

# **HHS Public Access**

Author manuscript *Dev Dyn.* Author manuscript; available in PMC 2015 October 01.

Published in final edited form as:

Dev Dyn. 2014 October ; 243(10): 1176-1186. doi:10.1002/dvdy.24155.

# The Gene Expression Database for Mouse Development (GXD): putting developmental expression information at your fingertips

Constance M. Smith, Jacqueline H. Finger, James A. Kadin, Joel E. Richardson, and Martin Ringwald<sup>\*</sup>

The Jackson Laboratory, 600 Main Street, Bar Harbor, ME 04609, USA

# Abstract

Because molecular mechanisms of development are extraordinarily complex, the understanding of these processes requires the integration of pertinent research data. Using the Gene Expression Database for Mouse Development (GXD) as an example, we illustrate the progress made towards this goal, and discuss relevant issues that apply to developmental databases and developmental research in general. Since its first release in 1998, GXD has served the scientific community by integrating multiple types of expression data from publications and electronic submissions and by making these data freely and widely available. Focusing on endogenous gene expression in wild-type and mutant mice and covering data from RNA *in situ* hybridization, *in situ* reporter (knock-in), immunohistochemistry, RT-PCR, northern blot and western blot experiments, the database has grown tremendously over the years in terms of data content and search utilities. Currently, GXD includes over 1.4 million annotated expression results and over 260,000 images. All these data and images are readily accessible to many types of database most effectively; discuss how we acquire, curate, and integrate developmental expression information; and describe how the research community can help in this process.

## Keywords

literature curation; data integration; online resource; *in situ* hybridization; immunohistochemistry; anatomy ontology

# INTRODUCTION

Gene expression data provide crucial insights into the molecular mechanisms of development, differentiation, and disease. However, the data are voluminous, complex, and heterogeneous. They are generated by many different laboratories and scattered through thousands of publications. Without the help of centralized databases, it is impossible to keep abreast of all this information, let alone to access and search these data in a cohesive and integrated way.

<sup>\*</sup>To whom correspondence should be addressed: Tel: +1 207 288 6436; Fax: +1 207 288 6132; Martin.Ringwald@jax.org.

The Gene Expression Database for Mouse Development (GXD) was one of the first databases to address these critical issues (Ringwald et al., 1994; Ringwald et al., 1999). As a mammalian model system, the mouse is heavily used for developmental research. Tissues from all developmental stages and from different mouse strains and mutants are subject to detailed expression studies. For many years, the GXD project has been curating mouse developmental expression data from the published literature, as well as acquiring data through direct submissions and collaboration with efforts that generate pertinent expression data from the EurExpress (Diez-Roux et al., 2011), GenePaint (Visel et al., 2004), GUDMAP (Genitourinary Molecular Anatomy Project; Harding et al., 2011), and BGEM (Brain Gene Expression Map; Magdaleno et al., 2006) projects. GXD integrates data from all these different sources and, as a major component of the Mouse Genome Informatics (MGI)

resource (www.informatics.jax.org), combines the expression information with genetic, functional, and phenotypic data. Therefore, these expression data are readily accessible to many types of database searches (Smith et al., 2014; Finger et al., 2011; Blake et al., 2014).

Here we describe the current status of GXD with a particular emphasis on its search utilities. Further, we illustrate issues of data curation and integration that apply to developmental research in general.

# CONCEPTS, SCOPE, AND EXPRESSION DATA CONTENT

GXD covers all developmental stages and all organ systems and comprises expression data from wild-type and mutant mice. The main focus is on endogenous gene expression data during development. As data accumulate, GXD aims to provide increasingly complete information about which RNA and protein products are made from a given gene, where and when these products are expressed, and how their expression varies in different mouse strains and mutants. Because there is no single assay type that can provide answers to all these questions, GXD is designed as a system that can integrate different types of expression data. At this point, GXD captures data from RNA *in situ* hybridization, *in situ* reporter (knock-in), immunohistochemistry, RT-PCR, northern blot and western blot experiments.

Expression patterns (i.e. the time and space of gene expression) are described in a standardized way by using an extensive anatomical ontology that has been developed in collaboration with the eMouseAtlas (EMAP) project (Hayamizu et al., 2013; Bard et al., 1998). The ontology is structured hierarchically, allowing the integrated description of expression patterns from experiments with differing spatial resolution, as well as enabling searches that include anatomical structures and their substructures (described in detail below).

As illustrated in Figure 1, each database record describes the results obtained for each specimen, including the level and pattern of expression for each anatomical structure examined, as well as the molecular probe and the experimental conditions used. Images of the original expression data accompany the annotations whenever possible. By capturing these elemental data, different types of expression data can be represented and integrated in a robust manner. Genes and mutant alleles are recorded using official nomenclature, and all

data are associated with a reference. Genes, probes, alleles, anatomical structures, and references are key points of data integration that tie genetic, genomic, expression, functional, and phenotypic data closely together, enabling search capabilities unique to GXD/MGI.

GXD currently includes detailed expression records for > 13,800 genes. The data come from > 67,000 expression assays and include > 1.4 million expression result annotations and > 260,000 images of primary expression data. 82 % of the data are from RNA *in situ* hybridization studies and 10 % from RT-PCR experiments, reflecting the detailed spatial resolution and sensitivity required in developmental expression studies. In addition to data from different strains of wild-type mice, GXD currently includes expression data from > 1,900 mouse mutants. In the following we illustrate different ways to effectively search these data.

# SEARCHING FOR EXPRESSION DATA

#### The GXD Home Page

One way to access the expression data for a given gene is to use the Quick Search, accessible from all MGI pages, in order to find the corresponding gene detail page and then follow the links in the "Expression" section (see Fig. 2). However, GXD's search tools allow you to do much more than look up expression data gene by gene. To take full advantage of GXD, we recommend the GXD Home Page as a starting point: http://www.informatics.jax.org/expression.shtml. This page gives access to GXD's search forms and provides more information about GXD, including user help, news announcements, and instructions for submitting data to GXD. We now describe the use of three of GXD's search forms in more detail.

# Gene Expression Data Query

The Gene Expression Data Query form (http://www.informatics.jax.org/gxd) is the most versatile and powerful search form for detailed expression data in GXD. It offers two different query utilities via the Standard Search and Differential Expression Search tabs.

The Standard Search tab (shown in Fig. 3) allows investigators to ask both broad and very specific questions pertinent to their research interests and quickly obtain matching expression results. Researchers can find expression data for specific genes, or for sets of genes as defined by their biological function or by association with annotated mouse phenotypes or human diseases. They can search for expression data for specific anatomical structures and/or specific developmental stages. Searches can be limited to expression data from wild-type mice or to expression data from mice that have been mutated in specific genes. Assay type(s) can also be chosen. Further, using combinations of the query parameters described above makes it possible to formulate complex queries. For example, one could search for genes associated with DiGeorge Syndrome expressed in heart; for genes involved in left/right asymmetry that are expressed in the primitive streak; or for genes involved in signaling pathways that are expressed in the eye of *Pax6* mutant mice.

The Differential Expression Search tab allows querying for genes that are expressed in one anatomical structure but not in another and/or at some developmental stages but not others. For example, one can search for genes that are expressed in the epithalamus but not in the hypothalamus; or for genes that are expressed at the morula stage (Theiler stage 3) but not at the blastocyst stages (Theiler stages 4 and 5). These searches will return a list of genes whose expression has been shown to be absent (not detected), as well as genes whose expression has not been analyzed or recorded in the database for the specified structures and stages. The two cases can be distinguished by filtering the results summaries for instances where expression was not detected (see below).

The Standard Search and Differential Expression Search return a results page with tabbed summaries for assay results, assays, genes, and images (see Fig. 4). This allows users to see the desired level of detail and focus on the data they are most interested in. The four tabs indicate the number of records returned, respectively. One can narrow down the returned results further by modifying the search or by filtering the expression results by Anatomical System, Assay Type, Detected/Not Detected, Theiler Stage, or Wild type/Mutant. Filters can be selected and de-selected to interactively revise and refine the data summaries. Most of the data columns of the summaries are sortable. Further, data from the Assay Results and Genes summaries can be downloaded in text or spreadsheet formats allowing upload into other applications.

Each row in the assays, assay results, and image summaries includes links to detailed expression records. Figure 1 shows, as an example, an entry for an immunohistochemistry experiment, illustrating the detail in which data in GXD are annotated. These Assay Detail pages display image panes together with their annotations. Each image pane is linked to the corresponding image detail page that shows the publication figure, which is often multipaned, thus presenting the image pane in context. Image detail pages might also include links to external resources. For example, detail pages for the EurExpress and GenePaint images link back to the corresponding records at these sites where utilities such as serialsection browsers and high-resolution images are available. Some image detail pages also have links to the Edinburgh Mouse Atlas and Gene Expression Database (EMAGE). GXD makes all its RNA in situ and immunohistochemistry images, together with their annotations, available to EMAGE (Richardson et al., 2014), so that the expression patterns can be mapped and queried spatially. If in situ images have been spatially mapped, GXD provides links from image detail pages to the corresponding mapped images in EMAGE. However, only a subset of the wild-type expression images can be spatially mapped (the 3D atlas is based on wild-type embryos). The standardized text-based description of expression patterns employed by GXD is essential as it allows the representation and integration of all types of expression data from wild-type and mutant mice, as well as the further integration with other data that relate to anatomy, such as mouse phenotype and human disease data.

In short, the Gene Expression Data Query form enables researchers to quickly find specific sets of expression data. Query summaries can be interactively refined and lead to the detailed expression records.

#### **Mouse Developmental Anatomy Browser**

As discussed above, GXD and EMAP have developed an extensive ontology for mouse developmental anatomy to describe the time and space of gene expression in a standardized way. This enables intuitive and comprehensive expression searches at variable anatomical resolution. The ontology is structured hierarchically. Each term can have multiple parents, allowing the anatomy to be represented and searched from different perspectives. For example, "brain" is represented as part of the "nervous system" and as part of the "head". Searches for expression in the "nervous system" or in the "head" will both return expression data for the brain.

The newest version of Mouse Developmental Anatomy comprises all 28 Theiler stages, including the embryonic (TS 1-26), newborn (TS 27), and postnatal mouse (TS 28). There is one "abstract" (non-stage specific) representation of the mouse anatomy that lists the anatomical structures for all Theiler stages, as well as the stage range during which each structure is present. We refer to these terms as EMAPA terms (A for abstract). In addition, there are 28 stage-specific representations (derived from the abstract version). Currently, the ontology includes more than 6500 EMAPA terms and more than 25,000 stage-specific terms (referred to as EMAPS terms). Expression data in GXD are annotated to the stage-specific anatomical terms.

The Mouse Developmental Anatomy Browser (http://www.informatics.jax.org/vocab/gxd/ anatomy) allows users to navigate through this anatomical ontology, view a specific anatomical structure, and to obtain the expression data associated with that structure and its substructures (see Fig. 5). The browser consists of three interactive sections: a search section for finding and selecting anatomical terms; a detail section that provides additional information for a selected term and lets users toggle between the abstract and stage-specific versions of the anatomical ontology; and a tree view section that allows users to view the terms in their hierarchical context, to expand and collapse branches of the hierarchy, and to retrieve the expression data for specific anatomical structures. The expression result summaries accessed from the Mouse Developmental Anatomy Browser have the same features and utilities as those obtained upon using the Gene Expression Data Query Form. They can be sorted and filtered and link to the detailed expression records, as described above.

Terms from the mouse developmental ontology are also being used to label the EMAP 3D atlas and to describe expression patterns in EMAGE (Armit et al., 2012). Efforts to establish cross-references to anatomical ontologies from other model organism and human databases are underway (Mungall et al., 2012; Dahdul et al., 2012; Hayamizu et al., 2012; Van Slyke et al., 2014; Segerdell et al., 2013, Costa et al., 2013). This will foster the comparative analysis of expression patterns between model organisms used in developmental research.

#### Gene Expression Literature Query

GXD provides researchers with an effective way to search the mouse embryonic expression literature. Our curators survey journals to find all publications that contain the types of data that GXD collects. As a first annotation step, they index all these publications with regard to

the genes that have been studied, the expression assay types used, and the ages analyzed. These annotations are then combined with bibliographic information from PubMed to generate the Gene Expression Literature Index. The index is complete and up-to-date from 1990 onwards for all major journals (~150). Currently, the index covers > 21,800 references reporting expression data for > 15,100 genes. An average of 1,200 papers are added to the index per year. All this information is available via the Gene Expression Literature Query form (http://www.informatics.jax.org/gxdlit). The query form allows researchers to quickly find publications that report specific sets of expression data (see Fig. 6). These searches are more effective and complete than PubMed searches because the index uses standard nomenclature for genes, assay types, and ages and because the annotations are based on the entire article, including supplemental data.

# ACQUIRING AND CURATING DATA

Data are acquired from the literature, via electronic data submissions, and through collaborations with projects that generate pertinent expression data at a large-scale. All data are reviewed by curators and annotated in standardized ways by making extensive use of controlled vocabularies and ontologies as illustrated in Fig. 1. This is a prerequisite for the data integration and search capabilities that GXD provides.

GXD is the only effort that curates mouse developmental expression data from the literature in a systematic way. The first step in this process is populating the Gene Expression Literature Index as described above. The next step is to annotate the details of the expression data from these articles, including supplemental data, as illustrated in Fig. 1. Papers are prioritized for detailed annotation based on the information in the Gene Expression Literature Index. Prioritization criteria include: genes for which there is no detailed data in the database; genes associated with human diseases; genes which, based on the number of publications, are underrepresented in the detailed portion of the database; publications that include a large amount of expression data; and publications that characterize the developmental expression pattern of a given gene in detail (often the first publications for that gene).

Large-scale electronic data sets are reviewed by a combination of computational and manual checks to make sure that the probe-to-gene assignments are up-to-date and that data entries are complete. Nomenclature issues, data ambiguities, and questions that might arise during the mapping of submitted data to ontologies are resolved together with the data provider before the data are loaded into GXD.

All data, including those from large-scale data sets, gain significant value when integrated with the other data in GXD and the larger MGI resource. All data can be explored together and searches can be done that are unavailable elsewhere. Further, GXD ensures that data and data connections are maintained and kept up-to-date after large-scale projects have ended and gene models or the gene names used in the literature have changed.

Authors base their conclusions on much more primary data than will appear in a publication, they are specialists in their fields, and they have detailed knowledge about specific experimental parameters and potential pitfalls that is not available to curators. For these

reasons, GXD curators rely on the text of the manuscript, or of data submissions, to derive annotations of expression patterns. These annotations are standardized by using terms from the anatomical ontology (which is expanded as required). However, curators do not interpret images themselves, thereby trying to derive additional expression results that have not been asserted in the paper. For the reasons discussed above, interpretation of images by curators to infer expression or absence of expression would be problematic and error-prone. Instead, GXD displays standardized text annotations together with the corresponding images so users can see the original expression data (see Fig. 1). We have obtained permissions to include images from all major developmental journals, as well as from many others. Currently, over 70% of the result annotations are accompanied by images. Also in cases where GXD does not have the permission to include images, we annotate the data based on the information in the manuscript and provide a reference to the corresponding figure panes.

It is thus important to note that the detail of expression annotations in GXD is determined by the details provided in the text of published articles and electronic data submissions. Detailed descriptions of expression results will lead to more fine-grained and complete annotations. Further, a clear correspondence in the publication between stated expression results, probes, specimens, and images facilitates data annotation. Concise, unambiguous descriptions of expression patterns result in robust annotations. Issues of completeness, consistency, data identity, and clarity apply not only to GXD but to all databases that curate data from the published scientific literature. This includes other developmental organism databases such as GEISHA (Antin et al., 2014), Xenbase (James-Zorn et al., 2013), ZFIN (Howe et al., 2013), FlyBase (St. Pierre et al., 2014), and Wormbase (Harris at al., 2014). Publications that present data, results, and interpretations clearly and identify genes, strains, reagents, and methods adequately can significantly facilitate data curation and dissemination, thus greatly benefiting the researchers who generated the data initially as well as improving data access to the research community at large.

# THE CASE FOR ELECTRONIC DATA SUBMISSION

Both journal publications and databases are essential for the research enterprise, and they fulfill complementary roles. Journal publications excel in the narrative descriptions of novel discoveries and discussions of data implications and future applications. However, they usually include only part of the data pertinent to a study due to space constraints or because authors report only the results most relevant to the papers' narrative. Expression (or non-expression) in anatomical systems peripheral to the narrative is often not reported. Further, journal publications cannot and do not provide a framework for data integration and regular updates, with the result that the data cannot be searched adequately. Databases, on the other hand, do not have space constraints or an incentive to focus on specific scientific narratives; and they excel at the handling, maintenance, and integration of data, and in making them accessible to searches. Currently, data generated from conventional (non large-scale) laboratories are primarily reported in free-text descriptions in journal publications. Unless database curators extract data from these publications and bring them into formats proper for integration and searching, these data will remain poorly integrated into our scientific knowledge base. This is clearly not a good solution for making research data accessible.

An obvious and effective solution to address this problem is to combine journal publications with electronic data submissions. Following the example of sequence and array expression data, the types of developmental expression data discussed here could be submitted to pertinent public databases in conjunction with publications. Submitters would receive accession numbers that can be cited in the publications. Without causing an undue burden on submitters, they could, for example, provide an expanded legend for each image that includes more complete descriptions of the expression patterns seen. Thus, electronic submission can include more primary data and results can be described in greater detail and in more standardized ways. While such submissions would still require review and annotation by database curators, it would significantly facilitate the acquisition, integration, and dissemination of data. Having the data widely accessible to many types of searches would benefit everyone: the journal (because all the data would be tied to the publication reference), the submitter (because their data would be more accessible), and the scientific community as a whole (because of the increased database content and utility).

GXD accepts electronic data submissions for the types of data it collects; see the "Send us your data" tab at the bottom of the GXD Home Page for instructions (http:// www.informatics.jax.org/mgihome/GXD/GEN/gxd\_submission\_guidelines.shtml). Other developmental databases, such as FlyBase, GEISHA, ZFIN and Xenbase, are welcoming electronic data submissions as well. The value of all these community resources is proportional to the amount and the quality of data they contain, and it is time for the research community to realize the potential of electronic data submissions.

# FUTURE DIRECTIONS

GXD will continue to acquire data from the literature and electronic data submissions and to improve its search and display capabilities. Later this year, we plan to add interactive matrix views of expression data. Tissue-by-developmental stage matrices will provide high-level overviews of the spatio-temporal expression patterns of genes. Tissue-by-gene matrices will enable a comparison of expression patterns. Both types of matrices can be expanded (and collapsed) along the tissue axis, based on the hierarchical organization of the anatomy. Thus, these matrix views will provide users with intuitive high-level summaries of expression results from where they can drill down to more detail. GXD and the larger MGI resource are also planning to implement additional links to other developmental organism databases. In the shorter term, gene-based links will enable users to look up and compare expression data (and other types of data) for orthologous genes. As described above, we are also working on establishing cross-references between anatomical ontologies to enable, in the longer term, an anatomy-based comparison of developmental gene expression patterns.

# USER SUPPORT AND OUTREACH

User Support and GXD curatorial staff actively seek to provide presentations, demonstrations and training sessions on GXD and the larger MGI resource at many meetings. Upon request user support personnel also provide on-site visits and training workshops, as well as remote interactive sessions. GXD is continually looking for ways to improve the user experience and, thus, direct user interactions, surveys and collaborations provide valuable feedback on the project from biologists, biomedical researchers, ontology developers and computational biologists who utilize our data. Further, the GXD Advisory Board provides critical input and guidance for the project.

# DATABASE ACCESS AND CONTACT INFORMATION

The GXD home page can be accessed directly at http://www.informatics.jax.org/ expression.shtml; via the MGI home page (http://www.informatics.jax.org/) by following the topic "Gene Expression Database (GXD)"; or from any other page within MGI by clicking the "Expression" tab of the navigation bar. For web-based access to GXD and MGI, we recommend Firefox, Chrome, or Safari. Online help is available via the FAQs on the GXD home page and by clicking on the question marks in the upper right corner of most GXD pages. User Support personnel can be contacted via email to mgi-help@jax.org or via the "Contact Us" link in the navigation bar. This article focuses on web-based access to the GXD database proper. Additional computational tools to explore GXD's expression data are available, such as the GXD BioMart (accessible via the GXD home page) and MouseMine (www.mousemine.org). MouseMine, in particular, offers advanced iterative search and filtering capabilities.

# Acknowledgments

We would like to thank our colleagues from the GXD project, as well as our colleagues from other MGI projects for their contributions to GXD and the larger MGI resource. In particularly, we would like to thank Janan Eppig and Joanne Berghout for their critical reading of the manuscript and the following individuals for their contributions to the most recent GXD release: Richard Baldarelli, Jonathan Beal, Olin Blodgett, Lori Corbani, Sharon Giannatto, Terry Hayamizu, Jill Lewis, Ingeborg McCright, Dave Miers, David Shaw, and Jingxia Xu.

#### FUNDING

Grant Sponsor: Eunice Kennedy Shriver National Institute of Child Health and Human Development (NICHD) of the National Institutes of Health (NIH)

Grant Number: HD062499

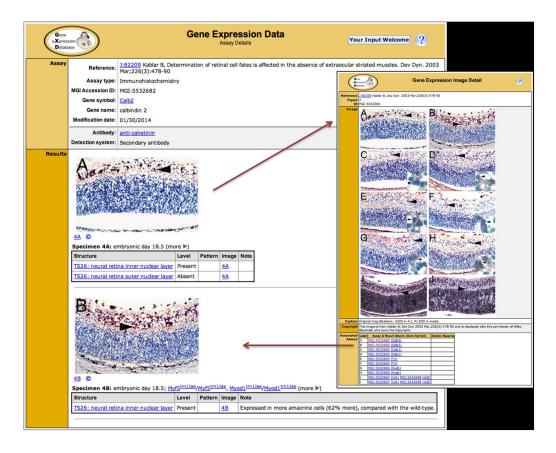
#### References

- Amberger J, Bocchini C, Hamosh A. A new face and new challenges for Online Mendelian Inheritance in Man (OMIM(R)). Hum Mutat. 2011; 32:564–567. [PubMed: 21472891]
- Antin PB, Yatskievych TA, Davey S, Darnell DK. GEISHA: an evolving gene expression resource for the chicken embryo. Nucleic Acids Res. 2014; 42:D933–937. [PubMed: 24150938]
- Armit C, Venkataraman S, Richardson L, Stevenson P, Moss J, Graham L, Ross A, Yang Y, Burton N, Rao J, Hill B, Rannie D, Wicks M, Davidson D, Baldock R. eMouseAtlas, EMAGE, and the spatial dimension of the transcriptome. Mamm Genome. 2012; 23:514–524. [PubMed: 22847374]
- Bard JBL, Kaufman MH, Dubreuil C, Brune RM, Burger A, Baldock RA, Davidson DR. An internetaccessible database of mouse developmental anatomy based on a systematic nomenclature. Mech Dev. 1998; 74:111–120. [PubMed: 9651497]
- Barrett T, Wilhite SE, Ledoux P, Evangelista C, Kim IF, Tomashevsky M, Marshall KA, Phillippy KH, Sherman PM, Holko M, Yefanov A, Lee H, Zhang N, Robertson CL, Serova N, Davis S, Soboleva A. NCBI GEO: archive for functional genomics data sets--update. Nucleic Acids Res. 2013; 41:D991–995. [PubMed: 23193258]
- Blake JA, Bult CJ, Eppig JT, Kadin JA, Richardson JE. The Mouse Genome Database Group. The Mouse Genome Database: integration of and access to knowledge about the laboratory mouse. Nucleic Acids Res. 2014; 42:D810–D817. [PubMed: 24285300]

- Costa M, Reeve S, Grumbling G, Osumi-Sutherland D. The Drosophila anatomy ontology. J Biomed Semantics. 2013; 4:32. [PubMed: 24139062]
- Dahdul WM, Balhoff JP, Blackburn DC, Diehl AD, Haendel MA, Hall BK, Lapp H, Lundberg JG, Mungall CJ, Ringwald M, Segerdell E, Van Slyke CE, Vickaryous MK, Westerfield M, Mabee PM. A unified anatomy ontology of the vertebrate skeletal system. PLoS One. 2012; 7:e51070. [PubMed: 23251424]
- Diez-Roux G, Banfi S, Sultan M, Geffers L, Anand S, Rozado D, Magen A, Canidio E, Pagani M, Peluso I, Lin-Marq N, Koch M, Bilio M, Cantiello I, Verde R, De Masi C, Bianchi SA, Cicchini J, Perroud E, Mehmeti S, Dagand E, Schrinner S, Nürnberger A, Schmidt K, Metz K, Zwingmann C, Brieske N, Springer C, Hernandez AM, Herzog S, Grabbe F, Sieverding C, Fischer B, Schrader K, Brockmeyer M, Dettmer S, Helbig C, Alunni V, Battaini MA, Mura C, Henrichsen CN, Garcia-Lopez R, Echevarria D, Puelles E, Garcia-Calero E, Kruse S, Uhr M, Kauck C, Feng G, Milyaev N, Ong CK, Kumar L, Lam M, Semple CA, Gyenesei A, Mundlos S, Radelof U, Lehrach H, Sarmientos P, Reymond A, Davidson DR, Dollé P, Antonarakis SE, Yaspo ML, Martinez S, Baldock RA, Eichele G, Ballabio A. A High-Resolution Anatomical Atlas of the Transcriptome in the Mouse Embryo. PLoS Biol. 2011; 9:e1000582. [PubMed: 21267068]
- Finger JH, Smith CM, Hayamizu TF, McCright IJ, Eppig JT, Kadin JA, Richardson JE, Ringwald M. The mouse Gene Expression Database (GXD): 2011 update. Nucleic Acids Res. 2011; 39:D835– D841. [PubMed: 21062809]
- Gene Ontology Consortium. The Gene Ontology in 2010: extensions and refinements. Nucleic Acids Res. 2010; 38:D331–D335. [PubMed: 19920128]
- Harding SD, Armit C, Armstrong J, Brennan J, Cheng Y, Haggarty B, Houghton D, Lloyd-MacGilp S, Pi X, Roochun Y, Sharghi M, Tindal C, McMahon AP, Gottesman B, Little MH, Georgas K, Aronow BJ, Potter SS, Brunskill EW, Southard-Smith EM, Mendelsohn C, Baldock RA, Davies JA, Davidson D. The GUDMAP database--an online resource for genitourinary research. Development. 2011; 138:2845–2853. [PubMed: 21652655]
- Harris TW, Baran J, Bieri T, Cabunoc A, Chan J, Chen WJ, Davis P, Done J, Grove C, Howe K, Kishore R, Lee R, Li Y, Muller HM, Nakamura C, Ozersky P, Paulini M, Raciti D, Schindelman G, Tuli MA, Van Auken K, Wang D, Wang X, Williams G, Wong JD, Yook K, Schedl T, Hodgkin J, Berriman M, Kersey P, Spieth J, Stein L, Sternberg PW. WormBase 2014: new views of curated biology. Nucleic Acids Res. 2014; 42:D789–793. [PubMed: 24194605]
- Hayamizu TF, de Coronado S, Fragoso G, Sioutos N, Kadin JA, Ringwald M. The mouse-human anatomy ontology mapping project. Database (Oxford). 2012; 2012:bar066. [PubMed: 22434834]
- Hayamizu TF, Wicks MN, Davidson DR, Burger A, Ringwald M, Baldock RA. EMAP/EMAPA ontology of mouse developmental anatomy: 2013 update. J Biomed Semantics. 2013; 4:15. [PubMed: 23972281]
- Heintz N. Gene expression nervous system atlas (GENSAT). Nature Neurosci. 2004; 7:483. [PubMed: 15114362]
- Howe DG, Bradford YM, Conlin T, Eagle AE, Fashena D, Frazer K, Knight J, Mani P, Martin R, Moxon SA, Paddock H, Pich C, Ramachandran S, Ruef BJ, Ruzicka L, Schaper K, Shao X, Singer A, Sprunger B, Van Slyke CE, Westerfield M. ZFIN, the Zebrafish Model Organism Database: increased support for mutants and transgenics. Nucleic Acids Res. 2013; 41:D854–860. [PubMed: 23074187]
- James-Zorn C, Ponferrada VG, Jarabek CJ, Burns KA, Segerdell EJ, Lee J, Snyder K, Bhattacharyya B, Karpinka JB, Fortriede J, Bowes JB, Zorn AM, Vize PD. Xenbase: expansion and updates of the Xenopus model organism database. Nucleic Acids Res. 2013; 41:D865–870. [PubMed: 23125366]
- Lein ES, Hawrylycz MJ, Ao N, Ayres M, Bensinger A, Bernard A, Boe AF, Boguski MS, Brockway KS, Byrnes EJ, Chen L, Chen L, Chen TM, Chin MC, Chong J, Crook BE, Czaplinska A, Dang CN, Datta S, Dee NR, Desaki AL, Desta T, Diep E, Dolbeare TA, Donelan MJ, Dong HW, Dougherty JG, Duncan BJ, Ebbert AJ, Eichele G, Estin LK, Faber C, Facer BA, Fields R, Fischer SR, Fliss TP, Frensley C, Gates SN, Glattfelder KJ, Halverson KR, Hart MR, Hohmann JG, Howell MP, Jeung DP, Johnson RA, Karr PT, Kawal R, Kidney JM, Knapik RH, Kuan CL, Lake JH, Laramee AR, Larsen KD, Lau C, Lemon TA, Liang AJ, Liu Y, Luong LT, Michaels J, Morgan JJ, Morgan RJ, Mortrud MT, Mosqueda NF, Ng LL, Ng R, Orta GJ, Overly CC, Pak TH, Parry

SE, Pathak SD, Pearson OC, Puchalski RB, Riley ZL, Rockett HR, Rowland SA, Royall JJ, Ruiz MJ, Sarno NR, Schaffnit K, Shapovalova NV, Sivisay T, Slaughterbeck CR, Smith SC, Smith KA, Smith BI, Sodt AJ, Stewart NN, Stumpf KR, Sunkin SM, Sutram M, Tam A, Teemer CD, Thaller C, Thompson CL, Varnam LR, Visel A, Whitlock RM, Wohnoutka PE, Wolkey CK, Wong VY, Wood M, Yaylaoglu MB, Young RC, Youngstrom BL, Yuan XF, Zhang B, Zwingman TA, Jones AR. Genome-wide atlas of gene expression in the adult mouse brain. Nature. 2007; 445:168–176. [PubMed: 17151600]

- Magdaleno S, Jensen P, Brumwell CL, Seal A, Lehman K, Asbury A, Cheung T, Cornelius T, Batten DM, Eden C, Norland SM, Rice DS, Dosooye N, Shakya S, Mehta P, Curran T. BGEM: an in situ hybridization database of gene expression in the embryonic and adult mouse nervous system. PLoS Biol. 2006; 4:e86. [PubMed: 16602821]
- Mungall CJ, Torniai C, Gkoutos GV, Lewis SE, Haendel MA. Uberon, an integrative multi-species anatomy ontology. Genome Biol. 2012; 13:R5. [PubMed: 22293552]
- Petryszak R, Burdett T, Fiorelli B, Fonseca NA, Gonzalez-Porta M, Hastings E, Huber W, Jupp S, Keays M, Kryvych N, McMurry J, Marioni JC, Malone J, Megy K, Rustici G, Tang AY, Taubert J, Williams E, Mannion O, Parkinson HE, Brazma A. Expression Atlas update--a database of gene and transcript expression from microarray- and sequencing-based functional genomics experiments. Nucleic Acids Res. 2014; 42:D926–932. [PubMed: 24304889]
- Richardson L, Venkataraman S, Stevenson P, Yang Y, Moss J, Graham L, Burton N, Hill B, Rao J, Baldock RA, Armit C. EMAGE mouse embryo spatial gene expression database: 2014 update. Nucleic Acids Res. 2014; 42:D835–844. [PubMed: 24265223]
- Ringwald M, Baldock R, Bard J, Kaufman M, Eppig JT, Richardson JE, Nadeau JH, Davidson D. A database for mouse development. Science. 1994; 265:2033–2034. [PubMed: 8091224]
- Ringwald M, Mangan ME, Eppig JT, Kadin JA, Richardson JE. GXD: a gene expression database for the laboratory mouse. The Gene Expression Database Group. Nucleic Acids Res. 1999; 27:106– 112. [PubMed: 9847152]
- Segerdell E, Ponferrada VG, James-Zorn C, Burns KA, Fortriede JD, Dahdul WM, Vize PD, Zorn AM. Enhanced XAO: the ontology of Xenopus anatomy and development underpins more accurate annotation of gene expression and queries on Xenbase. J Biomed Semantics. 2013; 4:31. [PubMed: 24139024]
- Smith CL, Eppig JT. The Mammalian Phenotype Ontology as a unifying standard for experimental and high-throughput phenotyping data. Mamm Genome. 2012; 23:653–668. [PubMed: 22961259]
- Smith CM, Finger JH, Hayamizu TF, McCright IJ, Xu J, Berghout J, Campbell J, Corbani LE, Forthofer KL, Frost PJ, Miers D, Shaw DR, Stone KR, Eppig JT, Kadin JA, Richardson JE, Ringwald M. The mouse Gene Expression Database (GXD): 2014 update. Nucleic Acids Res. 2014; 42:D818–D824. [PubMed: 24163257]
- St Pierre SE, Ponting L, Stefancsik R, McQuilton P. FlyBase Consortium. FlyBase 102--advanced approaches to interrogating FlyBase. Nucleic Acids Res. 2014; 42:D780–788. [PubMed: 24234449]
- Van Slyke CE, Bradford YM, Westerfield M, Haendel MA. The zebrafish anatomy and stage ontologies: representing the anatomy and development of Danio rerio. J Biomed Semantics. 2014; 5:12. [PubMed: 24568621]
- Visel A, Thaller C, Eichele G. GenePaint.org: an atlas of gene expression patterns in the mouse embryo. Nucleic Acids Res. 2004; 32:D552–D556. [PubMed: 14681479]



## Figure 1.

Left: GXD assay details pages provide detailed annotations of experimental parameters and expression results. Shown is an example of an Assay Detail page for an immunohistochemistry experiment illustrating the detailed content of expression results in GXD. The Assay section reports the reference from which the data were derived, the assay type, the gene analyzed, and the antibody used, with links to more details about the antibody, reference, and gene. The Results section reports the tissue (Theiler stage and anatomical structure) analyzed, as well as the level and pattern of expression, as described by the authors. Images of the original expression data are displayed together with the corresponding annotations whenever possible. Major specimen details such as the age and mutant alleles are always displayed on this page. Other information, such as genetic background, sex, and specimen preparation method, is accessible via the 'more' toggle. Right: Image detail pages are accessed by clicking on the image panes or pane labels shown in the assay details record. They show the entire figure, as published, providing the scientific context. As shown in the Associated Assays table of this example, several genes were studied in the same or similar tissue sections; the assay IDs and gene symbols link to the corresponding annotations for each image pane. While the image detail pages provide visual context, it is the detailed and standardized text annotations shown on the GXD assay detail pages (left) that make the expression data, including image data, accessible to searching.

Symbol	Otx2
Name	orthodenticle homolog 2 MGI:97451
	E130306E05Rik
	protein coding gene
Genetic Map	Chromosome 14 25.36 CM Detailed Genetic Map ± 1 CM Mapping data(9)
Sequence Map	Chr14:48657679-48667644 bp, - strand From VEGA annotation of GRCm38 Get FASTA 9966 bp ± 0 kb flank VEGA Genome Browser   Ensembl Genome Browser   UCSC Browser   NCBI Map Viewer Protein coding gene Mouse Genome Browser
	HomoloGene:11026 <u>Vertebrate Homology Class</u> 1 human; 1 mouse; 1 rat; 1 chimpanzee; 1 cattle; 1 dog; 1 chicken; 1 zebrafish Gene Tree: <u>Qbx2</u>
	Human Homolog         OTX2, orthodenticle homeobox 2           NCBI Gene ID         5015           nextProt AC         NX P32243           Human Synonyms         CPHD6, MCOP55           Human Chr (Location)         14q22.3; chrl4:57267425-57277194 (-)           Disease Associations         (2) Diseases Associated with Human OTX2
Alleles and phenotypes	All alleles(47) : Targeted(33) Gene trapped(14) Mice homozygous for a knock-out allele exhibit embryonic lethality during organogenesis due to abnormal gastrulation and embryonic patterning in the brain and heart.
Gene Ontology (GO) classifications	All GO classifications: (52 annotations) Process <u>anatomical structure development, anterior/posterior pattern specification,</u> Componen <u>cytoplasm, arowth cone,</u> Function <u>DNA binding, protein binding,</u> External Resources: <u>Functase</u>
Expression Concerning Concer	Data Summary: (404 records)         Th         Data Summary: Results (1370)       Tissues (410)       Images (466)         Theiler Stages: 2, 3, 4, 5, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 28         Assay Type       Results         Immunohistochemistry       55         RNA in situ       1116         In situ reporter (knock in)       81         C0       Northern blot       1         Ex       Western blot       9

#### Figure 2.

Gene Detail pages summarize, and provide access to, all the information about a given gene in MGI, together with extensive links to external resources. The upper portion of the Otx2 gene detail page is shown. The expression section (expanded) indicates the types and amount of expression information available for the gene and provides links to the corresponding summary pages. Links to databases that store mouse expression data not available in GXD are provided as well: the Allen Institute (Lein et al., 2007), GENSAT (Heintz, 2004), GEO (Barret at al., 2013) and ArrayExpress (Petryszak et al., 2014).

Gene eXpression Database	Gene Expression Data (?)
Standard Search D	ifferential Expression Search
Search Reset	
Genes	Find expression data for
	One gene e.g., Shh or kit oncogene       I       A set of genes defined by ()         Genes with similar nomenclature e.g., Hoxa*       OR       Function e.g., celi-celi signalling         I       Phenotype e.g., obese       Disease e.g., DiGeorge Syndrome
	transcription factor binding - Function
Anatomical structure or stage	Find assay results where expression is <ul> <li>Image: Construction of the expression of</li></ul>
	diencephalon         TS 15 (9.0-10.25 dpc) TS 16 (9.5-10.75 dpc) TS 16 (9.5-10.75 dpc) TS 18 (10.5-11.25 dpc) TS 18 (10.5-11.25 dpc) TS 20 (11.5-13.0 dpc) TS 20 (11.5-13.0 dpc)
Mutant / wild type	Find expression data in  Specimens mutated in gene:  Wild type specimens only  All specimens
Assay types	✓ Find expression data in any assay type         ✓ Immunohistochemistry       ✓ RNA in situ         ✓ In situ reporter (knock in)       ✓ RNase protection         ✓ Northern blot       ✓ RT-PCR         ✓ Nuclease S1       ✓ Western blot
Search Reset	

#### Figure 3.

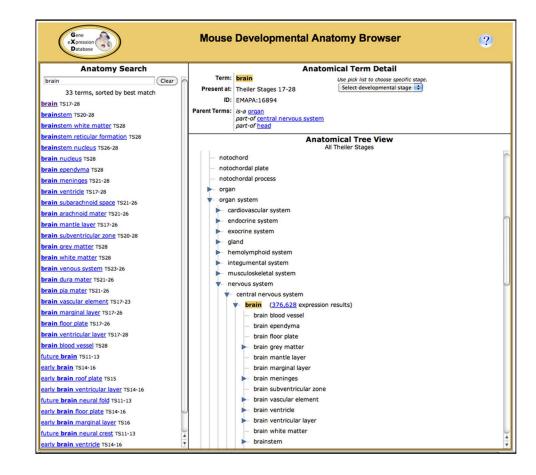
The Gene Expression Data Query Form features two search tabs: Standard and Differential Expression. The Standard Search, shown here, enables queries for expression data using one or more parameters. The Genes section allows users to find expression data for a specific gene or for a set of genes based on their function [as defined by Gene Ontology terms (Gene Ontology Consortium, 2010)], their association with mouse phenotypes [as defined by Mammalian Phenotype Ontology terms (Smith et al., 2012)], or their association with human diseases [as defined by Online Mendelian Inheritance in Man (OMIM) terms (Amberger et al., 2011)]. In the anatomical/stage section, one can search for expression data in specific anatomical structures and/or developmental stages, and one can specify whether (1) all results should be returned or only those where expression was (2) detected (i.e. present) or (3) not detected (i.e. absent). Anatomical searches combine word searching and hierarchical searching. For example, a search for expression in "diencephalon" would return expression annotations for all anatomical structures that have "diencephalon" as part of their name as well as for all their anatomical substructures such as "thalamus". In the mutant/wild type section one can limit the searches to expression data from wild-type mice or search for gene expression in specific mutants. The Assay types section allows selection of expression data types. Auto-fill utilities help to find appropriate search terms. The illustrated search asks for 'transcription factor binding' genes 'detected' in the 'diencephalon' at 'Theiler stages 17, 18, or 19'. The corresponding search results page is shown in Fig. 4. The Differential Expression Search (not shown) allows searching for genes that are expressed in

some anatomical structures but not others and/or at some developmental stages but not others.

eX	pression atabase					Gene Express	sion Data			?
Click to mo	dify search									
Results										
factor bin	thed for: otated to Function ding includes subters in diencephalon	ms	n	r expression by: Anatomic	cal Systen	Assay Type 7 Detected?	7 Theiler Stage 7	Wild type?	<< first < prev 1	2 3 next> last>> 100 Showing results(s) 1 - 100 of 264
substructures										
or TS:19)		15:17 of 15:18	5							
Genes (10	8) Assays (17)	7) Assay resul	lts(264)	Images (330)						
Export:	🖹 Text File 👘 Exc	el File					~			
Gene 🗘	Result Details	Assay Type	\$	Anatomical System 🗘	Age 🗘	Structure	Detected?	Images	Mutant Allele(s)	Reference
Arnt	data (MGI:4440508)	RNA in situ		nervous system	E11.5	TS19: diencephalon	Yes			J:81291 Aitola MH, et al. J Histochem Cytochem. 2003 Jan;51(1):41-54
Arnt2	data (MGI:4440509)	RNA in situ		nervous system	E11.5	TS19: diencephalon	Yes			<u>J:81291</u> Aitola MH, et al. J Histochem Cytochem. 2003 Jan;51(1):41-54
Ascl1	deta () Genes (108)	Assays (177) Assay	y results(264)	Images (330)			Yes			<u>J:156017</u> Yokoyama S, e al., Dev Cell. 2009 Dec;17(6):836-48
Ascl1	d 0 F	Expression	n images in MC	3I are copyrighted; click on an imag	e for details a	bout their use.	Yes	<u>3D</u>		J:14701 Guillemot F, et al., Mech Dev. 1993 Aug;42(3):171-85
	CGE	14	Gene	Assay Type	R	esult Details				
	1	622	Gsx2 Nkx2-1	Immunohistochemistry Immunohistochemistry	25					
	20	D CONTRACT								
	B	©					-			
	w g	and and	Gene	Assay Type		sult Details				
	w	·	Mef2a	Immunohistochemistry	38					
		vz Merge								
	G	vz wierge								
	G		Gene	Assay Type Immunohistochemistry	Re:	out Details				

#### Figure 4.

GXD data summaries can be viewed at different levels of detail and interactively refined and sorted. Searches using the Gene Expression Data Query form return a page with four tabbed summaries for the assay results, assays, genes, and images that match the search parameters. The assay results tab (upper) is displayed by default. It lists the gene studied, the assay type used, the anatomical system, age and tissue examined, indicates whether expression was detected, provides a link to the corresponding images, lists the mutant alleles of the specimen (if applicable), and provides the reference from which the data were derived. Links in the Result Details and Images columns lead to detailed expression records, such as the one shown in Fig. 1. Arrows in column headers indicate that the column is sortable (one set is circled). The assay results tab (as well as the genes tab) allows for the export of results in text and spread sheet formats (buttons in table header). The images tab (lower) shows all the images that match the search criteria, together with the gene(s) examined in that image and the assay type used and provides a link to the corresponding part of the detailed expression record. The expression summaries can be refined by using the 'click to modify search' button or by employing the filter options provided on the summary page. The content of all four tabbed summaries will change accordingly.



#### Figure 5.

The Mouse Developmental Anatomy Browser allows users to search for anatomical terms, to explore the anatomical hierarchies and locate specific anatomical structures in context, and to retrieve the expression data associated with these structures and their substructures. The anatomy search is facilitated by an auto-fill utility. As soon as a term is selected from the pick list, all matching anatomical structures are displayed in the search column, together with the developmental stage range during which these structures are present in the embryo. The best match is listed first and selected by default. Other matching terms can be selected by clicking. Upon selection, the Anatomical Tree View and the Anatomical Term Detail section are updated and the selected anatomical structure is highlighted. Using the Tree View, users can explore the ontology further by expanding and collapsing branches. Clicking on a term in the tree view will select (and highlight) that term. The number of expression results associated with each term is listed; following that link will lead to an expression summary page similar to the one shown in Fig. 4. The initial tree view shows the abstract version of the anatomy ontology. Accordingly, the associated expression results will include the annotations for all developmental stages at which the selected anatomical structure is present. The developmental stage pick list in the Anatomical Term Detail section allows users to toggle between stage-independent terms and tree views and stage-specific terms and tree views. Stage-specific terms will link to the expression results for the anatomical structure at that specific stage.

eXpression Database			Gene	e Exp	pression	Literature Search	2	Gene eXpression Database			G	ene E	xpre	ssic	on Lit	erat	ture S	umm	nary			?
Search Reset							You	searched for:														
Gene Symbol/Name Hoxb4					Examples	one gene e.g., Shh s: a set of genes with similar nomenclature e	a., Hoxa* Mark	er Symbol/Name: Hoxb4														
								7.5 or 8 or 8.5 or 9 or 9	.5 or	10 or												
Assay type ANY	rotein (sec	tion)	•					or 11 or 11.5 or 12 or 1		13 or												
In situ Ri In situ pi	NA (section rotein (who NA (whole	n) ole mount	)					or 14 or 14.5 or 15 or 1 6 matching records from		feren	ces.											
Age 14	(days po	ost conce	ption)				Sun	nmary by Age a	nd /	Assa	y: N	mbers	in the tal	ole ind	dicate the	e num	ber of res	sults ma	atching	the sear	ch criter	ria.
15							Age		E7.5	E8	8.5 E	9 E9.5	E10 E1	0.5	E11 E1	1.5 E	12 E12.	5 E13	E13.5	E14 E1	4.5 E1	5 E15
16 -							In sit	u protein (section)	1		3	2		3	1 2	2				1	1	1
Author						Author(s)	In sit	u RNA (section)		1	1	5	1	6	5	1	10		2		5	2
						Author Author	In sit	u protein (whole mount)			1	3	2	3	1							-
Journal				-	Examples	a: Proc Natl Acad Sci USA	In sit	u RNA (whole mount)	1		6			5	-	5	5		2		1	2
Year				-	(See ML)	M.) J Cell Mol Med 2008	1. C.	ern blot	-	$\vdash$			-	-			2		1		3	1
Year					Examples			ern blot	-	$\vdash$	-			-	-	·	-	+ +	-	1	·	1
						2009- (from 2009 through the present)	RT-PC			$\vdash$	-	1		3	1 1		1	1			2 2	_
Text						gastrulation, morphogenesis		dones	-	$\vdash$	1	-		-		-	-	-				-
lext					Examples			e protection	-	+	*	-		-+	-	-	1	+ +		1	+	+
	le 🗹 In Ab						RIVAS	e protection				_				-				*		_
iearch Reset							each n	mary by Gene						ndicat	tes the n	umbei	r of resul	ts matci	hing th	e search	criteria	record
Search Reset			<b>6</b>			- Literature Datall	each n * Indi Hoxb	eference. cates detailed expressi 4 homeobox B4 (Sync	on da	ta ent	ries a			ndicat	tes the n	umbei	r of resul	ts matci	hing th	e search	criteria .	record
	)		Gen	e Ex	pressio	n Literature Detail	each n * Indi Hoxb	eference. cates detailed expressi 4 homeobox B4 (Sync Its Reference J:33159 Akasaka 1	on da onyms r, Kani	ta ent Hox-	ries av 2.6) Balling	r <b>ailabl</b> e R, Miez	a MA, Tai	nigud	hi M, Kos	seki H,	, A role fo	or mel-1	.8, a Po	olycomb		
Gene eXpression Database	)		Gen	e Ex	pressio	n Literature Detail	each n * Indi Hoxb Resu 1*	eference. cates detailed expressi 4 homeobox B4 (Syno 15 Reference J:33159 Akasaka 1 vertebrate gene, di MAY;122(5):1513-1	on dat onyms f, Kani uring t 522	ta ent Hox- ho M, he an	ries av 2.6) Balling teropo	R, Miez	a MA, Tai specifical	nigud ion o	hi M, Kos f the axi	seki H, al ske	, A role fo	or mel-1 evelopm	.8, a Po tent. 1	olycomb 996	group-re	elated
Gene expression	)		Gen	e Ex	pressio	n Literature Detail	each n * Indi Hoxb 1* ف*	eference. cates detailed expressi 4 homeobox B4 (Synot its Reference J:33159 Akasaka 1 vertebrate gene, di MAY;122(5):1513-1 J:35305 Bogue CV foregut and lung. A	on dat onyms r, Kani uring t 522 V, Lou m J Re	ta ent Hox- ho M, he an LJ, Va spir C	ries an 2.6) Balling teropo savad ell Mol	R, Miez sterior a H, Wil Biol. 19	a MA, Tai specifical son CM, 96 Aug;:	nigud ion o Jacob 15(2):	hi M, Kos f the axi s HC, Ex :163-71	seki H, al ske press	, A role fo leton. De ion of Ho	or mel-1 evelopm oxb geno	8, a Po tent. 19 es in th	olycomb 996 he devel	group-re oping m	elated
Gene Expression Database Symbol Name homeobox 84 ID MGI:96185							* Indi * Indi Hoxb # S * 1* 5* 1*	eference. cates detailed expressi 4 homeobox B4 (Syno 133159 Akasaka T vertebrate gene, di MAY;122(5):1513-1 J:35305 Bogue CV	on dat onyms r, Kani uring t 522 V, Lou m J Re	ta ent Hox- ho M, he an L), Va spir C	ries av 2.6) Balling teropo savad ell Mol IR, Tar	R, Miez sterior a H, Wil Biol. 19 geted c	a MA, Tai specifical son CM, 96 Aug;:	nigud ion o Jacob 15(2):	hi M, Kos f the axi s HC, Ex :163-71	seki H, al ske press	, A role fo leton. De ion of Ho	or mel-1 evelopm oxb geno	8, a Po tent. 19 es in th	olycomb 996 he devel	group-re oping m	elated
Symbol Name Disbase Name box 84 MGI:96185 Balconno 2:35305 Bogu	e CW, Lo	ou LJ, Va	savada	H, Wils	son CM, Jaco	n Literature Detail	2 4 India 4 Noxh Resu 1* 5* 1*	eference. cates detailed expressi 4 homeobox B4 (Synot 1533159 Akasaka 1 vertebrate gene, di MAY;122(5):1513-1 J:35305 Bogue CV foregut and lung. A J:34198 Boulet AM	on dat onyms f, Kani uring t 522 V, Lou m J Re l, Cape Silthon	Hox- Hox- ho M, he and LJ, Va spir C ecchi I 1996	ries av 2.6) Balling teropo savad ell Mol IR, Tar Jul 10 umme	R, Miez sterior a H, Wil Biol. 19 geted c ;177(1) rbell D,	a MA, Tai specifical son CM, 96 Aug; isruptior :232-49 Rigby PV	higud ion o Jacob 15(2): of hi	hi M, Kos f the axi 163-71 pxc-4 ca tiple lev	seki H, al ske press uses e els of	, A role fo leton. De ion of Ho esophage transcrip	or mel-1 evelopm oxb gen eal defe tional a	8, a Po nent. 19 es in th ects and and pos	olycomb 996 he devel d verteb st-transc	group-re oping m ral riptional	elated
Symbol Hoxb4 Name homeobox 84 MGL:96185 Reference 2:35305 Bogu mouse foregu etailed expression data f	e CW, Lo it and lur for these	ou LJ, Va ng. Am J 2 assays	savada Respir : 20 <u>re</u> :	H, Wils Cell Mol	son CM, Jaco I Biol. 1996 A	obs HC, Expression of Hoxb genes in t lug;15(2):163-71	* Indi * Indi Hoxb # S * 1* 5* 1*	eference. cates detailed expressi 4 homeobox 84 (Sync ts Reference 33159 Akasaka vertebrate gene, di MAY;122(5):1513-1 3:35305 Bogue CV foregut and lung. A 3:34198 Boulet AM transformations. De 3:83257 Brend T, (3)	on dat onyms f, Kani uring t 522 V, Lou m J Re kv Biol Silthon ired to Nelso	Hox- Hox- he and LJ, Va spir C ecchi I 1996 De J, S defir n CE,	ries av 2.6) Balling teropo savad ell Mol IR, Tar Jul 10 umme e the Morga	R, Miez sterior a H, Wil Biol. 19 geted c ;177(1) rbell D, domain n BA, Ta	a MA, Tai specifical son CM, 96 Aug; isruptior :232-49 Rigby PV of Hoxb4	higud ion o Jacob 15(2): of he 2, Mul expr	hi M, Kos f the axi 163-71 oxc-4 ca ltiple lev ression.	seki H, al ske press uses e els of Develo	, A role fo leton. Do ion of Ho esophago transcrip opment.	or mel-1 evelopm exb gen eal defe tional a 2003 Ju	8, a Po ees in th ects and and pos in;130	blycomb 996 he devel d verteb st-transc (12):271	group-re oping m ral riptional 7-28	related
Symbol Hoxb4 Name homeobox 84 MGL:96185 Reference 1:35305 Bogu mouse foregu etailed expression data f D Indicates gene expression	e CW, Lo at and lur for these on was a	ou LJ, Va ng. Am J 2 assays	savada Respir ' : 20 <u>re</u> : but no	H, Wils Cell Mol <u>sults</u> t neces	son CM, Jaco I Biol. 1996 A Isarily detect	obs HC, Expression of Hoxb genes in t lug;15(2):163-71	each n° * Indi Hoxt I* I* S* I* S* I* I* I* I* I*	eference. defence. 1:3159 Akasaka 1 vertebrate gene, di Mari, 122(5):1513-1 1:35305 Bogue CV foregut and lung. A 1:34198 Boulet AM transformations. De 1:32323 Brend 1, ( regulation are requ 1:232135 Burke AC, Development. 1995 1:119560 Choi MY, expression survey i	on da onyms r, Kann uring t 522 V, Lou m J Re v Biol Dilthorn ired to Nelso Feb; J Rome dentifi	ta ent Hox- ho M, he an LJ, Va spir C ecchi I 1996 oe J, S o defir n CE, 21(2) rr AI, I	ries av 2.6) Balling teropo savad ell Mol IR, Tar Jul 10 umme e the Morga :333-4 tu M, L	R, Miez sterior a H, Wil Biol. 19 geted c ;177(1) rbell D, domain n BA, Ta 6 epource	a MA, Tai specifical son CM, 96 Aug; isruptior :232-49 Rigby PV of Hoxb4 ibin C, H elet M, M	higud ion o Jacob J5(2): i of h : expr : expr : expr : expr : expr : expr	hi M, Kos f the axi s HC, Es 163-71 oxc-4 ca tiple lev ression. nes and or A, Yes	seki H, al ske press uses e els of Develo the e ilaltay	, A role for eleton. De sion of Ho esophage transcrip opment. evolution A, Krieg	or mel-1 evelopm exb gen eal defe tional a 2003 Ju of verte er M, Gr	8, a Po tent. 19 ects and ects and pos in;130 ebrate ray PA,	olycomb 996 he devel d verteb st-transc (12):271 axial mo Shivdas.	group-re oping m ral riptional 7-28 rpholog	elated nouse al jy. A dyna
Symbol Name MGI:96185 Reference Indicates gene expression Indicates gene expression Indicates gene expression	e CW, Lo at and lur for these on was a	ou LJ, Va ng. Am J e assays malyzed	savada Respir ' : 20 <u>re</u> : but no	H, Wils Cell Mol <u>sults</u> t neces	son CM, Jaco I Biol. 1996 A Isarily detect	obs HC, Expression of Hoxb genes in t lug;15(2):163-71	eech n * Indi Hoxt Resu 1* 6* 1* 6* 1* 4* 2* 3	eference. actes detailed expressi 4 homeobox B4 (Sync ts Reference J:33159 Akasaka 1 vertebrate gene, di MAY;122(5):1513-1 J:35305 Boque CV foregut and lung. A J:34198 Boquet AM transformations. Do J:33257 Brend T, C Development. 1995 J:10560 Choi MY, expression survey in oct;133(20):4119-2	on da' phyms f, Kann uring t 522 V, Lou m J Re to S22 V, Lou V S2 V S2 V, Lou V S2 V S2 V S2 V S2 V S2 V S2 V S2 V S	ta enti Hox- ho M, he an LJ, Va spir C ecchi t 1996 o defir n CE, 21(2) rr AI, H es tra	ries av 2.6) Balling eeropo savad ell Mol lR, Tar Jul 10 umme e the Morga :333-4 Hu M, L Inscript	R, Miez sterior a H, Wil Biol. 19 geted o ;177(1) rbell D, domain n BA, Ta 6 epourco ion fact	a MA, Tai specifical son CM, 96 Aug; isruptior :232-49 Rigby PV of Hoxb4 bin C, H elet M, M ors relev	nigud ion o Jacob J5(2): o of h expr ox ge echoc ant ii	hi M, Kos f the axi is HC, Ex 163-71 pxc-4 car tiple lev ression. nes and or A, Yes n mouse	seki H, al ske press uses e els of Develo the e ilaltay diges	, A role fo leton. Do sion of Ho esophage transcrip opment. evolution A, Krieg stive trac	or mel-1 evelopm eal defe tional a 2003 Ju of verte er M, Gr	8, a Po nent. 19 es in th ects and and pos in; 1300 ebrate ay PA, opment	olycomb 996 he devel d verteb st-transc (12):271 axial mo Shivdas t. Develo	group-re oping m ral riptional 7-28 rphology ani RA, <i>A</i> pment.	related nouse al yy. A dyna 2006
Gene      Xpression      Arease     Symbol Hoxb4     Name homeobox 84     D MGI:96185     Reference <u>1:35305</u> Bogu     mouse foregu     tailed expression data f     Indicates gene expression     n situ protein (section)	e CW, Lo at and lur for these on was a	ou LJ, Va ng. Am J e assays malyzed	savada Respir ' : 20 <u>re</u> : but no	H, Wils Cell Mol <u>sults</u> t neces	son CM, Jaco I Biol. 1996 A Isarily detect	obs HC, Expression of Hoxb genes in t lug;15(2):163-71	eech n * Indi Hoxb Hoxb 1* £* 1* 1* 4* 3*	eference. defence. 1:3159 Akasaka 1 vertebrate gene, di Mari, 122(5):1513-1 1:35305 Bogue CV foregut and lung. A 1:34198 Boulet AM transformations. De 1:32323 Brend 1, ( regulation are requ 1:232135 Burke AC, Development. 1995 1:119560 Chei MY, expression survey i	on da' onyms r, Kani uring t 522 V, Lou m J Re 522 V, Lou m J Re 522 V, Lou m J Re 522 V, Lou M J Re 522 V, Lou Nelso Feb; 1 Rome dentifi 29 Lawr	ta enti Hox- ho M, he an LJ, Va spir C ecchi I 1996 oe J, S o defir n CE, 21(2) rr AI, I es tra ence I	ries an 2.6) 3alling teropo savad ell Mol IR, Tar Jul 10 umme e the :333-4 ku M, L nscripi	R, Miez sterior a H, Wil Biol. 19 geted c ;177(1) rbell D, domain n BA, Ta 6 epource ion fact gman C,	a MA, Tai specifical son CM, 96 Aug; isruptior :232-49 Rigby PV of Hoxb4 bin C, H elet M, M ors relev	nigud ion o Jacob J5(2): o of h expr ox ge echoc ant ii	hi M, Kos f the axi is HC, Ex 163-71 pxc-4 car tiple lev ression. nes and or A, Yes n mouse	seki H, al ske press uses e els of Develo the e ilaltay diges	, A role fo leton. Do sion of Ho esophage transcrip opment. evolution A, Krieg stive trac	or mel-1 evelopm eal defe tional a 2003 Ju of verte er M, Gr	8, a Po nent. 19 es in th ects and and pos in; 1300 ebrate ay PA, opment	olycomb 996 he devel d verteb st-transc (12):271 axial mo Shivdas t. Develo	group-re oping m ral riptional 7-28 rphology ani RA, <i>A</i> pment.	related nouse al gy. A dyna 2006
Symbol Hoxb4 Name homeobox 84 MGL:96185 Reference 2:35305 Bogu mouse foregu etailed expression data 1 P Indicates gene expression taide n situ protein (section) n situ RNA (section)	e CW, Lo It and lur for these on was a	ou LJ, Va ng. Am J e assays malyzed	savada Respir 20 res but no E11.5	H, Wils Cell Mol <u>sults</u> t neces	son CM, Jaco I Biol. 1996 A Issarily detect	obs HC, Expression of Hoxb genes in t lug;15(2):163-71	eech n * Indi Hoxt Resu 1* 6* 1* 6* 1* 4* 2* 3	eference. cates detailed expressi cates detailed expressi ts Reference J:33159 Akasaka 1 vertebrate gene, d MAY;122(5):1513-1 J:5305 Bogue CV foregut and lung. A J:34198 Boulet AM transformations. De J:33257 Brend T, Development. 1955 J:119506 Choi MY, expression survey oct;133(20):4119-2 J:14757 Detmer K, Invest Dermatol. 15 J:193244 Di Mediai	on da' nyms T, Kani T, Kani T, Kani S22 V, Lou m J Re V, Lou V, Lou V	ta enti Hox- ho M, he an LJ, Va spir C ecchi M 1996 be J, S o defir n CE, 21(2) r AI, H es tra ence H t;101	ries an 2.6) 3alling seropo savad ell Mol lumme e the .333-4 ku M, L mscrip I), Lar. (4):51: vil CF,	R, Miezz sterior a H, Wili Biol. 139 geted c (177(1) hold D, domain n BA, Ta 6 epource ion fact man C, -22 Vilain N	a MA, Tai specifical son CM, 96 Aug; isruptior :232-49 Rigby PV of Hoxb4 bin C, H elet M, M eors relev Express , Loche A	nigud ion o Jacob 5(2): o of he expr ox ge echoo rant ii ion o	hi M, Kos f the axi s HC, E> 163-71 oxc-4 ca htiple lev ression. nes and or A, Yes n mouse f class I bello A,	seki H, al ske press uses e els of Devek the e ilaltay diges home	, A role fe leton. De sion of Ho esophage transcrip opment. evolution A, Krieg stive trac obox ger hara K, H	or mel-1 evelopm eal defe tional a 2003 Ju of verte er M, Gr t develo nes in fe	8, a Po nent. 19 es in the es in the es in the est and post post post and post post and post post and post post and post and post	olycomb 996 he devel d verteb st-transc (12):271 axial mo Shivdas. Develo d adult n ca B, Petr	group-re oping m ral riptional 7-28 ani RA, 4 pment. hurine sl ers AH, E	elated nouse al 39. A dyna 2006 skin. J Eichm
Symbol Hoxb4 Name homeobx 84 ID MGI:96185 Reference 1:25305 Bogu mouse foregu etailed expression data f Indicates gene expressio de a situ protein (section) n situ protein (symbol) n situ protein (whole mou	for these on was a E9.5	ou LJ, Va ng. Am J e assays analyzed i E10.5	savada Respir 20 res but no E11.5	H, Wils Cell Mol <u>sults</u> t neces	son CM, Jaco I Biol. 1996 A Issarily detect	obs HC, Expression of Hoxb genes in t lug;15(2):163-71	each nr * Indi Hoxt Resu 1* 6* 1* 4* 2* 3 2*	eference. actes detailed expressi 4 homeobox B4 (Sync Its Reference J:33159 Akasaka 1 vertebrate gene, di MAY;122(5):1513-1 J:35305 Bogue CV foregut and lung. A J:34198 Boulet AM Transformations. De J:343257 Brend T, C Development. 1995 J:119560 Chai MY, expression survey i oct;133(20):4119- J:41757 Detmer K, Invest Dermatol. 15 J:193244 Di Megin A, Wellk O, Duret S	on dat nyms 7, Kani 522 V, Lou m J Re v Biol Silthon rired to Nelso Feb; 1 Rome dentifi 29 L Lawri 93 Oc 0 T, Kr, Kijli	ta enti Hox- Hox	2.6) Salling seropo savad ell Mol IR, Tar Jul 10 umme e the Morga 333-4 ku M, L nscripi D, Lan (4):51	R, Miez sterior a H, Will Biol. 19 geted c ;177(1) rbell D, domain n BA, Ta 6 epourcr ion fact yman C, 7-22 Vilain N hestrat	a MA, Tai specifical son CM, 96 Aug; isruptior :232-49 Rigby PV of Hoxb4 bin C, H elet M, M eors relev Express , Loche A	nigud ion o Jacob 5(2): o of he expr ox ge echoo rant ii ion o	hi M, Kos f the axi s HC, E> 163-71 oxc-4 ca htiple lev ression. nes and or A, Yes n mouse f class I bello A,	seki H, al ske press uses e els of Devek the e ilaltay diges home	, A role fe leton. De sion of Ho esophage transcrip opment. evolution A, Krieg stive trac obox ger hara K, H	or mel-1 evelopm eal defe tional a 2003 Ju of verte er M, Gr t develo nes in fe	8, a Po nent. 19 es in the es in the es in the est and post post post and post post and post post and post post and post and post	olycomb 996 he devel d verteb st-transc (12):271 axial mo Shivdas. Develo d adult n ca B, Petr	group-re oping m ral riptional 7-28 ani RA, 4 pment. hurine sl ers AH, E	elated nouse al 39. A dyna 2006 skin. J Eichm
Gene      Xpression     X	for these on was a E9.5	ou LJ, Va ng. Am J e assays analyzed i E10.5	savada Respir 20 res but no E11.5	H, Wils Cell Mol sults it neces E12.5	son CM, Jaco I Biol. 1996 A Issarily detect	obs HC, Expression of Hoxb genes in t lug;15(2):163-71	eech n * Indi Hoxt Resu 1* 6* 1* 4* 3* 3* 3* 3* 3* 4*	eference. actes detailed expressi 4 homeobox B4 (Sync its Reference J:33159 Akasaka 1 vertebrate gene, di MAY,122(5):1513-1 J:35305 Bouje CV foregut and lung, A J:34198 Boulet AM transformations. Du J:83257 Brend T, G Development. 1995 J:119560 Choi MY, expression survey in Ort;134(2):419-2 J:14757 Detmer K, Invest Dermatol. 15 J:193244 Di Meglin A, Wellik O, Duret & Science. 2013 Jan 1	on da' onyms r, Kanning t S22 V, Lou m J Re V, Lou M J Re V Re V J Re V Re V J Re V Re V Re V Re V Re V Re V Re V Re V	ta enti Hox- ho M, he an LJ, Vaspir C ecchi N 1996 o defir n CE, 21(2) r AJ, l es tra ence I t;101 tatochi FM, E: (6116	ries an 2.6) 3alling teropo savad lell Mol liR, Tar Jul 10 umme e the  Morga :333-4 du M, L Inscrip IJ, Lann (4):51 <sup>1</sup> Vil CF, h2 ord ):204-	R, Miez sterior a H, Will Biol. 19 geted c ;177(1) rbell D, domain n BA, Ta 6 eopurcr ion fact yman C, 7-22 Vilain N hestrat 7	a MA, Tai specifical son CM, 96 Aug; isruption :232-49 Rigby PW of Hoxb4 bin C, H elet M, M ors relev Express , Loche A es topog	higud ion o Jacob 5(2): i of hi expr ox ge echoo ant ii ion o , Vito	hi M, Kos f the axi s HC, E> :163-71 oxc-4 cai tiple lev ression. nes and or A, Yes n mouse f class I bello A, ic migrat	seki H, al ske press uses e els of Devek the e ilaltay diges home	, A role for leton. De tion of Ho esophage transcrip opment. evolution A, Krieg stive trac obox ger hara K, H and conne	or mel-1 evelopm hxb genu cal defe tional a 2003 Ju 2003 Ju 2005 Ju 20	.8, a Po eent. 19 es in th ects and poetrate ay PA, ppment 4, Rosk f mous	olycomb 996 he devel d verteb st-transc (12):271 axial mo Shivdas t. Develo d adult n ca B, Petre	group-re oping m riptional 7-28 rphologi ani RA, 4 pment. surine sl surine sl surine sl surine sl	elatec nouse al yy. A dyn: 2006 skin. J Eichm
Gere Xpression Xpression Xpression MoxD4 Name homeobox 84 D MGI:96185 Reference 1:35305 Bogu mouse foregu etailed expression data 1 Indicates gene expression data n situ protein (section) n situ RNA (section)	for these on was a E9.5	ou LJ, Va ng. Am J e assays analyzed i E10.5	savada Respir 20 res but no E11.5	H, Wils Cell Mol sults it neces E12.5	son CM, Jaco I Biol. 1996 A Issarily detect	obs HC, Expression of Hoxb genes in t lug;15(2):163-71	each nr * Indi Hoxt Resu 1* 6* 1* 4* 2* 3 2*	eference. cates detailed expressi cates detailed expressi transformations between the second market second the second temperature market second tempera	on da onyms T, Kann uring t 522 V, Lou m J Re v Biol Silthon ired to Nelso Feb; J Rome dentifi 29 Lawr 93 Oc 5, Kijli 1; 339 ux G, E antiel	ta enti Hox- Hox	ries a 2.6) 3alling teropo savad ell Mol umme e the Morga 333-4 tu M, L umme the 333-4 tu M, L umme the the 10 Jul 10 umme e the 10 Jul 10 U umme the 10 Jul 10 U umme the 10 Jul 10 U U U U U Larr (4):51 Vil CF, h2 orc ):204- , Sulta erde R	R, Miezz sterior a H, Wil Biol. 19 Biol. 19 geted c troff bell D, domain n BA, Ta 6 epourcci on fact gman C, -22 yulain N hestrat 7 n M, Ge	a MA, Tai specifical son CM, son CM, sisruption :232-49 PG Aug: :232-49 PG Aug	nigud ion o Jacob 15(2): of hi expr ox ge echoc ant ii ion o , Vito iraphi nand cchi S	hi M, Kos Is HC, Eb 163-71 Itiple lev ession. nes and r A, Yes f class I bello A, c Grigrat S, Roza A, Cicchi	seki H, al ske press uses e els of Develo the e ilaltay diges homeo Yoneh ion an do D, / ni J, P	, A role fr leton. De sion of Ho esophage transcrip opment. evolution A, Krieg stive trac obox gen hara K, H hara K, H d conne Magen A erroud E	or mel-1 evelopm txb gen- tional a 2003 Ju of verte er M, Grr develo trois of verte er sin fe rycaj SM trivity o'	8, a Po eent. 1 ees in th ects and posi- in; 1300 ebrate eray PA, opment 4, Rosk f mous io E, Pa	olycomb - 996 d vertebu st-transc (12):271 Shivdas t. Develo d adult n ca B, Pett agani M, agani M,	group-re oping m riptional 7-28 rphology ani RA, A prment.	elatec nouse al gy. A dyn. 2006 skin. J Eichm neuro I, Lin-Inner S,
Symbol Name D MGI:96185 Balance Lissa05 Bogu	for these on was a E9.5	ou LJ, Va ng. Am J e assays analyzed i E10.5	savada Respir 20 res but no E11.5	H, Wils Cell Mol sults it neces E12.5	son CM, Jaco I Biol. 1996 A Issarily detect	obs HC, Expression of Hoxb genes in t lug;15(2):163-71	eech n * Indi Hoxt Resu 1* 6* 1* 4* 3* 3* 3* 3* 3* 4*	eference. defen	on da onyms r, Kanu uring t 522 W, Lou W, Lou W	ta enti Hox- ho M, he an L), Va spir C ecchi N 1996 oe J, S o defir n CE, 21(2) r AI, H es tra ence H t;101 atoch FM, E: (6116 anfi S lo I, V wetz H	ries av 2.6) 3alling seropo savad ell Mol lumme e the o Morga :333-4 No Lar Work Morga :333-4 No Lar Work Morga Sal Sal Sal Sal Sal Sal Sal Sal Sal Sa	R, Miezz sterior a H, Wil Biol. 19 geted c (;177(1) rbell D, domain n BA, Ta 6 epourcc ion fact man C, -222 Vilain N, Ge De Ma 7 n M, Ge De De Ma	a MA, Tai specifical son CM, 96 Aug; isruptior 232-49 Rigby PW 232-49 Hoto Hoxb4 bin C, H express Loche A si C, Birask	nigud jacob Jacob J5(2): o of he echoo ant ii ion o , Vito raphi nand uchi S	hi M, Kot f the axi 163-71 oxc-4 cai tiple lev ession. nes and or A, Yess f class I bello A, c migrat S, Roza S, Roza	seki H, al ske press uses e els of Devek the e ilaltay diges home Yoneh ion an do D, J	, A role fc leton. Di iion of Hc esophage transcript opment. A, Kriegg trive trac obox ger nara K, H d conne Magen A erroud E	or mel-11 evelopm eal defe tional a 2003 Ju 2003 Ju of verte er M, Gr t develo rycaj SN rycaj SN rycaj SN Mehme Mehme	8, a Pro hent. 19 ess in the ess in the esst	plycomb - 996 d vertebi st-transcc (12):271 axial mo Shivdass d adult n :a B, Petti agani M, agand E rabbe	group-re opping m ral riptional 7-28 rpholog ani RA, / pment. uurine sl uurine sl uurine sl schrinn Peluso I	elated nouse al yy. A dyn, J Skin, J Eichm neuro I, Lin- iner S,
Control C	for these on was a E9.5	ou LJ, Va ng. Am J e assays analyzed i E10.5	savada Respir 20 res but no E11.5	H, Wils Cell Mol sults it neces E12.5	son CM, Jaco I Biol. 1996 A Issarily detect	obs HC, Expression of Hoxb genes in t lug;15(2):163-71	eech n * Indi Hoxt Resu 1* 6* 1* 4* 3* 3* 3* 3* 3* 4*	efference. dates detailed expression actes detailed expression yertebrate gene, di Warty 122(5):1513-1 13:35305 Bogue CV foregut and lung. A 13:35305 Bogue CV foregut and lung. A 13:34198 Boulet AM transformations. De J:83257 Brend T, C pevelopment. 1955 2:119560 Chei MY, expression survey j oct; 133(20):4119- 3:14757 Detmer K, Invest Dermatol. 15 3:193244 Di Megin A, Weilk O, Ducret Science. 2013 Jan J 1:15349 Diez-Rot, Nicother B, Schrader Echevaria D, Puelle	on da onyms T, Kann uring t S22 W, Lou W, Lou W	ta enti Hox- Hox	ries av 2.6) 3alling seropo savad ell Mol umme e the the the the the the the the the the	R, Miezz sterior a H, Will Biol. 19 g geted c for an a	a MA, Tai specificat son CM, 96 Aug; : sisruptior :232-49 of Hoxb4 bin C, H ibin C, H express : Loche A si C, Biar c, Braes si C, Biar S, Helbi	nigud jacob Jacob Jacob Jacob Jacob Jacob Sacob	hi M, Koi f the axi is HC, Eb Itiple lev tression. nes and pr A, Yese f class I ibello A, ic migrat S, Roza A, Cicchi Springer	seki H, al ske presss uses e els of Develo the e ilaltay diges homeo Yoneh ion an do D, I ni J, P C, He Battai	, A role fr leton. Do ision of Ho esophago transcrip opment. volution volution volution araa K, H ad conne Magen A erroud E errandez	or mel-1 veelopm eal defe tional a defe er M, Gr develo er M, Gr tovity o , Canidi , Mehme AM, Her	8, a Pc eent. 1 es in the es in the est and poperation and post in; 1300 ebrate ay PA, poperation at an in et a so f mous io E, Pa et i S, D	plycomb - 996 he devel d vertebu st-transcc (12):271 axial mo Shivdas c. Develo d adult n :a B, Petti agani M, agand E Grabbe Grabbe sen CN,	group-re opping m ral riptional ript	elatec nouse al yy. A dyn. Zooo skin. J Eichm neuro I, Lin- iner S, erding Lopez
Symbol Hoxb4 Name homeobox 84 MGL:96185 Reference 2:35305 Bogu mouse foregu etailed expression data f h Indicates gene expression data f h Indicates gene expression a situ protein (section) n situ RNA (section)	for these on was a E9.5	ou LJ, Va ng. Am J e assays analyzed i E10.5	savada Respir 20 res but no E11.5	H, Wils Cell Mol sults it neces E12.5	son CM, Jaco I Biol. 1996 A Issarily detect	obs HC, Expression of Hoxb genes in t lug;15(2):163-71	eech n K i Indi Hoxt Resu 1* 6* 1* 4* 2* 3 2* 4 1*	efference. 4 homeobox B4 (Sync. Cates detailed expression of the second seco	on da onyms r, Kann uring t S22 W, Lou m J Re l, Capte v Biol S22 Nelso Feb; 1 Rome dentif 29 Lawn Lawn S, Rijll 1;339 ux G, E antiel iidtK, I K, Bro S E, E 22	ta ent Hox- ho M, he an LJ, Va spir C spir C construction pe J, S o defir n CE, 21(2) r AI, I es tra ence I t;101 atochi FM, EE (6116 (6116 ckm) es tra ence I t;101 atochi FM, EE (6116 ckm) es tra ence I t;101 atochi f, S ence I f, S ence I ence I encen	ries av 2.6) 3alling teropo savad ell Mol IR, Tar Jul 10 umme e the 10, Lan 4):51 Vil CF, h2 or ):204- , Sulta erde R , Zwin erde R , Jwin erde R	R, Miezz sterior a H, Wil Biol. 15 geted c ;177(1) rbell D, domain n BA, T; 6 epourccion fact om A A man C, -222 Vilain N, Ge De Ma gmann Pettmeire resoluti	a MA, Tai specifical son CM, 96 Aug; 232-49 Rigby PV 232-49 Rigby PV Hoxb4 bbin C, H Lisz express Loche A si C, Birask S, Helbi S, S, Helbi S, S, Helbi	nigud ion o Jacob Jacob Jacob Jacob Jacob Jacob So So So So So So So So So So So So So	hi M, Kos f the axi 163-71 titple lev ession. nes and f class I bello A, c cmigrat S, Roza A, Cicchi S, Roza S, Roza S, Roza	seki H, al ske press uses e els of Develo the e ilaltay diges home yoneh ion an do D, / ni J, P. C, He Battai the tr	, A role fi leton. Do ision of Ho esophage transcript transcript transcript transcript transcript transcript transcript transcript	or mel-11 evelopm exal defe tional a 2003 Ju of verte ar M, Gr tivitz of tivitz of tivitz of , Canidi Mehm Mehm Mehm Mehm Jan M, Her ura C, H	.8, a Pc eent. 1 es in th ects and poin; 130i ebrate ay PA, ppment etal an- etal an-	olycomb 996 he devel d vertebi st-transcc 1(12):271 axial mo axial mo axiax	group-re pping m ral riptional 7-28 rphology ani RA, J, Pology ani	elated nouse al yy. A dyna 2006 skin. J Eichm neuro I, Lin-I, erding Lopez oS Bio
Symbol Hoxb4     Symbol Hoxb4     Name     homeobox 84     D     MGI:96185     Reference     1:35305 Bogu     mouse foregu     etailed expression data 1     Indicates gene expression     situ protein (section)     n situ protein (section)     n situ protein (section)     n situ protein (whole mount)     n situ reporter (snock in)     isrdivestern blot     Vestern blot     Vestern blot	for these on was a E9.5	ou LJ, Va ng. Am J e assays analyzed i E10.5	savada Respir 20 res but no E11.5	H, Wils Cell Mol sults it neces E12.5	son CM, Jaco I Biol. 1996 A Issarily detect	obs HC, Expression of Hoxb genes in t lug;15(2):163-71	eech n * Indi Hoxt Resu 1* 6* 1* 4* 3* 3* 3* 3* 3* 4*	efference. dates detailed expression actes detailed expression yertebrate gene, di Warty 122(5):1513-1 13:35305 Bogue CV foregut and lung. A 13:35305 Bogue CV foregut and lung. A 13:34198 Boulet AM transformations. De J:83257 Brend T, C pevelopment. 1955 2:119560 Chei MY, expression survey j oct; 133(20):4119- 3:14757 Detmer K, Invest Dermatol. 15 3:193244 Di Megin A, Weilk O, Ducret Science. 2013 Jan J 1:15349 Diez-Rot, Nicother B, Schrader Echevaria D, Puelle	on day onyms T, Kanni J, Capy M, Lou m J Re S22 V, Lou M J Re S25 V, Rijili M J Re S25 V, K, Bro S25 V, S2 V, N S25 V, K, Bro S25 V, S2 V, N M J Re M J Re M J Re M J Re S25 V, N M J Re M J Re S25 V, N M J Re M J Re S25 V, N M J Re M J Re M J Re M J Re M J Re M J Re S25 V, N M J Re M J R	ta enti Hox- Hox	ries an 2.6) 3alling savad ell Mol lR, Tar Jul 10 umme e the Morga 333-4 tu M, L Inscript U, Land (1:51; vil CF, 204- sulta erde R (2:0) 204- sulta erde R (1:51) vil 204- sulta erde R (1:51) vil 204- sulta (1:51) vil 204- sulta (1:51) vi	R, Miezz sterior a H, Wil geted co 1777(1), domain n BA, Ti 6 epourcci on fact gman C, -22 Vilain N hestrat 7 n M, Ge De Ma gmann M, Ge Settmer esoluti	a MA, Tai specifical son CM, y 96 Aug;: sruption :232-49 p6 Aug; sruption C, H elet M, M elet M, M elet M, M Express A es topoc C, Briesk S, Helbi on anato	nigud ion o Jacob J5(2): o of he expro- cox ge echoo raphi ion o , Vito raphi nand chi S e N, S g C, A mical ashav	hi M, Kos f the axi is HC, Eb 163-71 xxc-4 cai tiple lev ression. nes and yr A, Yes f class I bello A, c migrat S, Roza A, Cicchi springer S, Roza A, Cicchi springer atlas of y-Boris A	seki H, al ske press uses e els of Devek the e diges home Yoneh ion an do D, / ni J, P, Sher	, A role fe leton. Di ion of Hc esophagi opment. transcript obox ger nara K, H nd conne Magen A conne mande conne mande conne mande conne	or mel-1 evelopm axb genu- tional a 2003 Ju 2003 Ju 20	8, a Pc eent. 1: es in th ects ani- and pos- abrate ay PA, opment etal ani- etal ani- etal ani- etal ani- etal ani- teta S, D records and the mou- equirect	olycomb - 996 he devel d vertebi st-transc (12):271 Shivdass c. Develo d adult n :a B, Pett ie precer agani M, Sen CN, use emb	group-re opping m riptional 7-28 rpholog: ani RA, A pment. ani RA, A pment. schnin F, Sieve ryo. PLC ect oriel	elated nouse al yy. A dyna 2006 skin. J Eichm neuro I, Lin-I, erding Lopez oS Bio

#### Figure 6.

Querying the embryonic mouse expression literature. The Gene Expression Literature Search (top left) allows querying of the embryonic expression literature for genes and ages analyzed and expression assay types used, as well as querying for bibliographic information or specific words in the title or abstract. A portion of the summary return for the query formulated in the figure is displayed at right. The table at the top, "Index Results by Age and Assay", shows the number of matching records grouped by the age of the specimen and the assay type used. The lower portion of the page, "Index Results by Gene and Reference", lists the citations for the references where the matching index results were reported, as well as the number of matching results contained therein. Entries marked with an \* indicate they have been annotated in detail in GXD. Links on this summary page access detail pages (lower left). These pages display the expression information about the gene contained in the reference and provide links to gene and reference detail pages, as well as to the detailed expression data from the paper if they have already been annotated in GXD.