Resource Summary Report

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GEArray Expression Analysis Suite 2.0

RRID:SCR_000282
Type: Tool

Proper Citation

GEArray Expression Analysis Suite 2.0 (RRID:SCR_000282)

Resource Information

URL: http://saweb2.sabiosciences.com/manuals/GEArrayBrochure.pdf

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Description: THIS RESOURCE HAS BEEN DISCONTINUED, documented April 15, 2016. New GEArray Expression Analysis Suite 2.0 was released at Dec 21, 2006, please read Release Notices for details. SABiosciences' GEArray Analysis Suite uses advanced Java functionality. In order to experience full functionality of this Portal, the following free programs and upgrades for PC and Macs should be properly installed. PC Environment Downloads Browser compatibility is not an issue on Windows systems, so all operating systems running Windows 98 and above and either Internet explorer or Netscape should be fine. Java 1.4.1 or above is required--this should download automatically upon the first entry into the Portal. If this does not happen, Java 1.5 is available for download from the following URL: Java 1.5 Mac Environment Downloads Browser compatibility is an issue, and Mac Operating Systems prior to Panther are not able to fully take advantage of this Portal's functionality. These programs need to be downloaded and installed in a specific order as follows: Panther 10.3.5 (Operating System), Safari 1.2 (Compatible Internet Browser) and Java 1.4.2 (Java environment). Abstract. INTRODUCTION: Toll-like receptors (TLR) comprehend an emerging family of receptors that recognize pathogen-associated molecular patterns and promote the activation of leukocytes. Surgical trauma and ischemia-reperfusion injury are likely to provide exposure to endogenous ligands for TLR in virtually all kidney transplant recipients. METHODS: Macroarray (GEArray OHS-018.2 Series-Superarray) analyses of 128 genes involved in TLR signaling pathway were performed in nephrectomy samples of patients with chronic allograft nephropathy (CAN) and acute rejection (AR, vascular and non vascular). The analysis of each membrane was performed by GEArray Expression Analysis Suite 2.0. RESULTS: Macroarray profile identified a gene expression signature that could discriminate CAN and AR. Three genes were significantly expressed between CAN and vascular AR: Pellino 2; IL 8 and UBE2V1. In relation to vascular and non-vascular AR, there were only two genes with statistical significance: IL-6 and IRAK-3. CONCLUSION: Vascular and non-vascular AR and CAN showed different expression of a few genes in TLR pathway. The analysis of nephrectomy showed that activation of TLR pathway is present in AR and CAN. Sponsor. This work was

supported by the inconditional grant from Fundao de Amparo a Pesquisa do Estado de So Paulo (FAPESP, 04/08311-6), from Conselho Nacional de Pesquisa e Desenvolvimento (CNPq) and from Fundao Osvaldo Ramos.

Synonyms: GEArray

Resource Type: software resource

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GEArray Expression Analysis Suite 2.0

Resource ID: SCR_000282

Alternate IDs: nif-0000-30602

Record Creation Time: 20220129T080200+0000

Record Last Update: 20260808T185714+0000

Ratings and Alerts

No rating or validation information has been found for GEArray Expression Analysis Suite 2.0.

No alerts have been found for GEArray Expression Analysis Suite 2.0.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Mucci A, et al. (2018) iPSC-Derived Macrophages Effectively Treat Pulmonary Alveolar Proteinosis in Csf2rb-Deficient Mice. Stem cell reports, 11(3), 696.

Baldauf MC, et al. (2018) Systematic identification of cancer-specific MHC-binding peptides with RAVEN. Oncoimmunology, 7(9), e1481558.

Sanfilippo C, et al. (2017) CHI3L1 and CHI3L2 overexpression in motor cortex and spinal cord of sALS patients. Molecular and cellular neurosciences, 85, 162.

Moily NS, et al. (2017) Transcriptional profiles for distinct aggregation states of mutant Huntingtin exon 1 protein unmask new Huntington's disease pathways. Molecular and cellular neurosciences, 83, 103.

Yasuda K, et al. (2016) MAPK13 is preferentially expressed in gynecological cancer stem cells and has a role in the tumor-initiation. Biochemical and biophysical research communications, 472(4), 643.

Coppola A, et al. (2014) Cardiomyogenesis is controlled by the miR-99a/let-7c cluster and epigenetic modifications. Stem cell research, 12(2), 323.

Etzrodt M, et al. (2012) Regulation of monocyte functional heterogeneity by miR-146a and Relb. Cell reports, 1(4), 317.

Wang Z, et al. (2011) Fusion of core pathways reveals a horizontal synergistic mechanism underlying combination therapy. European journal of pharmacology, 667(1-3), 278.

Nanda SK, et al. (2009) Infection of bovine dendritic cells by rinderpest or measles viruses induces different changes in host transcription. Virology, 395(2), 223.