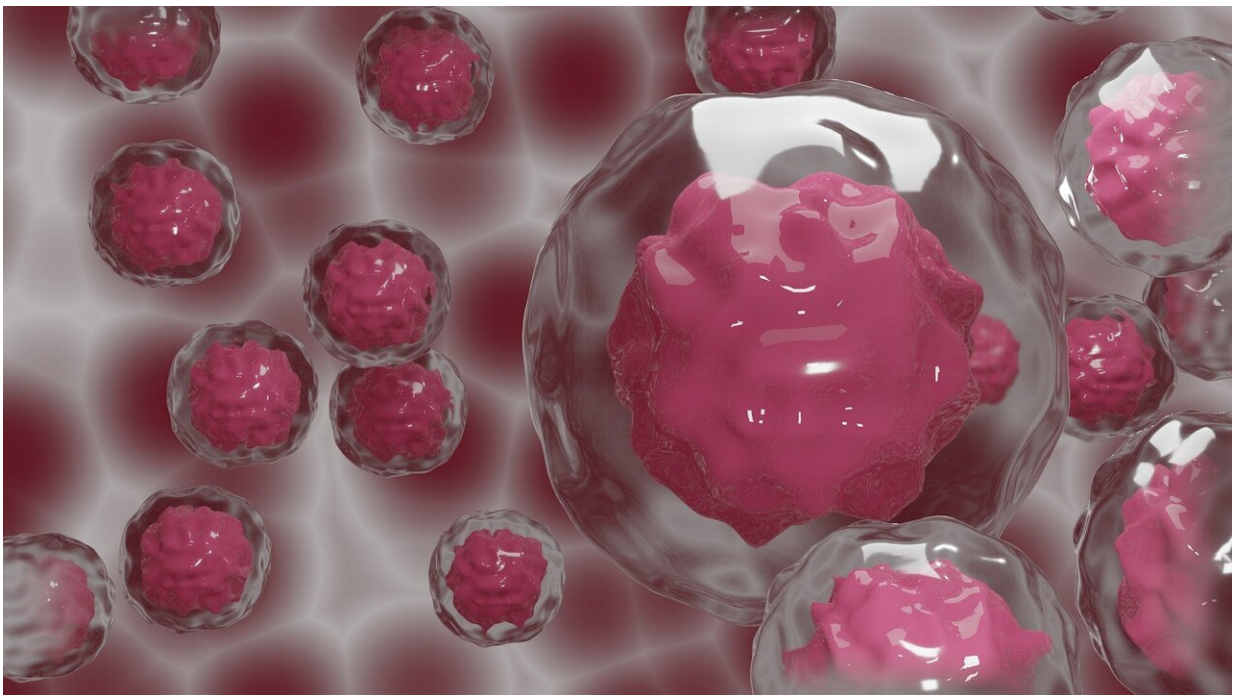


# Cancer-Immu: A data portal for predicting response to immune checkpoint blockade immunotherapy

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A new data portal called Cancer-Immu established by a team of Vanderbilt University Medical Center biostatisticians can help cancer clinicians and researchers predict which patients will respond to immune checkpoint inhibitors. With data from 3,652 samples for 16 cancer

types, Cancer-Immu is the largest immune checkpoint blockade-related data portal for exploring immunogenomic connections.

The team provided details about the open-access portal in a paper published Dec. 13 in *Cancer Research*. Cancer-Immu integrates large-scale multidimensional omics data, including genetic, bulk, and single-cell transcriptomic, proteomic and dynamic genomic profiles. It also integrates clinical phenotypes.

While immune checkpoint inhibitors can be lifesaving for some patients with cancer, most patients do not respond to the immunotherapies. Researchers are working to identify biomarkers that predict response, and Cancer-Immu offers a comprehensive functional portal for unraveling immune-genomic connections.

"It provides easy access to immunogenic data and empowers researchers to translate omics datasets into biological insights and clinical applications," said Yu Shyr, Ph.D., chair of the Department of Biostatistics at VUMC, Harold L. Moses Chair in Cancer Research and one of the paper's senior authors. According to Qi Liu, Ph.D., associate professor of Biostatistics and the paper's other senior author, "Cancer-Immu covers the greatest number of datasets and omics data types compared to existing databases with immune checkpoint blockade response outcome."

The [cancer types](#) in the data portal include melanoma, non-[small cell lung cancer](#), metastatic urothelial cancer, [renal cell carcinoma](#), [bladder cancer](#), glioma, [colorectal cancer](#), head and neck cancer, esophagogastric cancer, cancer of unknown primary cause, gastric cancer, breast cancer, hepatocellular carcinoma, prostate cancer, basal cell carcinoma and non-melanoma skin cancer.

With the Cancer-Immu portal, clinicians and researchers can upload and

analyze their own data or co-analyze with existing data simultaneously. They can use either a meta-analysis or a pan-cancer analysis. The portal has collections of three types of omics data: genetic, transcriptomics and single cell data. The pan-cancer module, which aggregates multiple datasets into one, enhances the detection and analysis of rare features. The biostatisticians noted in the study that while [meta-analysis](#)—the statistical evaluation of independent studies focused on the same question—failed to detect significant gene mutations, the pan-cancer analysis, which is a more expansive evaluation across multiple cancer types, detected 182 genes with mutations significantly associated with immune checkpoint inhibitors.

"Cancer-Immu helps address a lack and a challenge for evaluation of efficacy of known biomarkers and the discovery of new signatures," said the study's first author, Jing Yang, Ph.D., a postdoctoral fellow in the Shyr Research Lab.

**More information:** Jing Yang et al, A pan-cancer immunogenomic atlas for immune checkpoint blockade immunotherapy, *Cancer Research* (2021). [DOI: 10.1158/0008-5472.CAN-21-2335](https://doi.org/10.1158/0008-5472.CAN-21-2335)

Cancer-Immu: [129.59.197.30:3838/Cancer-Immu/](https://129.59.197.30:3838/Cancer-Immu/)

Provided by Vanderbilt University Medical Center

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