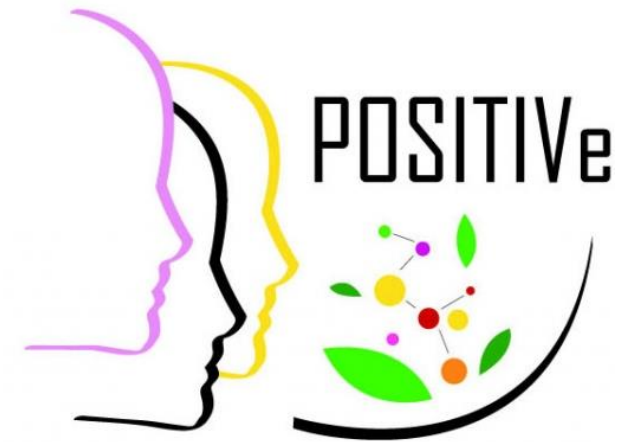


# ccost



**Bioinformatic analysis of  
nutrigenomics data of plant food  
bioactives extracted from *in vitro*  
and *in vivo* studies**

**STSM Report**

# General information



- STSM Grantee
- **Dr. Tatjana Ruskovska**
  - **Goce Delcev University, Stip**
  - **Faculty of Medical Sciences**
  - **Republic of Macedonia**



- STSM Host
- **Dr. Dragan Milenkovic**
  - **INRA**
  - **Centre de Clermont-Ferrand/Theix**  
**Unité de Nutrition Humaine**
  - **France**
- **Duration of the STSM: two weeks.**

# Gene symbols


GeneCardsSuite **GeneCards** MalaCards LifeMap Discovery PathCards TGex VarElect GeneAnalytics GeneALaCart GenesLikeMe

Free for academic non-profit institutions. Other users need a [Commercial license](#) WEIZMANN INSTITUTE OF SCIENCE  LifeMap SCIENCES 

Keywords   [Advanced](#)

Home | [User Guide](#) | [Analysis Tools](#) | [News And Views](#) | [About](#) | [My Genes](#) | [Log In / Sign Up](#)

**INSR** Gene (Protein Coding) ★  
Insulin Receptor

GCID: GC19M007112 ?  
GIFTS: 78 ?  



Genes  
Participants 

Jump to section

[Aliases](#) [Disorders](#) [Domains](#) [Drugs](#) [Expression](#) [Function](#) [Genomics](#) [Localization](#) [Orthologs](#)  
[Paralogs](#) [Pathways](#) [Products](#) [Proteins](#) [Publications](#) [Sources](#) [Summaries](#) [Transcripts](#) [Variants](#)

 Genes Peptides Proteins  
CRISPR

 Proteins Antibodies  
Assays Genes shRNA  
Primers CRISPR

 Genes (adenoviral)  
Genes (lentiviral) miRNA  
shRNA (AAV)

## Aliases for INSR Gene ?

### Aliases for INSR Gene

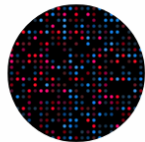
Insulin Receptor <sup>2 3 5</sup>  
EC 2.7.10.1 <sup>4 61</sup>  
**IR** <sup>3 4</sup>  
CD220 Antigen <sup>4</sup>  
EC 2.7.10 <sup>61</sup>  
CD220 <sup>3</sup>  
HHF5 <sup>3</sup>

# Pathways analysis

GeneTrail2 Home About Documentation Use cases Login

## GeneTrail2 1.5

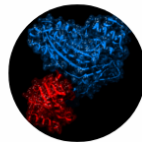
Statistical analysis of molecular signatures



### Transcriptomics

Upload *gene expression* data and perform enrichment analysis based on gene sets derived from popular databases like GO, KEGG and Reactome.

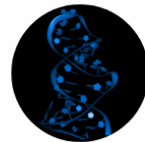
Start analysis



### Proteomics

Upload *protein* data and perform enrichment analysis based on protein datasets like SMPDB, or map proteins to corresponding genes and perform a gene set analysis.

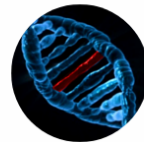
Start analysis



### miRNomics

Upload *miRNA* data and perform enrichment analysis based on miRNA categories like miRDB or miRTarBase, or map miRNAs to gene targets from popular databases and perform a gene set analysis.

Start analysis



### Genomics

Upload *SNP* data and perform enrichment analysis based on the popular GWAS and PheWAS catalogs. This will identify traits associated with your uploaded variants.

Start analysis

GeneTrail2 Home About Documentation Use cases Login

## GeneTrail2 1.5

Statistical analysis of molecular signatures



### Upload Data

Select your data source:


- a **GSE file** containing data of both, the sample and the reference group
- two GDS files** for the sample and the reference group
- a **text file** containing a list of identifier with or without scores in a tabular format
- a **list** of scores in a tabular format

### Help

Your options:

- a **GSE file** enter a valid GSE identifier (e.g., **GSE10072**). The corresponding GEO Series .soft file is then downloaded to the *GeneTrail 2* server automatically. In a next step, you may specify the sample and the reference group.
- **two GDS files** enter valid GDS identifiers (e.g., **GDS2161** and **GDS2162**) for the sample and reference group, respectively. The corresponding GEO Data Set .soft files are then downloaded to the *GeneTrail 2* server automatically.
- a **text file** upload a plain text file containing identifier with or without pre-computed scores. The values have to be whitespace separated. (identifier list, score list, matrix)
- a **list** paste a pre-computed list of scores. The values have to be whitespace separated

# Analysis of transcription factors



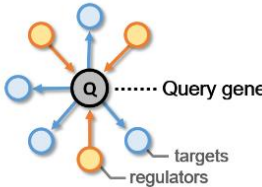
**TRRUST** version 2  
Transcriptional Regulatory Relationships  
Unraveled by Sentence-based Text mining

About TRRUST Search Download

**1. Search a gene in TRRUST database**

Submit a query gene below.

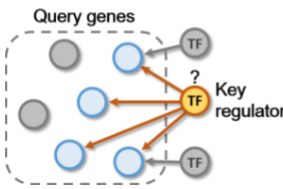
Tables for human genes and mouse genes included in TRRUST.

 Query gene  
targets  
regulators

Species:  Human  Mouse

TNF

**\*\*Examples\*\***



**2. Find key regulators for query genes**

Submit a set of genes for a function/pathway/phenotype. (Min=5, Max=500)

Each gene name must be separated by comma, tab, white space or new line.  
Input format: Entrez Gene ID (79923) or Gene Symbol (NANOG)

Species:  Human  Mouse

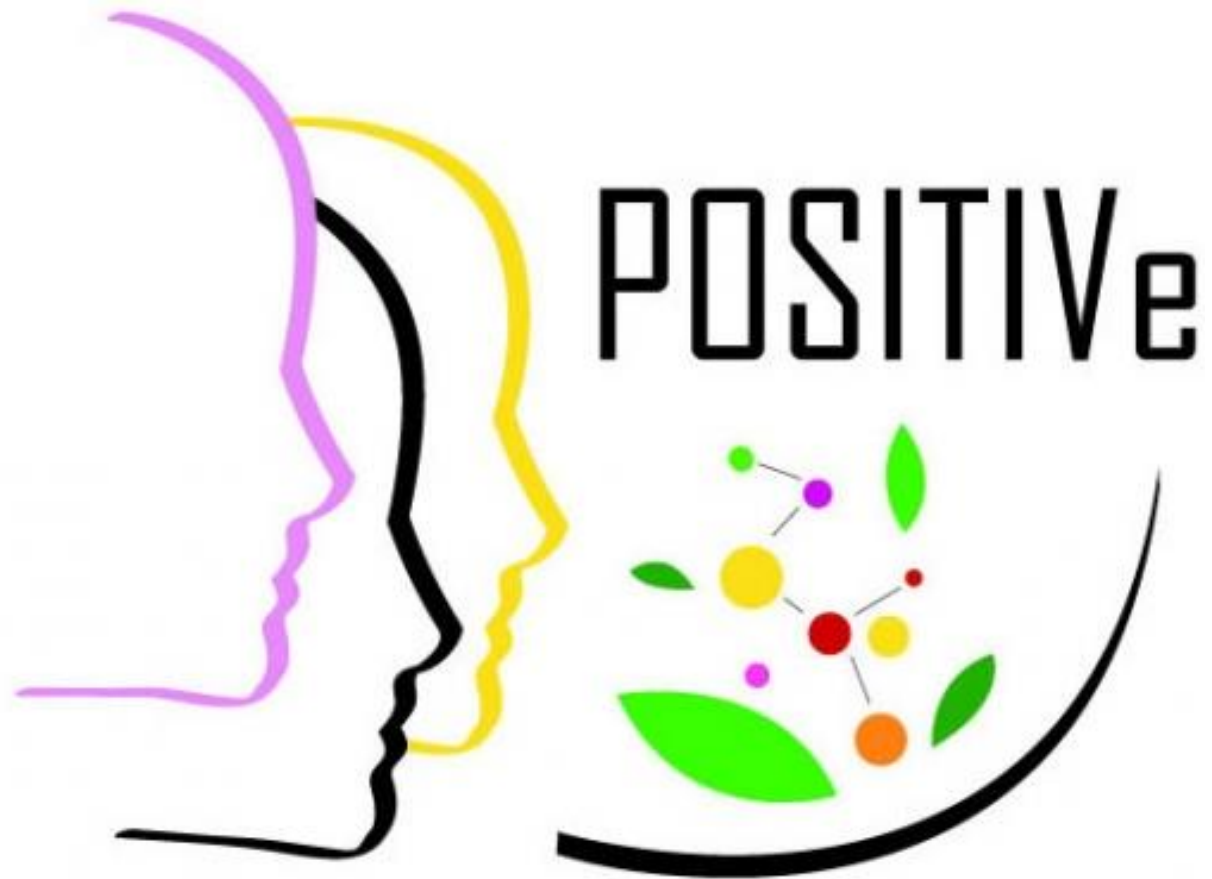
**\*\*Examples\*\***

Example gene sets

#1: 33 DEGs perturbed by ESR1 knockdown in human breast tumors.  
*Muthukaruppan et al., Clin Breast Cancer, 2017*

Copyright H3 Han

# COST Action FA1403 – POSITIVE





**Thank you for your attention**

