

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

Genome Network Platform

RRID:SCR_001737

Type: Tool

Proper Citation

Genome Network Platform (RRID:SCR_001737)

Resource Information

URL: https://cell-innovation.nig.ac.jp/GNP/index_e.html

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. Integrated database of experiment data generated by participating research institutes and public databases relating to: 1) transcription starting position of human genes in the human genome, 2) conjunction to control region on transcriptional factors and the human genome 3) protein-protein interaction with a central focus on transcription factors organized for use in genome level research. Gene Search is the function to search the integrated database by using keywords and public IDs. The search results can be visualized by: * Genome Explorer : provides annotation of landmarks (genes, transcription start sites, etc.) aligned in accordance with their genome locations. * PPI Network : provides a graphical view of protein-protein interaction (PPI) network from the experimental data generated under the project and the public datasets. * Expression Profile : clusters genes by expression pattern and display the result with heatmap. The function provides genes which have relation of coregulation and anti-coregulation. * Comparison Viewer : This function gives the view to compare the genomic regions between human and mouse homologous genes. The viewer shows the distribution of transcription start sites (TSS) as the way of separable by tissues or time points with other landmarks on genome region. * Gene Stock : This is the function to save the gene list that you are interested until the session is closed.

Abbreviations: GNP

Resource Type: data or information resource, database

Defining Citation: [PMID:24927841](#)

Keywords: gene, genome, chip, human, interaction, micro array, protein, protein-protein interaction, qrt-pcr, rat, rna, sequence, short rna, tiling array, transcription, transcription control, transcription factor, transcription starting position, yeast two hybrid, data set, cage, data analysis service

Availability: Free, Freely Available

Resource Name: Genome Network Platform

Resource ID: SCR_001737

Alternate IDs: nif-0000-10237

Old URLs: http://genomenetwork.nig.ac.jp/index_e.html

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260729T044015+0000

Ratings and Alerts

No rating or validation information has been found for Genome Network Platform.

No alerts have been found for Genome Network Platform.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Tanaka H, et al. (2021) HMGB1 signaling phosphorylates Ku70 and impairs DNA damage repair in Alzheimer's disease pathology. Communications biology, 4(1), 1175.

Fujita K, et al. (2018) Targeting Tyro3 ameliorates a model of PGRN-mutant FTLD-TDP via tau-mediated synaptic pathology. Nature communications, 9(1), 433.

Limviphuvadh V, et al. (2018) Discovering novel SNPs that are correlated with patient outcome in a Singaporean cancer patient cohort treated with gemcitabine-based chemotherapy. BMC cancer, 18(1), 555.

Tanaka H, et al. (2018) The intellectual disability gene PQBP1 rescues Alzheimer's disease pathology. Molecular psychiatry, 23(10), 2090.

Yamamoto T, et al. (2016) Transcriptome and Metabolome Analyses in Exogenous FABP4- and FABP5-Treated Adipose-Derived Stem Cells. PloS one, 11(12), e0167825.

Sakata K, et al. (2016) Loss of variation of state detected in soybean metabolic and human myelomonocytic leukaemia cell transcriptional networks under external stimuli. Scientific reports, 6, 35946.

Sakata K, et al. (2015) System-wide analysis of the transcriptional network of human myelomonocytic leukemia cells predicts attractor structure and phorbol-ester-induced differentiation and dedifferentiation transitions. *Scientific reports*, 5, 8283.

Akiyama T, et al. (2014) Mitochondria-nucleus shuttling FK506-binding protein 51 interacts with TRAF proteins and facilitates the RIG-I-like receptor-mediated expression of type I IFN. *PloS one*, 9(5), e95992.

Iwayanagi T, et al. (2012) TP Atlas: integration and dissemination of advances in Targeted Proteins Research Program (TPRP)-structural biology project phase II in Japan. *Journal of structural and functional genomics*, 13(3), 145.

Sugaya N, et al. (2012) Dr. PIAS 2.0: an update of a database of predicted druggable protein-protein interactions. *Database : the journal of biological databases and curation*, 2012, bas034.

Ohshima D, et al. (2011) RANK signaling induces interferon-stimulated genes in the fetal thymic stroma. *Biochemical and biophysical research communications*, 408(4), 530.

Miyamoto-Sato E, et al. (2010) A comprehensive resource of interacting protein regions for refining human transcription factor networks. *PloS one*, 5(2), e9289.

Kawaji H, et al. (2009) SDRF2GRAPH: a visualization tool of a spreadsheet-based description of experimental processes. *BMC bioinformatics*, 10, 133.

Kubosaki A, et al. (2009) Genome-wide investigation of in vivo EGR-1 binding sites in monocytic differentiation. *Genome biology*, 10(4), R41.

Fraser J, et al. (2009) Chromatin conformation signatures of cellular differentiation. *Genome biology*, 10(4), R37.

Severin J, et al. (2009) FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. *Genome biology*, 10(4), R39.

Kawaji H, et al. (2009) The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. *Genome biology*, 10(4), R40.

Tomaru Y, et al. (2009) Regulatory interdependence of myeloid transcription factors revealed by Matrix RNAi analysis. *Genome biology*, 10(11), R121.

Shimojo H, et al. (2008) Oscillations in notch signaling regulate maintenance of neural progenitors. *Neuron*, 58(1), 52.

Niwa Y, et al. (2007) The initiation and propagation of Hes7 oscillation are cooperatively regulated by Fgf and notch signaling in the somite segmentation clock. *Developmental cell*, 13(2), 298.