

Resource Summary Report

Generated by [dkNET](#) on Sep 1, 2026

Integrated Tumor Transcriptome Array and Clinical data Analysis

RRID:SCR_008182

Type: Tool

Proper Citation

Integrated Tumor Transcriptome Array and Clinical data Analysis (RRID:SCR_008182)

Resource Information

URL: <http://bioinfo-out.curie.fr/ittaca/>

Proper Citation: Integrated Tumor Transcriptome Array and Clinical data Analysis (RRID:SCR_008182)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on 6/12/25. ITTACA is a database created for Integrated Tumor Transcriptome Array and Clinical data Analysis. ITTACA centralizes public datasets containing both gene expression and clinical data and currently focuses on the types of cancer that are of particular interest to the Institut Curie: breast carcinoma, bladder carcinoma, and uveal melanoma. ITTACA is developed by the Institut Curie Bioinformatics group and the Molecular Oncology group of UMR144 CNRS/Institut Curie. A web interface allows users to carry out different class comparison analyses, including comparison of expression distribution profiles, tests for differential expression, patient survival analyses, and users can define their own patient groups according to clinical data or gene expression levels. The different functionalities implemented in ITTACA are: - To test if one or more gene, of your choice, is differentially expressed between two groups of samples exhibiting distinct phenotypes (Student and Wilcoxon tests). - The detection of genes differentially expressed (Significance Analysis of Microarrays) between two groups of samples. - The creation of histograms which represent the expression level according to a clinical parameter for each sample. - The computation of Kaplan Meier survival curves for each group. ITTACA has been developed to be a useful tool for comparing personal results to the existing results in the field of transcriptome studies with microarrays.

Abbreviations: ITTACA

Synonyms: ITTACA

Resource Type: data or information resource, database

Defining Citation: [PMID:16381943](#)

Keywords: expression, gene, analysis, array, bioinformatics, bladder, breast, cancer, carcinoma, clinical, integrated, melanoma, microarray, molecular, oncology, patient, phenotype, survival, transcriptome, tumor, uveal

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Integrated Tumor Transcriptome Array and Clinical data Analysis

Resource ID: SCR_008182

Alternate IDs: nif-0000-21227

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260829T183019+0000

Ratings and Alerts

No rating or validation information has been found for Integrated Tumor Transcriptome Array and Clinical data Analysis.

No alerts have been found for Integrated Tumor Transcriptome Array and Clinical data Analysis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Awan FM, et al. (2015) Identification of Circulating Biomarker Candidates for Hepatocellular Carcinoma (HCC): An Integrated Prioritization Approach. PloS one, 10(9), e0138913.

Moreaux J, et al. (2012) STEAP1 is overexpressed in cancers: a promising therapeutic target. Biochemical and biophysical research communications, 429(3-4), 148.

Bret C, et al. (2011) SULFs in human neoplasia: implication as progression and prognosis factors. Journal of translational medicine, 9, 72.

Malik A, et al. (2007) Databases and QSAR for cancer research. Cancer informatics, 2, 99.