

BIOMINA

BIOMEDICAL INFORMATICS NETWORK ANTWERP



Core facility UAntwerp

Active in Health & Environment

BIOMINA is the expertise hub for bioinformatics. Core facility manager Andrea Bours explains what makes this interdisciplinary network of data scientists and life scientists so unique and how the expertise that is brought together here helps companies move forward:

“New techniques in biomedical sciences, the shift towards digital healthcare and the rise of AI mean that we are increasingly confronted with ever larger and more complex data sets. But these are only valuable when they can be properly processed and interpreted. This requires specialized computer techniques, but of course not everyone who is active in the life sciences is also at home in the field of bioinformatics.

Whether it concerns data produced from biomedical, clinical or biological research, companies, hospitals and research centers can all come to us to transform their generated data into clear insights.

BIOMINA has been active at the interface between data and life sciences for years, resulting in a strong knowledge community of bioinformatics scientists. We can now offer the knowledge and specialized techniques

that we have developed during this time as a service to companies. We do this through research collaborations, through training or by providing support in the various phases of a project, ranging from experimental design and analysis to interpretation of results.

Finally, we are in a position to very closely follow innovations in the data science research field. That allows us to quickly translate them in light of new trends, assess their applications in life

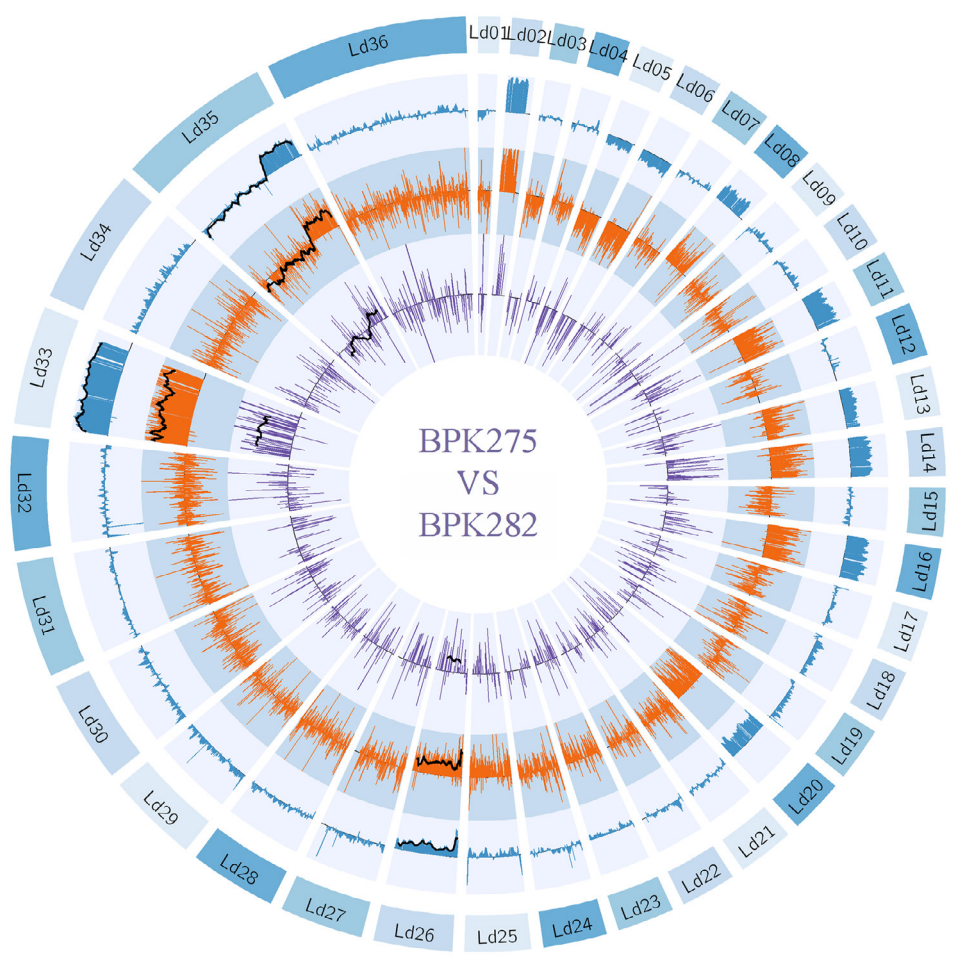
sciences topics and always apply the latest techniques.”


Curious how BIOMINA can help with the analysis and/or interpretation of your data? Andrea Bours would be happy to discuss it with you.

- ▶ Companies, hospitals and research centers can all come to us to transform their generated data into clear insights.

Through a multi-omics approach we can combine transcriptomics, proteomics and genomics, resulting in new insights.
© 2022 Cuypers, et al. PLOS Pathogens.

BIOMINA



 TCRex: a web tool for the prediction of TCR-epitope recognition

[TCRex](#) [Home](#) [Instructions](#) [New epitopes](#) [Statistics](#) [About](#) [Contact](#) [Release notes](#)

Welcome to TCRex!

TCRex predicts **TCR-epitope binding for human T cell receptors (TCRs)** using TCR beta chain information, i.e. the CDR3 amino acid sequence and the corresponding V/J genes. It is based on **random forest classifiers** trained on epitope-specific TCR data collected from the manually curated catalogue of pathology-associated T cell receptor sequences ([McPAS-TCR](#)), the VDJ database ([VDJdb](#)) and the [ImmuneCODE™](#) database. In total prediction models for 98 different epitopes, consisting of **93 viral** and **5 cancer epitopes**, are provided. Check the [statistics](#) page for detailed information about the performance of the individual prediction models.

Although TCRex supports a wide range of epitopes it might not include a prediction model for your epitope(s) of interest. However, in this case you can use our optimized machine learning and prediction workflow to train your own custom model using the [new epitopes](#) page.

In addition, TCRex can be used to perform epitope-specificity enrichment analyses to identify the epitopes that are targeted by the uploaded TCR data set.

Detailed information on how to use TCRex and interpret the results is provided on the [instructions](#) page.

Predict TCR-epitope binding

Select your TCR sequence data file: No file selected.

TCRex supports sequence data information in the TCRex format, the MIXCR format, and the immunoSEQ ANALYZER format (version 1 & 2).
Attention: TCRex only supports prediction files with at most 50 000 TCR sequences.

Select epitope(s)

Select the model version: 2022-12-06 ▾

| | | | | | |
|--------------------------------------|-------------------------------------|------------------------------------|---|-------------------------------------|-------------------------------------|
| <input type="checkbox"/> Viral | <input type="checkbox"/> Cancer | | | | |
| <input type="checkbox"/> CMV | <input type="checkbox"/> Melanoma | | | | |
| <input type="checkbox"/> IPSINVHHY | <input type="checkbox"/> NLVPMVATV | <input type="checkbox"/> QIKVRVKMV | <input type="checkbox"/> AMFWSVPTV | <input type="checkbox"/> EAAGIGILTV | <input type="checkbox"/> ELAGIGILTV |
| <input type="checkbox"/> QYDPVAALF | <input type="checkbox"/> VTEHDTLLY | <input type="checkbox"/> FLYNLLTRV | <input type="checkbox"/> Multiple Myeloma | | |
| <input type="checkbox"/> YSEHPTFTSQY | <input type="checkbox"/> TPRVTGGGAM | <input type="checkbox"/> LLLGIGILV | | | |

TCRex is a web tool that uses machine learning to recognize TCR epitomes, developed in collaboration with BIOMINA.
© 2018 Gielis, et al. TCRex.

BIOMINA is ...

Bio-informatica · Biomedical data sciences · Biomedical informatics ·
AI · Machine learning · Genomics · Transcriptomics · Proteomics · Big data ·
Digital Health · Software · Interdisciplinary network

BIOMINA

► **Biomina has truly revolutionised my work
and reshaped my research activities.**

Quote from Prof. dr. Benson Ogunjimi, Antwerp
University Hospital and VAXINFECTIO-PO (UAntwerp)

Research groups and expertise

BIOMINA was created by the University
of Antwerp and the Antwerp University
Hospital.

Within the university we combine
expertise from three faculties:

- Faculty of Medicine & Health
Sciences
- Faculty of Pharmaceutical,
Biomedical and Veterinary Sciences
- Faculty of Sciences

Because BIOMINA was founded as a
network, we transcend the boundaries
of the faculties, so to speak, thus
combatting the fragmentation of
expertise between faculties and
research groups. This means that for
every request that comes to BIOMINA,
someone can always be found within
the network who has the right expertise
and background.

In addition, there is close collaboration
with other core facilities and structures
within UAntwerp, including, for
example, the Centre for Proteomics
(processing of data they have
generated) and CalcUA / Flemish
Supercomputer Center (use of the
hardware they have available).

Collaborations have been in place with
the UZA for years, which has allowed
BIOMINA to build up a wealth of
experience with clinical practice. Finally,
certain collaborations have also resulted
in spin-offs, such as ImmuneWatch.

Collaboration is possible through...

Collaborative research · Contract research · Doctorates / postdoctorates
· Use of bioinformatic workflows · Master theses · Customized training ·
Service contracts · Internships

Unique features of our equipment

BIOMINA develops and has established a range of bioinformatic workflows that allow data to be processed into insights, and has the expertise to use these workflows and interpret the results.

Many of these workflows can be adapted to the needs of a company, or custom workflows can be devised.

BIOMINA currently has workflows for the analysis of genomic, transcriptomic and proteomic data, from bulk to single-cell sequencing. The workflows can integrate different data sets with each other and BIOMINA also uses machine learning and AI to analyze data.

BIOMINA collaborates with all kinds of (external) parties that have equipment to generate specific data.



Contact BIOMINA

Andrea Bours
Campus Middelheim
biomina@uantwerpen.be
www.biomina.be