

GUDMAP AN ONLINE GENITOURINARY RESOURCE



Armit, C.¹, Harding, S.², Davies, J.A.¹, Armstrong, J.¹, Brennan, J.¹, Lloyd-MacGilp, S.¹, Houghton, D.², Sharghi, M.², Pi, X.², Cheng, Y.², Aronow, B.³, Gaido, K.³, Grimmond, S.³, Koopman, P.³, Lessard, J.³, Little, M.³, McMahon, A.³, Mendelsohn, C.³, Potter, S.³, Southard-Smith, M.³ & Davidson, D.²

¹ GUDMAP Editorial Office, Centre for Integrative Physiology, University of Edinburgh, UK.
² GUDMAP Database Development Team, MRC Human Genetics Unit, Western General Hospital, Edinburgh, UK.
³ Other addresses - please see website (www.gudmap.org)

Introduction

The **GenitoUrinary Development Molecular Anatomy Project (GUDMAP)** is a consortium of laboratories working to provide the scientific and medical community with gene expression data and tools to facilitate research (www.gudmap.org).

GUDMAP Gene Expression Data

The data provided by GUDMAP include large in situ screens and expression microarray analysis of components of the developing mouse urogenital system. These data can be summarized as follows:

In situ data

- In situ hybridization screens (wholmount and section)
- In situ analysis of transgenic reporter screens (wholmount)
- Immunohistochemistry (section)

cDNA Microarray data

- Array analysis of laser-captured components of the developing GU system
- Array analysis of FACS-isolated cells from transgenic reporter mice

The screenshot shows two data tables side-by-side. The left table, 'In situ data', has columns for Gene, GUDMAP Entry Details, Assay Type, Stage, Lab, Specimen Type, and Images. The right table, 'cDNA Microarray data', has columns for GUDMAP Entry Details, Theliler Stage, Lab, Assay Type, Tissue Type, and Series ID. Both tables show a list of genes and their corresponding experimental details.

To facilitate integration of in situ data, microarray expression profiles, and disease associations, the GUDMAP Consortium has developed a Gene Strip interface that allows users to access these datasets easily. In addition, we are developing a range of tools that will allow users to collect and analyze these datasets.

The Gene Strip interface for the Jag1 gene shows a table with columns: Select, Gene, Synonyms, Disease, Theliler Stage, In situ expression profile, In situ expression images, Microarray expression profile, and Genesets. The 'In situ expression profile' column contains a bar chart showing expression levels across different stages. The 'Microarray expression profile' column shows a heatmap of expression data.

Disease Resource

A searchable database of associations between:

- Genes & OMIM Diseases (with GU component)
- Genes & Mammalian Renal/Urinary Phenotypes
- Genes & Mammalian Reproductive Phenotypes

1. To search for genes associated with a genitourinary disease:

Select the OMIM genitourinary disease of interest from the pull-down menu. Then click 'Search' - the query will bring back a table of genes that are associated with the chosen disease.

Select Disease:

Associations are obtained from

1. NCBI *mim2gene* file download <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA/>
2. Matching gene symbols in the main text of the OMIM entry

Disease-gene associations are searchable with results presented in a simple table.

The screenshot shows the 'GUDMAP Disease Database' search results for 'WILMS TUMOR 1'. It includes a table with columns: Disease Name, Gene Symbol, OMIM ID, and ISH data. The table lists several genes associated with Wilms tumor, such as Gpc3, Pax2, Pax3, Pax6, Sry, Wt1, and Brca2.

The **clinical synopsis** of OMIM disease entries is used to determine if the disease has implications for the **GU system**. It is searched for key GU terms such as 'renal', 'nepbro-', 'GU', and 'reproductive'.

The screenshot shows the NCBI OMIM clinical synopsis for 'WILMS TUMOR 1; WT1'. It includes sections for 'Clinical Synopsis', 'INHERITANCE', 'Pathogenesis', and 'GENITOURINARY'. The 'GENITOURINARY' section lists 'Kidneys' and 'Nephroblastoma'.

Submitting Data - Online Annotation Tool

The GUDMAP Editorial Office and Database Development Team has developed an Online Annotation Tool that simplifies in situ data submission through an ontology-based graphical user interface.

The screenshot shows the 'Annotation Tool' interface. It features a tree view of the anatomy ontology on the left, a central workspace for adding patterns, locations, and annotation notes, and a right-hand panel for managing these elements. A pop-up window is shown for adding a note.

- A high-resolution anatomy ontology has been developed by members of the GUDMAP consortium to describe the subcompartments of the developing murine genitourinary tract.
- This ontology is incorporated into the Online Annotation Tool where it is used to describe in situ gene expression patterns.

Using The Database

The screenshot shows the database query interface. It displays two Boolean queries: 'nephrogenic interstitium TS17 to: TS28' and 'renal capsule TS17 to: TS28'. Below the queries, there are sections for 'Collections' and 'Gene Collections'. The 'Gene Collections' section shows a table with columns: Select, Gene, and GUDMAP Entry Details. It lists 'Wnt2' with GUDMAP entry '10258'. Below this, there are buttons for 'Add to my Genes', 'Replace my Genes', and 'View my Genes (or other selections)'. A 'My Genes' section shows options to 'Get intersection with my Genes' and 'Get difference with my Genes'.

References

Little MH *et al.* (2007). A high-resolution anatomical ontology of the developing murine genitourinary tract. *Gene Expr Patterns*. 7(6):680-99.

Funding
 GUDMAP Genitourinary Development Molecular Anatomy Project (NIH-DK070200-05)

