CD70

- CD70 CAR-T cells empowered by TS-2021 through ex vivo transduction show potent antitumor efficacy against glioblastoma
- CD70 CAR T cells secreting an anti-CD33/anti-CD3 dual-targeting antibody overcome antigen heterogeneity in AML
- Construction of a Prognostic Model for Mitochondria and Macrophage Polarization Correlation in Glioma Based on Single-Cell and Transcriptome Sequencing
- The dual role of POSTN in maintaining glioblastoma stem cells and the immunosuppressive phenotype of microglia in glioblastoma
- Noninvasive prediction of CCL2 expression level in high-grade glioma patients
- Bioconjugated liquid-like solid enhances characterization of solid tumor - chimeric antigen receptor T cell interactions
- Integrated genetic analyses of immunodeficiency-associated Epstein-Barr virus- (EBV) positive primary CNS lymphomas
- Three-Dimensional Bioconjugated Liquid-Like Solid (LLS) Enhance Characterization of Solid Tumor - Chimeric Antigen Receptor T cell interactions

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The CD70 protein is expressed on highly activated lymphocytes (like in T- and B-cell lymphomas). It is therefore suggested that anti-CD70 antibodies might be a possible treatment for CD70 positive lymphomas as normal lymphocytes have low CD70 expression.

A study has shown that CAR T cells were effective in migrating to and attacking tumors that express a specific protein called CD70. This indicates that CAR T cells can be used against solid tumors, which have been historically difficult to treat using this therapy.

Chemotaxis and Immune Recruitment: The researchers analyzed cytokines and chemokines (signaling molecules in the immune system) and used in situ imaging to understand how immune cells are recruited to the tumor site. They found that immune cells were drawn to the tumors through a process called chemotaxis, which is a response to specific chemical signals. This suggests a mechanism by which CAR T cells can target solid tumors.

Effector to Target Ratio: The balance between the number of immune cells (effectors) and tumor cells (targets) is crucial for the overall effectiveness of CAR T cell therapy. This ratio was found to play a significant role in the therapy's anti-tumor function. It implies that having the right number of CAR T cells relative to the tumor cells is important for success.

Differential Gene Expression: By collecting single cells from the tumor environment and examining their genetic activity (transcriptomic profiling), the researchers identified differences in gene expression among different immune subpopulations. This suggests that not all immune cells in the tumor environment behave the same way, and understanding these differences can be valuable for optimizing CAR T cell therapy.

Statement of Significance: This section highlights the importance of the study's findings. It notes that while CAR T cells have been successful in treating blood cancers, their effectiveness in solid tumors

has been limited due to physical barriers in these tumors. The study's innovative three-dimensional in vitro model allows for a more detailed examination of how CAR T cells interact with solid tumors at the single-cell level. The research provides valuable insights into the complex dynamics of CAR T cell function in solid tumors, which can inform future research and development efforts to improve this promising cancer treatment approach.

In summary, this study demonstrates that CAR T cells can be effective against solid tumors expressing CD70 and sheds light on the mechanisms by which they work. It also underscores the importance of understanding the immune cell-tumor interactions at a detailed level for the development of better cancer therapies [1)].

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used a method called “unsupervised clustering” to analyze RNA sequencing data. This means they grouped the data without any prior knowledge or labels. As a result, they found that the data naturally fell into two distinct groups based on gene expression patterns.

Distinct Transcriptional Groups: Within these two groups, they noticed that certain genes, specifically CD70 and IL1R2, were strongly expressed. CD70 and IL1R2 are genes associated with a type of tumor microenvironment that is known to promote immune tolerance. In simpler terms, the expression of these genes suggests that the tumor has characteristics that help it evade the immune system.

Deconvolution of Bulk RNASeq Data: The researchers also conducted a process called “deconvolution” on bulk RNA sequencing data. Deconvolution is a method used to estimate the composition of different cell types within a tissue or sample based on gene expression data. In this case, they found higher proportions of certain immune cells in a type of lymphoma called EBV+ PCNSL (Epstein-Barr virus-positive primary central nervous system lymphoma).

Elevated Immune Cell Fractions: Specifically, they found higher fractions of M2-macrophages, T-regulatory cells, mast cells, and monocytes in EBV+ PCNSL. These are types of immune cells, and their increased presence in the tumor microenvironment suggests that the immune response against the tumor might be suppressed or skewed in a way that is conducive to tumor growth.

Rationale for Targeted Therapies: The data obtained from this study not only shed light on the underlying biology of EBV+ PCNSL but also provide a basis for considering specific treatment strategies. The mention of “JAK-, NOTCH-, and CD70-directed approaches” suggests that the researchers are proposing targeted therapies that could potentially disrupt the mechanisms or signals associated with these genes and immune cells. These therapies might aim to reverse the immunosuppressive environment within the tumor and improve treatment outcomes.

In summary, this statement summarizes findings from a study involving the analysis of gene expression data in the context of a specific type of lymphoma (EBV+ PCNSL). The study identified distinct gene expression patterns, highlighted genes associated with immune tolerance, and revealed the presence of certain immune cell types within the tumor. The data suggest that targeted therapies aimed at specific genes and immune cell types could be explored as potential treatments for this type of lymphoma [2)].

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2)
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