

OncoMX knowledgebase enables research of cancer biomarkers and related evidence

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Cancer cell during cell division. Credit: National Institutes of Health

The OncoMX knowledgebase will improve the exploration and research of cancer biomarkers in the context of related evidence, according to a recent article from the George Washington University (GW). The article

is published in the *Journal of Clinical Oncology Clinical Cancer Informatics* and is part of a special series called "Informatics Tools for Cancer Research and Care."

Cancer biomarkers, a sort of biological fingerprint, are molecules in bodily fluids or tissues that can indicate processes associated with various cancers. With increased research and funding, more potentially novel [cancer biomarkers](#) are being reported. However, challenges remain when it comes to reproducibility of initial findings, clinical validation, and access to harmonized biomarker data.

OncoMX, a knowledgebase and web portal for exploring cancer biomarker data and related evidence, was developed to integrate cancer biomarker and relevant data types into a meta-portal, enabling the research of cancer biomarkers side by side with other pertinent multidimensional data types.

"Many research groups and consortia have conducted studies reporting potentially actionable and available cancer biomarker data," said Hayley Dingerdissen, a Ph.D. student at the GW Institute for Biomedical Sciences and first author of the paper. "It seems reasonable that these data could be combined into a single meta-resource to facilitate more efficient cancer biomarker research and exploration, but the reality is there are numerous challenges to combining heterogeneously structured data in a unified way."

To address the challenges associated with [data collection](#) and access, the OncoMX team worked to integrate public cancer biomarker data from the Early Detection Research Network (EDRN) and the FDA, as well as additional related data around persistent identifiers, which are long-lasting references to a document, file, webpage, or other object. The team integrated information such as cancer mutation, cancer differential expression, cancer expression specificity, healthy gene expression from

human and mouse, and biomarker data.

The resulting data provides the foundation for integration of heterogeneous biomarker evidence, using the BioCompute Object framework, into OncoMX for improved cancer biomarker exploration.

"OncoMX is designed to combine existing biomarker-relevant data with newly generated data as it becomes available, establishing a resource customized for cancer biomarker research," said Raja Mazumder, Ph.D., professor of biochemistry and molecular medicine at the GW School of Medicine and Health Sciences, a member of the GW Cancer Center, and senior author on the study. "The focus on ontology-driven unification of [biomarker](#) data and cross comparison of various related experimental data, particularly inclusion of large-scale literature mining findings, NCI's EDRN and FDA biomarkers, and healthy gene expression data from Bgee are unique to OncoMX compared to other integrated cancer resources."

Moving forward, the OncoMX team is actively seeking new data types, such as imaging, glycan biomarkers, drug targets, alternative splicing, and more. They also continue to work on extending the data model to new types, integrating FDA data sets for additional cancers upon user request, and expanding cross references to key [cancer](#) resources.

More information: Hayley M. Dingerdissen et al, OncoMX: A Knowledgebase for Exploring Cancer Biomarkers in the Context of Related Cancer and Healthy Data, *JCO Clinical Cancer Informatics* (2020). [DOI: 10.1200/CCI.19.00117](https://doi.org/10.1200/CCI.19.00117)

Provided by George Washington University

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