LitDB - Tutorial

27.03.2017

Index

Create an account

First of all go to the LitDB webpage:
https://litdb.ikmb.uni-kiel.de

LitDB | Login Page

Please log in below...
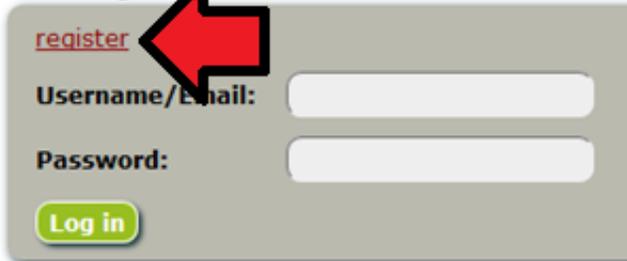
register

Username/Email:

Password:

Log in

To create a new LitDB account click the ‚register'-link on the login page.

LitDB

Registration Page

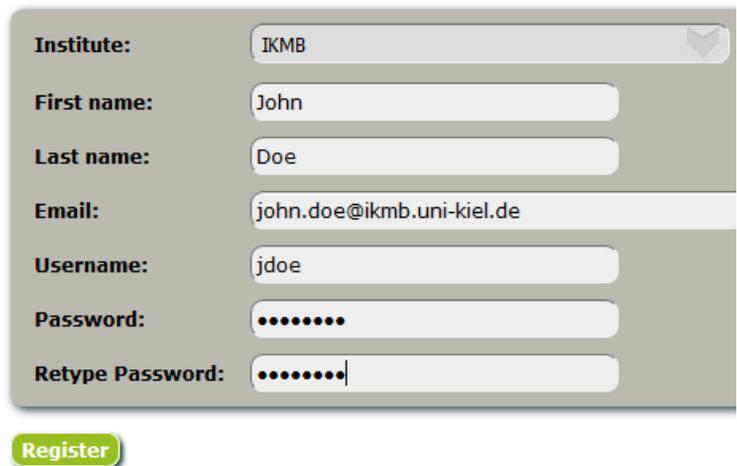| Institute:	IKMB
First name:	John
Last name:	Doe
Email:	john.doe@ikmb.uni-kiel.de
Username:	jdoe
Password:	••••••••
Retype Password:	••••••••

Register

Fill out the registration form and press the ‚Register'-button.

The newly created account will then be activated by an administrator.
After activation you will receive an email.

Logged in? And now?

After the first login perform the following steps:

1. Update your profile
2. Edit your aliases
3. Upload your papers
4. Associate papers with your account
5. Update your citations and statistic

Profile

To open the profile page click on the ‚PROFILE'-link in the menu-bar (1).
Hovering over the ‚PROFILE'-link also opens a sub-menu containing a link for changing your password (2).

You may set your ORCID identifier (3), to enable LitDB to connect to your ORCID account (but at the moment there are no ORCID related features available).

Aliases are very important, they are used for associating papers, contained in the LitDB, to your account. Press the ‚edit'-button (4) next to the alias list to add or remove aliases.

Aliases

Add Alias

Your aliases should encompass all possible variation of your name in an article author list.
For example: "Max Mustermann", "M Mustermann"

Alias List

	Fore Name	Last Name
✖	Lars	Kraemer
✖	L	Kraemer
✖	Lars	Krämer
✖	L	Krämer

Please enter a new alias below...

Fore Name:

Last Name:

add alias ⬅

You can find a link to the alias page on your ‚PROFILE'- and ‚My Space'-page.

Please make sure you enter all possible aliases of your name, which could appear in the author string of an article. This also means, that the ‚Fore Name'-field will contain only the first letter of your first and/or middle names for some aliases (look at the picture above).

My Space - Papers

To open the 'My Space'-page click on the „My Space'-link in the menu-bar (1).
Here you get an overview of your papers, grants, lists, patents, and teams.

On the 'Papers'-tab you will see a summary table of all your papers containing information about impact factors and citations. Furthermore you can associate papers with your account (2) and search/filter for papers already associated.

My Space - Statistics

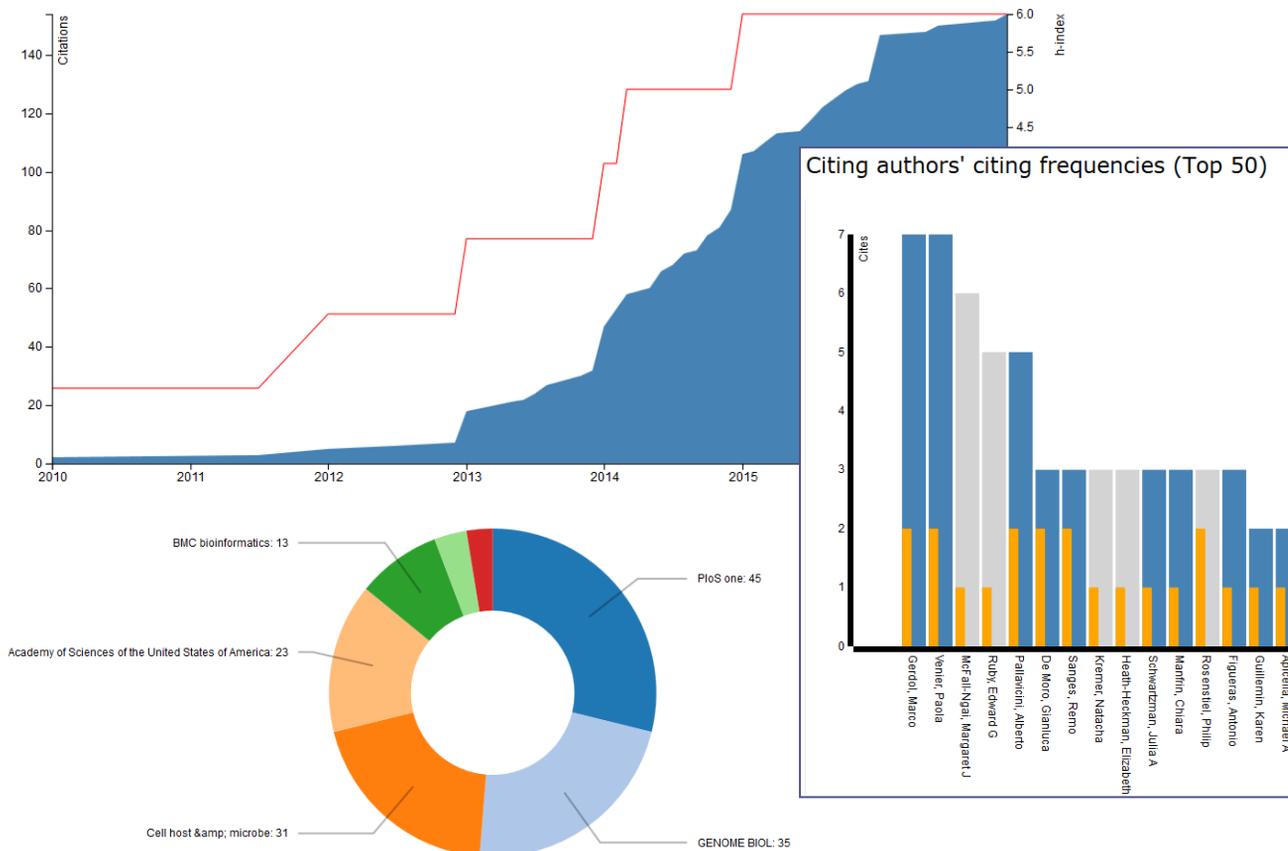The 'Statistics'-tab shows different diagrams regarding your papers, citations, impact factors, co- and citing-authors.
To recalculate the statistics press the 'update'-button.

You may double click on bars or pie slices to jump to a page with related data.

Paper

Original Article: The Transcriptome Analysis and Comparison Explorer--T-ACE: a platform-independent, graphical tool to process large RNAseq datasets of non-model organisms.

E E R Philipp, L Kraemer, D Mountfort, M Schilhabel, S Schreiber, P Rosenstiel 22285826

edit ← 1

Abstract:

MOTIVATION

Next generation sequencing (NGS) technologies allow a rapid and cost-effective compilation of large RNA sequence datasets in model and non-model organisms. However, the storage and analysis of transcriptome information from different NGS platforms is still a significant bottleneck, leading to a delay in data dissemination and subsequent biological understanding. Especially database interfaces with transcriptome analysis modules going beyond mere read counts are missing. Here, we present the Transcriptome Analysis and Comparison Explorer (T-ACE), a tool designed for the organization and analysis of large sequence datasets, and especially suited for transcriptome projects of non-model organisms with little or no a priori sequence information. T-ACE offers a TCL-based interface, which accesses a PostgreSQL database via a php-script. Within T-ACE, information belonging to single sequences or contigs, such as annotation or read coverage, is linked to the respective sequence and immediately accessible. Sequences and assigned information can be searched via keyword- or BLAST-search. Additionally, T-ACE provides within and between transcriptome analysis modules on the level of expression, GO terms, KEGG pathways and protein domains. Results are visualized and can be easily exported for external analysis. We developed T-ACE for laboratory environments, which have only a limited amount of bioinformatics support, and for collaborative projects in which different partners work on the same dataset from different locations or platforms (Windows/Linux/MacOS). For laboratories with some experience in bioinformatics and programming, the low complexity of the database structure and open-source code provides a framework that can be customized according to the different needs of the user and transcriptome project.

Citations: 5 (last update: Feb. 20, 2017, 2:45 p.m.)   2 → update citations

Type	Title	Journal	Year	ID Link
Original Article	Annocript: a flexible pipeline for the annotation of transcriptomes able to identify putative long noncoding RNAs. **Francesco Musacchia et al.**	Bioinformatics	2015	25701574
Original Article	TraV: a genome context sensitive transcriptome browser. **Sascha Dietrich et al.**	PloS one	2014	24709941
Original Article	Age-dependent expression of stress and antimicrobial genes in the hemocytes and siphon tissue of the Antarctic bivalve, Laternula elliptica, exposed to injury and starvation. **G Husmann et al.**	Cell stress & chaperones	2013	23666709
Original Article	TRAPID: an efficient online tool for the functional and comparative analysis of de novo RNA-Seq transcriptomes. **Michiel Van Bel et al.**	GENOME BIOL	2013	24330842
Original Article	Genome and low-iron response of an oceanic diatom adapted to chronic iron limitation. **Markus Lommer et al.**	GENOME BIOL	2012	22835381

Downloads:

- pdf_files/Bioinformatics-2012-Philipp-777-83.pdf ← 3

Journal	Volume	Issue	Pages	Publication Date	Cited Medium	ISSN	ESSN
Bioinformatics	28	6	-	14.03.2012	Internet	1367-4803	1367-4811

Event	Date
aheadofprint	27.01.2012
entrez	31.01.2012
pubmed	31.01.2012
DateCreated	20.03.2012
DateCompleted	04.09.2012
medline	05.09.2012
DateRevised	20.05.2013

Key	Identifier
pii	bts056
doi	10.1093/bioinformatics/bts056
pubmed	22285826

Third Party Project
Excellence Cluster - Inflammation at Interfaces

Team	Description
ZZ Stefan Schreiber (als Project)	Schreibers Publikationen - erstmal als Project

The 'Paper Details'-page displays most of the according papers information stored in the LitDB.

By pressing the 'edit'-button (1) you may add or alter certain paper data.

Here you can also update the paper citations (2) or download an PDF file of the article, if available.

Paper - Import

LitDB | Paper Import

PORTAL | My Space

Import Papers (via search or from files)

Third Party Projects

Institutes

Journals

Papers

Teams

Search   File Upload

Search: ℹ   Author ▽   [   ] search

import ⬅

add manually

To import new publications into the LitDB go to ‚Papers‘ in the side menu and choose the option ‚import‘.
There you may search for certain paper identifiers (PMID, PMCID, DOI), ORCID-Ids, or author names.

You may enter multiple values into the search field, separated by white space. When searching for an author you may enter the last name and first name separated by comma and in double quotes, e.g.: „doe,john".

Paper - Import

Import Papers (via search or from files)

| Search | File Upload |

Search: ⓘ | Author ▼ | "kraemer,l" | search |

Select papers for upload

☑	Title	Journal	Year	PMID
☑	Axiomatic Relation between Thermodynamic and Information-Theoretic Entropies. **Weilenmann M et al.**	Phys Rev Lett	2016	28059535
☑	Body size-dependent Cd accumulation in the zebra mussel Dreissena polymorpha from different routes. **Tang WL et al.**	Chemosphere	2017	27823784
☑	SiglecF+Gr1hi eosinophils are a distinct subpopulation within the lungs of allergen-challenged mice. **Percopo CM et al.**	J Leukoc Biol	2017	27531929

| upload to database | ⬅ 1

Papers already in database:

	Title	Journal	Year	PMID
2 ⬅ ⓘ	Vy-PER: eliminating false positive detection of virus integration events in next generation sequencing data. **Forster M et al.**	Sci Rep	2015	26166306
ⓘ	Initial symbiont contact orchestrates host-organ-wide transcriptional changes that prime tissue colonization. **Kremer N et al**	Cell Host Microbe	2013	23954157

After a search there may appear two lists of papers. The first list contains papers that can be imported into the LitDB. To do this just click the 'upload to database'-button (1).

The second list contains papers already available in the LitDB. If the paper you are searching for appears in this second list, but does not appear in the 'association'-list on your 'My Space'-site, please press the details button (2) to left of the paper title. This leads you to the details page of the paper. Here you can check the author string for your name and compare it to your aliases.

Paper - Import

Import Papers (via search or from files)

Search	**File Upload**

Only the PubMed IDs will be extracted from the uploaded file. Any article entry without such an ID tag cannot be inserted into the database.

File:	Durchsuchen... Keine Datei ausgewählt. (select)
File Formats:	☐ PubMed XML ☑ Mendeley BIB, EndNote XML or text file (with one ID per row)

When searching for a high number of PMIDs or DOIs it is possible to upload a .txt file containing the IDs (one ID per row).
Also PubMed XML, EndNote XML, or BIB files can be uploaded. In this case all PMIDs get extracted from the file and a normal search is performed on this ID list.

Paper - Association

To associate a paper with your account (or edit it) click on the pencil button (1) in the 'papers to associate'-list on your 'My Space'-page or the 'edit'-button on a 'Paper Details'-page.

The articles in the following table contain one of your aliases in the authorlist.

Please confirm/decline the association by clicking on the ✎-icon next to each article.

1	Articles for association:	PMID:
✎ ⓘ	Genome and low-iron response of an oceanic diatom adapted to chronic iron limitation.	22835381
✎ ⓘ	Gene expression and physiological changes of different populations of the long-lived bivalve Arctica islandica under low oxygen conditions.	23028566
✎ ⓘ	Initial symbiont contact orchestrates host-organ-wide transcriptional changes that prime tissue colonization.	23954157

This leads you to the 'Paper associate/edit'-page.

back to details | Upload PDF: [Durchsuchen...] Keine Datei au **upload** | Add to Team: [Biomedical Informatics and Genetic Redefinition of Phenotyp] **add**

Paper Type: [Original Article] **set**

Genome and low-iron response of an oceanic diatom adapted to chronic iron limitation. ⓘ

Markus Lommer, Michael Specht, Alexandra-Sophie Roy, Lars Kraemer, Reidar Andreson, Magdalena A Gutowska, Juliane Wolf, Sonja V Bergner, Markus B Schilhabel, Ulrich C Klostermeier, Robert G Beiko, Philip Rosenstiel, Michael Hippler, Julie LaRoche, Julie Laroche, 22835381

Please select your author position for this paper...

Author Position: [4] **associate** ...brings you back to 'My Space - Papers'

Please select third party projects for this paper...

Projects:
- ☐ DEEP - IHEC German Epigenome Programme
- ☐ e:Med e:AtheroSysMed
- ☐ e:Med sysINFLAME
- ☐ Excellence Cluster - Inflammation at Interfaces
- ☐ GRK1727 - Modulation of Autoimmunity
- ☐ IRTG1911 - Immunomodulation of Inflammation in Allergy and Infection
- ☐ PopGen 2.0 Network
- ☐ PopGen Biobank
- ☐ RTG1743/1 - Genes, Environment and Inflammation
- ☐ SFB 1182 - Origin and Function of Metaorganisms
- ☐ SFB 877 - Proteolysis as a Regulatory Event in Pathophysiology

associate

Here you may set your author position by selecting it from the dropdown-list and pressing the 'associate'-button.

Furthermore you may set paper type, upload a PDF file of the article, or associate it with third party projects and teams.

Paper - Search

The paper search can be reached by clicking the 'Papers'-button in the left menu.

Search:
You may enter multiple values separated by ',' into one search field. The field will always use '=' as search condition.
When using the 'LIKE' or '*LIKE*' condition, use '*' as wildcard for zero or more characters and '_' for a single character.
The '*LIKE*' condition adds wildcards on both sides automatically.