

Resource Summary Report

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Gene Expression Profiling in Spinal Cord Injury

RRID:SCR_003260

Type: Tool

Proper Citation

Gene Expression Profiling in Spinal Cord Injury (RRID:SCR_003260)

Resource Information

URL: <http://spine.rutgers.edu/microarray/>

Proper Citation: Gene Expression Profiling in Spinal Cord Injury (RRID:SCR_003260)

Description: Database which provides on-line searching of microarray datasets generated from rat spinal cord after contusion injury. Both the primary injury site and a site 5 mm distal to the injury site were assayed. Tissue was obtained from Long Evans rats subject to spinal cord contusion injury using the MASCIS impactor (formerly known as the NYU impactor). RNA expression was assayed at the site of injury and distal to the site of injury using the Affymetrix Rat Neuro U34 chip.

Resource Type: data set, database, data or information resource

Keywords: database, spinal cord, contusion, microarray data, FASEB list

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Gene Expression Profiling in Spinal Cord Injury

Resource ID: SCR_003260

Alternate IDs: nif-0000-00011

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260805T044051+0000

Ratings and Alerts

No rating or validation information has been found for Gene Expression Profiling in Spinal Cord Injury.

No alerts have been found for Gene Expression Profiling in Spinal Cord Injury.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 394 mentions in open access literature.

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

Yang J, et al. (2020) Upregulation of lncRNA LINC00460 Facilitates GC Progression through Epigenetically Silencing CCNG2 by EZH2/LSD1 and Indicates Poor Outcomes. Molecular therapy. Nucleic acids, 19, 1164.

Burska AN, et al. (2020) Dynamics of Early Signalling Events during Fracture Healing and Potential Serum Biomarkers of Fracture Non-Union in Humans. Journal of clinical medicine, 9(2).

Fong LY, et al. (2020) Abrogation of esophageal carcinoma development in miR-31 knockout rats. Proceedings of the National Academy of Sciences of the United States of America, 117(11), 6075.

González-Tablas M, et al. (2020) Heterogeneous EGFR, CDK4, MDM4, and PDGFRA Gene Expression Profiles in Primary GBM: No Association with Patient Survival. Cancers, 12(1).

Kumari S, et al. (2020) Musa balbisiana Fruit Rich in Polyphenols Attenuates Isoproterenol-Induced Cardiac Hypertrophy in Rats via Inhibition of Inflammation and Oxidative Stress. Oxidative medicine and cellular longevity, 2020, 7147498.

Hanamata S, et al. (2020) Impact of Autophagy on Gene Expression and Tapetal Programmed Cell Death During Pollen Development in Rice. Frontiers in plant science, 11, 172.

Dahmani MA, et al. (2020) Unearthing the Plant Growth-Promoting Traits of Bacillus megaterium RmBm31, an Endophytic Bacterium Isolated From Root Nodules of Retama monosperma. Frontiers in plant science, 11, 124.

Lv S, et al. (2020) High TXLNA Expression Predicts Favourable Outcome for Pancreatic Adenocarcinoma Patients. BioMed research international, 2020, 2585862.

Song F, et al. (2019) OVA66 promotes tumour angiogenesis and progression through enhancing autocrine VEGF-VEGFR2 signalling. EBioMedicine, 41, 156.

Deng H, et al. (2019) Coxsackievirus Type B3 Is a Potent Oncolytic Virus against KRAS-Mutant Lung Adenocarcinoma. Molecular therapy oncolytics, 14, 266.

Gehring F, et al. (2019) FOXO1 Confers Maintenance of the Dark Zone Proliferation and Survival Program and Can Be Pharmacologically Targeted in Burkitt Lymphoma. Cancers, 11(10).

Padella A, et al. (2019) Novel and Rare Fusion Transcripts Involving Transcription Factors and Tumor Suppressor Genes in Acute Myeloid Leukemia. *Cancers*, 11(12).

Gerace D, et al. (2019) Ex Vivo Expansion of Murine MSC Impairs Transcription Factor-Induced Differentiation into Pancreatic β -Cells. *Stem cells international*, 2019, 1395301.

Huang YH, et al. (2019) Decreased Steroid Hormone Receptor NR4A2 Expression in Kawasaki Disease Before IVIG Treatment. *Frontiers in pediatrics*, 7, 7.

Zhu B, et al. (2019) A clinical, biologic and mechanistic analysis of the role of ZNF692 in cervical cancer. *Gynecologic oncology*, 152(2), 396.

Dyberg C, et al. (2019) Inhibition of Rho-Associated Kinase Suppresses Medulloblastoma Growth. *Cancers*, 12(1).

Wang L, et al. (2019) Integrating genetic, transcriptional, and biological information provides insights into obesity. *International journal of obesity* (2005), 43(3), 457.

An X, et al. (2019) An Analysis of the Expression and Association with Immune Cell Infiltration of the cGAS/STING Pathway in Pan-Cancer. *Molecular therapy. Nucleic acids*, 14, 80.

Zhou J, et al. (2019) Identification of novel genes associated with a poor prognosis in pancreatic ductal adenocarcinoma via a bioinformatics analysis. *Bioscience reports*, 39(8).

Wu L, et al. (2019) GNPDA2 Gene Affects Adipogenesis and Alters the Transcriptome Profile of Human Adipose-Derived Mesenchymal Stem Cells. *International journal of endocrinology*, 2019, 9145452.