# Transcriptomine: The Nuclear Receptor Signaling Transcriptome Database

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**Abstract :** Understanding signaling by nuclear receptors (NRs) requires an appreciation of their cognate ligand- and tissue-specific transcriptomes. While target gene regulation data are abundant in this field, they reside in hundreds of discrete publications in formats refractory to routine query and analysis and, accordingly, their full value to the NR signaling community has not been realized. One of the mandates of the Nuclear Receptor Signaling Atlas (NURSA) is to facilitate access of the community to existing public datasets. Pursuant to this mandate we are developing a freely-accessible community web resource, Transcriptomine, to bring together the sum total of available expression array and RNA-Seq data points generated by the field in a single location. Transcriptomine currently contains over 25,000,000 gene fold change datapoints from over 1200 contrasts relevant to over 100 NRs, ligands and coregulators in over 200 tissues and cell lines. Transcriptomine is designed to accommodate a spectrum of end users ranging from the bench researcher to those with advanced bioinformatic training. Visualization tools allow users to build custom charts to compare and contrast patterns of gene regulation across different tissues and in response to different ligands. Our resource affords an entirely new paradigm for leveraging gene expression data in the NR signaling field, empowering users to query gene fold changes across diverse regulatory molecules, tissues and cell lines, target genes, biological functions and disease associations, and that would otherwise be prohibitive in terms of time and effort. Transcriptomine will be regularly updated with gene lists from future genome-wide expression array and expression-sequencing datasets in the NR signaling field.

**Keywords :** target gene database, informatics, gene expression, transcriptomics

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