

Insyght, a conserved synteny - homolog browser - Issues

| # | Tracker | Status | Priority | Subject | Author | Assignee | Updated | Category |
|------|--------------|-------------|----------|---|----------------|----------------|---------------------|----------|
| 8732 | Amélioration | Closed | Normal | Pipeline rev 471 ; improve the accessibility of the VM by simplifying the pipeline into 1 master script (keeping error handling proper) | Thomas Lacroix | Thomas Lacroix | 08/25/2017 12:09 PM | |
| 8731 | Bug | Closed | Normal | Pipeline rev 471 ; check_for_element_types_and_reorganize_elements_into_organisms.pl want to update already updated element type from previous run | Thomas Lacroix | Thomas Lacroix | 08/25/2017 12:08 PM | |
| 8730 | Bug | Closed | Normal | Pipeline rev 471 ; ObjectElement.pm -> setaccession -> deal with multiple digit in accnum name, do not file prefix and postfix | Thomas Lacroix | Thomas Lacroix | 08/25/2017 12:07 PM | |
| 8729 | Amélioration | Closed | Normal | Pipeline rev 471 ; check_db_consistency.pl : test that element lenght = sequence lenght | Thomas Lacroix | Thomas Lacroix | 08/25/2017 12:07 PM | |
| 8728 | Amélioration | Closed | Normal | Pipeline rev 471 ; check_db_consistency.pl : test that genes.residues = micado.prot.feats.residues | Thomas Lacroix | Thomas Lacroix | 08/25/2017 12:06 PM | |
| 8727 | Amélioration | Closed | Normal | Pipeline rev 471 ; script download_from_ncbi.pl : add the option -restrict_to_list_taxon_id_and_subnodes | Thomas Lacroix | Thomas Lacroix | 08/25/2017 12:05 PM | |
| 8726 | Feature | Closed | Normal | Pipeline rev 471 ; organize molecules into living organisms using assembly info | Thomas Lacroix | Thomas Lacroix | 08/25/2017 12:01 PM | |
| 8725 | Feature | Closed | Normal | adapt to database schema rev 2: additional links and info from ncbi, add columns for convenience when querying the database (avoid cross tables querying) | Thomas Lacroix | Thomas Lacroix | 08/25/2017 12:00 PM | |
| 8724 | Amélioration | Closed | Normal | Pipeline rev 471 ; Task_add_entry (insert of primary data) : Make the script more resilient to errors and re-run, faster (generator and integrator) | Thomas Lacroix | Thomas Lacroix | 08/25/2017 11:47 AM | |
| 8723 | Amélioration | Closed | Normal | Pipeline rev 471 ; fill_gene_entry.pl : generate data for table gene directly instead of after schema micado is filled w/ data | Thomas Lacroix | Thomas Lacroix | 08/25/2017 11:46 AM | |
| 8722 | Amélioration | Closed | Normal | Pipeline rev 471 ; fill_gene_entry.pl : infer correct type directly here instead of subsequent script | Thomas Lacroix | Thomas Lacroix | 08/25/2017 11:45 AM | |
| 8721 | Feature | Closed | Normal | Pipeline rev 471 ; add bmlink info on ncbi assembly id and accession, etc... for the table organisms (through element accnum) | Thomas Lacroix | Thomas Lacroix | 08/25/2017 11:44 AM | |
| 8720 | Feature | In Progress | Normal | Pipeline rev 471 ; avoid non essential redondant data, decrease total database size by around 2 fold | Thomas Lacroix | Thomas Lacroix | 08/28/2017 10:33 AM | |
| 8719 | Amélioration | Closed | Normal | Pipeline rev 471 ; improved analyse_stats_db.pl | Thomas Lacroix | Thomas Lacroix | 08/25/2017 11:34 AM | |
| 8718 | Feature | Closed | Normal | Pipeline rev 471 ; created script download_genome_files_from_ncbi.pl | Thomas Lacroix | Thomas Lacroix | 08/25/2017 11:33 AM | |
| 8717 | Amélioration | Closed | Normal | Pipeline rev 471 ; fill_gene_entry.pl : add Locus_tag directly in table genes | Thomas Lacroix | Thomas Lacroix | 08/25/2017 11:30 AM | |
| 8716 | Amélioration | Closed | Normal | Pipeline rev 471 ; Task_add_entry : cleaner option -GENOME_FILES_FORMAT | Thomas Lacroix | Thomas Lacroix | 08/25/2017 11:25 AM | |
| 8715 | Amélioration | Closed | Normal | Pipeline rev 471 ; Task_add_entry : added option -SKIP_NEIGHBOR_INFO as this info is not useful | Thomas Lacroix | Thomas Lacroix | 08/25/2017 11:23 AM | |
| 8714 | Bug | Closed | Normal | Navigation jumps when moving with >> or << in ortholog table or genomic organisation | Thomas Lacroix | Thomas Lacroix | 08/25/2017 10:58 AM | |
| 8713 | Bug | Closed | Normal | Compared organisms not sorted correctly for scope Whole organism | Thomas Lacroix | Thomas Lacroix | 08/25/2017 10:58 AM | |
| 8712 | Bug | Closed | Normal | Synteny symbol not displaying correct number of pairs, it was missing gene mismatch and insertion | Thomas Lacroix | Thomas Lacroix | 08/25/2017 10:57 AM | |

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| 8711 | Bug | Closed | Normal | When transferring q genes from synteny to ortholog table view, s_insertion genes were transeferd as well | Thomas Lacroix | Thomas Lacroix | 08/25/2017 10:57 AM | |
| 8710 | Bug | Closed | Normal | Error when the database was empty. Redirect user to use the guide to add data or check out http://genome.jouy.inra.fr/Insyght/ to test functionalities | Thomas Lacroix | Thomas Lacroix | 08/25/2017 10:57 AM | |
| 8709 | Amélioration | Closed | Normal | Modified user interface to deal with database changes in schema: removal of elements.description (-> sequences.definition), elements.date_seq (-> sequences.date_seq), elements.version (-> sequences.version), genes.residue (-> prot_feat.proteine) | Thomas Lacroix | Thomas Lacroix | 08/25/2017 10:56 AM | |
| 8708 | Bug | Closed | Normal | Fixed functionality to send email via smtp inra to report uncaught exception | Thomas Lacroix | Thomas Lacroix | 08/25/2017 10:55 AM | |
| 8707 | Bug | Closed | Normal | Fixed examples taxon ids for release Archaea | Thomas Lacroix | Thomas Lacroix | 08/25/2017 10:55 AM | |
| 8706 | Feature | Closed | Normal | Taxonomic browser, core / dispensable genome functionality : upon header selection, select all nodes in appropriate categories | Thomas Lacroix | Thomas Lacroix | 08/25/2017 10:55 AM | |
| 8705 | Bug | Closed | Normal | Sometimes 2 references genomes are selected in the taxonomic browser (2 nodes in yellow) ; impossible to change the group for them... | Thomas Lacroix | Thomas Lacroix | 08/25/2017 10:37 AM | |
| 8704 | Feature | Closed | Normal | Taxonomic browser, core / dispensable genome functionality : checkbox to select multiple genomes / nodes. Keyboard support. | Thomas Lacroix | Thomas Lacroix | 08/25/2017 10:36 AM | |
| 6924 | Feature | Closed | Normal | [Feature] PIPELINE: script integrate_taxo_data.pl : automatic management of the integration of the data for the tables micado.taxo and micado.taxo_names | Thomas Lacroix | Thomas Lacroix | 09/07/2016 02:38 PM | |
| 6923 | Feature | Closed | Normal | PIPELINE: script count_inserted_data.pl: utility to follow the data that have been inserted in the database | Thomas Lacroix | Thomas Lacroix | 09/07/2016 02:38 PM | |
| 6922 | Feature | Closed | Normal | PIPELINE: possibility to use Plast instead of Blast (Plast is ~5X faster than Blast) | Thomas Lacroix | Thomas Lacroix | 09/07/2016 02:35 PM | |
| 6506 | Bug | Closed | Normal | max connection idle : better configuration of the context.xml config file (max total 97 SQL request in parrallel) | Thomas Lacroix | Thomas Lacroix | 06/03/2016 03:14 PM | |
| 6505 | Feature | Closed | Normal | utilities to convert error report into stack trace with symbolMap file | Thomas Lacroix | Thomas Lacroix | 06/03/2016 03:13 PM | |
| 6504 | Feature | Closed | Normal | show info on PValue in ortholog table | Thomas Lacroix | Thomas Lacroix | 06/03/2016 03:13 PM | |
| 6503 | Feature | Closed | Normal | gene filter on PValue score if applicable | Thomas Lacroix | Thomas Lacroix | 06/03/2016 03:13 PM | |
| 6502 | Feature | Closed | Normal | over-representation (P-Value Fisher's Exact test) of orthologs whithin phenotype+ organisms in comparison to phenotype- organisms | Thomas Lacroix | Thomas Lacroix | 06/03/2016 03:11 PM | |
| 6501 | Bug | Closed | Normal | text above taxonomic browser search tab step 2 was not displaying properly | Thomas Lacroix | Thomas Lacroix | 06/03/2016 03:09 PM | |
| 6147 | Bug | Closed | Normal | color is not displayed correctly at first within the core / dispensable genome browser of the search page, it appears right after clicking on another node | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:45 PM | |
| 6146 | Bug | Closed | Normal | Uncaught exception: java.lang.IndexOutOfBoundsException when viewing resultq from core/ disp gene set directly in ortholog table | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:45 PM | |
| 6145 | Bug | Closed | Normal | FATAL: remaining connection slots are reserved for non-replication superuser connections | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:44 PM | |
| 6144 | Bug | Closed | Normal | the functionality "browse core / dispensable" genome" in the search tab is not longuer functioning correctly | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:44 PM | |

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| 6143 | Bug | Closed | Normal | The presence / absence homology filter did not work correctly with multiple organisms in the box : java.lang.Exception: could not parse orga id as integer : presence | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:43 PM | |
| 6142 | Feature | Closed | Normal | Better management of info panel: When we click on synteny info, we want to keep this disclosure panel open as we click on other synteny | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:43 PM | |
| 6141 | Feature | Closed | Normal | switch to no color for symbols q_gene_insertion or s_gene_insertion in genomic orga view when expanding a q or s insertion region | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:43 PM | |
| 6140 | Bug | Closed | Normal | The compared genomes list in the tab orthologs table and genomic organisation did contains public organisms with no element ; those organisms are now hidden from the result list | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:42 PM | |
| 6139 | Bug | Closed | Normal | In the search tab, the pre-made examples were not working properly | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:42 PM | |
| 6138 | Bug | Closed | Normal | some gene have qualifier protein_id with ref to other db (EMBL) enclosed in curly braces, this did pose a problem for the blast2seq link when it was the case ; exemple gene id 41305 metS of Listeria Monocytogenes strain 08-5578 (db origami_test) | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:41 PM | |
| 6137 | Bug | Closed | Normal | some genes have multiple qualifier protein_id, display them all in the info panel with correct link to external db | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:41 PM | |
| 6136 | Feature | Closed | Normal | direct link to GO, UniParc, PDB in the gene info panel (if available as annotation) | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:41 PM | |
| 6135 | Bug | Closed | Normal | some genes have multiple qualifier protein_id (some ref to other db such as tigr, start with REF), this did pose a problem for the blast2seq link when it was the case ; exemple gene id 5727 EF0944 of E faecalis v583 (db origami_test) | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:40 PM | |
| 6134 | Feature | Closed | Normal | different shade of grey to represent the alignment based on its %identity (>85% identity = black, between 50 to 85% = dark grey, etc.) | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:40 PM | |
| 6133 | Feature | Closed | Normal | Added support for url parameters: referenceSpecies, referenceStrain, referenceSubstrain, referenceAccnum, referenceGeneSetNames, referenceGeneSetLocusTag | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:39 PM | |
| 6132 | Feature | Closed | Normal | report 5 last history token in bug reporting tool | Thomas Lacroix | Thomas Lacroix | 04/06/2016 02:30 PM | |
| 5833 | Amélioration | Closed | Normal | Automatic and anonymous bug reporting tool | Thomas Lacroix | Thomas Lacroix | 02/09/2016 02:19 PM | |
| 5832 | Feature | Closed | Normal | PIPELINE: insertion of taxonomic data relevant to the dataset at hand only to save disk space. | Thomas Lacroix | Thomas Lacroix | 02/09/2016 11:16 AM | |
| 5831 | Feature | Closed | Normal | PIPELINE: support of .gbk files generated by prokka. | Thomas Lacroix | Thomas Lacroix | 02/09/2016 11:15 AM | |
| 5830 | Feature | Closed | Normal | PIPELINE: blast "organism vs all" instead of "element vs element" to be able to handle draft genomes with many contigs. | Thomas Lacroix | Thomas Lacroix | 02/09/2016 11:15 AM | |
| 5829 | Feature | Closed | Normal | PIPELINE: script to automatically correct elements types and group them into organisms. | Thomas Lacroix | Thomas Lacroix | 02/09/2016 11:15 AM | |
| 5828 | Feature | Closed | Normal | PIPELINE: option to recover from failure (computer shutdown, ...) without starting over for resources-consuming steps (blast and find synteny). | Thomas Lacroix | Thomas Lacroix | 02/09/2016 11:14 AM | |
| 5827 | Feature | Closed | Normal | PIPELINE: overall performance tuning : 2.5X faster (no bidirectional blasts, parallel insertion into the database), less intermediate files generated | Thomas Lacroix | Thomas Lacroix | 02/09/2016 11:14 AM | |

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| 5826 | Feature | Closed | Normal | PIPELINE: options to use an external cluster for resources-consuming steps (blast and find synteny) | Thomas Lacroix | Thomas Lacroix | 02/09/2016 11:12 AM | |
| 5824 | Feature | Closed | Normal | WEB APP: support of draft genomes with many contigs ; some queries regarding those genomes are still taking too much time though | Thomas Lacroix | Thomas Lacroix | 02/09/2016 10:33 AM | |
| 5823 | Feature | Closed | Normal | WEB APP: support of multiple organisms with identical taxo_id | Thomas Lacroix | Thomas Lacroix | 02/09/2016 10:33 AM | |
| 5822 | Feature | Closed | Normal | WEB APP: Select reference : functionality to have a direct access to the core / dispensable gene set for reference node | Thomas Lacroix | Thomas Lacroix | 02/09/2016 10:32 AM | |
| 5821 | Feature | Closed | Normal | WEB APP: taxonomic browser: automatic selection of the deeper node before branching | Thomas Lacroix | Thomas Lacroix | 02/09/2016 10:32 AM | |
| 5820 | Feature | Closed | Normal | WEB APP: export sequences of genes within a genomic region | Thomas Lacroix | Thomas Lacroix | 02/09/2016 10:31 AM | |
| 5819 | Bug | Closed | Normal | WEB APP: some special characters were not displaying correctly on some web browser, changed to more widely supported characters | Thomas Lacroix | Thomas Lacroix | 02/09/2016 10:30 AM | |
| 5818 | Feature | Closed | Normal | WEB APP: singleton synteny display the gene homology directly instead of a synteny of 1 to expand | Thomas Lacroix | Thomas Lacroix | 02/09/2016 10:30 AM | |
| 5817 | Feature | Closed | Normal | WEB APP: SELECT REFERENCE -> build your reference gene set among available molecules : new filter on protein lenght | Thomas Lacroix | Thomas Lacroix | 02/09/2016 10:29 AM | |
| 5816 | Feature | Closed | Normal | WEB APP: more distingasble colors for synteny ; ortholog not in synteny colored in grey to make the synyeny stand out more. | Thomas Lacroix | Thomas Lacroix | 02/09/2016 10:29 AM | |
| 5815 | Feature | Closed | Normal | WEB APP: export the ortholog table in .csv format ; simple output counting the number of orthologs per cell | Thomas Lacroix | Thomas Lacroix | 02/09/2016 10:28 AM | |
| 5814 | Feature | Closed | Normal | WEB APP: locus tag and functional annotation links to EnsemblGenomes, GOA, Interpro, Unipro, KEGG, PFAM, NCBI, blast2seq alignment viewer | Thomas Lacroix | Thomas Lacroix | 02/09/2016 10:27 AM | |
| 5813 | Feature | Closed | Normal | WEB APP: migrate to GWT 2.7 and GSS | Thomas Lacroix | Thomas Lacroix | 02/09/2016 10:24 AM | |
| 3794 | Bug | Feedback | Normal | find gene and go back to ortholog view | Thomas Lacroix | Thomas Lacroix | 01/14/2016 04:10 PM | |
| 3788 | Bug | Closed | Normal | transfert gene set from genomic orga to ortho table : some genes are missing sometime ? | Thomas Lacroix | | 01/14/2016 04:06 PM | |
| 3787 | Bug | Feedback | Normal | double click on empty cell in ortholog browser triggers error | Thomas Lacroix | Thomas Lacroix | 01/14/2016 04:10 PM | |
| 3756 | Bug | Closed | Normal | NullPointerException when navigating within a result page while data still loading | Thomas Lacroix | Thomas Lacroix | 07/31/2014 03:27 PM | |
| 3680 | Feature | Closed | Normal | improved browser history support | Thomas Lacroix | Thomas Lacroix | 07/31/2014 03:27 PM | |
| 3670 | Feature | Closed | Normal | automatic anonymous bug report on uncaughtException | Thomas Lacroix | Thomas Lacroix | 07/31/2014 03:27 PM | |
| 3661 | Feature | Closed | Normal | search tab : allow for a taxonomic node selection and easy access to core / dispensable genome | Thomas Lacroix | Thomas Lacroix | 07/31/2014 03:27 PM | |
| 3579 | Feature | Closed | Normal | add info on symbols and background color in detailed information stack | Thomas Lacroix | Thomas Lacroix | 07/31/2014 03:28 PM | |
| 3442 | Feature | New | Normal | display information if homology is 1-1, 1-n or n-n | Thomas Lacroix | Thomas Lacroix | 01/14/2016 04:10 PM | |
| 3409 | Bug | Closed | Normal | Ontologies comparator : genes aer not sorted according to bigger element as in other views | Thomas Lacroix | Thomas Lacroix | 04/30/2014 02:54 PM | |
| 3380 | Bug | Closed | Normal | exception on logout | Thomas Lacroix | Thomas Lacroix | 04/30/2014 02:56 PM | |
| 3379 | Feature | Closed | Normal | change pop up and internet text after registration | Thomas Lacroix | Thomas Lacroix | 04/30/2014 02:55 PM | |

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| 3211 | Feature | Rejected | Normal | rename "Annotations comparator" to "Ontologies comparator" | Thomas Lacroix | Thomas Lacroix | 04/16/2014 02:54 PM | |
| 3170 | Feature | Closed | Normal | taxonomic browser : auto-selection du noeud le plus profond dans la hiérarchie (auto-selection des noeuds enfant unique) | Thomas Lacroix | Thomas Lacroix | 04/30/2014 02:55 PM | |
| 3145 | Bug | Closed | Normal | navigation button when more rows displayed | Thomas Lacroix | Thomas Lacroix | 04/30/2014 02:54 PM | |
| 3134 | Bug | Rejected | Normal | when sorting the homolog table by a reference gene, bug in the result quick navigation ? | Thomas Lacroix | Thomas Lacroix | 04/18/2014 04:13 PM | |
| 3133 | Bug | Rejected | Normal | contextual menu find genes does not work for browse all homologs of an organism ? | Thomas Lacroix | Thomas Lacroix | 04/18/2014 04:02 PM | |
| 3131 | Bug | Rejected | Normal | IndexOutOfBoundsException ?? | Thomas Lacroix | Thomas Lacroix | 04/18/2014 03:48 PM | |
| 3130 | Bug | Rejected | Normal | NoSuchElementException ?? | Thomas Lacroix | Thomas Lacroix | 04/18/2014 03:26 PM | |
| 3129 | Bug | Closed | Normal | error if taxon id = 0 | Thomas Lacroix | Thomas Lacroix | 04/30/2014 02:55 PM | |
| 3128 | Feature | Closed | Normal | date and sequence version | Thomas Lacroix | Thomas Lacroix | 04/30/2014 02:55 PM | |
| 3127 | Bug | Rejected | Normal | taxon_id link | Thomas Lacroix | Thomas Lacroix | 04/17/2014 05:42 PM | |
| 3126 | Retour utilisateur | Rejected | Normal | load testing | Thomas Lacroix | Thomas Lacroix | 01/14/2016 04:09 PM | |
| 3125 | Feature | Rejected | Normal | fonctionnal tests | Thomas Lacroix | Thomas Lacroix | 07/30/2014 03:05 PM | |
| 3124 | Feature | Closed | Normal | add additional synteny info | Thomas Lacroix | Thomas Lacroix | 04/30/2014 02:56 PM | |
| 3123 | Bug | Closed | Normal | export sequence all genes of gene set | Thomas Lacroix | Thomas Lacroix | 04/30/2014 02:55 PM | |
| 3122 | Feature | New | Normal | change the result quick nav to be a cell widget that can handle a large quantity of data | Thomas Lacroix | Thomas Lacroix | 07/31/2014 03:07 PM | |
| 3117 | Bug | Closed | Normal | paper : homolog and synteny browser | Thomas Lacroix | Thomas Lacroix | 04/17/2014 05:43 PM | |
| 2500 | Feature | Closed | Normal | Possibility to select a subset of the taxonomic tree (node) while choosing the species that have(n't) homologs or should be featured / excluded in the result page | Thomas Lacroix | Thomas Lacroix | 08/14/2013 04:26 PM | |
| 2499 | Feature | Closed | Normal | [R1] : A person should be able to easily get to the system, i.e. there should be a list of supported genomes, and an example set. | Thomas Lacroix | Thomas Lacroix | 08/14/2013 04:26 PM | |