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.feat.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 bdlink info on ncbi assembly id and accession, etc... for the table organisms (trough element accnum)	Thomas Lacroix	Thomas Lacroix	08/25/2017 11:44 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	

#	Tracker	Status	Priority	Subject	Author	Assignee	Updated	Category
8711	Bug	Closed	Normal	When transfering 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	

#	Tracker	Status	Priority	Subject	Author	Assignee	Updated	Category
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 tocken 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, parralel insertion into the database), less intermediate files generated	Thomas Lacroix	Thomas Lacroix	02/09/2016 11:14 AM	

#	Tracker	Status	Priority	Subject	Author	Assignee	Updated	Category
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	
3756	Bug	Closed	Normal	NullPointer Exception 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 detailled information stack	Thomas Lacroix	Thomas Lacroix	07/31/2014 03:28 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	
3381	Bug	Closed	High	pb login genome privé uncaught exception (example S salivarius)	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:59 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	
3314	Feature	Closed	Low	favicon	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:58 PM	
3269	Bug	Closed	High	expand synteny show more genes than expected if those genes overlap	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:56 PM	

#	Tracker	Status	Priority	Subject	Author	Assignee	Updated	Category
3213	Retour utilisateur	Closed	Low	rename whole organism to reference organism in the sort result by options	Thomas Lacroix	Thomas Lacroix	01/14/2016 04:07 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	
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	
3209	Bug	Closed	High	when search page -> exclude genomes : ERROR: syntax error at or near ")"	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:59 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	
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	
3140	Support	Rejected	Low	fiche plume	Thomas Lacroix	Thomas Lacroix	01/14/2016 04:08 PM	
3138	Bug	Closed	Low	Export feature homolog table	Thomas Lacroix	Thomas Lacroix	07/31/2014 03:28 PM	
3137	Bug	Closed	Low	Export feature in the search tab	Thomas Lacroix	Thomas Lacroix	07/31/2014 03:28 PM	
3136	Feature	Rejected	Low	make private genomes appear in the taxonomic browser	Thomas Lacroix	Thomas Lacroix	04/17/2014 03:24 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	IndexOutOfBoundException ??	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	
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	
3119	Bug	Closed	High	alignment info is not displayed correctly	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:56 PM	
3118	Bug	Closed	High	paper and website: change gene to CDS	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:57 PM	
3117	Bug	Closed	Normal	paper : homolog and synteny browser	Thomas Lacroix	Thomas Lacroix	04/17/2014 05:43 PM	
3116	Feature	Closed	High	in the search tab, rename "clear selected / clear all"	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:57 PM	

#	Tracker	Status	Priority	Subject	Author	Assignee	Updated	Category
3115	Feature	Closed	High	not all genomic location have comma separating the thousands	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:57 PM	
3114	Bug	Rejected	High	no link to outside db for the compared gene annotations	Thomas Lacroix	Thomas Lacroix	04/16/2014 04:20 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	
3112	Bug	Closed	High	red stain marker in the proportional view	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:57 PM	
3111	Bug	Closed	High	remove update pipeline	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:58 PM	
3110	Support	Closed	High	public svn realease	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:58 PM	
3109	Bug	Rejected	High	locus tag can have multilpe feature id qualifiers	Thomas Lacroix	Thomas Lacroix	04/16/2014 02:47 PM	
3108	Bug	Closed	High	impossible to sort the homolog table by a reference gene	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:58 PM	
3107	Bug	Rejected	High	back button of the web browser -> error ?	Thomas Lacroix	Thomas Lacroix	04/11/2014 10:16 AM	
3106	Bug	Closed	High	resize web browser -> empty result page	Thomas Lacroix	Thomas Lacroix	04/30/2014 02:59 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	