

# INDIVIDUAL EXPRESSION DATA IN WILD TYPE CONDITION

(cf excel doc named "Expression\_data\_wild\_type.xls")

Thanks to this form, you can enter expression profile in wild type condition and the pattern of transcriptional activity of a cis-regulatory region.

One entry corresponds to one experiment (one excel line). You may have one or more pictures for an experiment. You have to name the pictures like below:

DevelopmentalStage\_clone.jpg or DevelopmentalStage\_construct.jpg (ex: [64c\\_cicl01i06.jpg](#)). Be careful, don't put any space in the name.

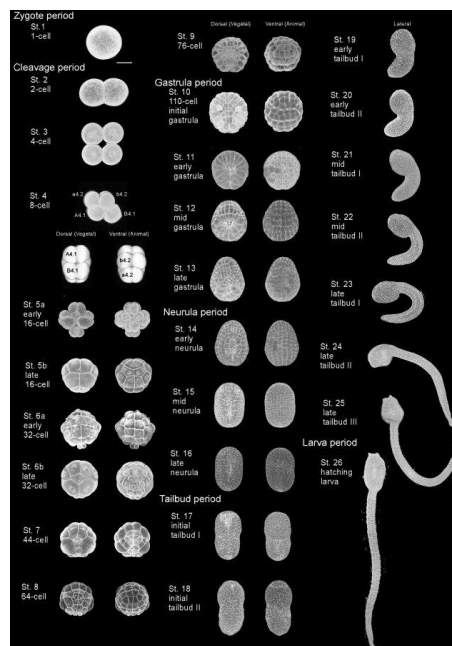
If you have more than one picture: 64c\_cicl01i06\_1.jpg; 64c\_cicl01i06\_2.jpg...

Pictures should be in jpg format.

Contact the ANISEED team ([aniseed@ibdm.univ-mrs.fr](mailto:aniseed@ibdm.univ-mrs.fr)) to organize transfers of pictures via FTP.

## Different columns in the form:

- **Developmental stage (mandatory):** developmental stage at which the expression was determined, according to the table of Hotta et al. (2007)



**Clone (mandatory):** clone(s) used to synthesize the in situ hybridization probes used in the experiment, transgenic construct in the case of electroporations, or antibody, with reference, used in immunohistochemistry.

**Annotation (mandatory):** use the ANISEED anatomical ontology to annotate your picture. For instance, if you want to annotate a 64-cell stage, you have to refer to the description of the 64-cell stage in Aniseed (explore the anatomy/ display the anatomical anatomy for a given stage/ choose the corresponding stage) and use the ontology to annotate the picture (*i.e. B7.6 cell pair*).

**Comments (not mandatory)**

## INDIVIDUAL EXPRESSION DATA IN DEREGULATED MOLECULE CONTEXT

(cf excel doc named "Expression\_data\_molecular\_perturbation.xls")

The system allows submission and annotation of experimental expression data in response to molecule deregulation.

Same rules as above, one entry corresponds to one experiment. The name of the picture: DevelopmentalStage\_Clone\_DeregulatedGene.jpg (*i.e. 64c\_cicl01i06\_Deregulatedci0100151552.jpg*). Be careful, don't put any space in the name.

Pictures should be in jpg format.

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You will find the same columns as the description patterns in wild type condition. In addition, you have to specify the deregulated gene, the type of regulation, the molecular tool used and the time of injection:

**Deregulated molecule (mandatory):** identity of the deregulated molecule: The biological name of the gene can be ambiguous. It is preferable to indicate the corresponding gene/transcript model deregulated with a preference for KH (Satou et al., 2008) models, followed by JGI v1.0 and ENSEMBL models (for example, [ci0100151552](#)).

**Type of interference (mandatory):** type of interference with gene function -> gain-of-function or loss-of-function.

***Molecular tool (mandatory):*** put the molecular tool used to deregulate the gene. Molecular tool used to deregulate the gene, with either reference of a previous study using this tool (for instance, *FGF9/16/20 Imai's 25 mer MO described in Imai et al., 2006*), or the precise sequence (MOs, mRNAs) or origin (Small molecules) of the tool.

***Stage of onset of the perturbation (mandatory):*** eg. time of injection for morpholinos.

## INDIVIDUAL EXPRESSION DATA IN ANATOMICAL PERTURBED CONTEXT

(cf excel doc named "Expression\_data\_anatomical\_perturbation.xls")

The system allows submission and annotation of experimental expression data in response anatomical perturbation (ablation, explant).

Same rules for picture as above.

You will find the same columns as the description patterns in wild type condition. In addition, you have to specify the time of perturbation and the removed anatomy part:

***Time of perturbation (mandatory):*** Hotta stage when the structure(s) was/were removed or when the explants(s) was/were isolated.

***Removed anatomical part or explants (mandatory):*** use the ANISEED anatomical dictionary to describe the removed anatomy part(s) or the type of explant isolated.

## MORPHOLOGICAL PHENOTYPE

(cf excel doc named "Phenotype")

The idea here is to be able to describe phenotypes that cannot be described in terms of alteration of genetic programs

Same rules for picture as above.

### Different columns in the form:

***Name (mandatory):*** add a name to describe the morphogenetic process observed (*e.g. short tail, disorganised body plan...*)

***Developmental stage (mandatory):*** developmental stage at which the expression of the phenotype was examined, according to the developmental table of Hotta et al. (2007)

**Transcript model downregulated (mandatory):** Here enter the transcript model responsible of the affectation (JGI V1.0 or KYOTOGRAIL or ENSEMBL)

**Comments (mandatory):** describe in detail the experiment.

## REGULATORY REGION

(cf excel doc named "Regulatory region")

### Different columns in the form:

**Name of the region (mandatory):** we ask you to respect the following format for region names: ci-"gene name" "start of region "bp" end of region "bp" *e.g. ci-ZicL - 4037bp/313bp.*

**Natural (mandatory):** the region is either Natural (if it can be associated to the genome of a given Species) or Artificial. Put yes or no.

**Artificial (mandatory):** yes or no.

**Comments (not mandatory):** enter a general comment describing the region, the different modules and motifs that are important to regulate the gene.

**Type of regulation (mandatory):** enter the type of regulatory activity displayed by this region according to the following definitions:

*A Basal Promoter* is a region that only binds to the basal transcription machinery and should always require other elements to induce expression.

*An Extended Promoter* is a region that is able to drive expression by itself, thus it should include basal promoter and enhancer(s)

*An Enhancer* is a region that drives expression, when put in front of a basal promoter.

*A Silencer* is a region that blocks transcription.

*An Insulator* is a region that prevents the activity of another regulatory region over different genes.

*A Complex Regions* are regions that are able to drive expression but nothing is known about its inner elements.

*No Activity* is used to annotate regions that do not seem to be able to drive expression.

*Unknown Activity* should be the last resource to annotate a region, only when nothing is known.

***Regulated gene(s) (not mandatory):*** use a transcript model to describe the gene (when known) (*e.g. ci0100147513*).

***Name of the construct (mandatory):*** you should add a "p" (for plasmid) in front of the name, the basal promoter name and the reporter *e.g. pfog -214/-74 pbra::NLS LacZ*.

***Basal promoter of the construct (mandatory):*** basal promoter used

***Reporter gene of the construct (mandatory):*** LacZ or GFP

***Sequence of the construct (mandatory):*** sequence tested in electroporation constructs.

*Thanks to take time to contribute to ANISEED project.*

*The ANISEED team*