



MetaCore

## Integrated pathway analysis for multi-OMICs data

Gain greater insight into disease understanding — *MetaCore* delivers high-quality biological systems content in context, giving you essential data and analytics to accelerate your scientific research.

### Integrated pathway analysis for multi-OMICs data

*MetaCore* is an integrated software suite for functional analysis of Next Generation Sequencing, microarray, metabolic, proteomics, siRNA, microRNA, and screening data. *MetaCore* is based on a high-quality, manually curated database of

- transcription factors, receptors, ligands, kinases, drugs, and endogenous metabolites, as well as other molecular classes;
- species-specific directional interactions between protein-protein, protein-DNA and protein-RNA interactions, drug targeting, and bioactive molecules and their effects;
- signaling and metabolic pathways represented on maps and networks;
- rich ontologies for diseases and processes with hierarchical or graphic output.

### Trusted content

The data contained within *MetaCore* is industry leading in accuracy, reliability, and comprehensiveness, manually curated by PhD- and MD-level research professionals. There are more than a million small-scale experiment interactions, defined with directionality, effect, and mechanism, and supported by literature for ease of reference.

### Seize the opportunity next-generation sequencing (ngs) presents in improving disease understanding

Our extended DNA NGS capability is fully integrated with *MetaCore*. The Genomic Analysis tools help you identify potentially significant variants with 27 filters, including functional predictions, conservation scores, population frequencies, and biological and clinical evidence.

- Embedded workflows for combining VCF variant files with other OMICs data
- Easy-to-use comprehensive filters to build up complex queries to identify variants of significance, integrated with 1,000 Genomes and Exome Sequencing Project (ESP) data
- Trusted, manually annotated gene variant associations in the context of human health, rigorously controlled for quality
- Gene variant content is extracted from global patents and conferences, as well as from clinically actionable sources such as published clinical trial registries, multiple clinical guidelines, and approval documents from FDA, EMA, and Japan
- Workflows for defining Cochran-Armitage Trend Test significance in a cohort analysis, Somatic Mutations, and inheritance patterns in a trio analysis

### MetaCore highlights

- Integrated analysis of gene expression and gene variant data with copy number, microarray, metabolic, proteomics, siRNA, microRNA, and screening data
- Industry-leading advanced analytics, such as overconnectivity and causal reasoning algorithms, for identifying key hubs and pathways associated with your data
- More than 1.6 million trusted, manually annotated molecular interactions, rigorously controlled for quality from human, mouse, and rat small-scale experiments
- More than 1,600 pathway maps, including more than 700 disease-specific maps

For more information, visit [clarivate.com](http://clarivate.com)

#### North America

Philadelphia: +1 800 336 4474  
+1 215 386 0100

#### Latin America

Brazil: +55 11 8370 9845  
Other countries: +1 215 823 5674

07.2017

© 2017 Clarivate Analytics

#### Europe, Middle East and Africa

London: +44 20 7433 4000

#### Asia Pacific

Singapore: +65 6775 5088  
Tokyo: +81 3 5218 6500

[clarivate.com](http://clarivate.com)

### Use MetaCore for

- Pathway analysis of OMICs data for drug discovery
- Overlay of public information to enhance interpretation and accuracy
- Knowledge mining of the database for hypothesis generation
- Target and biomarker identification and validation
- Disease pathway modeling and investigation of causal mechanisms
- Patient stratification and mechanism of action (MoA) reconstruction

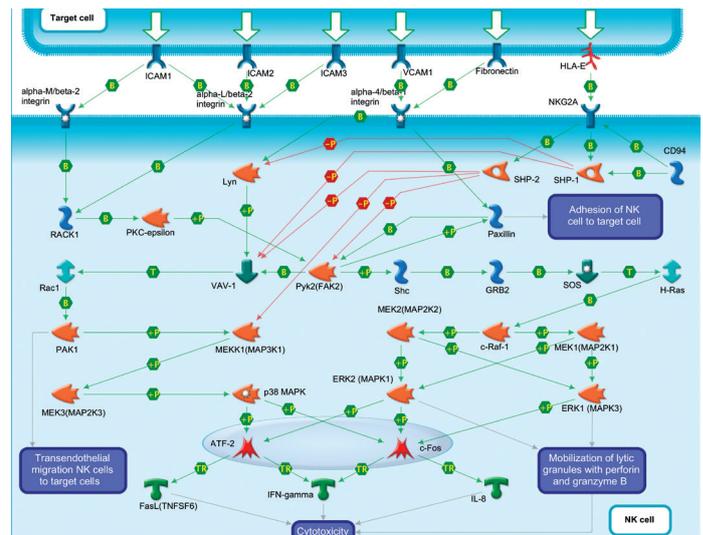
### Who can benefit

- Biological researchers
- Discovery biologists
- Bioinformaticians
- Biomarker groups and preclinical researchers
- Heads of therapy area
- Principal investigators
- Translational researchers

### Tech specs

Web browser

- Internet Explorer® version 9.0
- Firefox® 17
- Safari® 6 or higher
- Chrome 33
- Macromedia Flash Player 8 or higher
- Java Runtime Environment (JRE) 1.5.0



Example of a *MetaCore* canonical pathway map showing “the role of integrins in Natural Killer (NK) cell cytotoxicity” in immune response. Pathway maps in *MetaCore* are manually reconstructed by our experts based on findings from peer-reviewed literature references and are fully interactive.

- Save time on literature research (some pathway maps represent a collection of over 300 references).
- Overlay your own experimental data to visualize results and generate actionable hypotheses.