

Insyght, a conserved synteny - homolog browser - Issues

#	Tracker	Status	Priority	Subject	Author	Assignee	Updated	Category
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	
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 redundant data, decrease total database size by around 2 fold	Thomas Lacroix	Thomas Lacroix	08/28/2017 10:33 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	
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	
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	
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 within phenotype+ organisms in comparison to phenotype- organisms	Thomas Lacroix	Thomas Lacroix	06/03/2016 03:11 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	
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	
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	
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	

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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, parralel insertion into the database), less intermediate files generated	Thomas Lacroix	Thomas Lacroix	02/09/2016 11:14 AM	
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	
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	
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	
3379	Feature	Closed	Normal	change pop up and internet text after registration	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:55 PM	
3314	Feature	Closed	Low	favicon	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:58 PM	
3212	Feature	Closed	Low	clean server side servlet to transfert some methods in CallForInfo	Thomas Lacroix	Thomas Lacroix	07/30/2014 03:19 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	
3210	Feature	Closed	High	View "Annotation comparator" : add comparison of "Product" et "Note"	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:56 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	
3142	Feature	Rejected	Low	search genes for all genomes under a taxonomic node	Thomas Lacroix	Thomas Lacroix	07/30/2014 03:19 PM	
3141	Feature	Rejected	Low	lien vers blast ? blink ?	Thomas Lacroix	Thomas Lacroix	07/30/2014 03:09 PM	
3136	Feature	Rejected	Low	make private genomes appear in the taxonomic browser	Thomas Lacroix	Thomas Lacroix	04/17/2014 03:24 PM	
3135	Feature	New	Low	center display on a reference gene in the middle of the screen	Thomas Lacroix	Thomas Lacroix	12/03/2013 05:45 PM	
3128	Feature	Closed	Normal	date and sequence version	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:55 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	
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	
3121	Feature	Closed	High	copyright INRA	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:58 PM	
3120	Feature	Closed	High	remove 100 organisms limit	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:56 PM	
3116	Feature	Closed	High	in the search tab, rename "clear selected / clear all"	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:57 PM	
3115	Feature	Closed	High	not all genomic location have comma separating the thousands	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:57 PM	
3113	Feature	Closed	High	button Add all in the search tab when building the gene set	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:57 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	