GMOD-DBSF,biosoftware_benchandgenes4all

2.0

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Chapter 1

Todo List

Member gmod_dbsf_chado_name2id($name, $table_type, $reverse=FALSE, $reconnect=TRUE) expand this function for all tables and also make it work with Drupal too, then move it to gmod_dbsf.module

Member gmod_dbsf_get_defined_dbs() currently, we are following the est2assembly nomenclature, however in the future we should make a connection to each database explictly and check for a specific table (it will be much slower but can be controlled by a switch)

Member gmod_dbsf_getspecies($limit=NULL, $all_orgs=NULL) move into gmod_dbsf_get_add_organism();

Member gmod_dbsf_validate_seq_dna($seq=NULL, $strip=FALSE) support FASTQ

Chapter 2

Bug List

File gmod_dbsf.module The Chado database must be aliased as 'chado' in the settings.ini and the database name MUST contain chado (case insensitive) (Drupal requires us to have the module name as a prefix to all tables, but Chado has no prefix. Since Drupal has no function to give us the alias of the active database, we have to strpos the db_name

Chapter 3

File Index

3.1 File List

Here is a list of all documented files with brief descriptions:

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Chapter 4

File Documentation

4.1 biosoftware_bench/biosoftware_bench.module File Reference

Functions

- biosoftware_bench_init ()
- biosoftware_bench_perm ()
- biosoftware_bench_theme ()
- biosoftware_bench_menu ()
- biosoftware_bench_software_select_page ()
- biosoftware_bench_check_software_active ($software)
- biosoftware_bench_get_role ($limit=NULL)
- biosoftware_bench_generate_options ($software_name)
- biosoftware_bench_formatdb_fastafile ($infile, $file_type= 'protein')
- biosoftware_bench_get_user_datasets ($software_name= 'blastall')
- biosoftware_bench_cron ()
- biosoftware_bench_get_software ($limit=NULL, $name_as_key=NULL)
- biosoftware_bench_get_resource_roles ($resource, $name_as_key=NULL)
- biosoftware_bench_get_dataset_path ($dataset)
- biosoftware_bench_software_result_form (&$form)

4.1.1 Detailed Description

Drupal Bioinformatic Server framework Module

A BLAST dataset must be formated with formatdb -o T in order to use the fastacmd fetching of accession IDs.

Developed by Alexie Papanicolaou University of Exeter.

See also

http://insectacentral.org

caution. Tabs needs the following settings to be set at /admin/settings/tabs due to tabs' bugs navigation buttons: enabled ; descriptive tab URLs: enabled. internet explorer 7 has a bug with double row tabs. use IE8

Definition in file biosoftware_bench.module.

4.1.2 Function Documentation

4.1.2.1 biosoftware_bench_check_software_active ($ *software*)

Helper function to check if a software is active

Parameters

$software ID or uniquename of software to check.

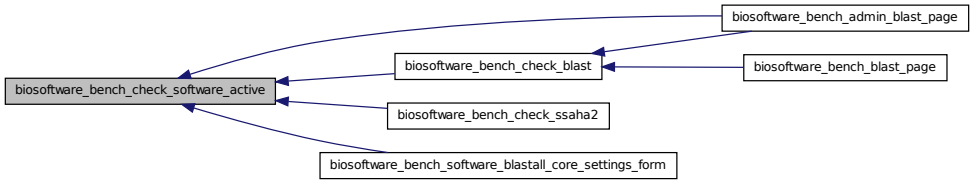
Returns

TRUE if software is active, FALSE otherwise or on failure

Definition at line 192 of file biosoftware_bench.module.

Referenced by biosoftware_bench_admin_blast_page(), biosoftware_bench_check_blast(), biosoftware_-bench_check_ssaha2(), and biosoftware_bench_software_blastall_core_settings_form().

Here is the caller graph for this function:



4.1.2.2 biosoftware_bench_cron ( )

Implement hook_cron()

Finds & deletes temporary files

Definition at line 405 of file biosoftware_bench.module.

4.1.2.3 biosoftware_bench_formatdb_fastafile ($ *infile,* $ *file_type* = `'protein'`)

Format a FASTA file for BLAST

Parameters

$infile Full path to file to format.

$file_type Either 'protein' or 'nucleotide'

Returns

Returns output of formatdb, or FALSE upon failure

Definition at line 303 of file biosoftware_bench.module.

4.1.2.4 biosoftware_bench_generate_options ($ *software_name*)

Get software options, their values and the FAPI type

Parameters

$software_name Name of software to generate options for

Returns

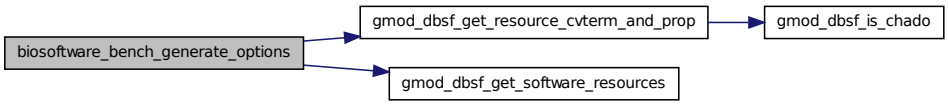
An 2D associative array. Primary key is option name and 2nd key is 'options' and 'type'. Content of options is a list array and type is a string.

Definition at line 257 of file biosoftware_bench.module.

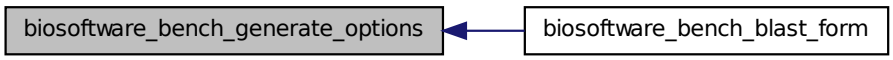
References gmod_dbsf_get_resource_cvterm_and_prop(), and gmod_dbsf_get_software_resources().

Referenced by biosoftware_bench_blast_form().

Here is the call graph for this function:



Here is the caller graph for this function:



4.1.2.5 biosoftware_bench_get_dataset_path ($ *dataset*)

Get full path to a dataset

Parameters

$dataset Dataset to get path for

Returns

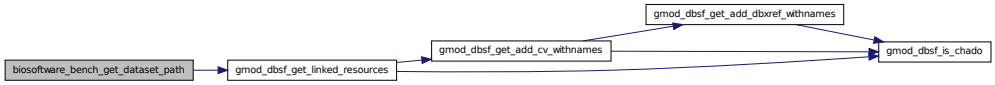
Full path to directory.

Definition at line 526 of file biosoftware_bench.module.

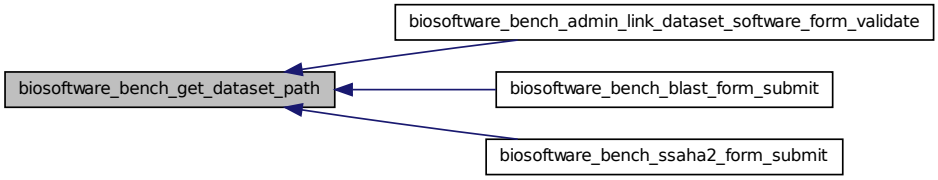
References gmod_dbsf_get_linked_resources().

Referenced by biosoftware_bench_admin_link_dataset_software_form_validate(), biosoftware_bench_-blast_form_submit(), and biosoftware_bench_ssaha2_form_submit().

Here is the call graph for this function:



Here is the caller graph for this function:



4.1.2.6 biosoftware_bench_get_resource_roles ($ *resource*, $ *name_as_key* = `NULL`)

Get roles linked to a specific resource

Parameters

$resource id ID or uniquename of resource to get data for
$name_as_key If TRUE, return array is not indexed by id but by the name of roles

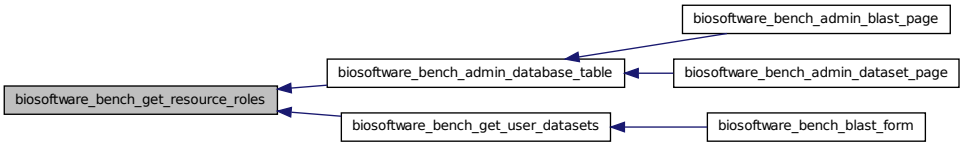
Returns

An associative array with id and name of roles. The key is controlled by $name_as_key

Definition at line 485 of file biosoftware_bench.module.

Referenced by biosoftware_bench_admin_database_table(), and biosoftware_bench_get_user_datasets().

Here is the caller graph for this function:



4.1.2.7 biosoftware_bench_get_role ($ *limit* = *NULL*)

Get drupal roles, optionally with a limit

Parameters

$limit Optionally add a limit. It can be a two element array with first element to act as the column name and second as the value. or it can be a string to be added after WHERE.

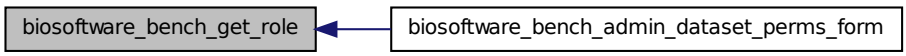
Returns

FALSE on failure or an associative array of names with role.rid as key

Definition at line 223 of file biosoftware_bench.module.

Referenced by biosoftware_bench_admin_dataset_perms_form().

Here is the caller graph for this function:



4.1.2.8 biosoftware_bench_get_software ($ *limit* = *NULL*, $ *name_as_key* = *NULL*)

Get all software

Parameters

$limit Optionally add a limit. It can be an assoc. array where key is column, value is constraint or a string to append with an AND

$name_as_key If TRUE then return array has uniquename as the key and id as the value.

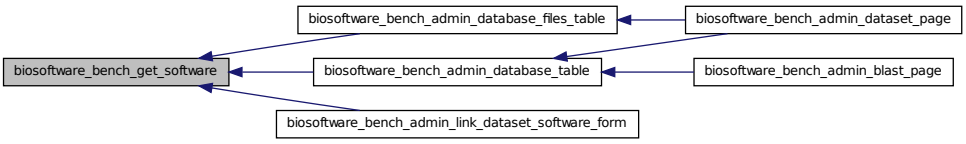
Returns

An associative array of data with ID as key unless $name_as_key is set. FALSE on failure

Definition at line 431 of file biosoftware_bench.module.

Referenced by biosoftware_bench_admin_database_files_table(), biosoftware_bench_admin_database_-table(), and biosoftware_bench_admin_link_dataset_software_form().

Here is the caller graph for this function:



4.1.2.9 biosoftware_bench_get_user_datasets ($ *software_name* = *'blastall'*)

Get software datasets available to visitor/user

Parameters

$software_name Name of software to get datasets for

Returns

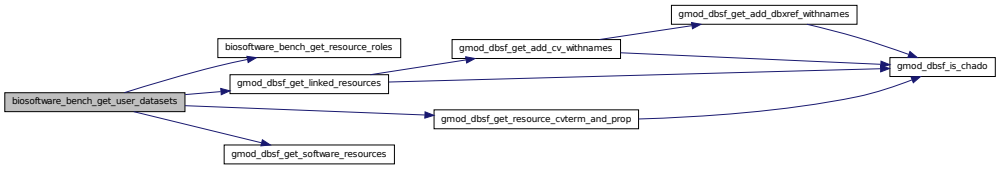
FALSE on failure and a 3D associative array if successful. The array structure is like so: [dbtype][dbgroup][id] = name

Definition at line 338 of file biosoftware_bench.module.

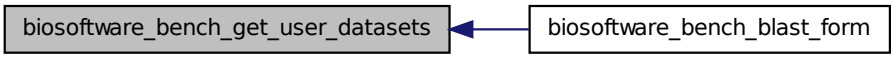
References biosoftware_bench_get_resource_roles(), gmod_dbsf_get_linked_resources(), gmod_dbsf_get_resource_cvterm_and_prop(), and gmod_dbsf_get_software_resources().

Referenced by biosoftware_bench_blast_form().

Here is the call graph for this function:



Here is the caller graph for this function:



4.1.2.10 biosoftware_bench_init ( )

Implements hook_init().

Definition at line 26 of file biosoftware_bench.module.

4.1.2.11 biosoftware_bench_menu ( )

Implements hook_menu().

If it finds plugin files, it adds them too.

Definition at line 80 of file biosoftware_bench.module.

4.1.2.12 biosoftware_bench_perm ( )

Implements hook_perm().

Definition at line 33 of file biosoftware_bench.module.

4.1.2.13 biosoftware_bench_software_result_form (&$ *form*)

Theme software result form

See also

biosoftware_bench_blast_result_form()

Parameters

$form Form API form variable which will be themed.

Returns

String with HTML of themed form.

Definition at line 803 of file biosoftware_bench.module.

4.1.2.14 biosoftware_bench_software_select_page ( )

Produce HTML for the 'select software page'.

Menu biosoftware_bench/select

Definition at line 156 of file biosoftware_bench.module.

4.1.2.15 biosoftware_bench_theme ( )

Implement hook_theme()

Definition at line 54 of file biosoftware_bench.module.

4.2 biosoftware_bench/includes/biosoftware_bench_admin.inc File Reference

Functions

- biosoftware_bench_software_form ($form_state)
- biosoftware_bench_software_form_validate ($form, &$form_state)
- biosoftware_bench_software_form_submit ($form, &$form_state)
- biosoftware_bench_admin_database_files_table ()
- biosoftware_bench_admin_database_table ($software=NULL)
- biosoftware_bench_admin_dataset_page ()
- biosoftware_bench_admin_edit_dataset_form ($form_state)
- biosoftware_bench_admin_edit_dataset_form_validate ($form, &$form_state)
- biosoftware_bench_admin_edit_dataset_form_submit ($form, &$form_state)

- biosoftware_bench_admin_software_page ()
- biosoftware_bench_admin_dataset_perms_form ($form_state)
- biosoftware_bench_admin_dataset_perms_form_submit ($form, &$form_state)
- biosoftware_bench_admin_dataset_variables_form ($form_state)
- biosoftware_bench_admin_dataset_variables_form_validate ($form, &$form_state)
- biosoftware_bench_admin_dataset_variables_form_submit ($form, &$form_state)
- biosoftware_bench_admin_newdataset_form ($form_state)
- biosoftware_bench_admin_newdataset_form_validate ($form, &$form_state)
- biosoftware_bench_admin_newdataset_form_submit ($form, &$form_state)
- biosoftware_bench_admin_link_dataset_software_form ($form_state, $software=NULL)
- biosoftware_bench_admin_link_dataset_software_form_validate ($form, &$form_state)
- biosoftware_bench_admin_link_dataset_software_form_submit ($form, &$form_state)
- biosoftware_bench_admin_page ()

4.2.1 Detailed Description

Administration interface for biosoftware_bench

Definition in file biosoftware_bench_admin.inc.

4.2.2 Function Documentation

4.2.2.1 biosoftware_bench_admin_database_files_table ( )

Builds a table with all files which could be added as datasets

Returns

HTML of a table

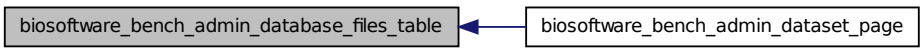
Definition at line 142 of file biosoftware_bench_admin.inc.

References biosoftware_bench_get_software(), gmod_dbsf_get_add_resource(), and gmod_dbsf_get_-softwareprop().

Referenced by biosoftware_bench_admin_dataset_page().

Here is the call graph for this function:

Here is the caller graph for this function:



4.2.2.2 biosoftware_bench_admin_database_table ($ *software* = *NULL*)

Builds a table containing all datasets that have been uploaded

Parameters

$software Optionally, software to create the table for. Defaults to NULL i.e. all

Returns

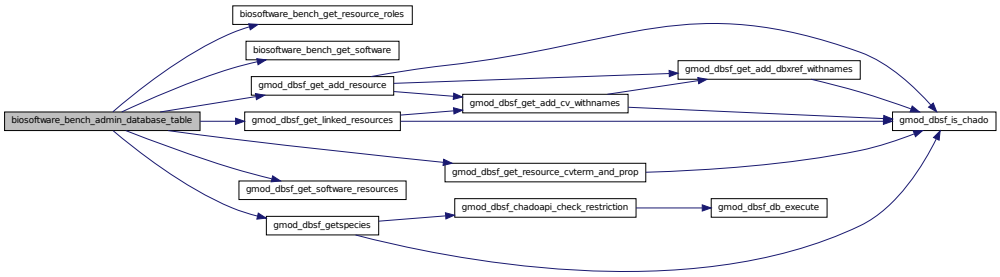
HTML of a table

Definition at line 202 of file biosoftware_bench_admin.inc.

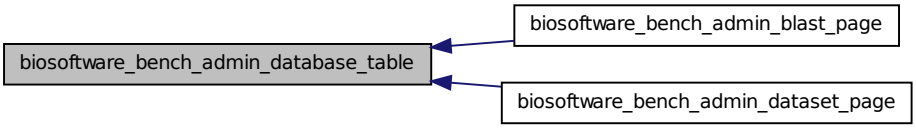
References biosoftware_bench_get_resource_roles(), biosoftware_bench_get_software(), gmod_dbsf_get_add_resource(), gmod_dbsf_get_linked_resources(), gmod_dbsf_get_resource_cvterm_and_prop(), gmod_dbsf_get_software_resources(), and gmod_dbsf_getspecies().

Referenced by biosoftware_bench_admin_blast_page(), and biosoftware_bench_admin_dataset_page().

Here is the call graph for this function:



Here is the caller graph for this function:



4.2.2.3 biosoftware_bench_admin_dataset_page ( )

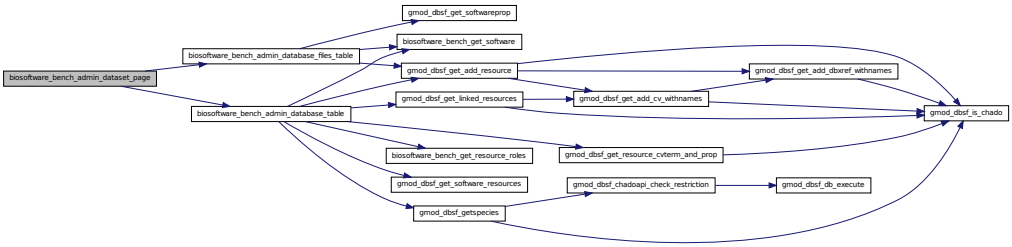
Produce HTML for the 'administrate dataset page'.

Menu admin/bench/dataset

Definition at line 296 of file biosoftware_bench_admin.inc.

References biosoftware_bench_admin_database_files_table(), and biosoftware_bench_admin_database_-table().

Here is the call graph for this function:



4.2.2.4 biosoftware_bench_admin_dataset_perms_form ($ *form_state*)

Implements hook_form()

See also

biosoftware_bench_admin_dataset_perms_form_validate()
biosoftware_bench_admin_dataset_perms_form_submit()

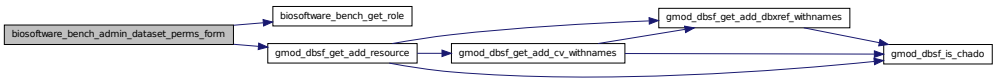
Parameters

$form_state hook_form data

Definition at line 647 of file biosoftware_bench_admin.inc.

References biosoftware_bench_get_role(), and gmod_dbsf_get_add_resource().

Here is the call graph for this function:



4.2.2.5 biosoftware_bench_admin_dataset_perms_form_submit ($ *form*, &$ *form_state*)

Implements hook_form_submit()

See also

biosoftware_bench_admin_dataset_perms_form()
biosoftware_bench_admin_dataset_perms_form_validate()

Parameters

$form hook_form data

$form_state hook_form data

Definition at line 702 of file biosoftware_bench_admin.inc.

References gmod_dbsf_link_unlink_resource_role().

Here is the call graph for this function:

4.2.2.6 biosoftware_bench_admin_dataset_variables_form ($ *form_state*)

Implements hook_form()

See also

biosoftware_bench_admin_dataset_variables_form_validate()
biosoftware_bench_admin_dataset_variables_form_submit()

Parameters

$form_state hook_form data

Definition at line 750 of file biosoftware_bench_admin.inc.

4.2.2.7 biosoftware_bench_admin_dataset_variables_form_submit ($ *form*, &$ *form_state*)

Implements hook_form_submit()

See also

biosoftware_bench_admin_dataset_variables_form_validate()
biosoftware_bench_admin_dataset_variables_form()

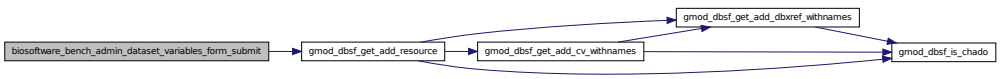
Parameters

$form hook_form data
$form_state hook_form data

Definition at line 843 of file biosoftware_bench_admin.inc.

References gmod_dbsf_get_add_resource().

Here is the call graph for this function:



4.2.2.8 biosoftware_bench_admin_dataset_variables_form_validate ($ *form*, &$ *form_state*)

Implements hook_form_validate()

See also

biosoftware_bench_admin_dataset_variables_form()
biosoftware_bench_admin_dataset_variables_form_submit()

Parameters

$form hook_form data

$form_state hook_form data

Definition at line 804 of file biosoftware_bench_admin.inc.

4.2.2.9 biosoftware_bench_admin_edit_dataset_form ($ *form_state*)

Implements of hook_form()

Used to edit dataset properties

See also

biosoftware_bench_admin_edit_dataset_form_validate()
biosoftware_bench_admin_edit_dataset_form_submit()

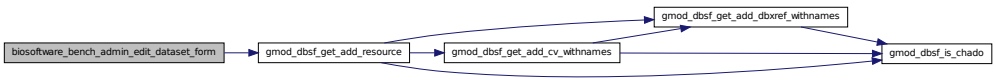
Parameters

$form_state hook_form data

Definition at line 381 of file biosoftware_bench_admin.inc.

References gmod_dbsf_get_add_resource().

Here is the call graph for this function:



4.2.2.10 biosoftware_bench_admin_edit_dataset_form_submit ($ *form*, &$ *form_state*)

Implements of hook_form()

Used to edit dataset properties

See also

biosoftware_bench_admin_edit_dataset_form()
biosoftware_bench_admin_edit_dataset_form_validate()

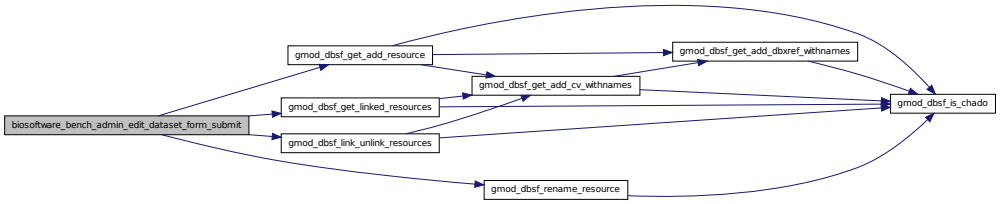
Parameters

$form_state hook_form data

Definition at line 517 of file biosoftware_bench_admin.inc.

References gmod_dbsf_get_add_resource(), gmod_dbsf_get_linked_resources(), gmod_dbsf_link_-unlink_resources(), and gmod_dbsf_rename_resource().

Here is the call graph for this function:



4.2.2.11 biosoftware_bench_admin_edit_dataset_form_validate ($ *form*, &$ *form_state*)

Implements of hook_form()

Used to edit dataset properties

See also

biosoftware_bench_admin_edit_dataset_form()
biosoftware_bench_admin_edit_dataset_form_submit()

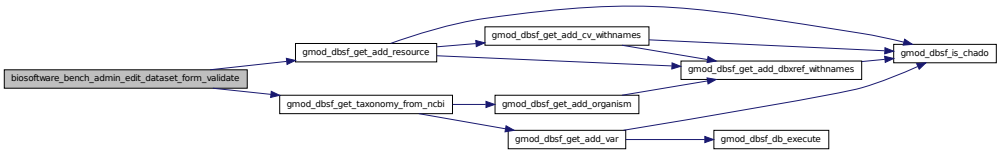
Parameters

$form_state hook_form data

Definition at line 451 of file biosoftware_bench_admin.inc.

References gmod_dbsf_get_add_resource(), and gmod_dbsf_get_taxonomy_from_ncbi().

Here is the call graph for this function:



4.2.2.12 biosoftware_bench_admin_link_dataset_software_form ($ *form_state*, $ *software* = ***NULL***)

Implements hook_form()

See also

biosoftware_bench_admin_link_dataset_software_form_validate()
biosoftware_bench_admin_link_dataset_software_form_submit()

Parameters

$form_state hook_form data

$software Which software to produce form for

Definition at line 1155 of file biosoftware_bench_admin.inc.

References biosoftware_bench_get_software(), and gmod_dbsf_get_add_resource().

Here is the call graph for this function:

4.2.2.13 biosoftware_bench_admin_link_dataset_software_form_submit ($ *form*, &$ *form_state*)

Implements hook_form_submit()

See also

biosoftware_bench_admin_link_dataset_software_form()
biosoftware_bench_admin_link_dataset_software_form_validate()

Parameters

$form hook_form data

$form_state hook_form data

Definition at line 1282 of file biosoftware_bench_admin.inc.

References gmod_dbsf_link_unlink_software_resource().

Here is the call graph for this function:

4.2.2.14 biosoftware_bench_admin_link_dataset_software_form_validate ($ *form*, &$ *form_state*)

Implements hook_form_validate()

See also

biosoftware_bench_admin_link_dataset_software_form()
biosoftware_bench_admin_link_dataset_software_form_submit()

Parameters

$form hook_form data

$form_state hook_form data

Definition at line 1224 of file biosoftware_bench_admin.inc.

References biosoftware_bench_get_dataset_path(), and gmod_dbsf_get_softwareprop().

Here is the call graph for this function:

4.2.2.15 biosoftware_bench_admin_newdataset_form ($ *form_state*)

Implements hook_form()

See also

biosoftware_bench_admin_newdataset_form_validate()
biosoftware_bench_admin_newdataset_form_submit()

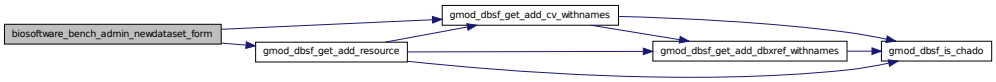
Parameters

$form_state hook_form data

Definition at line 883 of file biosoftware_bench_admin.inc.

References gmod_dbsf_get_add_cv_withnames(), and gmod_dbsf_get_add_resource().

Here is the call graph for this function:



4.2.2.16 biosoftware_bench_admin_newdataset_form_submit ($ *form*, &$ *form_state*)

Implements hook_form_submit()

See also

biosoftware_bench_admin_newdataset_form()
biosoftware_bench_admin_newdataset_form_validate()

Parameters

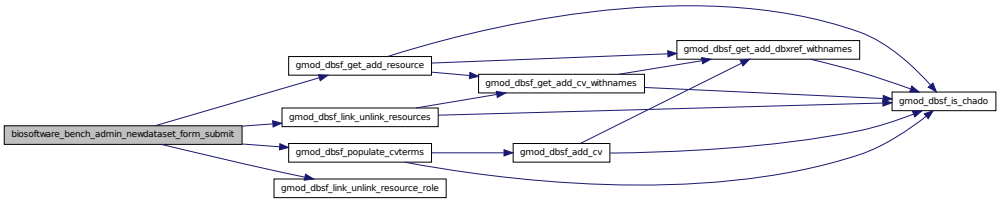
$form hook_form data

$form_state hook_form data

Definition at line 1104 of file biosoftware_bench_admin.inc.

References gmod_dbsf_get_add_resource(), gmod_dbsf_link_unlink_resource_role(), gmod_dbsf_link_-unlink_resources(), and gmod_dbsf_populate_cvterms().

Here is the call graph for this function:



4.2.2.17 biosoftware_bench_admin_newdataset_form_validate ($ *form*, &$ *form_state*)

Implements hook_form_validate()

See also

biosoftware_bench_admin_newdataset_form()
biosoftware_bench_admin_newdataset_form_submit()

Parameters

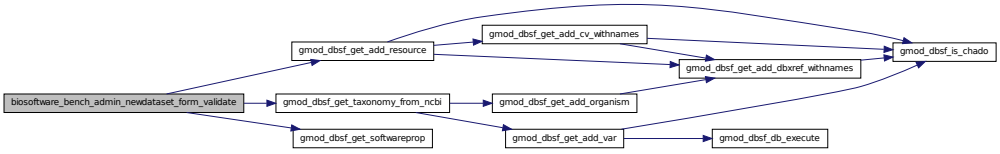
$form hook_form data

$form_state hook_form data

Definition at line 968 of file biosoftware_bench_admin.inc.

References gmod_dbsf_get_add_resource(), gmod_dbsf_get_softwareprop(), and gmod_dbsf_get_-taxonomy_from_ncbi().

Here is the call graph for this function:



4.2.2.18 biosoftware_bench_admin_page ( )

Produce HTML for the 'administrate software page'.

Menu admin/settings/bench

Definition at line 1332 of file biosoftware_bench_admin.inc.

4.2.2.19 biosoftware_bench_admin_software_page ( )

Produce HTML for the 'administrate software page'.

Menu admin/bench/software Grabs available plugins as well.

See also

biosoftware_bench_software_form()
biosoftware_bench_software_blastall_core_settings_form()

Definition at line 585 of file biosoftware_bench_admin.inc.

4.2.2.20 biosoftware_bench_software_form ($ *form_state*)

Implements of hook_form()

Used when selecting which software to make available

See also

biosoftware_bench_software_form_submit()

Parameters

$form_state hook_form data

Definition at line 19 of file biosoftware_bench_admin.inc.

4.2.2.21 biosoftware_bench_software_form_submit ($ *form*, &$ *form_state*)

Implements hook_form_submit()

See also

biosoftware_bench_software_form()

Parameters

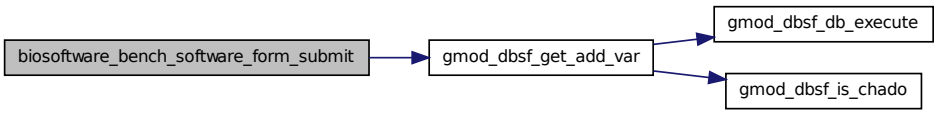
$form hook_form data

$form_state hook_form data

Definition at line 106 of file biosoftware_bench_admin.inc.

References gmod_dbsf_get_add_var().

Here is the call graph for this function:



4.2.2.22 biosoftware_bench_software_form_validate ($ *form*, &$ *form_state*)

Implements hook_validate

Definition at line 83 of file biosoftware_bench_admin.inc.

4.3 biosoftware_bench/includes/biosoftware_bench_annot8r.inc File Reference

Functions

- biosoftware_bench_annot8r_result_page ($submission_uid=NULL, $level=1)
- biosoftware_bench_annot8r_result_form ($form_state, $uid, $resultfile, $level=1, $suid=NULL)

4.3.1 Detailed Description

Universal Search Server Module plugin A Drupal module to implement annot8r usage via the Universal Search Server Developed by Alexie Papanicolaou. Licensed under GPLv3 University of Exeter. Licensed under GPLv3

See also

http://insectacentral.org/

This module requires annot8r to be properly installed annot8r: GO, EC and KEGG annotation of EST datasets by Ralf Schmid and Mark L Blaxter BMC Bioinformatics 2008, 9:180doi:10.1186/1471-2105-9-180 http://www.biomedcentral.com/1471-2105/9/180

Definition in file biosoftware_bench_annot8r.inc.

4.3.2 Function Documentation

4.3.2.1 biosoftware_bench_annot8r_result_form ($ *form_state*, $ *uid*, $ *resultfile*, $ *level* = *1*, $ *suid* = *NULL*)

Implements hook_form()

Used to produce a table of results with checkboxes which we can then select for processing (e.g. downloading). This form is themed.

See also

biosoftware_bench_theme_blast_result_form()
biosoftware_bench_blast_result_page()

Parameters

$form_state Form API variable

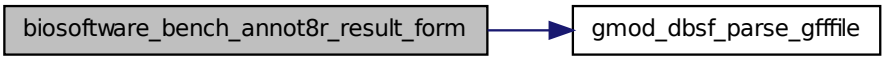
$uid Unique Identifier of algorithm's BLAST search

$blastfile Full path to BLAST results as an XML file

Definition at line 866 of file biosoftware_bench_annot8r.inc.

References gmod_dbsf_parse_gfffile().

Here is the call graph for this function:



4.3.2.2 biosoftware_bench_annot8r_result_page ($ *submission_uid* = `NULL`, $ *level* = `1`)

Present software results by providing the UID

This function must be customized

Definition at line 769 of file biosoftware_bench_annot8r.inc.

4.4 biosoftware_bench/includes/biosoftware_bench_annot8r_-install.inc File Reference

4.4.1 Detailed Description

Installs annot8r

Definition in file biosoftware_bench_annot8r_install.inc.

4.5 biosoftware_bench/includes/biosoftware_bench_blastall.inc File Reference

Functions

- biosoftware_bench_admin_blast_page ()
- biosoftware_bench_software_blastall_core_settings_form ($form_state)

- biosoftware_bench_software_blastall_core_settings_form_validate ($form, &$form_state)
- biosoftware_bench_software_blastall_core_settings_form_submit ($form, &$form_state)
- biosoftware_bench_check_blast ($software= 'blastall')
- biosoftware_bench_blast_page ($switch= 'nophylo')
- biosoftware_bench_blast_form ($form_state, $switch= 'nophylo')
- biosoftware_bench_blast_form_validate ($form, &$form_state)
- biosoftware_bench_blast_form_submit ($form, &$form_state)
- biosoftware_bench_blastall_software_pars ($data, $algorithm)
- biosoftware_bench_blastall_batch_finished ($success, $results, $operations)
- biosoftware_bench_blast_result_xml ($outfile=NULL)
- biosoftware_bench_blast_result_page ($submission_uid=NULL, $level=1)
- biosoftware_bench_blast_result_form ($form_state, $uid, $resultfile, $level=1, $suid=NULL)

4.5.1 Detailed Description

BLAST include file

Definition in file biosoftware_bench_blastall.inc.

4.5.2 Function Documentation

4.5.2.1 biosoftware_bench_admin_blast_page ( )

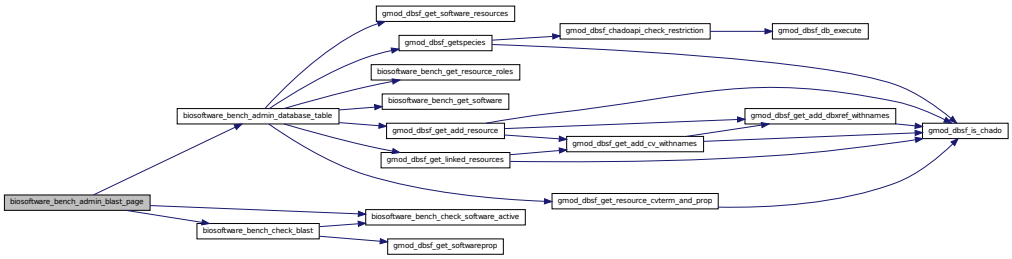
Create HTML for the administration BLAST page

Menu as admin/bench/blastall

Definition at line 43 of file biosoftware_bench_blastall.inc.

References biosoftware_bench_admin_database_table(), biosoftware_bench_check_blast(), and biosoftware_bench_check_software_active().

Here is the call graph for this function:



4.5.2.2 biosoftware_bench_blast_form ($ *form_state*, $ *switch* = `'nophylo'`)

Implements hook_form()

See also

biosoftware_bench_blast_form_validate()
biosoftware_bench_blast_form_submit()

Parameters

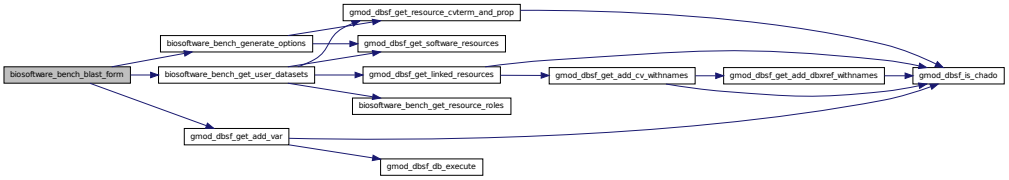
$form_state hook_form data

$sample_data Boolean, if TRUE then fill form with sample data

Definition at line 383 of file biosoftware_bench_blastall.inc.

References biosoftware_bench_generate_options(), biosoftware_bench_get_user_datasets(), and gmod_dbsf_get_add_var().

Here is the call graph for this function:



4.5.2.3 biosoftware_bench_blast_form_submit ($ *form*, &$ *form_state*)

Implements hook_form_submit()

See also

biosoftware_bench_blast_form()
biosoftware_bench_blast_form_validate()

Parameters

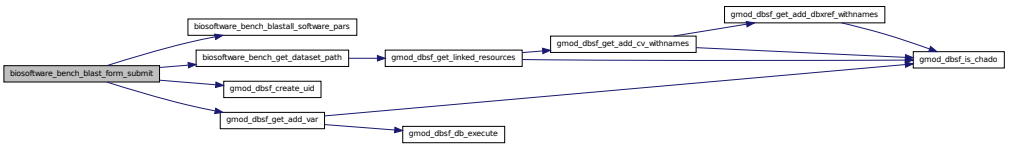
$form hook_form data

$form_state hook_form data

Definition at line 819 of file biosoftware_bench_blastall.inc.

References biosoftware_bench_blastall_software_pars(), biosoftware_bench_get_dataset_path(), gmod_dbsf_create_uid(), and gmod_dbsf_get_add_var().

Here is the call graph for this function:



4.5.2.4 biosoftware_bench_blast_form_validate ($ *form*, &$ *form_state*)

Implements hook_form_validate()

See also

biosoftware_bench_blast_form()
biosoftware_bench_blast_form_submit()

Parameters

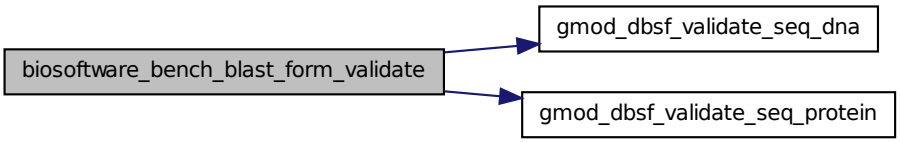
$form hook_form data

$form_state hook_form data

Definition at line 730 of file biosoftware_bench_blastall.inc.

References gmod_dbsf_validate_seq_dna(), and gmod_dbsf_validate_seq_protein().

Here is the call graph for this function:



4.5.2.5 biosoftware_bench_blast_page ($ *switch* = *'nophylo'*)

Creates HTML for the BLAST page

Menu as bench/blastall

Parameters

$sample_data If true then the form will be prefilled with sample data

Returns

HTML of BLAST page

Definition at line 317 of file biosoftware_bench_blastall.inc.

References biosoftware_bench_check_blast().

Here is the call graph for this function:

4.5.2.6 biosoftware_bench_blast_result_form ($ *form_state*, $ *uid*, $ *resultfile*, $ *level* = *1*, $ *suid* = *NULL*)

Implements hook_form()

Used to produce a table of results with checkboxes which we can then select for processing (e.g. downloading). This form is themed.

See also

biosoftware_bench_software_result_form()
biosoftware_bench_blast_result_page()

Parameters

$form_state Form API variable

$uid Unique Identifier of algorithm's BLAST search

$resultfile Full path to BLAST results as an XML file

Definition at line 1341 of file biosoftware_bench_blastall.inc.

References biosoftware_bench_blast_result_xml().

Here is the call graph for this function:

4.5.2.7 biosoftware_bench_blast_result_page ($ *submission_uid* = *NULL*, $ *level* = *1*)

Produces HTML results for a BLAST

See also

biosoftware_bench_blast_result_form()

Parameters

$submission_uid The UID relating to the submission. This is not the same as the individual BLAST algorithm UID as users can perform multiple algorithm searches from one form

Returns

HTML of results, include a table and graph of hits.

Definition at line 1239 of file biosoftware_bench_blastall.inc.

4.5.2.8 biosoftware_bench_blast_result_xml ($ *outfile* = *NULL*)

Parses a BLAST XML file.

Parameters

$resultfile Full path to BLAST XML file

Returns

An associative array of the parsed XML, suitable for downstream processing

Definition at line 1106 of file biosoftware_bench_blastall.inc.

Referenced by biosoftware_bench_blast_result_form().

Here is the caller graph for this function:

4.5.2.9 biosoftware_bench_blastall_batch_finished ($ *success*, $ *results*, $ *operations*)

Implements hook_batch_finish

Handles the final operations of the BATCH API

See also

http://api.drupal.org/api/group/batch

Parameters

$success See Drupal's BATCH API

$results See Drupal's BATCH API

$operations See Drupal's BATCH API

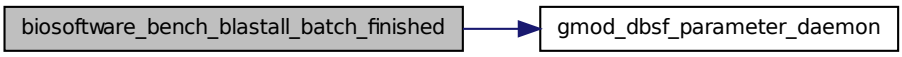
Returns

FALSE on failure

Definition at line 1041 of file biosoftware_bench_blastall.inc.

References gmod_dbsf_parameter_daemon().

Here is the call graph for this function:



4.5.2.10 biosoftware_bench_blastall_software_pars ($ *data*, $ *algorithm*)

Prepares the BLAST software cmdline parameters

They will then be return to a file for parsing by the daemon

See also

gmod_dbsf_parameter_daemon Use this as a template for plugins

Parameters

$data Associative array with BLAST option key/values for parsing into a parameter string

$algorithm The BLAST algorithm used TODO: Integrate it into $data

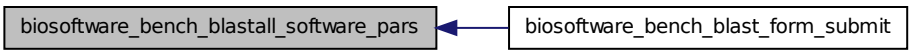
Returns

A string with all the parameters, suitable to be used with cmdline interface. FALSE on failure.

Definition at line 969 of file biosoftware_bench_blastall.inc.

Referenced by biosoftware_bench_blast_form_submit().

Here is the caller graph for this function:



4.5.2.11 biosoftware_bench_check_blast ($ *software* = `'blastall'`)

Checks if BLAST is setup correctly

Use this function as a template for plugins.

Parameters

$software The name of software to check

Returns

TRUE if software is correctly setup. Otherwise it return a string depending what is wrong:

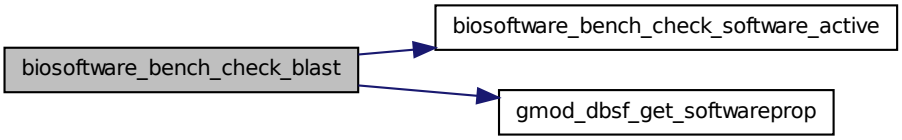
- variables: One of the variables such as execuutable path
- datasets: Not enough datasets have been linked to the software
- active: It has not been activated in the main settings page

Definition at line 275 of file biosoftware_bench_blastall.inc.

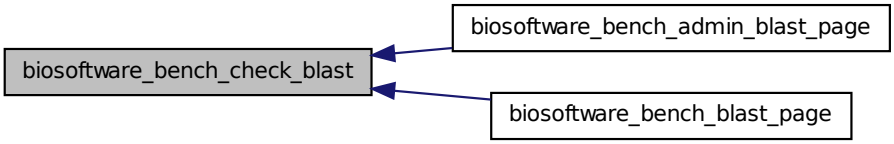
References biosoftware_bench_check_software_active(), and gmod_dbsf_get_softwareprop().

Referenced by biosoftware_bench_admin_blast_page(), and biosoftware_bench_blast_page().

Here is the call graph for this function:



Here is the caller graph for this function:



4.5.2.12 biosoftware_bench_software_blastall_core_settings_form ($ *form_state*)

Implements hook_form()

See also

biosoftware_bench_software_blastall_core_settings_form_validate()
biosoftware_bench_software_blastall_core_settings_form_submit()

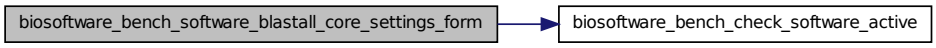
Parameters

$form_state hook_form data

Definition at line 93 of file biosoftware_bench_blastall.inc.

References biosoftware_bench_check_software_active().

Here is the call graph for this function:



4.5.2.13 biosoftware_bench_software_blastall_core_settings_form_submit ($ *form*, &$ *form_state*)

Implements hook_form_submit()

See also

biosoftware_bench_software_blastall_core_settings_form_validate()
biosoftware_bench_software_blastall_core_settings_form()

Parameters

$form hook_form data
$form_state hook_form data

Definition at line 221 of file biosoftware_bench_blastall.inc.

4.5.2.14 biosoftware_bench_software_blastall_core_settings_form_validate ($ *form*, &$ *form_state*)

Implements hook_form_validate()

See also

biosoftware_bench_software_blastall_core_settings_form()
biosoftware_bench_software_blastall_core_settings_form_submit()

Parameters

$form hook_form data
$form_state hook_form data

Definition at line 160 of file biosoftware_bench_blastall.inc.

4.6 biosoftware_bench/includes/biosoftware_bench_blastall_-install.inc File Reference

Functions

- biosoftware_bench_add_software_blastall ()

4.6.1 Detailed Description

Installs BLASTALL

Definition in file biosoftware_bench_blastall_install.inc.

4.6.2 Function Documentation

4.6.2.1 biosoftware_bench_add_software_blastall ( )

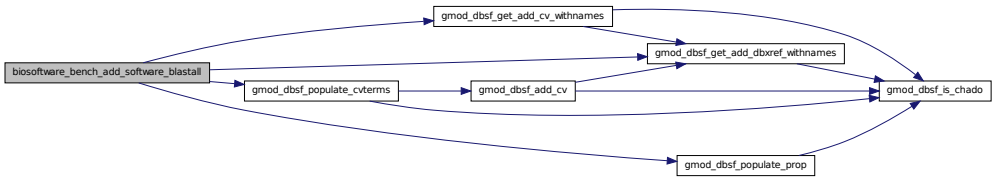
Helper function to add BLAST software

Use it as a template for adding plugins

Definition at line 15 of file biosoftware_bench_blastall_install.inc.

References gmod_dbsf_get_add_cv_withnames(), gmod_dbsf_get_add_dbxref_withnames(), gmod_dbsf_populate_cvterms(), and gmod_dbsf_populate_prop().

Here is the call graph for this function:



4.7 biosoftware_bench/includes/biosoftware_bench_get_seq.inc File Reference

Functions

- biosoftware_bench_get_sequence ($uid=NULL, $database=NULL)

4.7.1 Detailed Description

Fetch sequences from various programs using a indexed database

Definition in file biosoftware_bench_get_seq.inc.

4.7.2 Function Documentation

4.7.2.1 biosoftware_bench_get_sequence ($ *uid* = ***NULL***, $ *database* = ***NULL***)

Retrieve the sequence from a formatdb-ed dataset

Used when retrieving hits of BLAST reports

Parameters

$uid the UID of the BLAST report, used to grab the database

$database Explicitly set the database to get the sequence from. It can be a string or a list array.

Returns

HTML text of sequences in FASTA format plus a link to download a text file

Definition at line 23 of file biosoftware_bench_get_seq.inc.

4.8 biosoftware_bench/includes/biosoftware_bench_iprscan.inc File Reference

Functions

- biosoftware_bench_iprscan_result_page ($submission_uid=NULL, $level=1)
- biosoftware_bench_iprscan_result_form ($form_state, $uid, $resultfile, $level=1, $suid=NULL)

4.8.1 Detailed Description

Universal Search Server Module plugin A Drupal module to implement iprscan (InterProScan) usage via the Universal Search Server Developed by Alexie Papanicolaou. Licensed under GPLv3 University of Exeter. Licensed under GPLv3

See also

http://insectacentral.org/

This module was built using iprscan V 4.5

by Zdobnov E.M. and Apweiler R. "InterProScan - an integration platform for the signature-recognition methods in InterPro." Bioinformatics, 2001, 17(9): 847-8.

[1] The InterPro Consortium (∗R.Apweiler, T.K.Attwood, A.Bairoch, A.Bateman, E.Birney, M.Biswas, P.Bucher, L.Cerutti, F.Corpet, M.D.R.Croning, R.Durbin, L.Falquet, W.Fleischmann, J.Gouzy, H.Hermjakob, N.Hulo, I.Jonassen, D.Kahn, A.Kanapin, Y.Karavidopoulou, R.Lopez, B.Marx, N.J.Mulder, T.M.Oinn, M.Pagni, F.Servant, C.J.A.Sigrist, E.M.Zdobnov). "The InterPro database, an integrated documentation resource for protein families, domains and functional sites." Nucleic Acids Research, 2001, 29(1): 37-40.

Definition in file biosoftware_bench_iprscan.inc.

4.8.2 Function Documentation

4.8.2.1 biosoftware_bench_iprscan_result_form ($ *form_state*, $ *uid*, $ *resultfile*, $ *level* = *1*, $ *suid* = *NULL*)

Implements hook_form()

Used to produce a table of results with checkboxes which we can then select for processing (e.g. downloading). This form is themed.

See also

biosoftware_bench_theme_blast_result_form()
biosoftware_bench_blast_result_page()

Parameters

$form_state Form API variable

$uid Unique Identifier of algorithm's BLAST search

$blastfile Full path to BLAST results as an XML file

Definition at line 680 of file biosoftware_bench_iprscan.inc.

References gmod_dbsf_parse_gfffile().

Here is the call graph for this function:

4.8.2.2 biosoftware_bench_iprscan_result_page ($ *submission_uid* = *NULL*, $ *level* = *1*)

Present software results by providing the UID

This function must be customized

Definition at line 539 of file biosoftware_bench_iprscan.inc.

4.9 biosoftware_bench/includes/biosoftware_bench_iprscan_-install.inc File Reference

4.9.1 Detailed Description

Installs InterProScan

Definition in file biosoftware_bench_iprscan_install.inc.

4.10 biosoftware_bench/includes/biosoftware_bench_ssaha2.inc File Reference

Functions

- biosoftware_bench_check_ssaha2 ($software)
- biosoftware_bench_ssaha2_form_submit ($form, &$form_state)

- biosoftware_bench_ssaha2_parse_result ($outfile)
- biosoftware_bench_ssaha2_result_form ($form_state, $uid, $outfile, $level=1, $suid=NULL)

4.10.1 Detailed Description

Please use this file as a template to make new modules You will need to search for lines which have PLUGIN_EDIT_HERE and follow the instructions you will also need to rename the functions. I suggest you pick a name for your software (e.g. iprscan) and search and replace ssaha2 with e.g. iprscan. then continue editing.

Universal Search Server Module plugin A Drupal module to implement SSAHA2 usage via the Universal Search Server

A SSAHA dataset must have the following to be allowed 1) The actual raw fasta file (eg dmel_genome_-5.16) 2) formatted with index_fasta.pl (in scripts; a BioPerl script) e.g. index_fasta.pl -d dmel_genome_-5.16 3) hash table build with the ssaha2Build -rtype abi as -save dmel_genome_5.16_sanger 4) hash table build with the ssaha2Build -rtype 454 as -save dmel_genome_5.16_454 5) hash table build with the ssaha2Build -rtype solexa as -save dmel_genome_5.16_solexa 6) ALL the ∗.head files produced by ssaha2Build MUST be compressed; use gzip -1 as it is fast. so that for a dataset 'dmel' we have the files

- dmel, dmel.index
- dmel_sanger.base,dmel_sanger.body,dmel_sanger.head.gz,dmel_sanger.name,dmel_sanger.size
- dmel_454.base,dmel_454.body,dmel_454.head.gz,dmel_454.name,dmel_454.size,
- dmel_solexa.basedmel_solexa.body,dmel_solexa.head.gz,dmel_solexa.name,dmel_solexa.size Symbolic links are also allowed but must be set in your Apache configuration file as allowed ("follow symlinks" etc) NB The run-user of biosoftware_bench_daemon.pl must have permission to write in the directory where the .head.gz file resides

Drupal module developed by Alexie Papanicolaou. University of Exeter

See also

http://insectacentral.org/

This module was built using SSAHA2 v2.4.1

SSAHA2 is a package combining SSAHA with cross_match developed by Phil Green at the University of Washington. Reference: Ning Z, Cox AJ, Mullikin JC. SSAHA: a fast search method for large DNA-databases. Genome Res. 2001 Oct;11(10):1725-9.

Definition in file biosoftware_bench_ssaha2.inc.

4.10.2 Function Documentation

4.10.2.1 biosoftware_bench_check_ssaha2 ($ *software*)

Check if the ssaha2 software is setup correctly

Parameters

$software software name

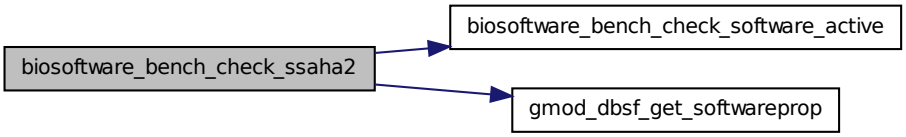
Returns

boolean TRUE if everything is ok, a string signifying what is wrong otherwise

Definition at line 254 of file biosoftware_bench_ssaha2.inc.

References biosoftware_bench_check_software_active(), and gmod_dbsf_get_softwareprop().

Here is the call graph for this function:



4.10.2.2 biosoftware_bench_ssaha2_form_submit ($ *form*, &$ *form_state*)

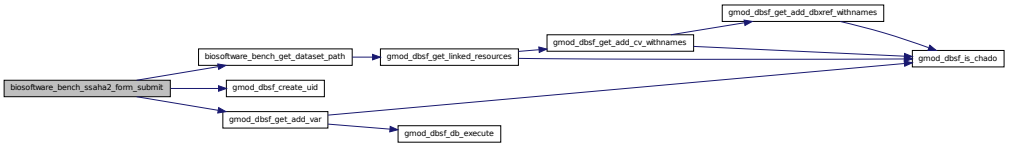
Submit the search form

This form does all the work, including the batch processing

Definition at line 550 of file biosoftware_bench_ssaha2.inc.

References biosoftware_bench_get_dataset_path(), gmod_dbsf_create_uid(), and gmod_dbsf_get_add_-var().

Here is the call graph for this function:



4.10.2.3 biosoftware_bench_ssaha2_parse_result ($ *outfile*)

Parse a ssaha result of a software run

Parameters

$file full path to file

Returns

array with data

Definition at line 848 of file biosoftware_bench_ssaha2.inc.

Referenced by biosoftware_bench_ssaha2_result_form().

Here is the caller graph for this function:

4.10.2.4 biosoftware_bench_ssaha2_result_form ($ *form_state*, $ *uid*, $ *outfile*, $ *level* = *1*, $ *suid* = *NULL*)

Implements hook_form()

Used to produce a table of results with checkboxes which we can then select for processing (e.g. downloading). This form is themed.

See also

biosoftware_bench_software_result_form()
biosoftware_bench_blast_result_page()

Parameters

$form_state Form API variable
$uid Unique Identifier of algorithm's BLAST search
$blastfile Full path to BLAST results as an XML file

Definition at line 1042 of file biosoftware_bench_ssaha2.inc.

References biosoftware_bench_ssaha2_parse_result().

Here is the call graph for this function:

4.11 biosoftware_bench/includes/biosoftware_bench_ssaha2_-install.inc File Reference

4.11.1 Detailed Description

Installs SSAHA2

Definition in file biosoftware_bench_ssaha2_install.inc.

4.12 genes4all/genes4all.module File Reference

Functions

- genes4all_get_lib_info ($lib_data)

4.12.1 Detailed Description

The genes4all module contains functions shared between genes4all sub_modules

Developed by Alexie Papanicolaou

See also

http://insectacentral.org

Definition in file genes4all.module.

4.12.2 Function Documentation

4.12.2.1 genes4all_get_lib_info ($ *lib_data*)

Get data on a stored library and return it as a themed table

Originally developed for the dbEST database of NCBI. We are performing some cleanup so that the data makes sense to humans.

Parameters

$lib_data Either the data to present (in an associative array with the 'id', 'name', 'type', 'organism' and 'accession' variables or the library identifier (or uniquename) given as a string

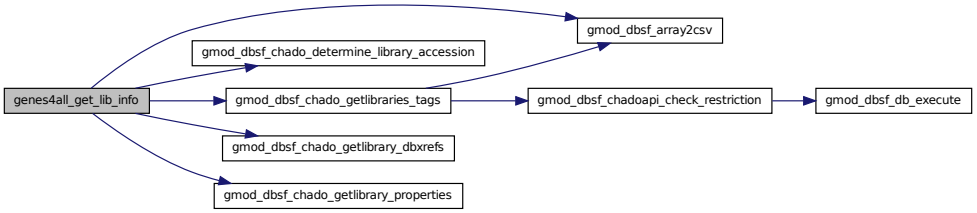
Returns

HTML of a table with the stored information

Definition at line 40 of file genes4all.module.

References gmod_dbsf_array2csv(), gmod_dbsf_chado_determine_library_accession(), gmod_dbsf_chado_getlibraries_tags(), gmod_dbsf_chado_getlibrary_dbxrefs(), and gmod_dbsf_chado_getlibrary_properties().

Here is the call graph for this function:



4.13 genes4all/includes/genes4all_autocomplete.inc File Reference

Functions

- genes4all_feature_autocomplete ($string= ”)
- genes4all_curate_autocomplete_custom_term ($string=NULL)
- genes4all_curate_autocomplete_library_cvterm ($string=NULL)
- genes4all_curate_autocomplete_library_dbname ($string=NULL)
- genes4all_curate_autocomplete_genus ($string=NULL)
- genes4all_curate_autocomplete_species ($string=NULL)
- genes4all_experiment_publication_autocomplete ($string= ”)
- genes4all_experiment_dbname_autocomplete ($string=NULL)
- genes4all_experiment_targetdb_autocomplete ($string= ”)
- genes4all_experiment_constructdb_autocomplete ($string= ”)
- genes4all_experiment_resourcedb_autocomplete ($string= ”)
- genes4all_experiment_studydb_autocomplete ($string= ”)

4.13.1 Detailed Description

Autocomplete functions use in genes4all and submodules

Definition in file genes4all_autocomplete.inc.

4.13.2 Function Documentation

4.13.2.1 genes4all_curate_autocomplete_custom_term ($ *string* = `NULL`)

Autocomplete curation terms

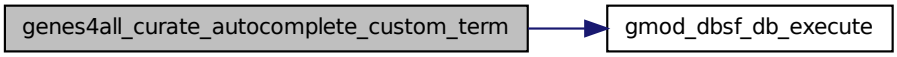
See also

user_autocomplete

Definition at line 44 of file genes4all_autocomplete.inc.

References gmod_dbsf_db_execute().

Here is the call graph for this function:



4.13.2.2 genes4all_curate_autocomplete_genus ($ *string* = ***NULL***)

Autocomplete genus of organism

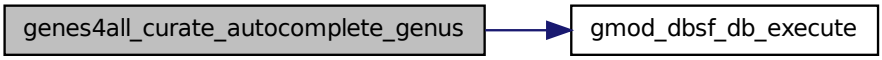
See also

user_autocomplete

Definition at line 143 of file genes4all_autocomplete.inc.

References gmod_dbsf_db_execute().

Here is the call graph for this function:



4.13.2.3 genes4all_curate_autocomplete_library_cvterm ($ *string* = ***NULL***)

Autocomplete library

See also

user_autocomplete

Definition at line 77 of file genes4all_autocomplete.inc.

References gmod_dbsf_db_execute().

Here is the call graph for this function:

4.13.2.4 genes4all_curate_autocomplete_library_dbname ($ *string* = ***NULL***)

Autocomplete library dbname

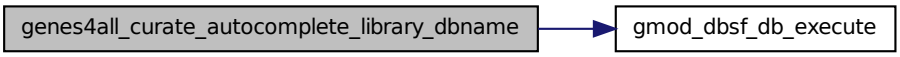
See also

user_autocomplete

Definition at line 110 of file genes4all_autocomplete.inc.

References gmod_dbsf_db_execute().

Here is the call graph for this function:



4.13.2.5 genes4all_curate_autocomplete_species ($ *string* = ***NULL***)

Autocomplete species of organism

See also

user_autocomplete

Definition at line 176 of file genes4all_autocomplete.inc.

References gmod_dbsf_db_execute().

Here is the call graph for this function:

4.13.2.6 genes4all_experiment_constructdb_autocomplete ($ *string* = '')

Autocomplete construct database

See also

user_autocomplete

Definition at line 284 of file genes4all_autocomplete.inc.

4.13.2.7 genes4all_experiment_dbname_autocomplete ($ *string* = `NULL`)

Autocomplete dbname of experiment

See also

user_autocomplete

Definition at line 233 of file genes4all_autocomplete.inc.

4.13.2.8 genes4all_experiment_publication_autocomplete ($ *string* = '')

Autocomplete publication of experiment

See also

user_autocomplete

Definition at line 209 of file genes4all_autocomplete.inc.

4.13.2.9 genes4all_experiment_resourcedb_autocomplete ($ *string* = '')

Autocomplete resource database

See also

user_autocomplete

Definition at line 312 of file genes4all_autocomplete.inc.

4.13.2.10 genes4all_experiment_studydb_autocomplete ($ *string* = '')

Autocomplete study database

See also

user_autocomplete

Definition at line 340 of file genes4all_autocomplete.inc.

4.13.2.11 genes4all_experiment_targetdb_autocomplete ($ *string* = '')

Autocomplete target database

See also

user_autocomplete

Definition at line 256 of file genes4all_autocomplete.inc.

4.13.2.12 genes4all_feature_autocomplete ($ *string* = '')

Autocomplete features

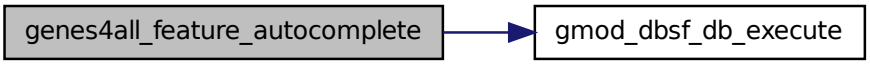
See also

user_autocomplete

Definition at line 15 of file genes4all_autocomplete.inc.

References gmod_dbsf_db_execute().

Here is the call graph for this function:



4.14 genes4all/modules/genes4all_download/genes4all_-download.module File Reference

Functions

- genes4all_download_menu ()
- genes4all_download_perm ()

- genes4all_download_download_page ()
- genes4all_download_download_form ($form_state)
- genes4all_download_download_form_validate ($form, &$form_state)
- genes4all_download_download_form_submit ($form, &$form_state)
- genes4all_download_bulk_get ($variables)
- genes4all_download_cron ()

4.14.1 Detailed Description

The genes4all_download module provides an interface for downloading sequences from the Chado database Developed by Alexie Papanicolaou

See also

http://insectacentral.org

Definition in file genes4all_download.module.

4.14.2 Function Documentation

4.14.2.1 genes4all_download_bulk_get ($ *variables*)

Get data from Chado as GFF or FASTA

Parameters

$variables associative array with data which includes 'organism', 'type','format' and 'outfile'. Also 'no_constituents'

Returns

unknown_type

Definition at line 244 of file genes4all_download.module.

4.14.2.2 genes4all_download_cron ( )

Implement hook_cron()

Finds temporary files

Definition at line 503 of file genes4all_download.module.

4.14.2.3 genes4all_download_download_form ($ *form_state*)

Implements hook_form()

Form for downloading data from database

See also

genes4all_download_download_form_validate()
genes4all_download_download_form_submit()

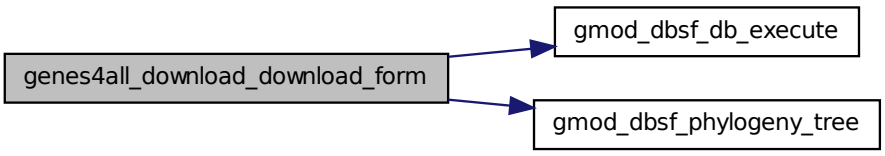
Parameters

$form_state hook_form data

Definition at line 104 of file genes4all_download.module.

References gmod_dbsf_db_execute(), and gmod_dbsf_phylogeny_tree().

Here is the call graph for this function:



4.14.2.4 genes4all_download_download_form_submit ($ *form*, &$ *form_state*)

Implements hook_form_submit()

Form for downloading data from database

See also

genes4all_download_download_form_validate()
genes4all_download_download_form()

Parameters

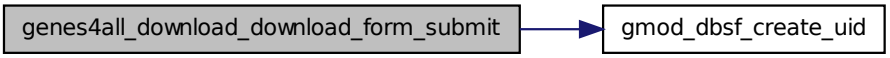
$form hook_form data

$form_state hook_form data

Definition at line 208 of file genes4all_download.module.

References gmod_dbsf_create_uid().

Here is the call graph for this function:



4.14.2.5 genes4all_download_download_form_validate ($ *form*, &$ *form_state*)

Implements hook_form_validate()

Form for downloading data from database

See also

genes4all_download_download_form()
genes4all_download_download_form_submit()

Parameters

$form hook_form data

$form_state hook_form data

Definition at line 164 of file genes4all_download.module.

References gmod_dbsf_db_execute().

Here is the call graph for this function:

4.14.2.6 genes4all_download_download_page ( )

Produce HTML for the 'download page'.

Menu genes4all/download

Definition at line 69 of file genes4all_download.module.

4.14.2.7 genes4all_download_menu ( )

Implementation of hook_menu

Definition at line 37 of file genes4all_download.module.

4.14.2.8 genes4all_download_perm ( )

Implementation of hook_perm().

Definition at line 60 of file genes4all_download.module.

4.15 genes4all/modules/genes4all_experiment/genes4all_-experiment.module File Reference

Functions

- genes4all_experiment_menu ()
- genes4all_experiment_init ()
- genes4all_experiment_perm ()
- genes4all_experiment_forms ($form_id, $args=NULL)
- genes4all_experiment_reset_session_form ($form_state, &$todestroy=NULL)
- genes4all_experiment_get_authorships ($pub_id)

4.15.1 Detailed Description

TODO: consider creating arrays for form building (e.g. $purification_method_array) via the database. Module for adding experiments into InsectaCentral Developed by Alexie Papanicolaou

See also

http://insectacentral.org

All SQLs here are aimed for Drupal, not Chado

Definition in file genes4all_experiment.module.

4.15.2 Function Documentation

4.15.2.1 genes4all_experiment_forms ($ *form_id*, $ *args* = `NULL`)

Allow for rewriting form names so that multiple forms can be generated in one page from same function

Parameters

$form_id

$args

Returns

unknown_type

Definition at line 469 of file genes4all_experiment.module.

4.15.2.2 genes4all_experiment_get_authorships ($ *pub_id*)

Unused function genes4all_experiment_publication_verify($uname) { $passkey = check_plain($_-SESSION['passkey']); $uname = check_plain(trim($uname)); $check_pass = "SELECT passkey from {gmod_dbsf_pub} WHERE uniquename='$uname'"; $res_pass = db_fetch_array(db_query($check_-pass)); if (!empty($res_pass['passkey']) && $res_pass['passkey'] !== $passkey) { return FALSE; } else { return TRUE; } }

Definition at line 595 of file genes4all_experiment.module.

4.15.2.3 genes4all_experiment_init ( )

Implementation of hook_init()

Definition at line 115 of file genes4all_experiment.module.

4.15.2.4 genes4all_experiment_menu ( )

Implementation of hook_menu

Definition at line 17 of file genes4all_experiment.module.

4.15.2.5 genes4all_experiment_perm ( )

Implementation of hook_perm().

Definition at line 125 of file genes4all_experiment.module.

4.15.2.6 genes4all_experiment_reset_session_form ($ *form_state*, &$ *todestroy* = `NULL`)

Used to unset a session variable and hence reset a specific form

Definition at line 485 of file genes4all_experiment.module.

4.16 genes4all/modules/genes4all_experiment/includes/genes4all_experiment_add.inc File Reference

Functions

- genes4all_experiment_page_add ()
- genes4all_experiment_publication_add ($data=NULL)
- genes4all_experiment_feature_add_gene ($feature_id, $data, $cvterms=NULL)
- genes4all_experiment_feature_add_construct ($feature_id, $data, $cvterms=NULL)

4.16.1 Detailed Description

include file for adding new experiments

Definition in file genes4all_experiment_add.inc.

4.16.2 Function Documentation

4.16.2.1 genes4all_experiment_feature_add_construct ($ *feature_id*, $ *data*, $ *cvterms* = `NULL`)

Parameters

$feature_id feature_id

$data data from user

$cvterms data from database (if any)

Definition at line 2176 of file genes4all_experiment_add.inc.

4.16.2.2 genes4all_experiment_feature_add_gene ($ *feature_id*, $ *data*, $ *cvterms* = ***NULL***)

Parameters

$feature_id feature_id

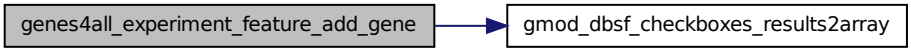
$data data from user

$cvterms data from database

Definition at line 2108 of file genes4all_experiment_add.inc.

References gmod_dbsf_checkboxes_results2array().

Here is the call graph for this function:



4.16.2.3 genes4all_experiment_page_add ( )

Add new experiments

Parameters

$lib_id

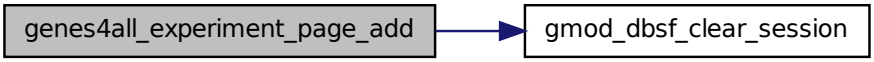
Returns

unknown_type

Definition at line 25 of file genes4all_experiment_add.inc.

References gmod_dbsf_clear_session().

Here is the call graph for this function:



4.16.2.4 genes4all_experiment_publication_add ($ *data* = ***NULL***)

Add data to pub table(s) if one does not exist already.

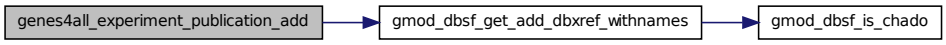
Returns

$pub_id string integer

Definition at line 1783 of file genes4all_experiment_add.inc.

References gmod_dbsf_get_add_dbxref_withnames().

Here is the call graph for this function:



4.17 genes4all/modules/genes4all_experiment/includes/genes4all_-experiment_search.inc File Reference

4.17.1 Detailed Description

include file for searching for particular experiments

Definition in file genes4all_experiment_search.inc.

4.18 genes4all/modules/genes4all_experiment/includes/genes4all_-experiment_view.inc File Reference

Functions

- genes4all_experiment_page_view_experiment_all ($round=0)
- _genes4all_experiment_experiment_details ($experiment_id)
- genes4all_experiment_page_view_experiment ($experiment_id=0)

4.18.1 Detailed Description

include file for viewing experiments

Definition in file genes4all_experiment_view.inc.

4.18.2 Function Documentation

4.18.2.1 _genes4all_experiment_experiment_details ($ *experiment_id*)

Helper function to get experiment details

Parameters

$experiment_id Can be a numerical identifier or uniquename

Returns

Tabulated HTML

Definition at line 91 of file genes4all_experiment_view.inc.

Referenced by genes4all_experiment_page_view_experiment().

Here is the caller graph for this function:

4.18.2.2 genes4all_experiment_page_view_experiment ($ *experiment_id = 0*)

View experiments

Parameters

$experiment_id Can be an array or string. Can be a numerical identifier or uniquename

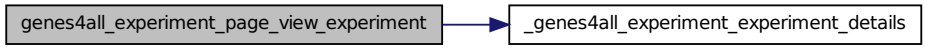
Returns

Tabulated HTML

Definition at line 156 of file genes4all_experiment_view.inc.

References _genes4all_experiment_experiment_details().

Here is the call graph for this function:



4.18.2.3 genes4all_experiment_page_view_experiment_all ($ *round = 0*)

View all experiments

Parameters

$round Integer for page to view. Each page has $how_many experiments

Returns

unknown_type

Definition at line 17 of file genes4all_experiment_view.inc.

4.19 genes4all/modules/genes4all_nextgen/genes4all_-nextgen.module File Reference

Functions

- genes4all_nextgen_menu ()
- genes4all_nextgen_perm ()
- genes4all_nextgen_theme ()
- genes4all_nextgen_theme_result_form ($form)

4.19.1 Detailed Description

Supports Illumina, SAM/BAM for JBrowse and more Developed by Alexie Papanicolaou

See also

http://insectacentral.org

Definition in file genes4all_nextgen.module.

4.19.2 Function Documentation

4.19.2.1 genes4all_nextgen_menu ( )

Implementation of hook_menu

Definition at line 14 of file genes4all_nextgen.module.

4.19.2.2 genes4all_nextgen_perm ( )

Implementation of hook_perm

Definition at line 33 of file genes4all_nextgen.module.

4.19.2.3 genes4all_nextgen_theme ( )

Implementation of hook_theme

Returns

unknown_type

Definition at line 41 of file genes4all_nextgen.module.

4.19.2.4 genes4all_nextgen_theme_result_form ($ *form*)

Implementation of hook_form

Definition at line 54 of file genes4all_nextgen.module.

4.20 genes4all/modules/genes4all_nextgen/includes/genes4all_-nextgen_admin.inc File Reference

4.20.1 Detailed Description

Admin functions for genes4all_nextgen Developed by Alexie Papanicolaou

See also

http://insectacentral.org

TODO Add new SAM or BAM data; allow gzip or bz2 Allow upload or server link if SAM, format as BAM, sort & index

Actions update chado library and genes4all_nextgen validate and toggle verified flag

other: link to add new library

Definition in file genes4all_nextgen_admin.inc.

4.21 gmod_dbsf/gmod_dbsf.module File Reference

Functions

- gmod_dbsf_menu ()
- gmod_dbsf_is_chado ()
- gmod_dbsf_init ()
- gmod_dbsf_encode ($variable)
- gmod_dbsf_decode ($encoded, $check=NULL)
- gmod_dbsf_array2csv ($array=NULL, $quote=NULL, $separator= ',', $key=FALSE)
- gmod_dbsf_db_execute ($db=NULL, $function=NULL, $variables=NULL)
- gmod_dbsf_validate_ic_id ($accession=NULL)
- gmod_dbsf_validate_seq_dna ($seq=NULL, $strip=FALSE)
- gmod_dbsf_validate_seq_protein ($seq=NULL, $strip=FALSE)
- gmod_dbsf_checkboxes_results2array ($results)
- gmod_dbsf_add_cv ($cv, $cvterm_array)
- gmod_dbsf_delete_cv ($cv, $cvterm_array=NULL)
- gmod_dbsf_populate_prop ($table_type, $object_name, $cvterm_id, $property_array)
- gmod_dbsf_populate_cvterms ($table_type, $object_name, $cvname, $cvterm_array=NULL, $pub_id=NULL)
- gmod_dbsf_get_add_cv_withnames ($cv_name, $cvterm_name=NULL, $name_as_key=FALSE, $definition=FALSE, $force_update_def=FALSE)
- gmod_dbsf_get_add_dbxref_withnames ($dbname, $accession=NULL, $description=NULL, $name_as_key=NULL)
- gmod_dbsf_get_add_pub ($pub_type_category, $type_name, $data=NULL, $add=FALSE, $name_-as_key=FALSE)
- gmod_dbsf_clear_session ($var=NULL)
- gmod_dbsf_create_uid ($sessionid=NULL, $timestamp=NULL, $string=NULL)
- gmod_dbsf_get_resource_name_id ($resource, $name_as_key=FALSE)
- gmod_dbsf_get_add_resource ($type_name, $data=NULL, $add=FALSE, $name_as_key=FALSE)
- gmod_dbsf_get_resource_cvterm_and_prop ($resource)

- gmod_dbsf_rename_resource ($old_name, $new_name)
- gmod_dbsf_link_unlink_resources ($subject, $rel, $object=NULL, $replace=FALSE)
- gmod_dbsf_get_linked_resources ($resource, $relationship_name=NULL, $name_as_key=FALSE, $limit=NULL)
- gmod_dbsf_link_unlink_features ($data)
- gmod_dbsf_get_feature_name_id ($feature, $name_as_key=FALSE)
- gmod_dbsf_get_change_feature ($type_name=NULL, $data=NULL, $change=FALSE, $name_as_-key=FALSE)
- gmod_dbsf_get_feature_data ($feature)
- gmod_dbsf_get_feature_cvterm_and_prop ($feature)
- gmod_dbsf_rename_feature ($old_name, $new_name)
- gmod_dbsf_write_fastafile ($infile=NULL, $outfile=NULL, $delete=NULL, $definition=NULL)
- gmod_dbsf_phylogeny_tree ($phylogeny_array, $button=NULL)
- gmod_dbsf_form_clear ($form, &$form_state)
- gmod_dbsf_delete_temp ($file=NULL, $deftime=604800)
- gmod_dbsf_decypher_organism_id ($organism_id)
- gmod_dbsf_chadoapi_check_restriction ($restrict_type, $resource_type, $id, $reconnect=TRUE)
- gmod_dbsf_getspecies ($limit=NULL, $all_orgs=NULL)
- gmod_dbsf_install_pgfunction ($name, $sql)
- gmod_dbsf_install_dbviews ($variables)
- gmod_dbsf_db_key ($db_name=NULL)
- gmod_dbsf_drupal_set_message ($message, $type='status', $repeat=TRUE)
- gmod_dbsf_t ($string, $args=array(), $langcode=NULL)
- gmod_dbsf_chadoapi_add_mat_view ($data)
- gmod_dbsf_install_dbtable ($variables)
- gmod_dbsf_store_feature ($data)
- gmod_dbsf_get_add_organism ($data)
- gmod_dbsf_batch_save_data ($data=NULL, &$context)
- gmod_dbsf_batch_upload_fasta ($batch_file_data, &$context)
- gmod_dbsf_parameter_daemon ($uid, $dir, $par, $software= 'blastall', $more_data=NULL, $cmd_-vars=NULL)
- gmod_dbsf_translate_DNA_to_protein ($seq, $genetic_code)
- gmod_dbsf_get_add_library ($data=NULL)
- gmod_dbsf_decypher_library_id ($library_id, $limit=NULL, $full_access=FALSE)
- gmod_dbsf_feature2gff3 ($feature_id, $outfile)
- gmod_dbsf_count_gfffile ($infile)
- gmod_dbsf_parse_gfffile ($infile)
- gmod_dbsf_get_users_roles ($name_as_key=NULL)
- gmod_dbsf_add_cv_only ($cvname, $definition=NULL)
- gmod_dbsf_get_defined_dbs ()
- gmod_dbsf_link_unlink_resource_role ($resource, $role, $switch=FALSE)
- gmod_dbsf_link_unlink_software_resource ($software, $resource, $switch=FALSE)
- gmod_dbsf_get_softwareprop ($limit=NULL, $name_as_key=FALSE)
- gmod_dbsf_get_software_resources ($limit=NULL, $name_as_key=FALSE)
- gmod_dbsf_get_add_var ($name=NULL, $value=NULL, $db_reconnect= 'chado')
- gmod_dbsf_get_taxonomy_from_ncbi ($ncbi_taxid)

4.21.1 Detailed Description

gmod_dbsf is an API for other bioinformatic Drupal modules making use of Chado it is meant to hold all the essential functions used elsewhere.

In the settings.php this database is needed: 'chado' -> read only access 'chado_edit' -> read/write access

Developed by Alexie Papanicolaou

See also

http://insectacentral.org

Bug

The Chado database must be aliased as 'chado' in the settings.ini and the database name MUST contain chado (case insensitive) (Drupal requires us to have the module name as a prefix to all tables, but Chado has no prefix. Since Drupal has no function to give us the alias of the active database, we have to strpos the db_name

Definition in file gmod_dbsf.module.

4.21.2 Function Documentation

4.21.2.1 gmod_dbsf_add_cv ($ *cv*, $ *cvterm_array*)

Populate a CV table using a CV name and a list of CVTERMS

Can be used with a Chado or Drupal database

Parameters

$cv Name of CV

$cvterm_array A list array of cvterm names to add

Returns

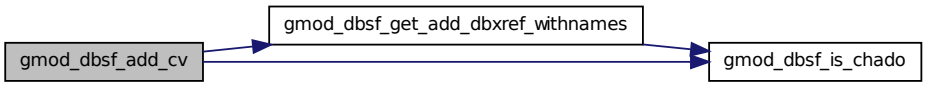
FALSE on failure, the (int) cv_id on success

Definition at line 454 of file gmod_dbsf.module.

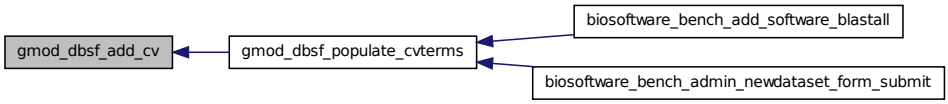
References gmod_dbsf_get_add_dbxref_withnames(), and gmod_dbsf_is_chado().

Referenced by gmod_dbsf_populate_cvterms().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.2 gmod_dbsf_add_cv_only ($ *cvname*, $ *definition* = `NULL`)

Add a new CV, if it does not exist, return ID

Works with Drupal and Chado Used for making a new CV without any associated cvterms or just getting the CV ID of an existing one

Parameters

$cvname the name to give to your CV

$definition optionally, a definition to store for the CV

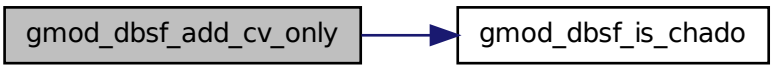
Returns

integer the internal ID of the CV or FALSE if it failed.

Definition at line 4439 of file gmod_dbsf.module.

References gmod_dbsf_is_chado().

Here is the call graph for this function:



4.21.2.3 gmod_dbsf_array2csv ($ *array* = `NULL`, $ *quote* = `NULL`, $ *separator* = `','`, $ *key* = `FALSE`)

Convert an array to a quoted string, suitable for SQL queries

Essentially implode() with bells and whistles

See also

implode()

Parameters

$array a list array of elements to ocnvert to a comma delimited string

$quote give TRUE to include quotes around element or pass any string to include left and right of element

$separator character to separate elements in list

$key Boolean, if true then return the keys of the $array.

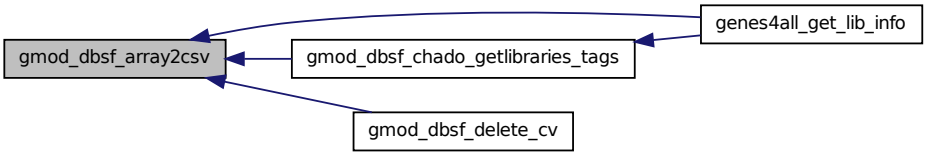
Returns

A String of comma delimited values, optionally quoted.

Definition at line 157 of file gmod_dbsf.module.

Referenced by genes4all_get_lib_info(), gmod_dbsf_chado_getlibraries_tags(), and gmod_dbsf_delete_cv().

Here is the caller graph for this function:



4.21.2.4 gmod_dbsf_batch_save_data ($ *data* = ***NULL***, &$ *context*)

Save an array to be used for the batch API. see batch_set()

Parameters

$data A variable to store to $context

$context The variable used by batch API to store data

Definition at line 3631 of file gmod_dbsf.module.

4.21.2.5 gmod_dbsf_batch_upload_fasta ($ *batch_file_data*, &$ *context*)

Upload FASTA as used in a batch operation.

Needed because we use the same create_fasta function more than once

See also

gmod_dbsf_write_fastafile()
dbsf_formatdb_fastafile()

Parameters

$batch_file_data Associative array with following keys.

- infile: all the infiles to be passed to gmod_dbsf_write_fastafile()
- outfile: likewise, all outfiles
- filetype: likewise all file types
- format: whether to run format this file via dbsf_formatdb_fastafile()

$context Array FROM batch_api

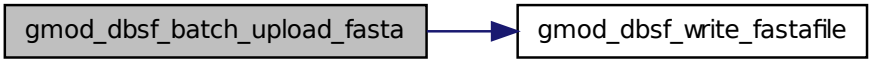
Returns

It does not return anything, it updates $context instead by altering $context['finished']

Definition at line 3655 of file gmod_dbsf.module.

References gmod_dbsf_write_fastafile().

Here is the call graph for this function:



4.21.2.6 gmod_dbsf_chadoapi_add_mat_view ($ *data*)

Create a new materialized view in chado

Uses the materialized_view table to add views. It is not part of the _chado submodule because the _chado.install uses it.

Parameters

$data An associative array with 'refresh_time','name','mv_schema','mv_table', 'indexed','query' and 'special_index' relating to the relevant Chado columns

Returns

unknown_type

Definition at line 3131 of file gmod_dbsf.module.

4.21.2.7 gmod_dbsf_chadoapi_check_restriction ($ *restrict_type*, $ *resource_type*, $ *id*, $ *reconnect* = ***TRUE***)

Check if the user has access to a Chado resource

This is a Chado specific function. It will connect to Chado internally. Like all chadoapi functions it must not be part of _chado.module as it is used in a dependency (in this case, the gmod_dbsf.module itself) implement it for Drupal as well

Parameters

$restrict_type The type of restriction sought, e.g. 'select','update','create','delete' see CV ic_data_-restrictions

$resource_type What kind of resource: library, organism or feature

$id The internal Chado id of the resource.

$reconnect If true then it will reconnect to Drupal. Otherwise stay in Chado (careful!)

Returns

TRUE on pass, FALSE otherwise

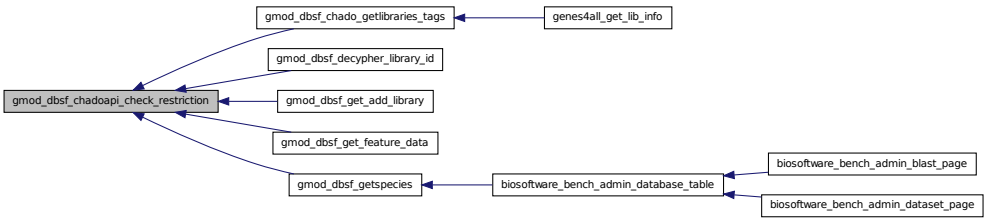
Definition at line 2687 of file gmod_dbsf.module.

References gmod_dbsf_db_execute().

Referenced by gmod_dbsf_chado_getlibraries_tags(), gmod_dbsf_decypher_library_id(), gmod_dbsf_-get_add_library(), gmod_dbsf_get_feature_data(), and gmod_dbsf_getspecies().

Here is the call graph for this function:

Here is the caller graph for this function:



4.21.2.8 gmod_dbsf_checkboxes_results2array ($ *results*)

Cleans and decomposes a checkbox FAPI result array

Parameters

$results FAPI Checkboxes result as an associative array

Returns

A list array of results

Definition at line 425 of file gmod_dbsf.module.

Referenced by genes4all_experiment_feature_add_gene().

Here is the caller graph for this function:

4.21.2.9 gmod_dbsf_clear_session ($ *var* = ***NULL***)

Clear all or part of $_SESSION

For example, this is used in the genes4all_experiment module to empty the user session variables.

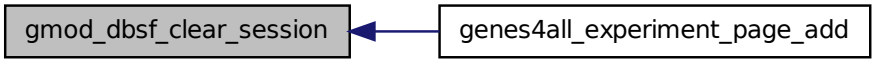
Parameters

$var A string or a list array of $_SESSION parameter names(s) to empty. If no $var is provided, then the whole of $_SESSION is emptied (use with care)

Definition at line 1232 of file gmod_dbsf.module.

Referenced by genes4all_experiment_page_add().

Here is the caller graph for this function:



4.21.2.10 gmod_dbsf_count_gfffile ($ *infile*)

Count results in a GFF file

Parameters

$infile

Returns

Definition at line 4301 of file gmod_dbsf.module.

4.21.2.11 gmod_dbsf_create_uid ($ *sessionid* = *NULL*, $ *timestamp* = *NULL*, $ *string* = *NULL*)

Create a Unique Identifier using SESSIONID, time and, optionally, a string

Heavily used by the dbsf module to create unique identifiers. It is not meant to be decoded.

Uses the md5 algorithm to generate a hexadecimal unique identifier.

See also

session_id()
time()
md5()

Parameters

$sessionid the session id to include in the calculation. If empty, it is retrieved.

$timestamp Unix timestamp (integer) to include in md5 calculation. If empty, it's retrieved.

$string Optionally, add a string to the md5 calculation. This allows you to generate multiple UIDs with the same timestamp.

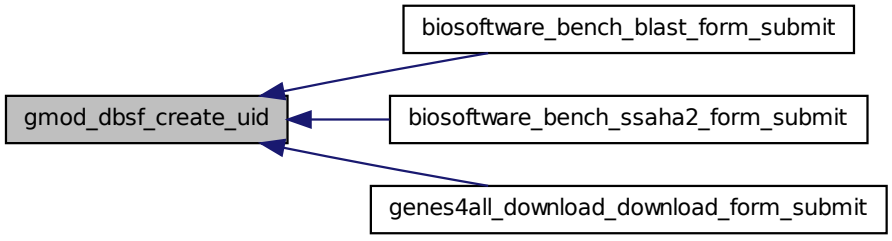
Returns

A 32 letter long hexadecimal string. e.g. d0bfa38422474be81a716e3dbe7ad21e

Definition at line 1273 of file gmod_dbsf.module.

Referenced by biosoftware_bench_blast_form_submit(), biosoftware_bench_ssaha2_form_submit(), and genes4all_download_download_form_submit().

Here is the caller graph for this function:



4.21.2.12 gmod_dbsf_db_execute ($ *db* = *NULL*, $ *function* = *NULL*, $ *variables* = *NULL*)

Seamlessly execute a connection to an non-drupal database

Parameters

$db Name of database to connect to as in settings.php. If empty it connects to default

$function Function to execute to $db. If empty, it only just connects to $db but does not re-connect to Drupal. Use with care!!!

$variables variables to pass to above function. Can be an associative array or you can specify up to 7 arguments after $db and $function

Returns

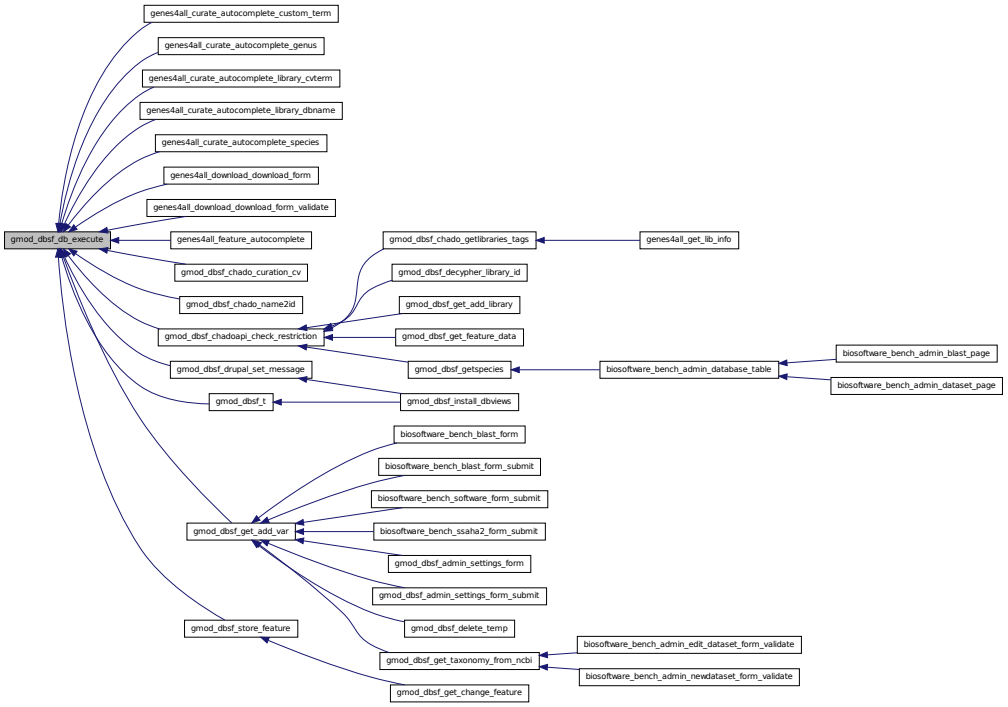
array of results or if none expected FALSE/TRUE on failure/success respectively

allow connection to any other database upon completion (not backwards compatible)

Definition at line 208 of file gmod_dbsf.module.

Referenced by genes4all_curate_autocomplete_custom_term(), genes4all_curate_autocomplete_genus(), genes4all_curate_autocomplete_library_cvterm(), genes4all_curate_autocomplete_library_dbname(), genes4all_curate_autocomplete_species(), genes4all_download_download_form(), genes4all_download_download_form_validate(), genes4all_feature_autocomplete(), gmod_dbsf_chado_curation_cv(), gmod_dbsf_chado_name2id(), gmod_dbsf_chadoapi_check_restriction(), gmod_dbsf_drupal_set_message(), gmod_dbsf_get_add_var(), gmod_dbsf_store_feature(), and gmod_dbsf_t().

Here is the caller graph for this function:



4.21.2.13 gmod_dbsf_db_key ($ *db_name* = ***NULL***)

Get database key in $db_url using a database name

Parameters

$db_name,defaults to current connection

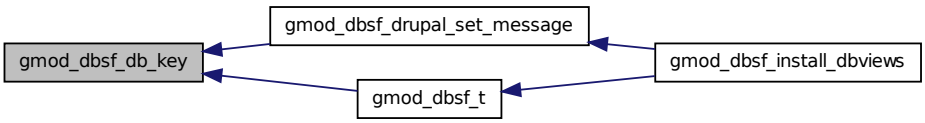
Returns

string database key

Definition at line 3045 of file gmod_dbsf.module.

Referenced by gmod_dbsf_drupal_set_message(), and gmod_dbsf_t().

Here is the caller graph for this function:



4.21.2.14 gmod_dbsf_decode ($ *encoded*, $ *check* = `NULL`)

Decodes gmod_dbsf_encode function

See also

gmod_dbsf_encode()

Parameters

$encoded Variable to be decoded

Returns

Decoded and unserialized variable

Definition at line 127 of file gmod_dbsf.module.

4.21.2.15 gmod_dbsf_decypher_library_id ($ *library_id*, $ *limit* = `NULL`, $ *full_access* = `FALSE`)

Get library data using an library id or binomial name

Allows for Drupal library table which does not exist (yet)

Parameters

$library_id The id, name, uniquename or dbEST code to get data for

$limit Can be library_id, uniquename, name or dbEST in order to force search only in that property

$full_access Return data, even if user is not allowed. Useful to find out if a uniquename is already taken.

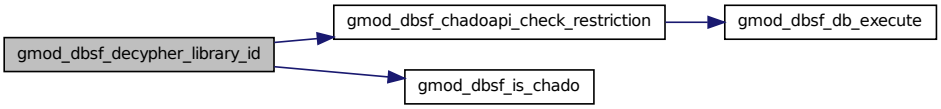
Returns

FALSE on failure or in success an associative array with 'uniquename','name','library_id' as keys

Definition at line 4130 of file gmod_dbsf.module.

References gmod_dbsf_chadoapi_check_restriction(), and gmod_dbsf_is_chado().

Here is the call graph for this function:



4.21.2.16 gmod_dbsf_decypher_organism_id ($ *organism_id*)

Get organism data using an organism id or binomial name

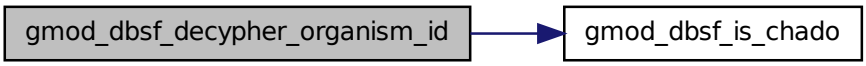
Parameters

$organism_id The internal organism ID or latin name or NCBI taxonomy ID if in form of NCBI\d+

Definition at line 2623 of file gmod_dbsf.module.

References gmod_dbsf_is_chado().

Here is the call graph for this function:



4.21.2.17 gmod_dbsf_delete_cv ($ *cv*, $ *cvterm_array* = ***NULL***)

Delete an entire CV or specific terms

Parameters

$cv CV to delete

$cvterm_array If present, only delete these terms FROM $cv

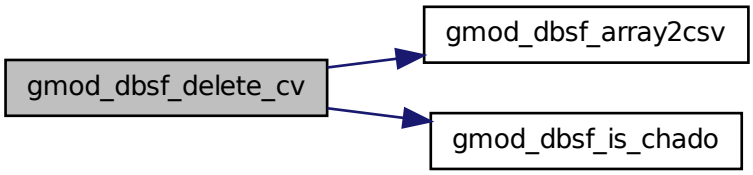
Returns

TRUE on success

Definition at line 509 of file gmod_dbsf.module.

References gmod_dbsf_array2csv(), and gmod_dbsf_is_chado().

Here is the call graph for this function:



4.21.2.18 gmod_dbsf_delete_temp ($ *file* = `NULL`, $ *deftime* = `604800`)

Delete a file if older than 7 days.

Used with cron

See also

gmod_dbsf_download_cron()
biosoftware_bench_cron()

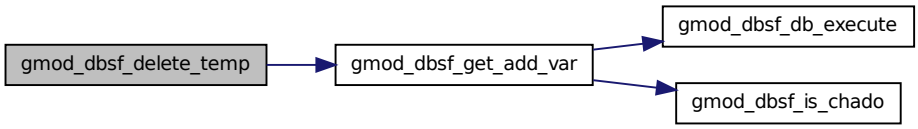
Parameters

$file File to delete

Definition at line 2590 of file gmod_dbsf.module.

References gmod_dbsf_get_add_var().

Here is the call graph for this function:



4.21.2.19 gmod_dbsf_drupal_set_message ($ *message*, $ *type* = `'status'`, $ *repeat* = `TRUE`)

Helper function to set_message when connected to a secondary database

See also

drupal_set_message() This ensures that the proper connection to the Drupal database is connected before attempting to store a message. The connection to the original database is restored. The input parameters are exactly as in drupal_set_message

Parameters

$message

$type

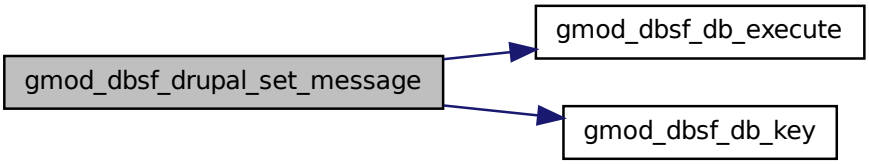
$repeat

Definition at line 3079 of file gmod_dbsf.module.

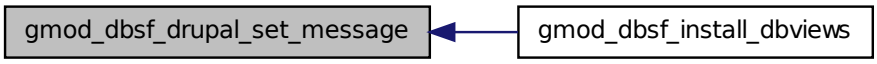
References gmod_dbsf_db_execute(), and gmod_dbsf_db_key().

Referenced by gmod_dbsf_install_dbviews().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.20 gmod_dbsf_encode ($ *variable*)

Encode a variable using base64,serialize and gzcompress

Allows encoding of more than 2000 characters (IE6 problem)

See also

gmod_dbsf_decode()

Parameters

$variable Variable to be encoded

Returns

Encoded variable as a serialized string

Definition at line 109 of file gmod_dbsf.module.

4.21.2.21 gmod_dbsf_feature2gff3 ($ *feature_id*, $ *outfile*)

Create a GFF3 file for a feature

Parameters

$feature_id the feature ID or uniquename

$outfile the output filename

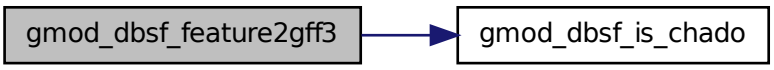
Returns

boolean True on success

Definition at line 4196 of file gmod_dbsf.module.

References gmod_dbsf_is_chado().

Here is the call graph for this function:



4.21.2.22 gmod_dbsf_form_clear ($ *form*, &$ *form_state*)

This submit button will clear any form which calls it, incl. storage and values

Used as a hook_form_validate

Parameters

$form hook_form data

$form_state hook_form data

Definition at line 2574 of file gmod_dbsf.module.

4.21.2.23 gmod_dbsf_get_add_cv_withnames ($ *cv_name*, $ *cvterm_name* = **NULL**, $ *name_as_key* = **FALSE**, $ *definition* = **FALSE**, $ *force_update_def* = **FALSE**)

Get cvterm_id for a CV, add it first if it does not exist.

If $cvterm_name (second argument) is not given, it will return all cvterm_id/cvterm_names for the CV specified in $cv_name (first arg). $name_as_key controls the return array

See also

gmod_dbsf_get_add_dbxref_withnames

Parameters

$cv_name The name of the CV to which the cvterm belong.

$cvterm_name The name of the cvterm to look for or add. Not needed if just want to retrieve all cvterms

$name_as_key TRUE, FALSE or BOTH. False gives cvterm_id as key to return array; TRUE gives name with ID as value; BOTH gives name both as key and value (useful for FAPI)

$definition if provided, then it updates the definition for the added term if there is none stored currently

$force_update_def If true, then definition is updated even if empty

Returns

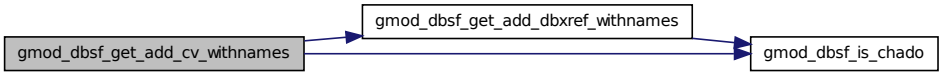
FALSE on failure. If cvterm has been provided, then an integer of the cvterm_id is returned. If no cvterm, then return is an associative array WHERE keys are controlled by $name_as_key.

Definition at line 837 of file gmod_dbsf.module.

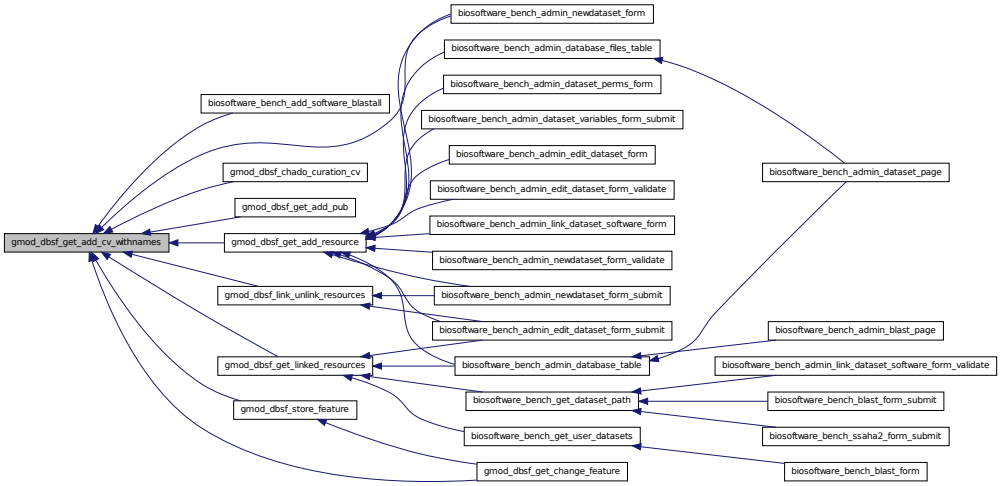
References gmod_dbsf_get_add_dbxref_withnames(), and gmod_dbsf_is_chado().

Referenced by biosoftware_bench_add_software_blastall(), biosoftware_bench_admin_newdataset_form(), gmod_dbsf_chado_curation_cv(), gmod_dbsf_get_add_pub(), gmod_dbsf_get_add_resource(), gmod_dbsf_get_change_feature(), gmod_dbsf_get_linked_resources(), gmod_dbsf_link_unlink_resources(), and gmod_dbsf_store_feature().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.24 gmod_dbsf_get_add_dbxref_withnames ($ *dbname*, $ *accession* = *NULL*, $ *description* = *NULL*, $ *name_as_key* = *NULL*)

Get dbxref_id for a dbxref; add it first if it doesn't exist

If $accession is not given, it returns all dbxref_id and names for the database you specify with $dbname

See also

gmod_dbsf_get_add_cv_withnames

Parameters

$dbname Name of db to link dbxref

$accession Accession/uniquename for dbxref to get and/or add. If empty return all accessions for $dbname

$name_as_key TRUE, FALSE or BOTH. False gives cvterm_id as key to return array; TRUE gives name with ID as value; BOTH gives name both as key and value (useful for FAPI)

$definition if provided, then it updates the definition for the added term if there is none stored currently

$force_update_def If true, then definition is updated even if empty

Returns

FALSE on failure or an integer with the dbxref_id on success.

Definition at line 973 of file gmod_dbsf.module.

References gmod_dbsf_is_chado().

Referenced by biosoftware_bench_add_software_blastall(), genes4all_experiment_publication_add(), gmod_dbsf_add_cv(), gmod_dbsf_get_add_cv_withnames(), gmod_dbsf_get_add_library(), gmod_dbsf_-get_add_organism(), gmod_dbsf_get_add_resource(), and gmod_dbsf_get_change_feature().

Here is the call graph for this function:

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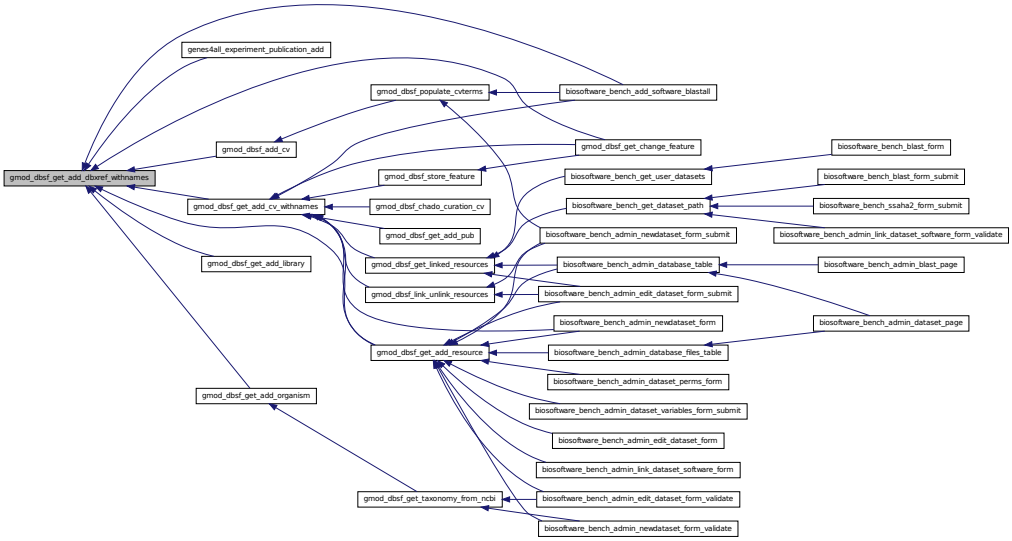


4.21.2.25 gmod_dbsf_get_add_library ($ *data* = ***NULL***)

Get or add library data

under-construction Chado Libraries have a type_id/cvterm.name, a name and a uniquename In est2assembly, the name is the friendly name aimed for users. The uniquename varies: if the library is derived FROM dbest, then the name is accession of the dbest. We also add the accession in library_dbxref. Otherwise, we have chosen a uniquename ourselves. If adding, then it must be verified as unique before continuing.

Parameters

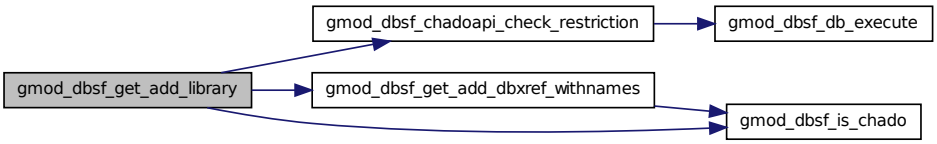
$data If empty, return ID, type and name of all libraries user has access to.

Returns

Definition at line 3957 of file gmod_dbsf.module.

References gmod_dbsf_chadoapi_check_restriction(), gmod_dbsf_get_add_dbxref_withnames(), and gmod_dbsf_is_chado().

Here is the call graph for this function:



4.21.2.26 gmod_dbsf_get_add_organism ($ *data*)

Get or add data for an organism

Uses the chado organism schema instead of the gmod_dbsf

Parameters

$data if $data['organism_id'] is present, then it is an organism id and we we want to get the data for it. Otherwise, we want to store the data and return the new organism_id. The $data['pgtype'] can be either drupal or chado (case sensitive). This regulates which schema is being used

Returns

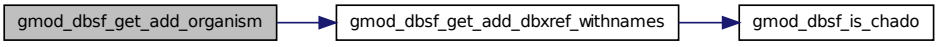
FALSE on failure, TRUE on adding success or an associative array with the columns as keys if you wanted to fetch.

Definition at line 3478 of file gmod_dbsf.module.

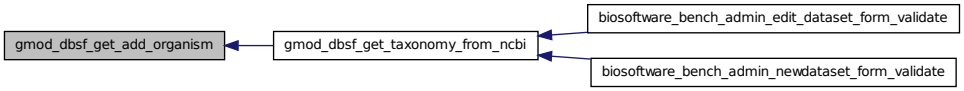
References gmod_dbsf_get_add_dbxref_withnames().

Referenced by gmod_dbsf_get_taxonomy_from_ncbi().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.27 gmod_dbsf_get_add_pub ($ *pub_type_category*, $ *type_name*, $ *data* = ***NULL***, $ *add* = ***FALSE***, $ *name_as_key* = ***FALSE***)

Get a list of pubs, replace or add a new one

Parameters

$pub_type_category what kind of publication you're aiming to add, governs which CV is used. Currently 'annotation' sets CV as Evidence Codes and 'dbxref' sets CV as publications

$type_name Name of the cvterm which defines the pub type

$data (optional) An assoc. array to limit SELECT queries: the keys are used as column and values as the condition. Further, when adding/replacing, $data has to contain keys with 'uniquename' and 'dbxref_name'

$add Switch which can be FALSE/NULL, ADD, DELETE or REPLACE

$name_as_key A boolean. If TRUE the return array has uniquename as keys and pub_id as values.

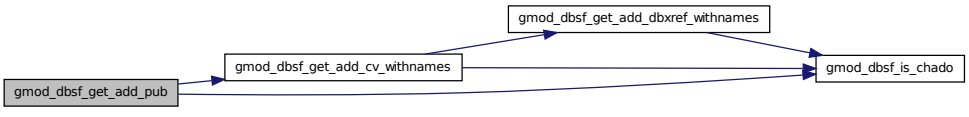
Returns

An associative array with pub_id as the keys and uniquename as values. Or FALSE on failure.

Definition at line 1093 of file gmod_dbsf.module.

References gmod_dbsf_get_add_cv_withnames(), and gmod_dbsf_is_chado().

Here is the call graph for this function:



4.21.2.28 gmod_dbsf_get_add_resource ($ *type_name*, $ *data* = ***NULL***, $ *add* = ***FALSE***, $ *name_as_key* = ***FALSE***)

Get a list of resources, replace or add a new one

Parameters

$type_name Name of the cvterm which defines the resource type

$data (optional) An assoc. array to limit SELECT queries: the keys are used as column and values as the condition. Further, when adding/replacing, $data has to contain keys with 'uniquename' and 'dbxref_name'

$add Switch which can be FALSE/NULL, ADD, DELETE or REPLACE

$name_as_key A boolean. If TRUE the return array has uniquename as keys and resource_id as values. if ALL then all data is returned in associative array

Returns

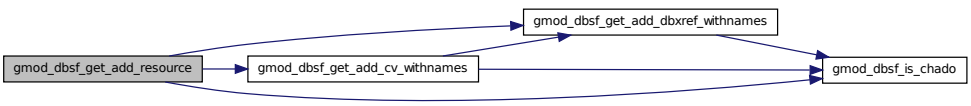
An associative array with resource_id as the keys and uniquename as values but see $name_as_key Or FALSE on failure.

Definition at line 1348 of file gmod_dbsf.module.

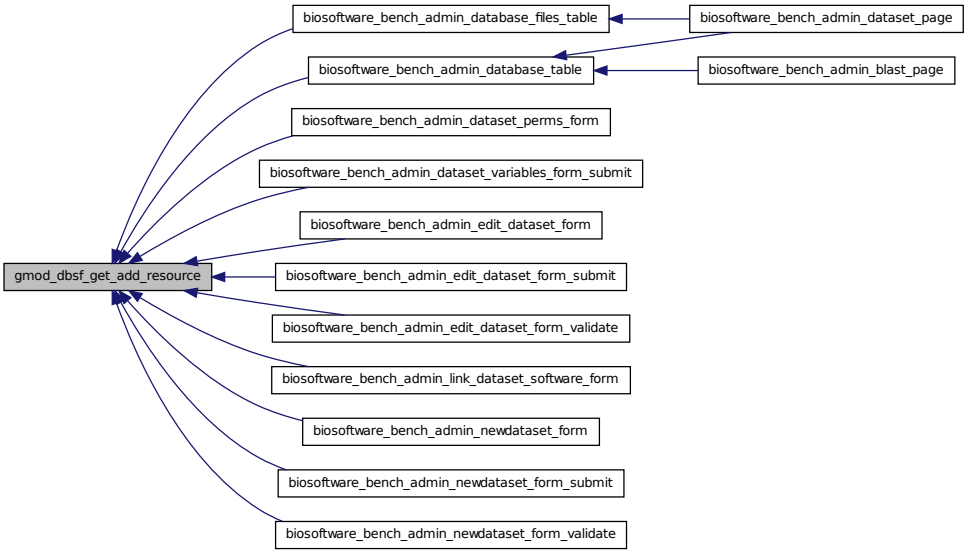
References gmod_dbsf_get_add_cv_withnames(), gmod_dbsf_get_add_dbxref_withnames(), and gmod_dbsf_is_chado().

Referenced by biosoftware_bench_admin_database_files_table(), biosoftware_bench_admin_database_table(), biosoftware_bench_admin_dataset_perms_form(), biosoftware_bench_admin_dataset_variables_form_submit(), biosoftware_bench_admin_edit_dataset_form(), biosoftware_bench_admin_edit_dataset_form_submit(), biosoftware_bench_admin_edit_dataset_form_validate(), biosoftware_bench_admin_link_dataset_software_form(), biosoftware_bench_admin_newdataset_form(), biosoftware_bench_admin_newdataset_form_submit(), and biosoftware_bench_admin_newdataset_form_validate().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.29 gmod_dbsf_get_add_var ($ *name* = `NULL`, $ *value* = `NULL`, $ *db_reconnect* = `'chado'`)

Manipulate the Drupal variable table

You can add, get, delete and update variables with one go. It checks if the active db is chado and then it reconnects to chado

See also

variable_del
variable_get
variable_set

Parameters

$name The name field

$value The value field. If empty, it performs a GET, if it is set as DELETE then it deletes the entry

$db_reconnect If provided, this is the alias of the db to reconnect back to. defaults to chado

Returns

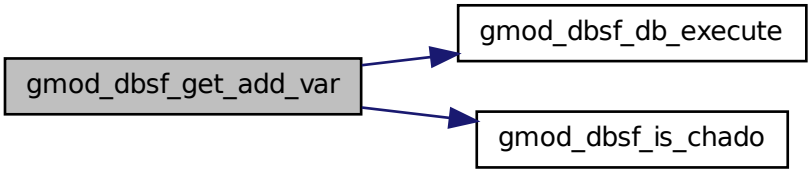
boolean TRUE on success, FALSE on failure

Definition at line 4905 of file gmod_dbsf.module.

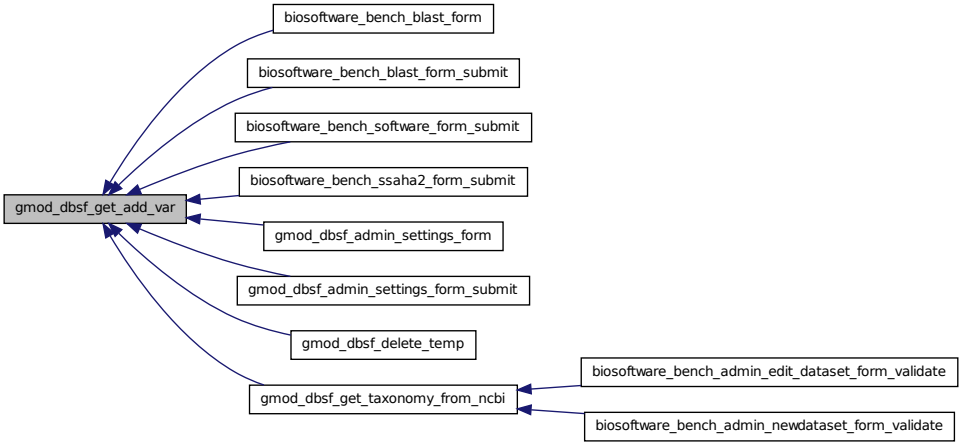
References gmod_dbsf_db_execute(), and gmod_dbsf_is_chado().

Referenced by biosoftware_bench_blast_form(), biosoftware_bench_blast_form_submit(), biosoftware_bench_software_form_submit(), biosoftware_bench_ssaha2_form_submit(), gmod_dbsf_admin_settings_form(), gmod_dbsf_admin_settings_form_submit(), gmod_dbsf_delete_temp(), and gmod_dbsf_get_taxonomy_from_ncbi().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.30 gmod_dbsf_get_change_feature ($ *type_name* = ***NULL***, $ *data* = ***NULL***, $ *change* = ***FALSE***, $ *name_as_key* = ***FALSE***)

Get a list of features, replace or delete one

This is a general function name. Does not add new features.

See also

gmod_dbsf_store_feature()

Parameters

$type_name Name of the cvterm which defines the feature type

$data (optional) An assoc. array to limit SELECT queries: the keys are used as column and values as the condition. Further, when adding/replacing, $data has to contain keys with 'uniquename' and 'dbxref_name'

$change Switch which can be FALSE/NULL, ADD, DELETE or REPLACE

$name_as_key A boolean. If TRUE the return array has uniquename as keys and feature_id as values.

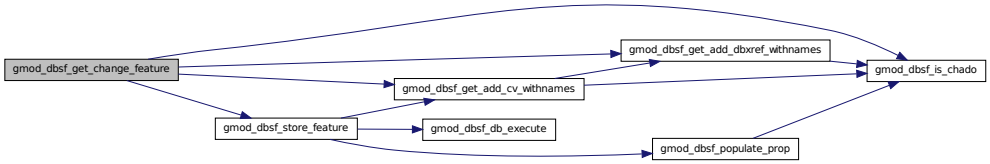
Returns

An associative array with feature_id as the keys and uniquename as values. Or FALSE on failure.

Definition at line 1966 of file gmod_dbsf.module.

References gmod_dbsf_get_add_cv_withnames(), gmod_dbsf_get_add_dbxref_withnames(), gmod_dbsf_is_chado(), and gmod_dbsf_store_feature().

Here is the call graph for this function:



4.21.2.31 gmod_dbsf_get_defined_dbs ( )

Get databases registered in settings.ini according to their type

Todo

currently, we are following the est2assembly nomenclature, however in the future we should make a connection to each database explictly and check for a specific table (it will be much slower but can be controlled by a switch)

Returns

associative array with 'SeqFeature', 'Chado' and 'Drupal' for the databases which follow the pattern [a-z]{2}_+ , /chado/i or everything else respectively. Note that the seqfeature database

Definition at line 4511 of file gmod_dbsf.module.

4.21.2.32 gmod_dbsf_get_feature_cvterm_and_prop ($ *feature*)

Get cvterms and properties for a feature

Parameters

$feature ID or name of feature to get cvterms and properties for.

Returns

An associative array WHERE the primary key is 'cvterm' and 'prop' for cvterms and properties respectively. 'cvterm' is has cvterm.names in a list array foreach cv_name. 'prop' does likewise for values of each cvterm.name

Definition at line 2178 of file gmod_dbsf.module.

References gmod_dbsf_is_chado().

Here is the call graph for this function:

4.21.2.33 gmod_dbsf_get_feature_data ($ *feature*)

Get all data regarding a feature and the uniquenames of its parents

This functions on both Drupal and Chado

Parameters

$feature The feature_id or uniquename

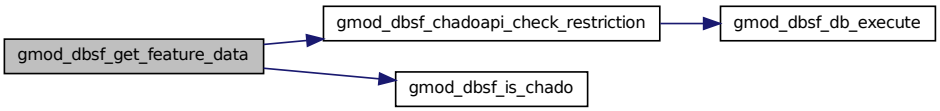
Returns

associative array with keys the columns of the feature table (and also type_name for the cvterm.name of type_id) also the 'parent' key is the for a list of the uniquename(s) of the parent(s) according to featureloc. If there is only one parent, then not a list but a string is the value of 'parent'

Definition at line 2114 of file gmod_dbsf.module.

References gmod_dbsf_chadoapi_check_restriction(), and gmod_dbsf_is_chado().

Here is the call graph for this function:



4.21.2.34 gmod_dbsf_get_feature_name_id ($ *feature*, $ *name_as_key* = **FALSE**)

Get 1+ feature names/IDs by providing 1+ feature IDs/names

Parameters

$feature A string or list array of IDs or uniquename of features to fetch

$name_as_key A boolean, if true then the key of the returned array is the uniquename.

Returns

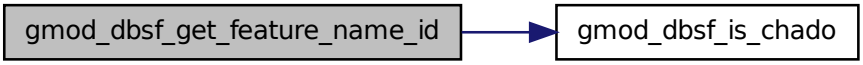
An associative array with the ID and uniquename of each feature The key is the ID unless $name_as_-key is set.

Definition at line 1905 of file gmod_dbsf.module.

References gmod_dbsf_is_chado().

Referenced by gmod_dbsf_link_unlink_features().

Here is the call graph for this function:



Here is the caller graph for this function:

4.21.2.35 gmod_dbsf_get_linked_resources ($ *resource*, $ *relationship_name* = ***NULL***, $ *name_as_key* = ***FALSE***, $ *limit* = ***NULL***)

Get all object resources stored in the resource_resource table

Parameters

$resource id ID or uniquename of subject resource

$relationship_name Optionally delimit by relationship type by providing the type name

$name_as_key A boolean, if TRUE then the return array has uniquename as key

$limit A string. Optionally pass a string to add as LIMIT to the query.

Returns

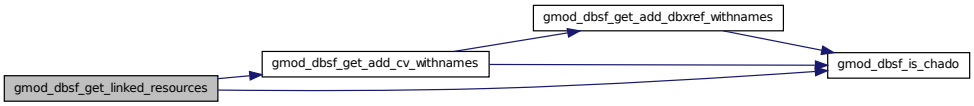
A 2D associative array with primary key the object_id and secondary the column names object_-type,object_name for each object resource

Definition at line 1742 of file gmod_dbsf.module.

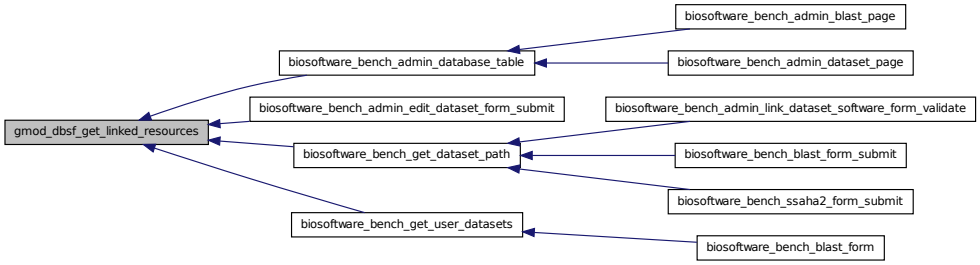
References gmod_dbsf_get_add_cv_withnames(), and gmod_dbsf_is_chado().

Referenced by biosoftware_bench_admin_database_table(), biosoftware_bench_admin_edit_dataset_-form_submit(), biosoftware_bench_get_dataset_path(), and biosoftware_bench_get_user_datasets().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.36 gmod_dbsf_get_resource_cvterm_and_prop ($ *resource*)

Get cvterms and properties for a resource

Parameters

$resource ID or name of resource to get cvterms and properties for.

Returns

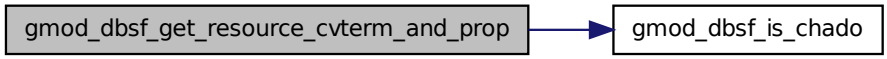
An associative array WHERE the primary key is 'cvterm' and 'prop' for cvterms and properties respectively. 'cvterm' is has cvterm.names in a list array foreach cv_name. 'prop' does likewise for values of each cvterm.name

Definition at line 1486 of file gmod_dbsf.module.

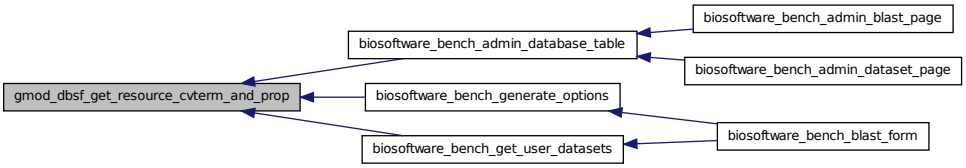
References gmod_dbsf_is_chado().

Referenced by biosoftware_bench_admin_database_table(), biosoftware_bench_generate_options(), and biosoftware_bench_get_user_datasets().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.37 gmod_dbsf_get_resource_name_id ($ *resource*, $ *name_as_key* = ***FALSE***)

Get 1+ resource names/IDs by providing 1+ resource IDs/names

Parameters

$resource A string or list array of IDs or uniquename of resources to fetch

$name_as_key A boolean, if true then the key of the returned array is the uniquename.

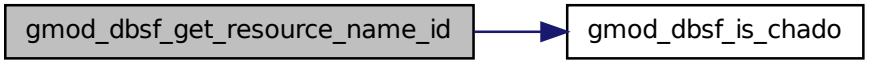
Returns

An associative array with the ID and uniquename of each resource The key is the ID unless $name_-as_key is set.

Definition at line 1297 of file gmod_dbsf.module.

References gmod_dbsf_is_chado().

Here is the call graph for this function:



4.21.2.38 gmod_dbsf_get_software_resources ($ *limit* = **NULL**, $ *name_as_key* = **FALSE**)

Get all resources linked for a specific software

Parameters

$limit Aptionally an array or string to add a constraint. NB: The software table is aliased as s; resource as r; software_resource as sr and cvterm (linked with resource) as rcvterm

$name_as_key A boolean, if TRUE then return array uses names instead of IDs

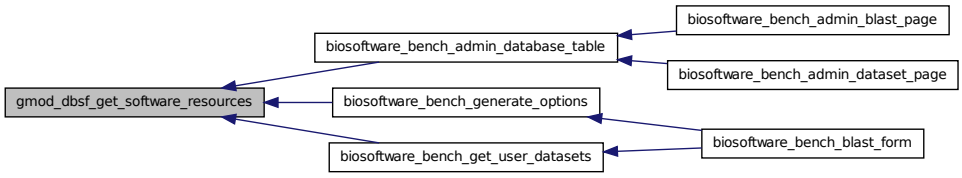
Returns

An associative array WHERE first keys is the software id/name, second key is the resource id/name. The value is the name of the resource type.

Definition at line 4826 of file gmod_dbsf.module.

Referenced by biosoftware_bench_admin_database_table(), biosoftware_bench_generate_options(), and biosoftware_bench_get_user_datasets().

Here is the caller graph for this function:



4.21.2.39 gmod_dbsf_get_softwareprop ($ *limit* = **NULL**, $ *name_as_key* = **FALSE**)

Get the properties FROM the softwareprop table

Parameters

$limit Optionally add a limit. It can be a string to be added after WHERE or an array WHERE they keys are the column names

$name_as_key If TRUE, set the return array to use the software uniquename as the key

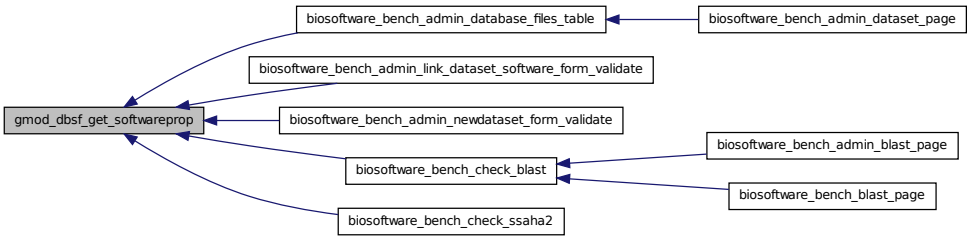
Returns

A 3D associative array. First key is ID or name (controlled by $name_as_key); second key is the type_name and third is the rank (an integer). The value of the property is the value of the array.

Definition at line 4781 of file gmod_dbsf.module.

Referenced by biosoftware_bench_admin_database_files_table(), biosoftware_bench_admin_link_-dataset_software_form_validate(), biosoftware_bench_admin_newdataset_form_validate(), biosoftware_-bench_check_blast(), and biosoftware_bench_check_ssaha2().

Here is the caller graph for this function:



4.21.2.40 gmod_dbsf_get_taxonomy_from_ncbi ($ *ncbi_taxid*)

Get an organism ID after storing the complete taxonomy using NCBI

Parameters

$ncbi_taxid the NCBI Taxonomy ID to retrieve

Returns

associative array of results

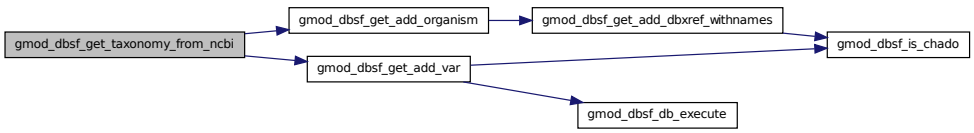
- 'organism_id' Organism ID
- 'common_name' Common name
- 'species' Species
- 'genus' Genus
- 'class' Class
- 'order' Order
- 'family' Family
- 'ncbi_taxid' NCBI taxonomy ID

Definition at line 4986 of file gmod_dbsf.module.

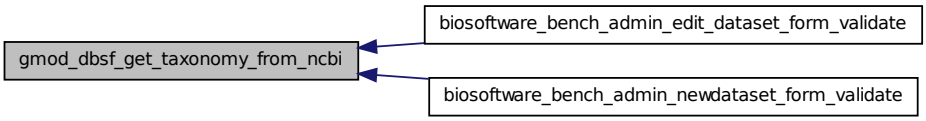
References gmod_dbsf_get_add_organism(), and gmod_dbsf_get_add_var().

Referenced by biosoftware_bench_admin_edit_dataset_form_validate(), and biosoftware_bench_admin_-newdataset_form_validate().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.41 gmod_dbsf_get_users_roles ($ *name_as_key* = *NULL*)

Get the roles of any user

This is a Drupal-specific function

Parameters

$name_as_key if TRUE then the name of the user will be the key of the array, ID the value if BOTH then then both key and value will be the username else the userid is the key of the array with the username as the value

Returns

associative array

Definition at line 4387 of file gmod_dbsf.module.

4.21.2.42 gmod_dbsf_getspecies ($ *limit* = *NULL*, $ *all_orgs* = *NULL*)

Get species

We want to use genus/species instead of organism_id in order to allow potential future taxonomic searches Unless $all_orgs is given, it gives only organisms with features

See also

gmod_dbsf_get_add_organism()

Todo

move into gmod_dbsf_get_add_organism();

Parameters

$limit a string of comma delimited numbers or an array of organism_id

$all_orgs if not empty, it gets all organisms, even those without contigs or other features. This is only for Chado, as Drupal always gets all organisms.

This function checks for restrictions if the connection is to the Chado db

Returns

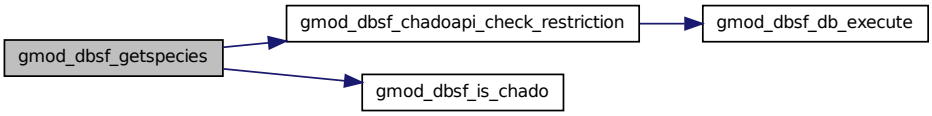
associative array: 'species_array' and 'phylogeny_array' as keys

Definition at line 2825 of file gmod_dbsf.module.

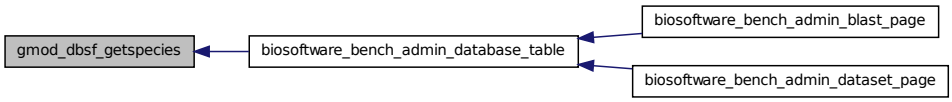
References gmod_dbsf_chadoapi_check_restriction(), and gmod_dbsf_is_chado().

Referenced by biosoftware_bench_admin_database_table().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.43 gmod_dbsf_init ( )

Load any CSS used by all other modules

Definition at line 90 of file gmod_dbsf.module.

4.21.2.44 gmod_dbsf_install_dbtable ($ *variables*)

Install a new table without producing errors

Parameters

$variables

Returns

Definition at line 3171 of file gmod_dbsf.module.

4.21.2.45 gmod_dbsf_install_dbviews ($ *variables*)

Install a views on your database

Parameters

$variables Associative array WHERE 'view_name' is name of the view and 'spec' is the SQL which builds the view

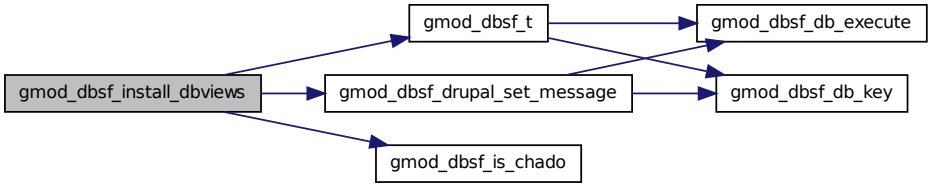
Returns

FALSE on failure, TRUE on success

Definition at line 2994 of file gmod_dbsf.module.

References gmod_dbsf_drupal_set_message(), gmod_dbsf_is_chado(), and gmod_dbsf_t().

Here is the call graph for this function:



4.21.2.46 gmod_dbsf_install_pgfunction ($ *name*, $ *sql*)

Install a postgres function unless it already exists

Parameters

$name Name of function to check if it already exists

$sql Complete SQL to create function (include 'CREATE')

Definition at line 2967 of file gmod_dbsf.module.

4.21.2.47 gmod_dbsf_is_chado ( )

Check if the current database is a chado one

Look for database name, not db alias in settings.ini (don't know how to get that) Search is case insensitive. We use it to rewrite SQL commands, since Chado has no prefixes, neither as db_prefix or due to module

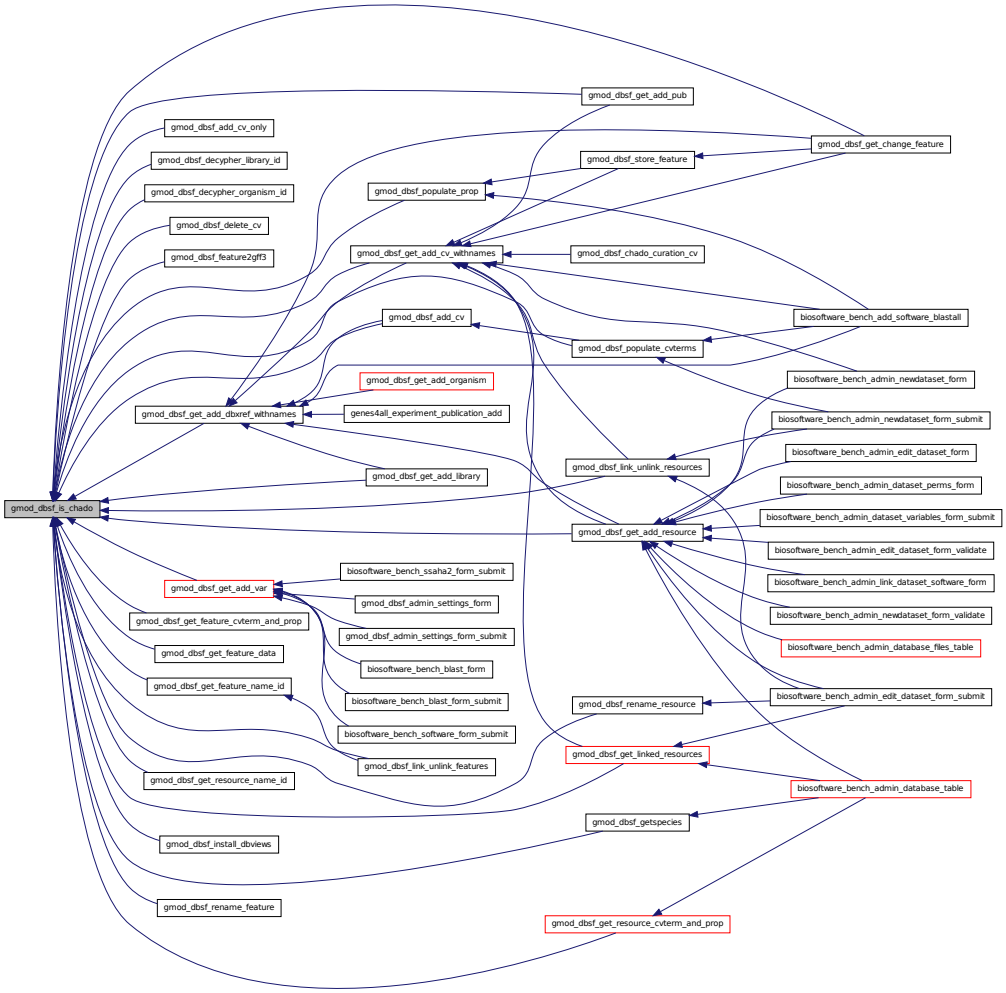
Returns

boolean TRUE if active db is Chado, FALSE otherwise.

Definition at line 76 of file gmod_dbsf.module.

Referenced by gmod_dbsf_add_cv(), gmod_dbsf_add_cv_only(), gmod_dbsf_decypher_library_id(), gmod_dbsf_decypher_organism_id(), gmod_dbsf_delete_cv(), gmod_dbsf_feature2gff3(), gmod_dbsf_get_add_cv_withnames(), gmod_dbsf_get_add_dbxref_withnames(), gmod_dbsf_get_add_library(), gmod_dbsf_get_add_pub(), gmod_dbsf_get_add_resource(), gmod_dbsf_get_add_var(), gmod_dbsf_get_change_feature(), gmod_dbsf_get_feature_cvterm_and_prop(), gmod_dbsf_get_feature_data(), gmod_dbsf_get_feature_name_id(), gmod_dbsf_get_linked_resources(), gmod_dbsf_get_resource_cvterm_and_prop(), gmod_dbsf_get_resource_name_id(), gmod_dbsf_getspecies(), gmod_dbsf_install_dbviews(), gmod_dbsf_link_unlink_features(), gmod_dbsf_link_unlink_resources(), gmod_dbsf_populate_cvterms(), gmod_dbsf_populate_prop(), gmod_dbsf_rename_feature(), and gmod_dbsf_rename_resource().

Here is the caller graph for this function:



4.21.2.48 gmod_dbsf_link_unlink_features ($ *data*)

Link two resources with a relationship

A bit different FROM the _link_unlink_resources function.

See also

gmod_dbsf_link_unlink_resources This function accepts a single variable as an associative array with the following keys: 'start', 'end' for start and end respectively; 'phase' and 'strand' as used by GFF3 (defaults to NULL and + respectively) 'feature' for the subject feature's ID as internal numeric or uniquename and likewise with 'parent' for the parental ID. Further, 'delete' actually deletes a relationship instead of adding it.

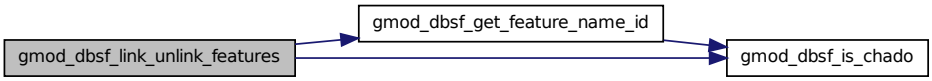
Returns

The function uses the featureloc table to attach the 'feature' to the 'parent' using the 'start' and 'end' coordinates provided. TRUE on success, FALSE on failure.

Definition at line 1817 of file gmod_dbsf.module.

References gmod_dbsf_get_feature_name_id(), and gmod_dbsf_is_chado().

Here is the call graph for this function:



4.21.2.49 gmod_dbsf_link_unlink_resource_role ($ *resource*, $ *role*, $ *switch* = **FALSE**)

Link a Drupal role with a resource

Parameters

$resource The ID or uniquename of the resource to link

$role The ID or name of the Drupal role to link

$switch Boolean of whether to delete instead of linking an association. TRUE deletes. Also, TOGGLE links if unlinked and deletes if linked.

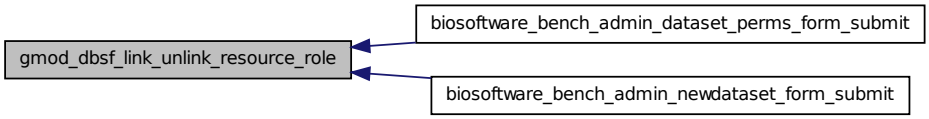
Returns

FALSE on failure, GRANTED/REVOKED on success

Definition at line 4544 of file gmod_dbsf.module.

Referenced by biosoftware_bench_admin_dataset_perms_form_submit(), and biosoftware_bench_admin_newdataset_form_submit().

Here is the caller graph for this function:



4.21.2.50 gmod_dbsf_link_unlink_resources ($ *subject*, $ *rel*, $ *object* = ***NULL***, $ *replace* = ***FALSE***)

Link two resources with a relationship

See also

gmod_dbsf_link_unlink_features

Parameters

$subject The resource_ID or uniquename of the subject of the relationship

$rel The name of a relationship such as 'part_of' or 'uses'

$object The resource_ID or uniquename object of the relationship

$replace Whether to fail if an existing relationship exists (FALSE), replace it (REPLACE) or simply delete it ('DELETE'). If $object is NULL and $replace is DELETE then all relationships $rel for $subject are removed.

Returns

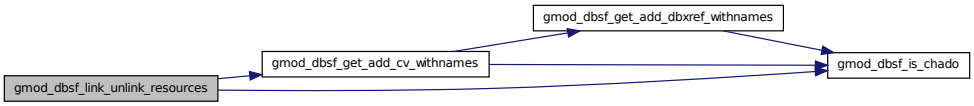
TRUE on success.

Definition at line 1593 of file gmod_dbsf.module.

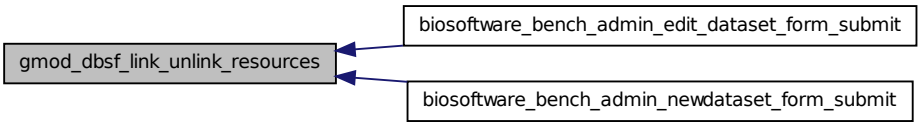
References gmod_dbsf_get_add_cv_withnames(), and gmod_dbsf_is_chado().

Referenced by biosoftware_bench_admin_edit_dataset_form_submit(), and biosoftware_bench_admin_-newdataset_form_submit().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.51 gmod_dbsf_link_unlink_software_resource ($ *software*, $ *resource*, $ *switch* = **FALSE**)

Link a software with a specific resource

Parameters

$software The ID or uniquename of the software to link

$resource The id or name of the resource to link

$switch Boolean of whether to delete instead of linking an association. TRUE deletes. Also, TOGGLE links if unlinked and deletes if linked.

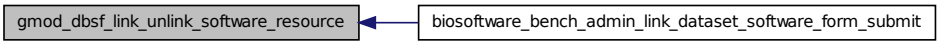
Returns

FALSE on failure, GRANTED/REVOKED on success

Definition at line 4664 of file gmod_dbsf.module.

Referenced by biosoftware_bench_admin_link_dataset_software_form_submit().

Here is the caller graph for this function:



4.21.2.52 gmod_dbsf_menu ( )

Implements hook_menu().

Definition at line 39 of file gmod_dbsf.module.

4.21.2.53 gmod_dbsf_parameter_daemon ($ *uid*, $ *dir*, $ *par*, $ *software* = **'blastall'**, $ *more_data* = **NULL**, $ *cmd_vars* = **NULL**)

Create parameter file for daemon

Parameters

$uid A unique identifier

$dir Directory of WHERE to create the file

$par Contents to print, such as the parameters to be used by the software. This can now be an array

$software Name of software used

$more_data A string or array with any other data which should be written. If it is an associative array, the data are printed as $key : $value

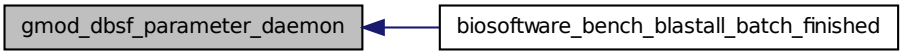
Returns

TRUE on success..

Definition at line 3705 of file gmod_dbsf.module.

Referenced by biosoftware_bench_blastall_batch_finished().

Here is the caller graph for this function:



4.21.2.54 gmod_dbsf_parse_gfffile ($ *infile*)

Parse a GFF3 file

Parameters

$infile the full path to the GFF file

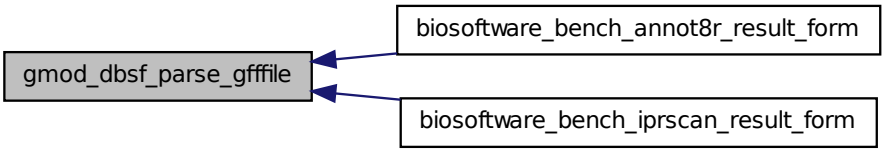
Returns

associative array Each element in the array is an array with the keys 'source', 'type', 'start', 'end', 'score', 'strand', 'phase', and 'attributes'. The latter is an associative array with keys being the tag names returned in a fashion similar to BioPerl's FeatureIO get_tag_values

Definition at line 4333 of file gmod_dbsf.module.

Referenced by biosoftware_bench_annot8r_result_form(), and biosoftware_bench_iprscan_result_form().

Here is the caller graph for this function:



4.21.2.55 gmod_dbsf_phylogeny_tree ($ *phylogeny_array*, $ *button* = `NULL`)

Create a checkbox tree of species and their phylogeny

Parameters

$phylogeny_array Phylogeny array FROM gmod_dbsf_getspecies

$button If set then give data for a button. Keys are description (used during hovering),title and validate The $button can be TRUE or a validation function callback

See also

genes4all_explore_select_species_form

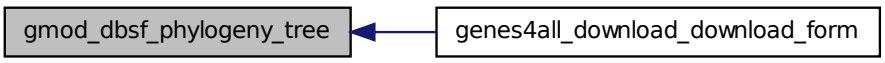
Returns

form API item;

Definition at line 2422 of file gmod_dbsf.module.

Referenced by genes4all_download_download_form().

Here is the caller graph for this function:



4.21.2.56 gmod_dbsf_populate_cvterms ($ *table_type*, $ *object_name*, $ *cvname*, $ *cvterm_array* = `NULL`, $ *pub_id* = `NULL`)

Populate a _cvterm Chado table

This function populates a _cvterm table in chado or Drupal

See also

gmod_dbsf_populate_prop

Parameters

$table_type Type of table linked to teh _cvterm table Currently, only feature and resource table sets are supported

$object_name Name of reference feature/resourc

$cvname Name of CV to which the cvterms belong to

See also

gmod_dbsf_add_cv()

Parameters

$cvterm_array A list array of cvterms to add to the _cvterm table

See also

gmod_dbsf_add_cv()

Parameters

$pub_id The publication ID or uniquenames which defines how the CVterm was derived

Returns

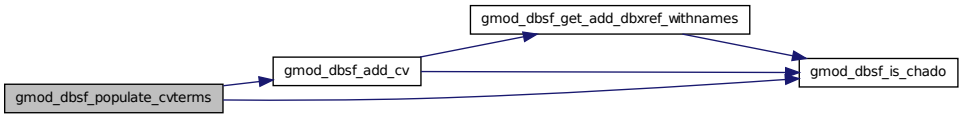
FALSE on failure, TRUE on success

Definition at line 691 of file gmod_dbsf.module.

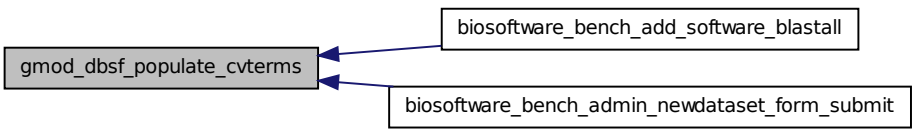
References gmod_dbsf_add_cv(), and gmod_dbsf_is_chado().

Referenced by biosoftware_bench_add_software_blastall(), and biosoftware_bench_admin_newdataset_-form_submit().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.57 gmod_dbsf_populate_prop ($ *table_type,* $ *object_name,* $ *cvterm_id,* $ *property_array*)

Populate a IC Chado property table

This function allows you to populate a property table of feature, resource, organism, library or software type in Chado or Drupal.

Parameters

$table_type Type of table linked to the -prop table. Currently only organism, library, software, feature and resource are allowed

$object_name Name or ID of reference feature/resource etc

$cvterm_id CV term ID used to link the property

$property_array An array of property values to insert with the above cvterm and reference

Returns

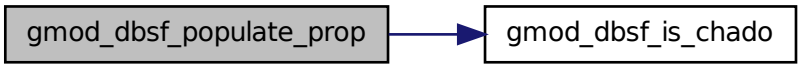
FALSE on failure, TRUE on success

Definition at line 579 of file gmod_dbsf.module.

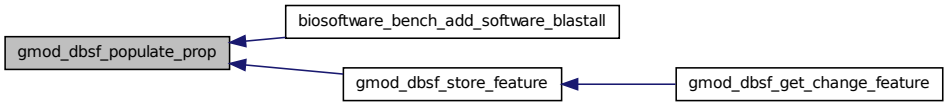
References gmod_dbsf_is_chado().

Referenced by biosoftware_bench_add_software_blastall(), and gmod_dbsf_store_feature().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.58 gmod_dbsf_rename_feature ($ *old_name,* $ *new_name*)

Rename a feature

Parameters

$old_name feature's current uniquename

$new_name New uniquename to set for $old_name feature

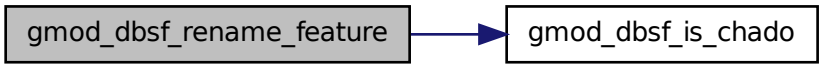
Returns

TRUE on success and FALSE on failure. On failure it also sets a message.

Definition at line 2237 of file gmod_dbsf.module.

References gmod_dbsf_is_chado().

Here is the call graph for this function:



4.21.2.59 gmod_dbsf_rename_resource ($ *old_name*, $ *new_name*)

Rename a resource

Parameters

$old_name Resource's current uniquename

$new_name New uniquename to set for $old_name resource

Returns

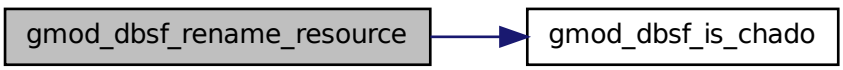
TRUE on success and FALSE on failure. On failure it also sets a message.

Definition at line 1545 of file gmod_dbsf.module.

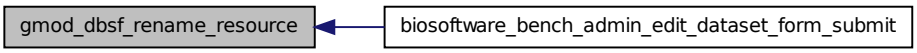
References gmod_dbsf_is_chado().

Referenced by biosoftware_bench_admin_edit_dataset_form_submit().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.60 gmod_dbsf_store_feature ($ *data*)

Store a feature in the feature table

Allows for organism data to be in a second database (it syncs them) Uses the est2assembly model (which does not use Parent but a placeholder; this should be changed in the next version) orf == orf_0 placeholder (no seq) pep == pep_0 placeholder (no seq) Further it uses the est2assembly multi-reference data model for featureloc: contig -> contig orf -> orf pep -> pep con -> orf_0 (not orf) orf -> pep_0 (not pep)

Parameters

$data is an assoc. array with the following keys

- pgdb: settings.ini postgres database name to store this feature.
- uniquename: the internal est2assembly name. Required.
- name: an alias given by the user. Optional.
- organism_id: relates to the organism table. Required.
- organism_db: settings.ini postgres database name which hold data on your organism. Defaults to default. It checks if it is the same as pgdb and if not then it translates the organism data.
- residues: the sequence of the feature. Optional.
- type: The name or ID FROM the cvterm. Becomes type_id. Required.
- parent: associative array with following keys: 'parent_id','start','end','phase','strand'

Returns

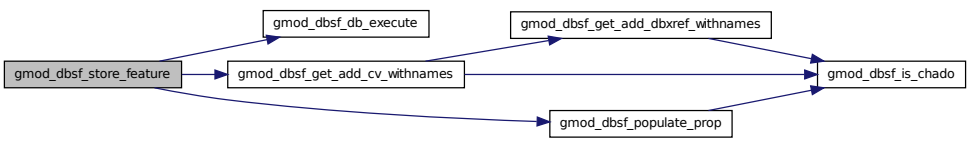
FALSE on failure. EXISTS on feature already existing

Definition at line 3226 of file gmod_dbsf.module.

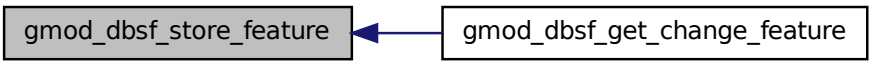
References gmod_dbsf_db_execute(), gmod_dbsf_get_add_cv_withnames(), and gmod_dbsf_populate_prop().

Referenced by gmod_dbsf_get_change_feature().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.61 gmod_dbsf_t ($ *string*, $ *args* = `array()`, $ *langcode* = `NULL`)

Helper function to t() when connected to a secondary database

See also

t() This ensures that the proper connection to the Drupal database is connected before attempting to t(). The connection to the original database is restored. The input parameters are exactly as in t()

Parameters

$string

$args

$langcode

Returns

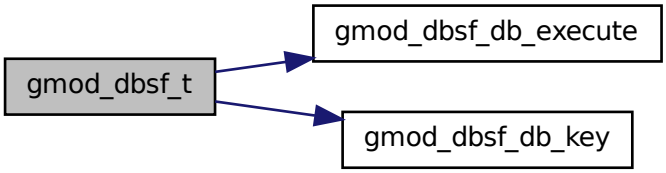
unknown_type

Definition at line 3105 of file gmod_dbsf.module.

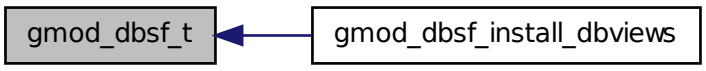
References gmod_dbsf_db_execute(), and gmod_dbsf_db_key().

Referenced by gmod_dbsf_install_dbviews().

Here is the call graph for this function:



Here is the caller graph for this function:



4.21.2.62 gmod_dbsf_translate_DNA_to_protein ($ *seq*, $ *genetic_code*)

Translate a DNA to a protein sequence

Borrowed FROM the biophp project

Parameters

$seq The Sequence to translate as a string

$genetic_code An integer for the genetic code which defines the codon table to use.

- 1 => Standard
- 2 => Vertebrate Mitochondrial
- 3 => Yeast Mitochondrial
- 4 => Mold, Protozoan and Coelenterate Mitochondrial. Mycoplasma, Spiroplasma
- 5 => Invertebrate Mitochondrial
- 6 => Ciliate Nuclear; Dasycladacean Nuclear; Hexamita Nuclear
- 9 => Echinoderm Mitochondrial
- 10 => Euplotid Nuclear
- 11 => Bacterial and Plant Plastid
- 12 => Alternative Yeast Nuclear
- 13 => Ascidian Mitochondrial
- 14 => Flatworm Mitochondrial
- 15 => Blepharisma Macronuclear
- 16 => Chlorophycean Mitochondrial
- 21 => Trematode Mitochondrial
- 22 => Scenedesmus obliquus mitochondrial
- 23 => Thraustochytrium mitochondrial code

Returns

string of the protein sequence

Definition at line 3822 of file gmod_dbsf.module.

4.21.2.63 gmod_dbsf_validate_ic_id ($ *accession* = ***NULL***)

Validate and InsectaCentral accession ID.

Parameters

$accession ID to validate

Returns

Returns correct/cleaned part of accession or FALSE on failure

Definition at line 280 of file gmod_dbsf.module.

4.21.2.64 gmod_dbsf_validate_seq_dna ($ *seq* = ***NULL***, $ *strip* = ***FALSE***)

Validate that a sequence is with IUPAC DNA alphabet only

Xs are allowed

See also

gmod_dbsf_validate_seq_protein()

Todo

support FASTQ

Parameters

$seq string of sequence to validate

$strip Boolean; whether to remove any FASTA definition line from the sequence. Default to FALSE

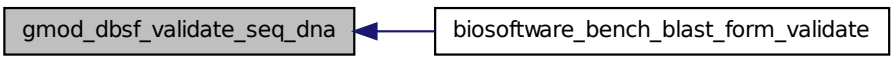
Returns

Cleaned sequence or (int) number of errors detected (or FALSE on failure)

Definition at line 308 of file gmod_dbsf.module.

Referenced by biosoftware_bench_blast_form_validate().

Here is the caller graph for this function:



4.21.2.65 gmod_dbsf_validate_seq_protein ($ *seq* = ***NULL***, $ *strip* = ***FALSE***)

Validate a protein sequence using IUPAC amino acids

Xs are allowed

See also

gmod_dbsf_validate_seq_dna()

Parameters

$seq Sequence string to validate

$strip Boolean; whether to remove any FASTA definition line from the sequence. Default to FALSE

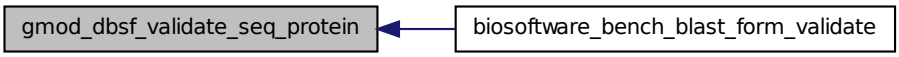
Returns

Returns cleaned string or number of errors found (or FALSE on failure)

Definition at line 371 of file gmod_dbsf.module.

Referenced by biosoftware_bench_blast_form_validate().

Here is the caller graph for this function:



4.21.2.66 gmod_dbsf_write_fastafile ($ *infile* = ***NULL***, $ *outfile* = ***NULL***, $ *delete* = ***NULL***, $ *definition* = ***NULL***)

Write a FASTA file to a destination

Used when uploading FROM a form

Parameters

$infile Full path to input file, e.g. one uploaded into temp dir /tmp/temp.txt

$outfile Desired destination (including filename) for FASTA file.

$delete A boolean of whether to delete the input file after transfer.

$definition If there is no definition line, you can provide one here

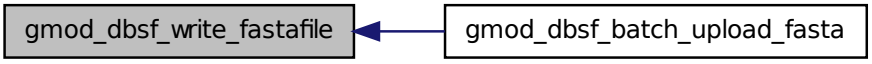
Returns

TRUE on success

Definition at line 2283 of file gmod_dbsf.module.

Referenced by gmod_dbsf_batch_upload_fasta().

Here is the caller graph for this function:



4.22 gmod_dbsf/includes/gmod_dbsf_admin.inc File Reference

Functions

- gmod_dbsf_admin_page ()
- gmod_dbsf_admin_settings_form ($form_state)
- gmod_dbsf_admin_settings_form_validate ($form, &$form_state)
- gmod_dbsf_admin_settings_form_submit ($form, &$form_state)

4.22.1 Detailed Description

Administration pages for gmod_dbsf

Definition in file gmod_dbsf_admin.inc.

4.22.2 Function Documentation

4.22.2.1 gmod_dbsf_admin_page ( )

Prepare administration page

Definition at line 12 of file gmod_dbsf_admin.inc.

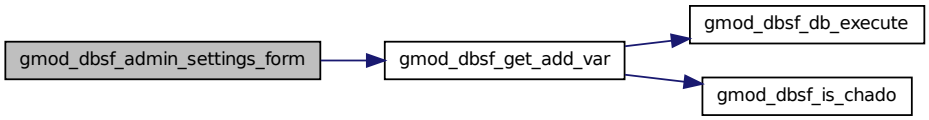
4.22.2.2 gmod_dbsf_admin_settings_form ($ *form_state*)

Implement hook_form

Definition at line 19 of file gmod_dbsf_admin.inc.

References gmod_dbsf_get_add_var().

Here is the call graph for this function:



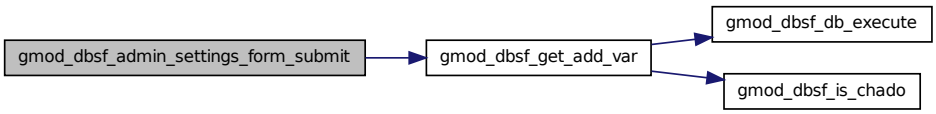
4.22.2.3 gmod_dbsf_admin_settings_form_submit ($ *form*, &$ *form_state*)

Implement hook_form_submit

Definition at line 63 of file gmod_dbsf_admin.inc.

References gmod_dbsf_get_add_var().

Here is the call graph for this function:



4.22.2.4 gmod_dbsf_admin_settings_form_validate ($ *form*, &$ *form_state*)

Implement hook_form_validate

Definition at line 45 of file gmod_dbsf_admin.inc.

4.23 gmod_dbsf/modules/gmod_dbsf_chado/gmod_dbsf_-chado.module File Reference

Functions

- gmod_dbsf_chado_name2id ($name, $table_type, $reverse=FALSE, $reconnect=TRUE)
- gmod_dbsf_chado_get_ncbi_taxid ($organism_id)
- gmod_dbsf_chado_latest_assembly_serial ($variables)
- gmod_dbsf_chado_add_library_dbxref ($lib_id, $dbxref_id)
- gmod_dbsf_chado_add_library_cvterm ($lib_id, $cvterm_id, $pub_id)
- gmod_dbsf_chado_curation_cv ($limit=NULL, $reverse=FALSE, $required=TRUE)
- gmod_dbsf_chado_determine_library_accession ($id)

- gmod_dbsf_chado_getlibrary_properties ($lib_id)
- gmod_dbsf_chado_getlibrary_dbxrefs ($lib_id)
- gmod_dbsf_chado_getlibraries_tags ($variables)
- gmod_dbsf_chado_feature2gff ($feature_id, $advanced=FALSE)
- gmod_dbsf_chado_gff2chado ($dsn, $gff_files, &$context)
- gmod_dbsf_chado_gff2seqfeature ($db_array, $gff_files, &$context)
- gmod_dbsf_chado_get_assembly ($variables)
- gmod_dbsf_chado_assembly2gff ($ref_names)
- gmod_dbsf_chado_get_fasta ($variables)
- gmod_dbsf_chado_get_feature_blastdbs ($feature_id, $limit=NULL)
- gmod_dbsf_chado_get_featuregff_blastdbs ($feature_id)
- gmod_dbsf_chado_get_feature_blast_values ($feature_id, $limit=NULL)

4.23.1 Detailed Description

Chado integration and helper function

Most of these methods are running on the chado database via gmod_dbsf_db_execute, therefore only have one input variable, or one an assoc. array. This is for historical reasons before the function was changed to accept extra arguments directly (w/o an assoc. array)

Also the drupal {tablename} convention is not used here as all functions run on the Chado database (which cannot have any prefixes).

Definition in file gmod_dbsf_chado.module.

4.23.2 Function Documentation

4.23.2.1 gmod_dbsf_chado_add_library_cvterm ($ *lib_id,* $ *cvterm_id,* $ *pub_id*)

Add a library controlled vocabulary term

Parameters

$lib_id The internal library_id

$cvterm_id The CV term ID

$pub_id The publication ID for storing this CVterm

Returns

integer; the library_cvterm_id

Definition at line 172 of file gmod_dbsf_chado.module.

4.23.2.2 gmod_dbsf_chado_add_library_dbxref ($ *lib_id,* $ *dbxref_id*)

Add a library database cross-reference

Parameters

$lib_id The internal library_id

$dbxref_id The internal dbxref_id

Returns

integer; the library_dbxref_id

Definition at line 141 of file gmod_dbsf_chado.module.

4.23.2.3 gmod_dbsf_chado_assembly2gff ($ *ref_names*)

Get an assembly as GFF

helper function used by exploration module

See also

gmod_dbsf_chado_get_assembly
gmod_dbsf_download_bulk_get

Parameters

string or array of reference name(s)

Returns

HTML

Definition at line 799 of file gmod_dbsf_chado.module.

References gmod_dbsf_chado_get_assembly().

Here is the call graph for this function:

4.23.2.4 gmod_dbsf_chado_curation_cv ($ *limit* = ***NULL***, $ *reverse* = ***FALSE***, $ *required* = ***TRUE***)

Produde a $form API variable for evidence codes

This is used every time we ask the user to provide a CV term for an annotation they wish to store.

Parameters

$limit a string limit to apply when fetching the evidence codes. this is a partial case insensitive search using stripos. $limit is the codes not returned

$reverse Default is FALSE; if TRUE then limit is the evidence codes to fetch

$required if set to TRUE (default) then the form does not have a "None" option. Otherwise it does

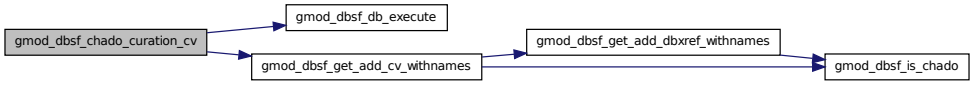
Returns

a variable according to the Drupal form API.

Definition at line 208 of file gmod_dbsf_chado.module.

References gmod_dbsf_db_execute(), and gmod_dbsf_get_add_cv_withnames().

Here is the call graph for this function:



4.23.2.5 gmod_dbsf_chado_determine_library_accession ($ *id*)

Decide if an accession is a chado library id or a library name TODO: decide how to support dbest (a prefix -> dbEST:+)?

Parameters

$id

Returns

array

Definition at line 255 of file gmod_dbsf_chado.module.

Referenced by genes4all_get_lib_info().

Here is the caller graph for this function:

4.23.2.6 gmod_dbsf_chado_feature2gff ($ *feature_id*, $ *advanced* = **FALSE**)

Convert a feature to GFF

This function is slower than the ones using materialized views but it does not depend on them.

Parameters

$feature_id the feature internal ID or uniquename

$advanced UNUSED. A placeholder for future ability to fetch data in a more advanced and complete way

Returns

associative array with 'gff' and 'fsa' as keys. Each value is the relevant data stored as a string

Definition at line 432 of file gmod_dbsf_chado.module.

4.23.2.7 gmod_dbsf_chado_get_assembly ($ *variables*)

Get assembly in a format suitable for GFF

See also

Parameters

$features (unique)names of features.

Returns

unknown_type

Definition at line 659 of file gmod_dbsf_chado.module.

Referenced by gmod_dbsf_chado_assembly2gff().

Here is the caller graph for this function:

4.23.2.8 gmod_dbsf_chado_get_fasta ($ *variables*)

Parameters

$features

Returns

unknown_type

Definition at line 854 of file gmod_dbsf_chado.module.

4.23.2.9 gmod_dbsf_chado_get_feature_blast_values ($ *feature_id*, $ *limit* = `NULL`)

Get keywords that appeared on BLAST.

utilize gmod_dbsf_get_feature_cvterm_and_prop()

Parameters

$feature_id

$limit

Returns

unknown_type

Definition at line 1024 of file gmod_dbsf_chado.module.

4.23.2.10 gmod_dbsf_chado_get_feature_blastdbs ($ *feature_id*, $ *limit* = `NULL`)

Get BLAST databases that were used for searching

utilize gmod_dbsf_get_feature_cvterm_and_prop()

Parameters

$feature_id

$limit

Returns

unknown_type

Definition at line 926 of file gmod_dbsf_chado.module.

4.23.2.11 gmod_dbsf_chado_get_featuregff_blastdbs ($ *feature_id*)

Get BLAST databases that were used for searching

utilize gmod_dbsf_get_feature_cvterm_and_prop()

Parameters

$feature_id

$limit

Returns

unknown_type

Definition at line 978 of file gmod_dbsf_chado.module.

4.23.2.12 gmod_dbsf_chado_get_ncbi_taxid ($ *organism_id*)

Get NCBI taxonomy id for an organism

Parameters

$organism_id The organism_id FROM organism table

Definition at line 86 of file gmod_dbsf_chado.module.

4.23.2.13 gmod_dbsf_chado_getlibraries_tags ($ *variables*)

Parameters

$variables

Returns

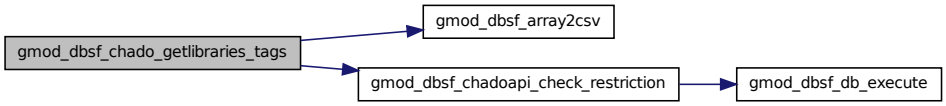
unknown_type

Definition at line 350 of file gmod_dbsf_chado.module.

References gmod_dbsf_array2csv(), and gmod_dbsf_chadoapi_check_restriction().

Referenced by genes4all_get_lib_info().

Here is the call graph for this function:



Here is the caller graph for this function:

4.23.2.14 gmod_dbsf_chado_getlibrary_dbxrefs ($ *lib_id*)

Get library database cross-references as a URL

Parameters

$lib_id the library internal ID

Returns

associative array with the name and url as consecutive keys. the value is the url prefix + the accession

Definition at line 328 of file gmod_dbsf_chado.module.

Referenced by genes4all_get_lib_info().

Here is the caller graph for this function:

4.23.2.15 gmod_dbsf_chado_getlibrary_properties ($ *lib_id*)

Get properties of a library

Parameters

$lib_id the library internal ID

Returns

associative array with the type name as key

Definition at line 305 of file gmod_dbsf_chado.module.

Referenced by genes4all_get_lib_info().

Here is the caller graph for this function:

4.23.2.16 gmod_dbsf_chado_gff2chado ($ *dsn*, $ *gff_files*, &$ *context*)

Upload GFF3 annotation files to Chado

This function is not new sequence data, the reference must already exist in Chado. It prepares the commandline program ic_chado_loadcv.pl (part of est2assembly) so the data must be compatible to that one (BLAST, EC, KEGG, InterProScan) This function is used as part of the BATCH API

See also

batch_set
genes4all_curate_load_approved in genes4all_curate_feature.inc

Parameters

$dsn The database DSN to connect to

$gff_files One or more GFF files as 2D-associative array with the first key being the ID from the batch relevant functions.

$context The batch_set $context variable is automatically parsed when this function is called via a batch-implementing function

Returns

updates the $context['results'] variable which is eventually parsed into $results in the batch API. The associative has the 'chado']['par' and 'chado']['out elements set to the cmdline arguments and output file respectively

Definition at line 566 of file gmod_dbsf_chado.module.

4.23.2.17 gmod_dbsf_chado_gff2seqfeature ($ *db_array*, $ *gff_files*, &$ *context*)

Import a GFF3 to a seqfeature database

See also

gmod_dbsf_chado_gff2chado

Parameters

$db_array
$gff_files
$context

Returns

unknown_type

Definition at line 609 of file gmod_dbsf_chado.module.

4.23.2.18 gmod_dbsf_chado_latest_assembly_serial ($ *variables*)

Get latest est2assembly accession ID

Parameters

$organism_id The organism_id from organism table

Returns

Associative array with 'latest_assembly' (e.g. Ab) and 'next_serial' (int) the next free serial

Definition at line 105 of file gmod_dbsf_chado.module.

4.23.2.19 gmod_dbsf_chado_name2id ($ *name*, $ *table_type*, $ *reverse* = ***FALSE***, $ *reconnect* = ***TRUE***)

Convert a Chado uniquename to an ID

Used by for variety of Chado tables

Todo

expand this function for all tables and also make it work with Drupal too, then move it to gmod_-dbsf.module

Parameters

$name uniquename to fetch

$table_type resource, feature, organism,pub or library

$reverse assume that $name is an internal ID and fetch the uniquename

$reconnect whether to reconnect to Drupal or leave the connection in Chado

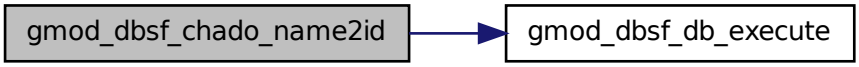
Returns

unknown_type the internal ID or the uniquename if $reverse was used

Definition at line 36 of file gmod_dbsf_chado.module.

References gmod_dbsf_db_execute().

Here is the call graph for this function:



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