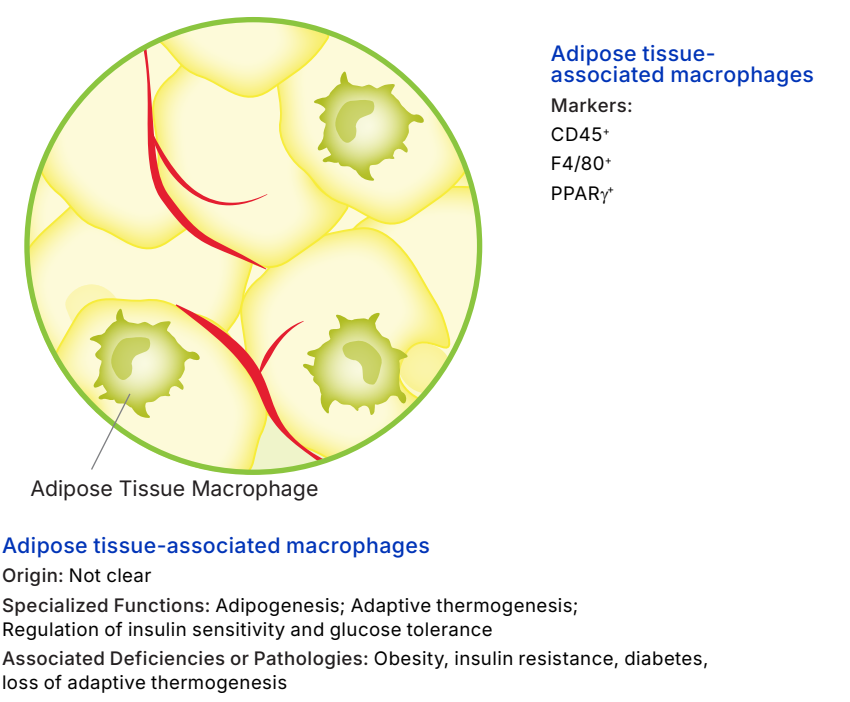
The Origins of Mouse Tissue-Resident Macrophages Redefined

During development and throughout life, macrophages reside in many tissues of the body, contributing to both the maintenance of tissue homeostasis and the immune response following injury or pathogenic insult. In the late 1960s, van Furth and Cohn proposed that tissue-resident macrophages develop primarily from circulating, bone marrow-derived monocytes. This model was widely accepted until recent fate-mapping studies demonstrated that several tissue-resident macrophage populations in mice arise from HSC-independent embryonic precursors and are maintained by self-renewal. The earliest macrophages or primitive progenitors arise from early and late erythro-myeloid progenitors (EMPs) generated in the extra-embryonic yolk sac during primitive hematopoiesis at embryonic age 7.5 and 8.25 (E7.5 and E8.25). These EMPs can give rise to yolk sac-derived macrophages without passing through a monocytic intermediate and are the first to seed the fetal tissues following initiation of the blood circulation. With the exception of microglial cells in the brain, the primitive macrophages in most fetal tissues are subsequently replaced either partially or completely by fetal liver-derived monocytes. Fetal liver monocytes are generated from EMPs derived from either the yolk sac or hemogenic endothelium of the placenta and umbilical cord, or from hematopoietic stem cells (HSCs) generated in the para-aortic splanchnopleura (P-Sp) and aorta-gonad-mesonephros (AGM) regions of the embryo. These progenitors migrate to the fetal liver in two successive waves around E9.5 (EMPs) and E10.5/E11 (immature and mature HSCs) and expand, giving rise to fetal liver monocytes, which enter the circulation and differentiate into macrophages in peripheral tissues. In some tissues, including the liver, lung, skin, spleen, and peritoneum, fetal liver monocyte-derived macrophages maintain the ability to self-renew into adulthood and establish the tissue-resident population. In other tissues, such as the dermis and gut, fetal liver monocyte-derived macrophages are gradually replaced by the recruitment of bone marrow-derived monocytes generated from adult hematopoiesis beginning around E17.5.

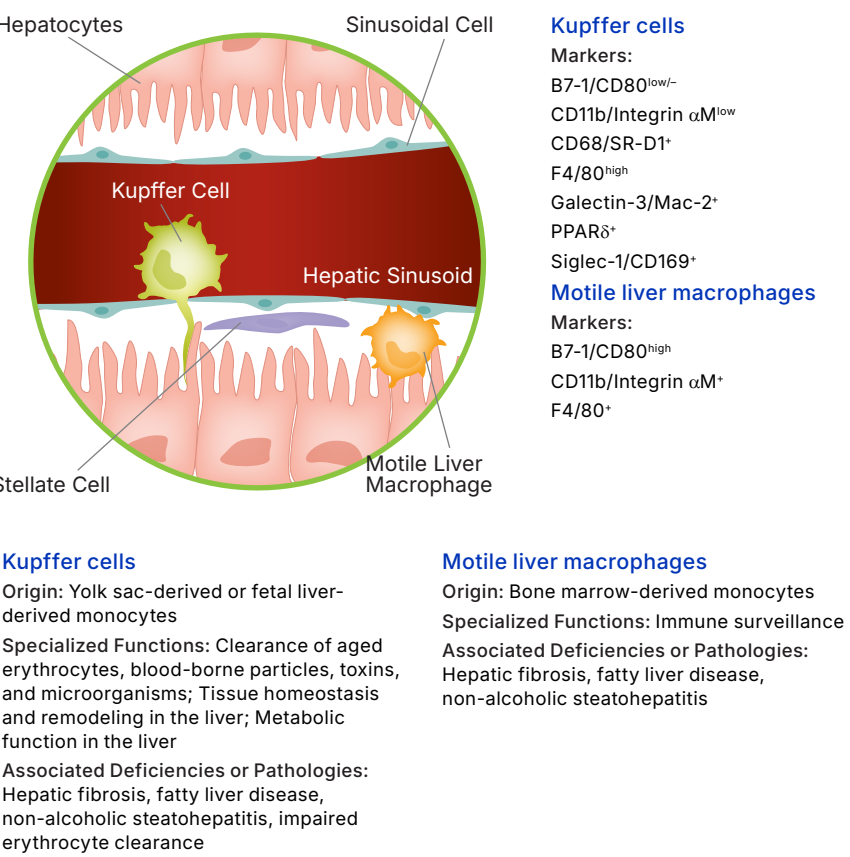
Tissue-resident macrophages are a versatile, heterogeneous group of cells that support multiple tissue functions. Most of our knowledge about these cells has come from studies in mice, which suggest that the phenotypes and functional programs of tissue macrophages are determined by signals that they receive in their tissue microenvironments. Aside from providing the first line of defense against invading pathogens, tissue-resident macrophages have a fundamental role in maintaining tissue integrity and homeostasis. In addition, they may have specialized functions based on their locations and distinct gene expression profiles. For example, osteoclasts are bone-resident macrophages that specialize in bone resorption, while red pulp macrophages in the spleen specialize in heme degradation and iron recycling. Abnormalities in macrophage functions have been associated with a wide range of chronic inflammatory and autoimmune diseases including obesity and type II diabetes, asthma, atherosclerosis, fibrosis, cancer, inflammatory bowel disease, multiple sclerosis, and rheumatoid arthritis, suggesting that macrophages may serve as therapeutic targets. This possibility, however, requires a greater understanding of the differences in the development, phenotypes, and functions of tissue-resident macrophages.

Markers, Origins, & Specialized Functions of Select Mouse Tissue-resident Macrophages

Adipose Tissue

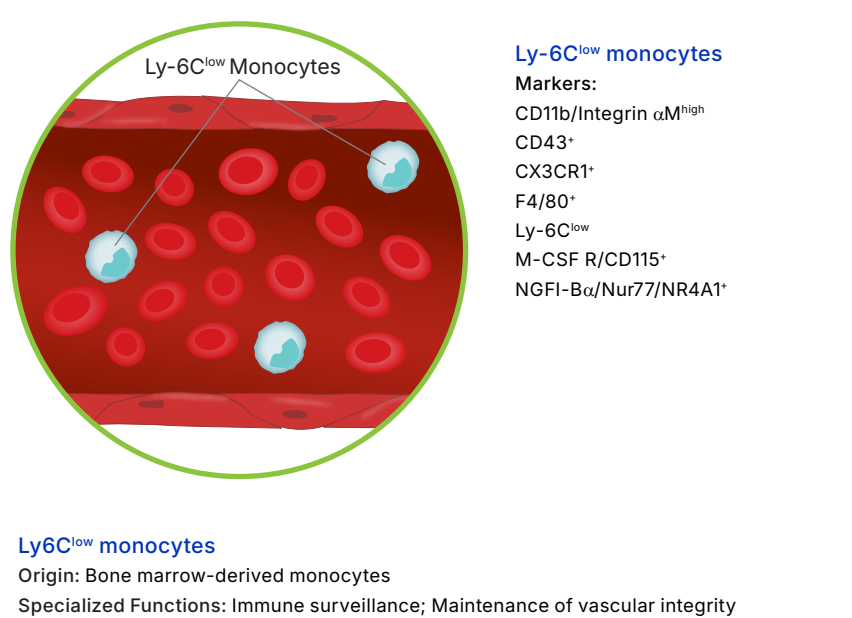


Liver

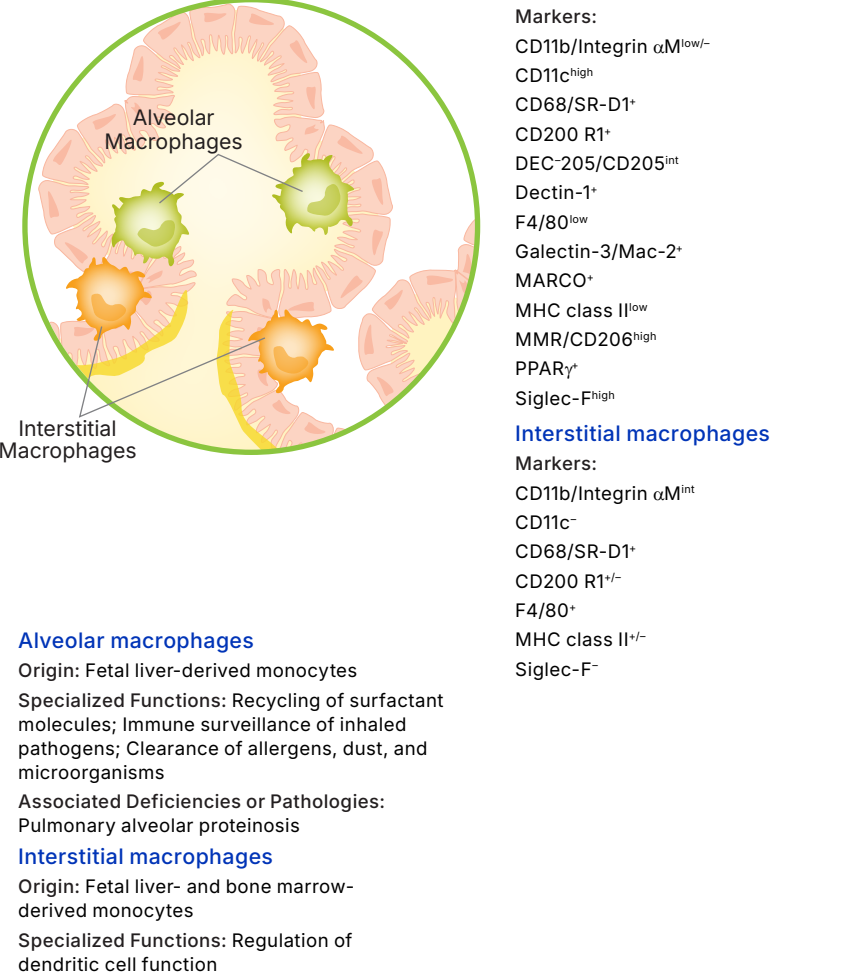


Associated Deficiencies or Pathologies: Hepatic fibrosis, fatty liver disease, non-alcoholic steatohepatitis, impaired erythrocyte clearance

Blood

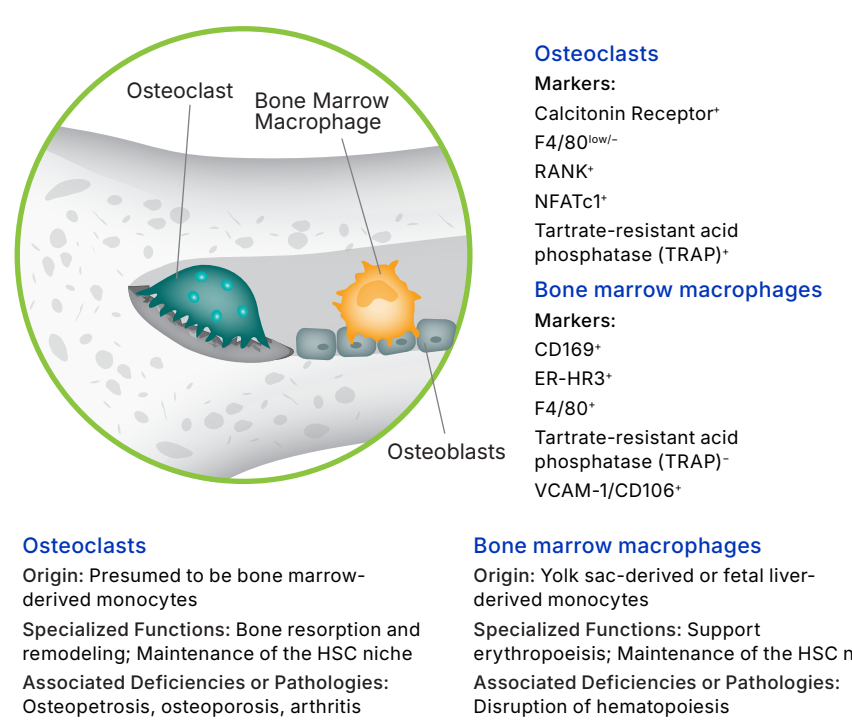


Lung

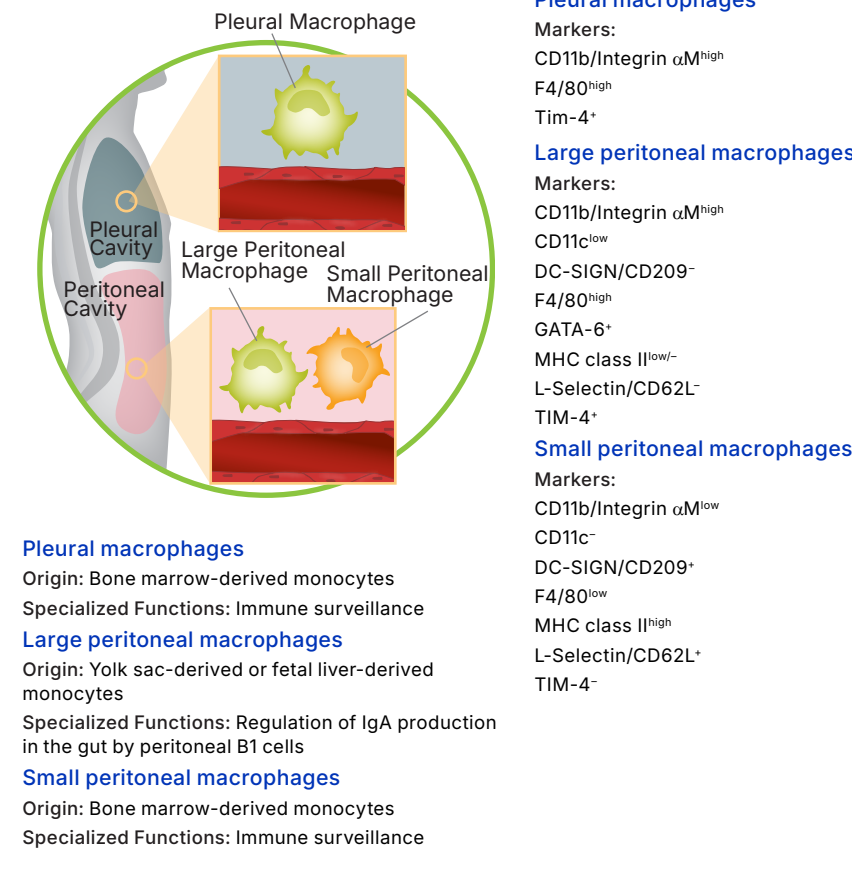


Specialized Functions: Regulation of dendritic cell function

Bone

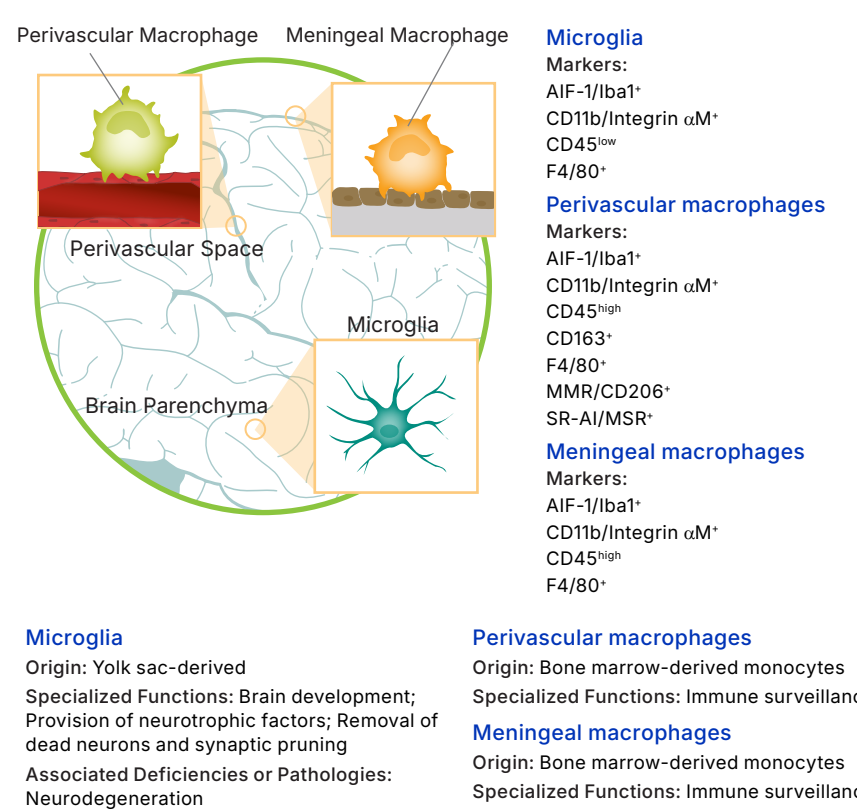


Serosal Tissues

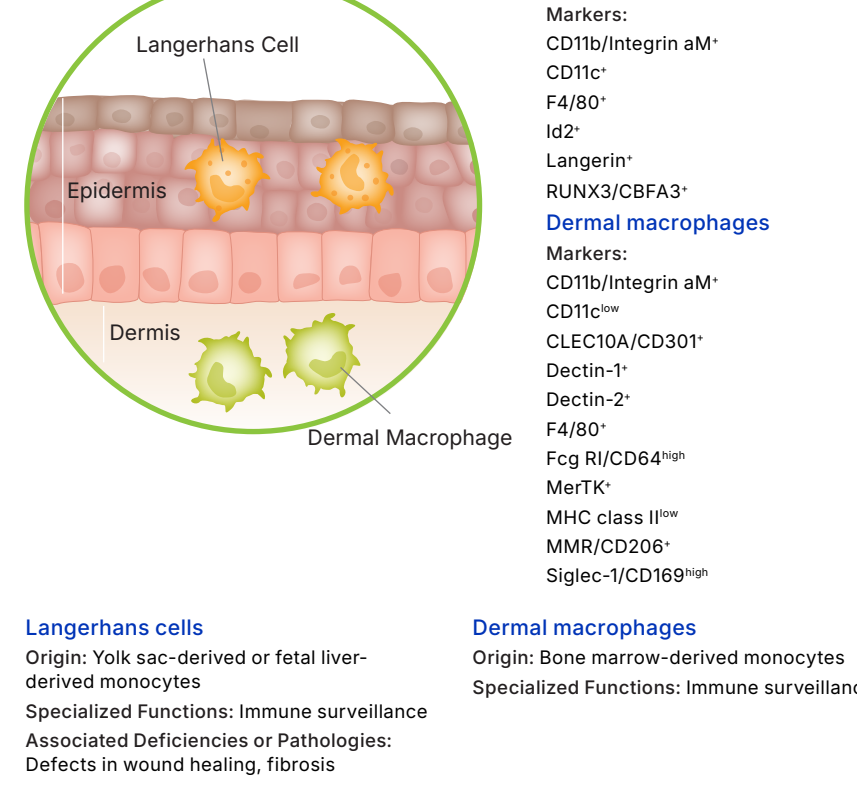


Specialized Functions: Regulation of IgA production in the gut by peritoneal B1 cells

Central Nervous System

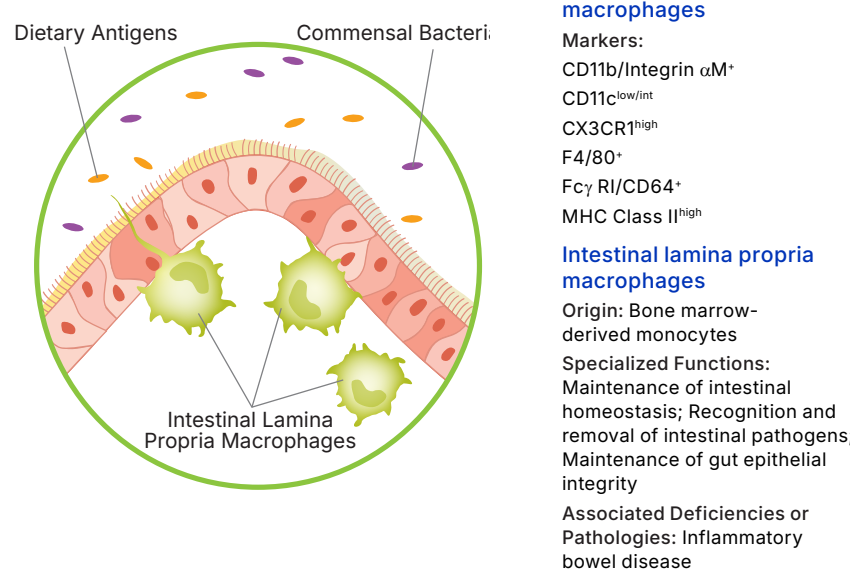


Skin

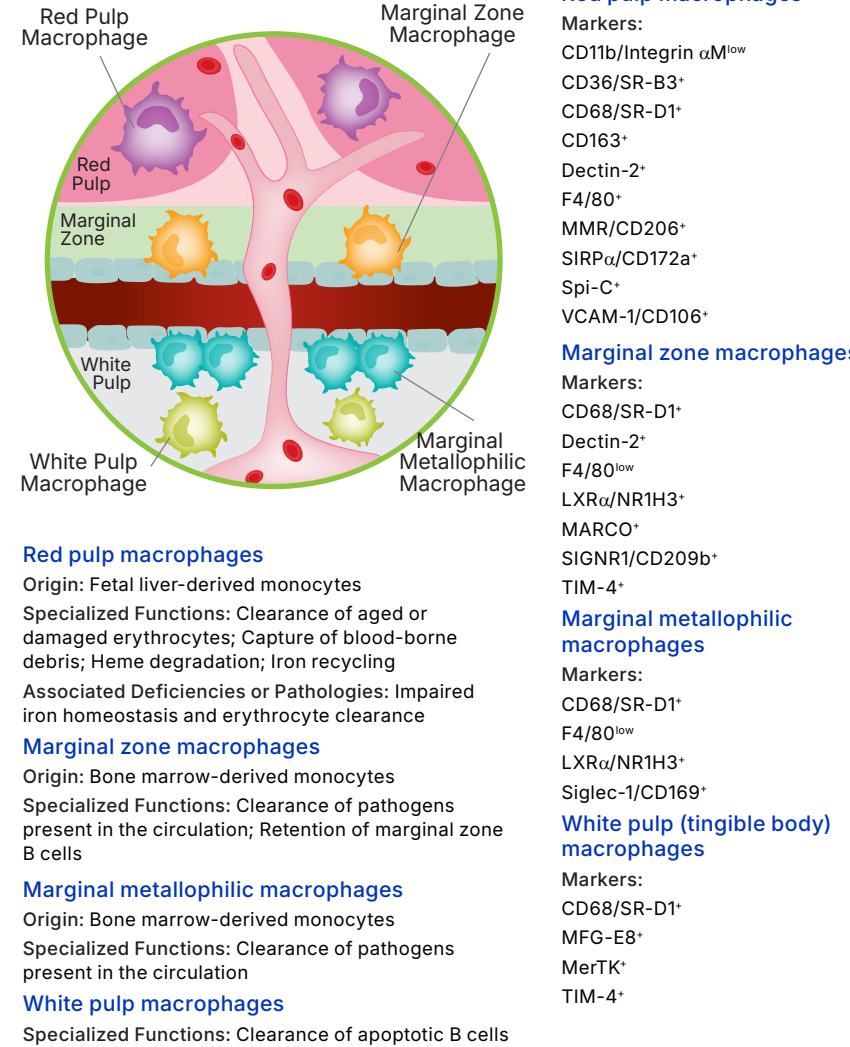


Specialized Functions: Immune surveillance

Gastrointestinal Tract



Spleen

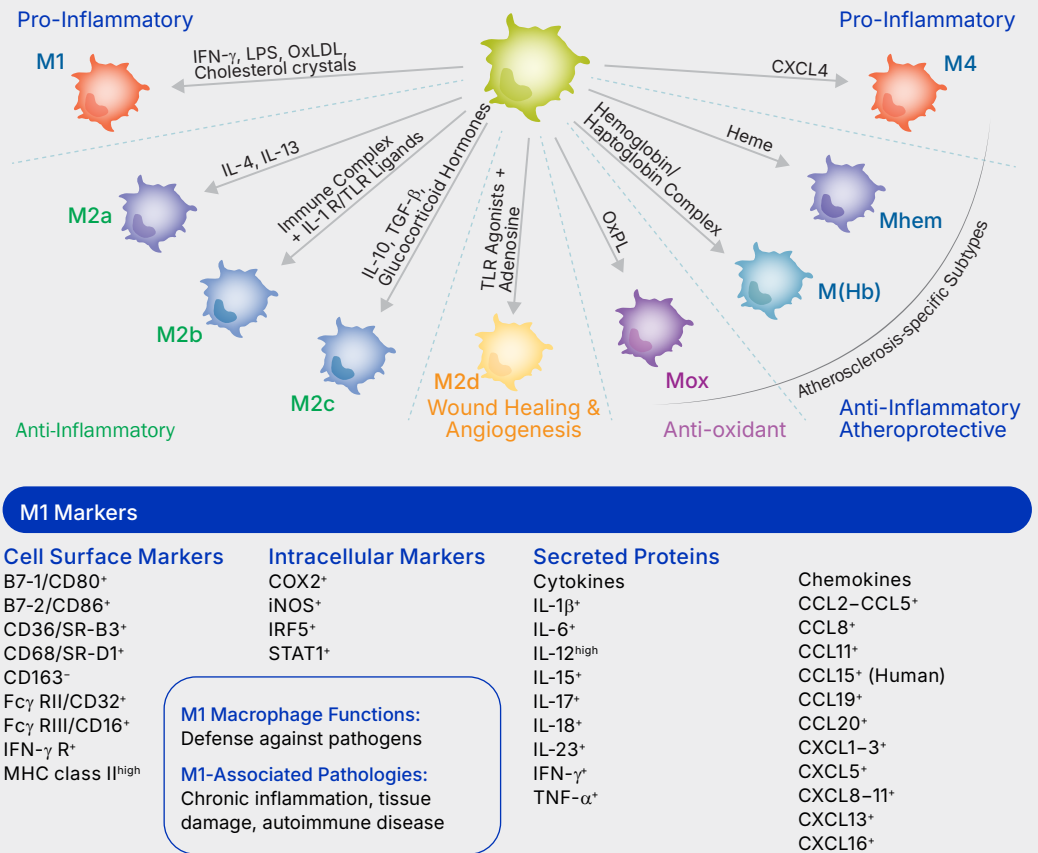


Specialized Functions: Clearance of apoptotic B cells

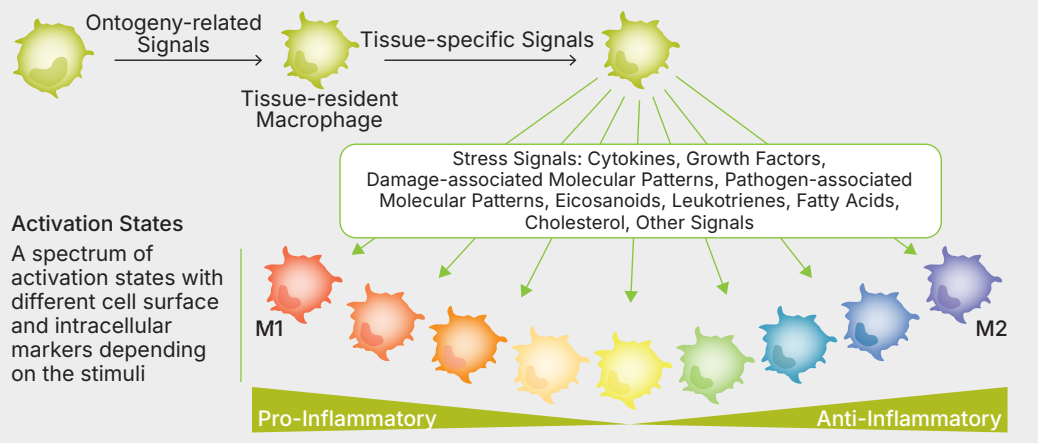
Models of Macrophage Activation

Following development, macrophages encounter diverse stimuli, which can alter their transcriptional programs leading to an activated state. The classic view of macrophage activation is described in a dichotomous model. According to this model, classical (M1) macrophage activation is induced by IFN-γ or lipopolysaccharide (LPS) and promotes a pro-inflammatory response, while alternative (M2) macrophage activation is induced by IL-4, IL-10, or IL-13 and stimulates an anti-inflammatory response. Slight phenotypic variations noted in the M2 phenotype, subsequently led to the description of different M2 subsets known as M2a, M2b, M2c, and M2d, which were defined based on the stimuli used for activation (top below). It has been widely recognized however, that even this expanded model of macrophage activation is too simplistic to account for the range of phenotypes observed in macrophages under different homeostatic and pathological conditions. For this reason, a new multidimensional model of macrophage activation has recently been proposed based on extensive gene expression analysis (bottom below). This model suggests that a spectrum of activation states spanning the M1/M2 states can occur in response to diverse signals including ontogeny-related signals, tissue-specific signals, and stress signals, which are integrated to determine the macrophage response.

Classical/Alternative Model of Macrophage Activation



New Multidimensional Model of Macrophage Activation



NOTE: This poster conveys a general overview and should be considered neither comprehensive nor definitive. The details of this information are understood to be subject to interpretation.



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