Dear all,

Full ORF Gateway-compatible clones and KH transcript models are now accessible from the Aniseed website, in addition to their representation in the Aniseed Genome browser.

The following instructions will help you to find information concerning Gateway-compatible clones and KH transcript models. Don't hesitate to send us feedback or comments, especially if you find some bugs or inconsistencies.

Information available in Aniseed:

Full ORF gateway-compatible clones (Rothbächer et al., in preparation)

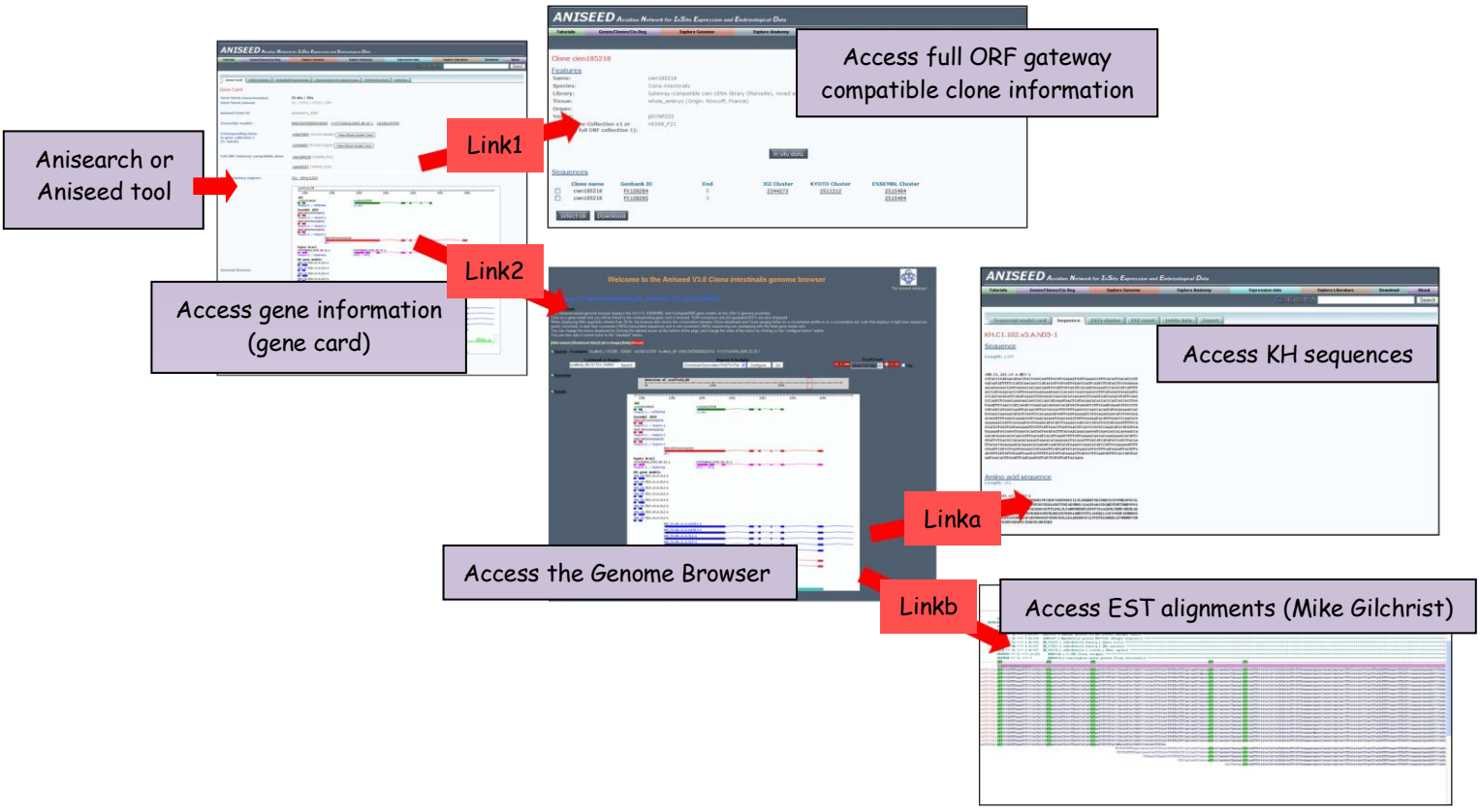
- Library clone name (e.g. cima810896 ; cien56376)
- JGI/Gilchrist clone name (e.g. CBWU10896 ; XABT56376)
- Plate position (e.g. VES58_F02)
- Genbank entry (e.g. FF864681)
- Sequence
- Library/Origin
- Vector

KH transcript models (Satou et al., 2008)

- DNA sequence
- Amino acid sequence

How to access this information?

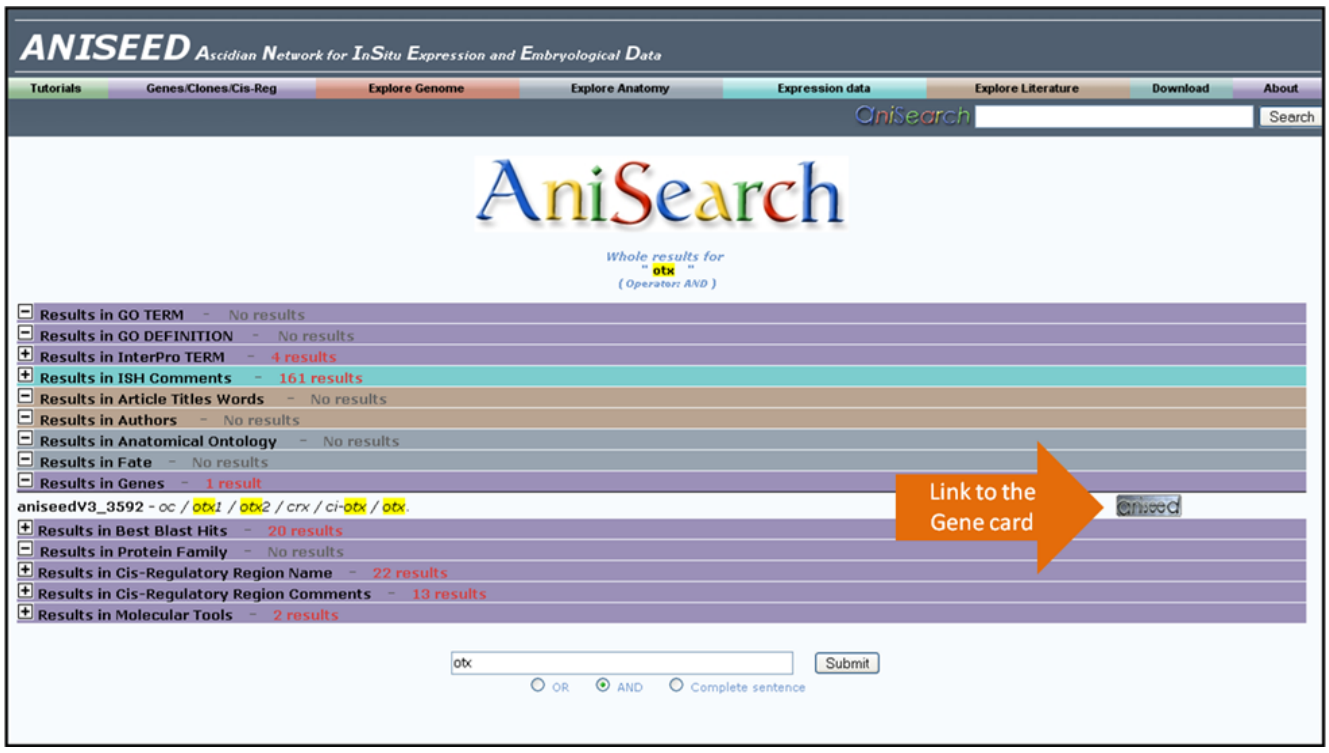
Access this information in Aniseed (http://crfb.univ-mrs.fr/aniseed/)
Schematic overview:



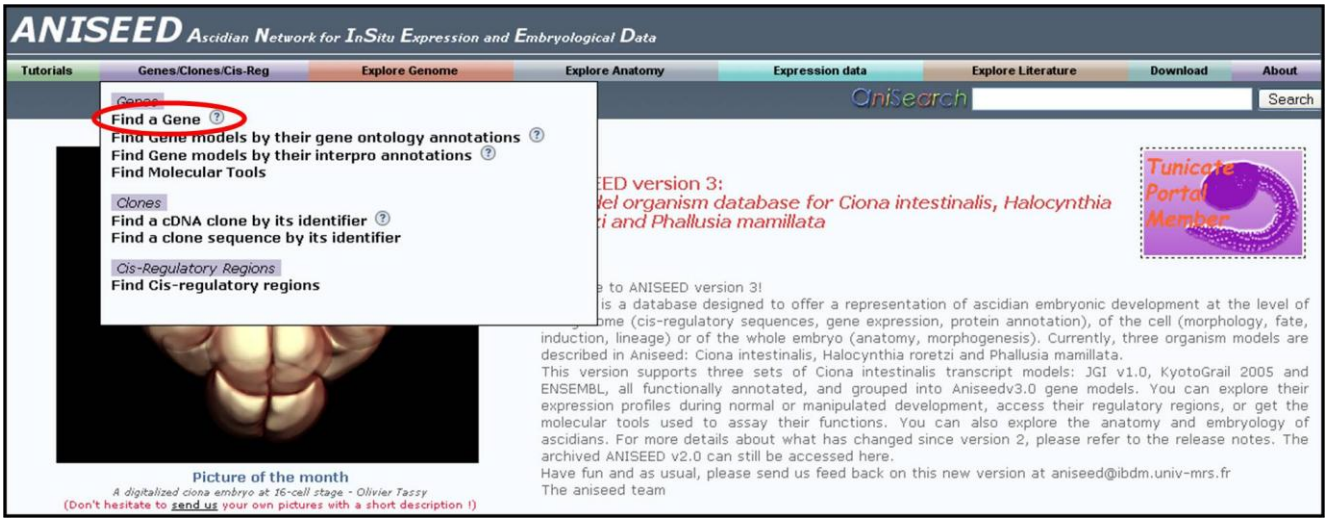
Access gene information (gene card)

You can access gene features (gene card) using AniSearch or using the menu "Genes/Clones/Cis-reg menu".

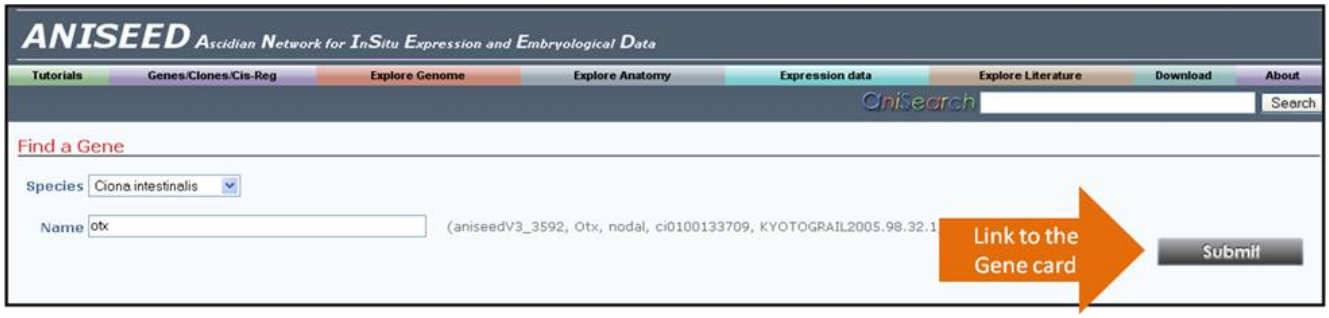
- Using AniSearch:



- Using the Genes/Clones/Cis-reg menu, select the "Find a gene" link:

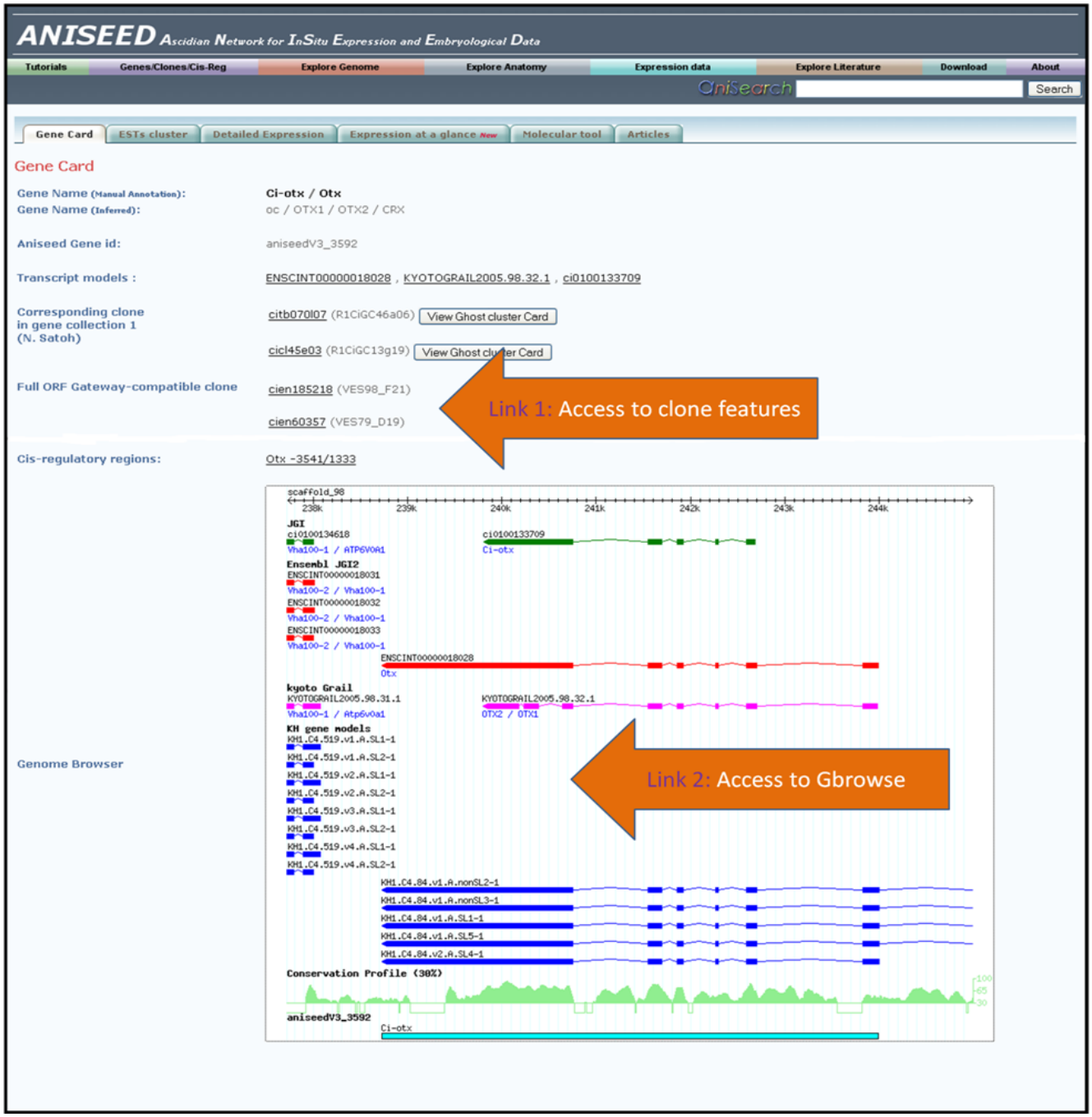


- Choose an "Ascidian species" from the menu by clicking on the arrows and scrolling down.
- Enter the biological name (otx) or the identifier of the gene model (ENSEMBL, JGI v1.0, KYOTOGRAIL2005, KH) you are looking for and click on the "Submit" button to access the gene card.



The gene card gives access to functional annotation of the gene (name, ortholog in mouse, human and Drosophila, interpro domains and Gene Ontology classification), corresponding transcript models, clones and regulatory regions and to an overview of the Genome browser. Thus, you can access from the gene card to corresponding full ORF gateway-compatible clone information and to the Genome browser:

Otx Gene card

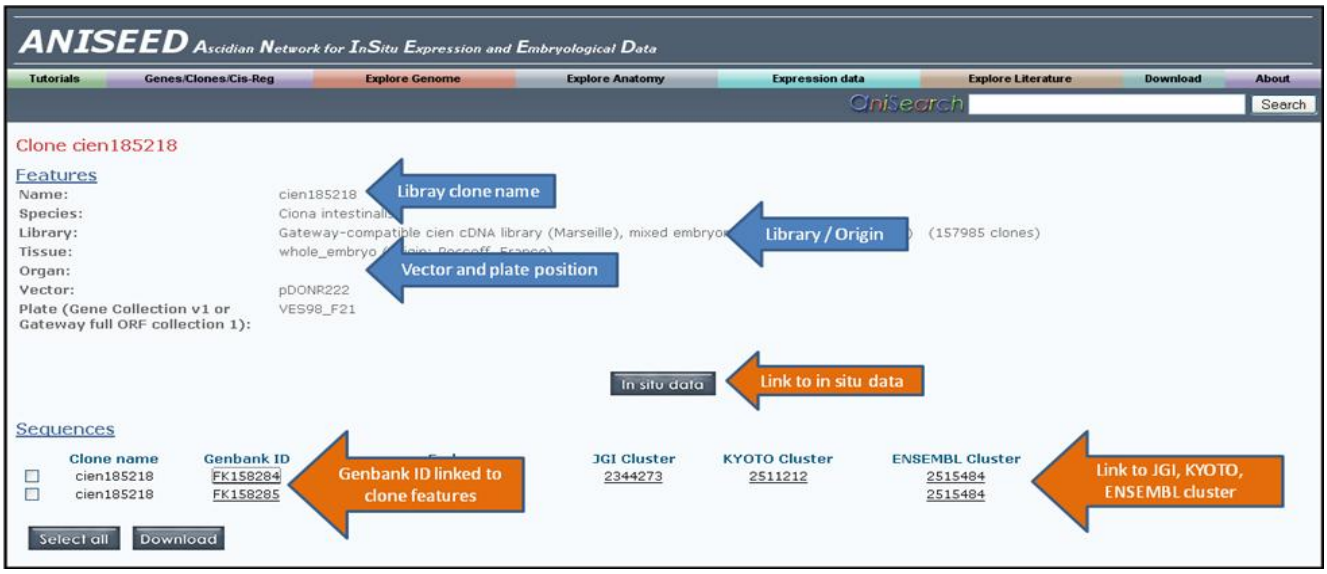


Access full ORF gateway compatible clone information from the gene card (link 1)

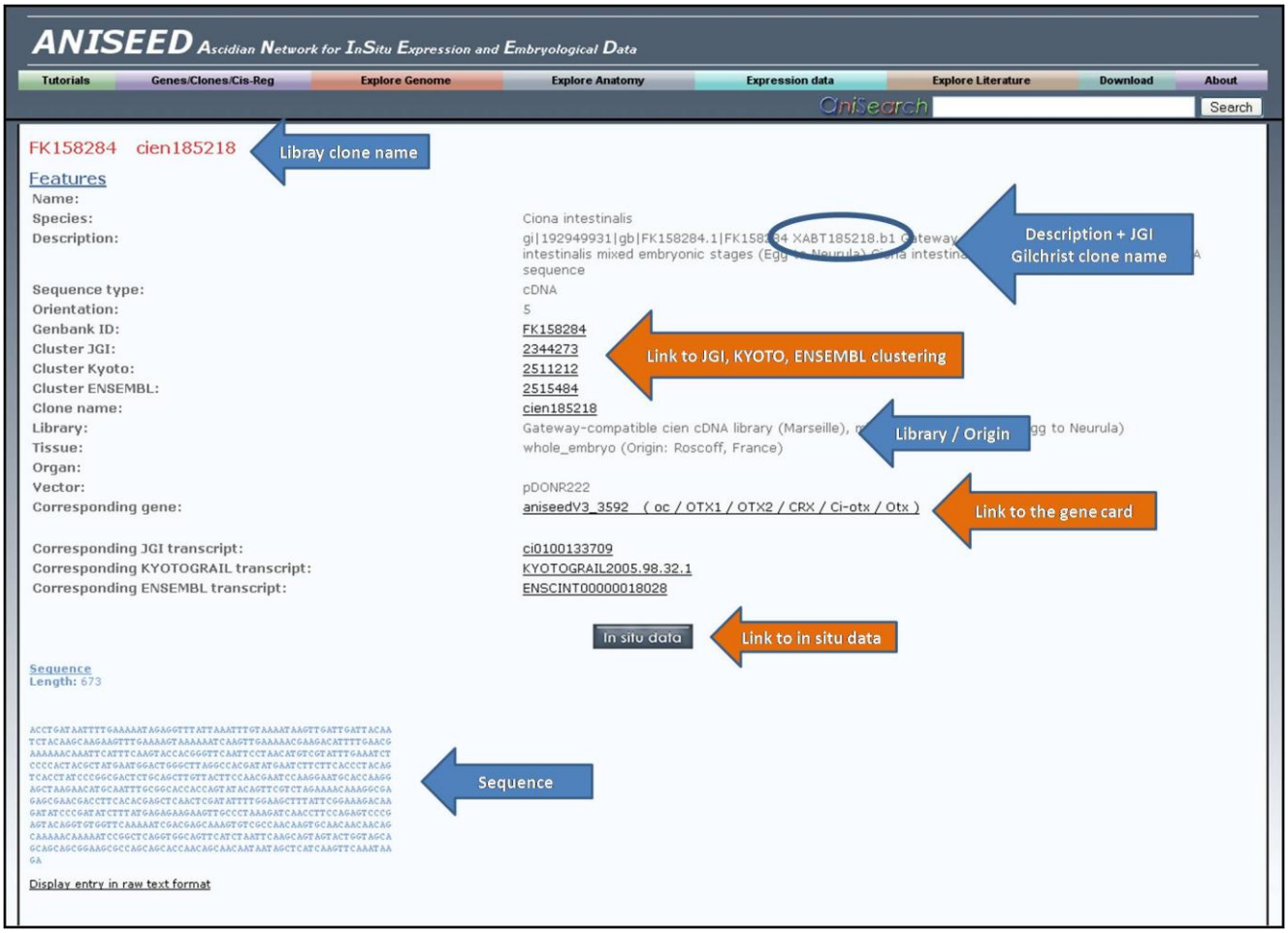
"Link 1" will give you access to clone features: the corresponding page displays some features like the library where the clone came from, the vector used, the plate position in the Unigene collection. You will also find the different clone sequences corresponding to the clone and the cluster that the clone belongs to from the three assemblies.

Otx Gene card

Link 1

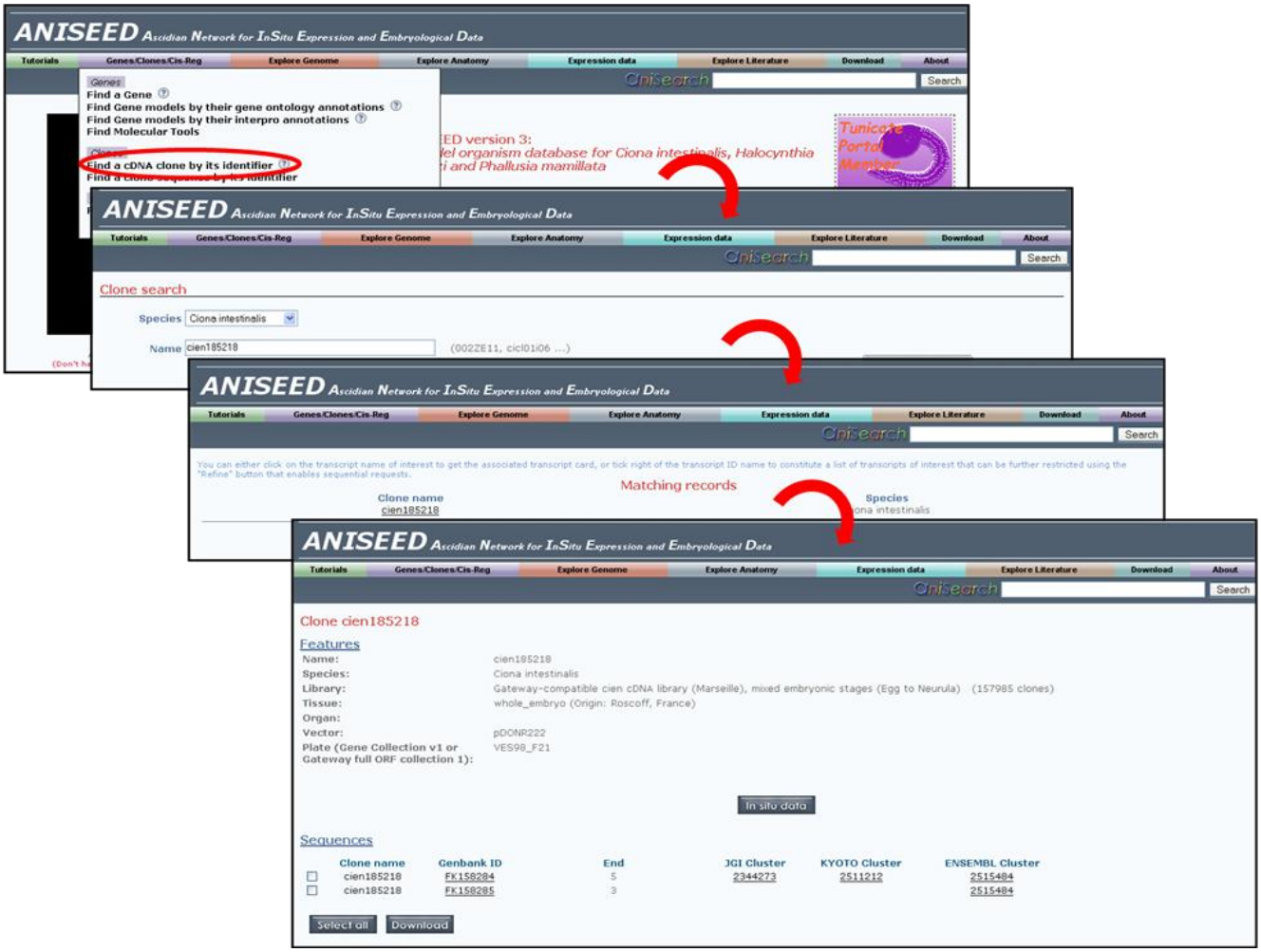


If you click on the Genbank ID:



This page gives you an access point to clone features including a brief description (including the JGI/Gilchrist clone name), the type of sequence (EST or cDNA) and corresponding orientation (5' or 3' end). You can also directly link to Genbank information by clicking on the Genbank ID. You retrieve the library used, the vector used, the tissue or the organ that it comes from. There are also the gene model corresponding to the clone sequence and when available, a link to the in situ data. Finally, you can find the sequence. All the information of this page can be exported in raw text format by clicking on "Display entry in raw text format" at the bottom.

PS: you can also access clone features using the Genes/Clones/Cis-reg link in the Aniseed menu. Note that if you use the "find a cDNA clone by its identifier" link, you have to enter the exact clone name in the corresponding field (e.g. cien177890) and if you use the "find a clone sequence" link, you have to enter the Genbank ID (e.g. FK050052) :

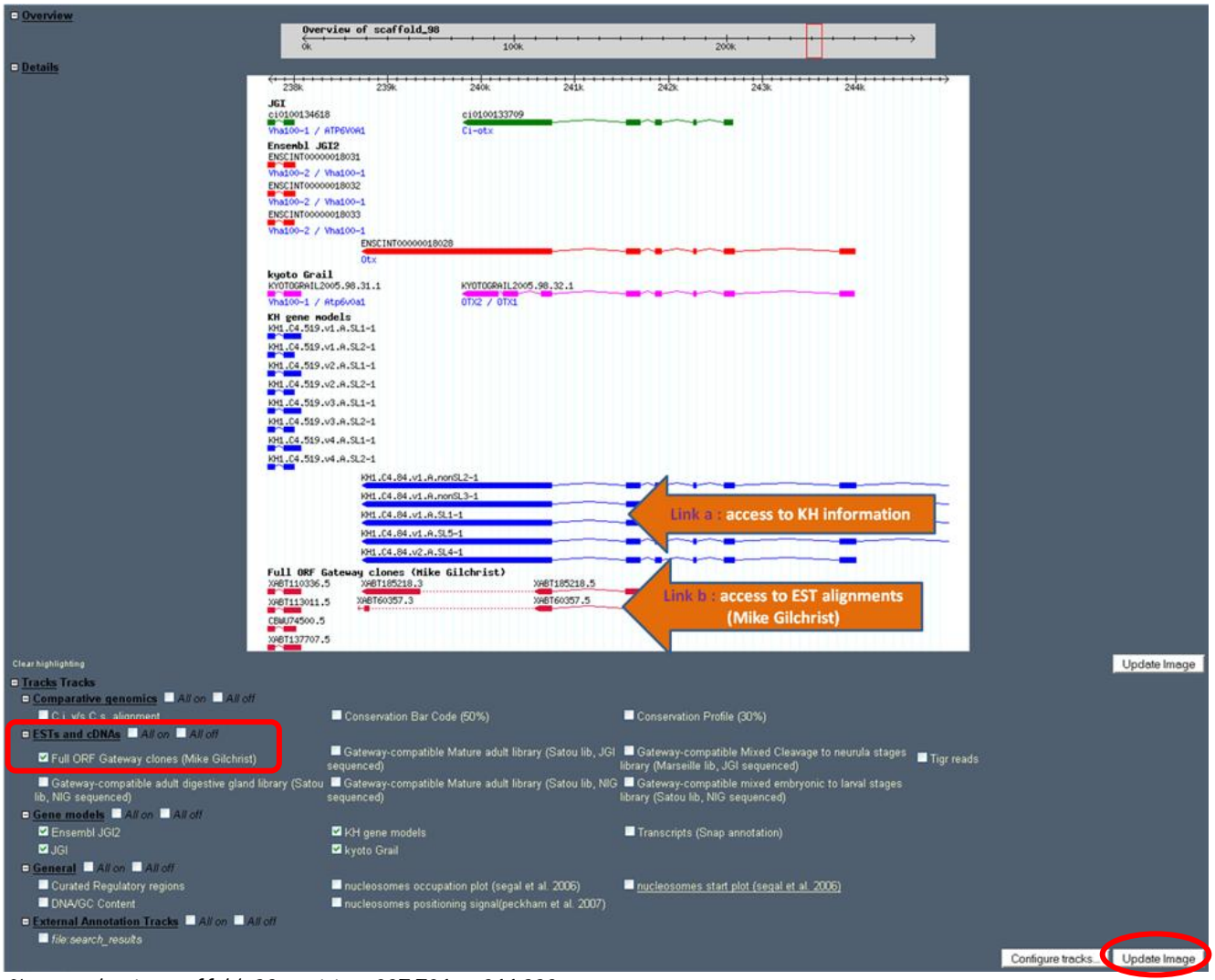


Access the Genome Browser from the gene card (link 2)

"Link 2" will give you access to the Genome Browser: the corresponding page displays the JGI v1.0, ENSEMBL Kyotograil2005 and KH gene models on the JGIv1.0 genome assembly. Click on a gene model and you will be linked to the corresponding gene card in Aniseed (see "link a" in the following figures). Move down to the « tracks » section and tick the 'Full ORF Gateway clones (Mike Gilchrist)' in the « ESTs and cDNAs (and other Gene models) » section. Update the image to show the track on the browser and then you can visualize Full ORF gateway clones. Click on a clone and you will be linked to the EST alignments of Mike Gilchrist (see "link b" in the following figures).

Otx Gene card

Link 2

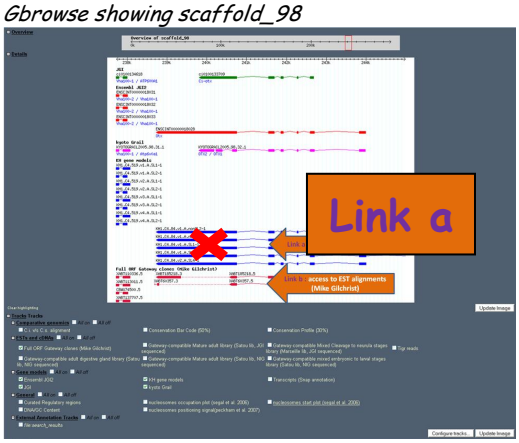


Gbrowse showing scaffold_98, positions 237.724 to 244.993

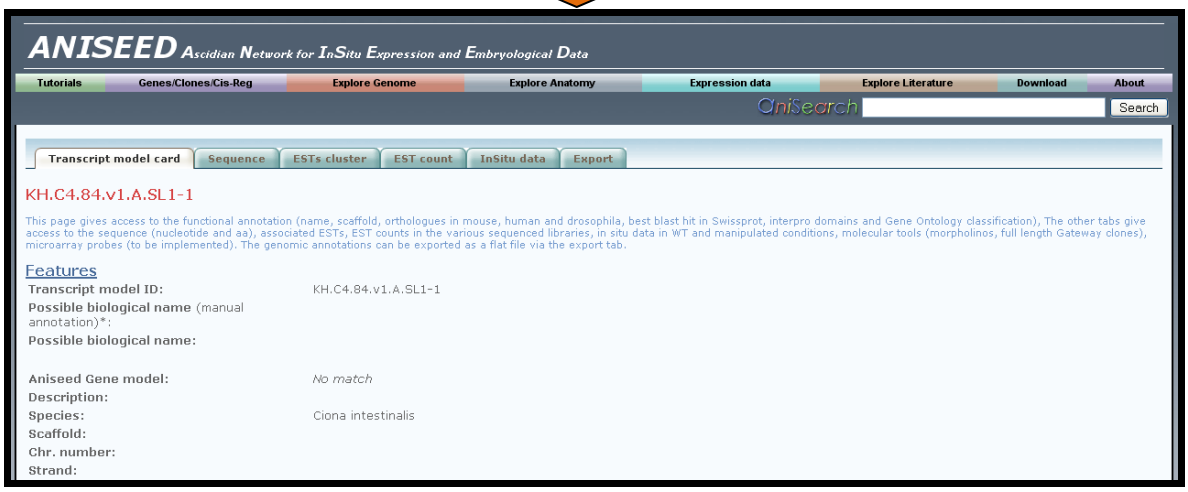
Access KH information (gene card) from Gbrowse (link a)

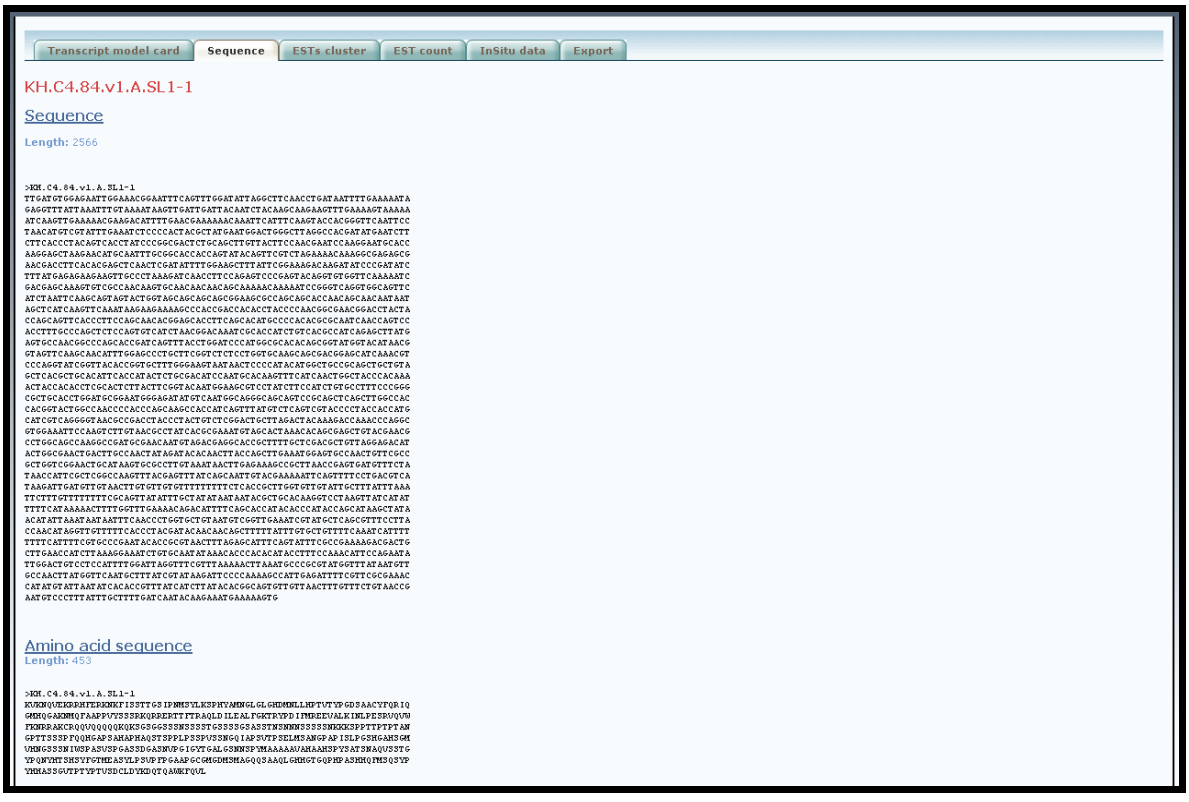
"Link a" will give you access to corresponding gene card. Here, you can access the sequence (nucleotide and amino acid).

Gbrowse showing scaffold_98



Link a



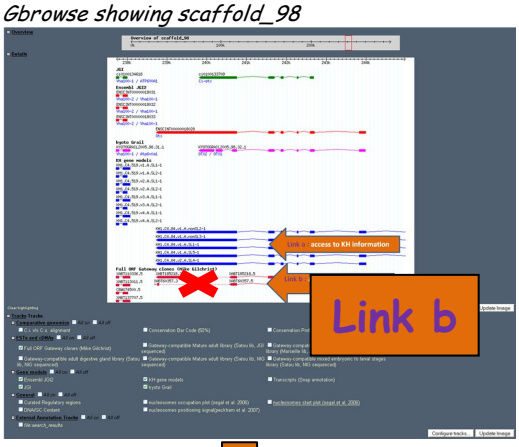


PS: you can also access the KH features using the "find a gene" link in the Genes/Clones/Cis-reg menu and entering the KH identifier in the corresponding box (see the "access gene information" section).

Access EST alignments from Gbrowse (link b)

"Link b" will give you access to the EST alignments of Mike Gilchrist.

Gbrowse showing scaffold_98



Don't hesitate to ask us if you cannot place a request you would like on ANISEED.

Delphine Dauga, 20th january 2009
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