

## **Atlas of Cancer Signaling Network: a resource of multi-scale biological maps to study disease mechanisms**

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We present here the second edition of Atlas of Cancer Signaling Network (ACSN2.0, <https://acsn.curie.fr>). ACSN is a web-based resource of multi-scale biological maps depicting molecular processes in cancer cell and tumor microenvironment. The core of the Atlas is a set of interconnected cancer-related signaling and metabolic network maps. Molecular mechanisms are depicted on the maps at the level of biochemical interactions, forming a large seamless network of above 8000 reactions covering close to 3000 proteins and 800 genes and based on more than 4500 scientific publications. Constructing and updating ACSN involves careful manual curation of molecular biology literature and the participation of experts in the corresponding fields.

The maps of ACSN2.0 are interconnected, the regulatory loops within cancer cell and between cancer cell and tumor microenvironment are systematically depicted. The cross-talk between signaling mechanisms and metabolic processes in the cancer cells is explicitly depicted thanks to new feature of the Atlas: ACSN2.0 is now connected to RECON metabolic network, the largest graphical representation of human metabolism.

The Atlas is a "geographic-like" interactive "world map" of molecular interactions leading the hallmarks of cancer as described by Hanahan and Weinberg. The Atlas is created with the use of systems biology standards and amenable for computational analysis. As of today, ACSN2.0 is composed of 13 comprehensive maps of molecular interactions. There are six maps covering signalling processes involved in cancer cell and four maps describing tumor microenvironment. In addition, there are 3 cell type-specific maps describing signaling within different cells types frequently surrounding and interacting with cancer cells. This feature of ACSN2.0 reflects the complexity of tumor microenvironment.

The resource includes tools for map navigation, visualization and analysis of molecular data in the context of signaling network maps.