



## Emma Ricart

Bioinformatician & Developer

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## Hard-skills

Data analysis 9+ yrs

Software development 8+ yrs.

Web development 7+ yrs.

## Soft-skills

- ▶ Learning agility
- ▶ Teamwork
- ▶ Communication skills
- ▶ Critical thinking
- ▶ Enthusiasm
- ▶ Initiative
- ▶ Trustworthiness
- ▶ Presentation skills

## Languages

English C1

French B1

Spanish & Catalan C2

## Profile

Bioinformatician in the intersection of data analysis, pipeline design and software development. In the era of big data, my goal is to formulate data-driven hypothesis and validate them. I achieve this by 1) performing statistical analyses, 2) creating tools for data visualization, 3) developing pipelines or 4) building computational infrastructures such as databases. I hold a PhD in Bioinformatics and I conducted interdisciplinary research working with biologists, physicists and software engineers. I'm deeply committed to promoting best programming practices for shareable and reproducible research!

## Work experience

### Bioinformatician | Database administrator

02/2021 - 02/2024

Bassani Lab (Prof. Michal Bassani)

AGORA Cancer Research Center - Lausanne

- Developed a workflow for large-scale identification and quantification of HLA/HLAII peptides from mass spectrometry experiments
- Implemented an ETL process for the creation of an immunopeptidomics data warehouse which included +1.000.000 peptides identified with the workflow
- Used the collected data to create a scoring system for the prioritization of neoantigens, directly impacting the clinical trials
- Build a web interface for querying and visualizing the database

*Python - R - Bash - Nextflow - HPC - Immunopeptidomics - Mass spectrometry - Data Visualization - Biological Data Analysis - Docker - Software development - Git*

### Ph.D. Student

09/2015 - 09/2019

Proteomic Informatics Group (Frederique Lisacek)

Swiss Institute of Bioinformatics (SIB) - Geneva

- Developed rBAN, a java package and web application tool for the retro biosynthesis of non-ribosomal peptides
- Developed NRPro, a web application tool for the identification and annotation of tandem mass spectra from peptidic natural products
- Worked with SMILES format and graph structures for the substructures search and the fragmentation algorithms used by the tools
- Build a NoSQL database for the backend of NRPro integrating data from Norine, ChEBI and Natural Products Atlas

*Java - R - Maven - MongoDB - AngularJS - Mass spectrometry - Peptidomics - Data Visualization - Biological Data Analysis - Software development - Git*

### Junior Bioinformatician

02/2015 - 09/2015

The Chuang Lab (Prof. Jeffrey H. Chuang)

JAX Cancer Center - Connecticut

- Analyzed iCLIP data from ENCODE project to study RNA-protein binding sides

*Python - R - Perl - Bash - HPC - Biological Data Analysis - Statistics - Data Visualization - Transcriptomics*

### Bioinformatics researcher

09/2014 - 02/2015

Computational Genomics group (Prof. Eduardo Eyras)

PRBB - Barcelona

- Analyzed and quantified iTRAQ mass spectrometry data from the TCGA project to validate findings identified at RNA level

## Programming

- Python
- R
- Bash
- Nextflow
- Java
- Perl
- Javascript
- HTML & CSS

## Server side

- Docker & Conda
- MongoDB & PostgreSQL
- Tomcat
- Node.js
- REST API
- HPC

## Frameworks/Libs

- Django
- AngularJS
- React & Next.js
- Bootstrap & MaterialUI
- JUnit

## Development tools

- Maven
- Git
- Jenkins

### Master's Student

Computational Proteomics group (Fredrik Levander)

📍 Lund University - Sweden

- Identified and quantified of protein variants using a combination of shotgun proteomics and DIA LC-MS
- Applied statistical analysis to the proteins identified for biomarkers discovery

02/2014 - 06/2014

## Education

### Ph.D. in Bioinformatics

Swiss Institute of Bioinformatics (SIB)

University of Geneva

09/2015 - 09/2019

### Master's degree in Biomedical engineering

University of Barcelona

Polytechnic University of Catalonia

Lund University

09/2012 - 09/2014

### Bachelor's degree in Biotechnology

University of Vic - Central University of Catalonia

09/2007 - 09/2011

## Awards

### Winner Best Lighting Talk Award

SIB Days Awards 2018

2018

### SIB PhD Fellowship Laureate

SIB Fellowship Program 2015

2015

### Fundació Agrupació Master's Degree Grant

Fundació Agrupació Awards 2013

2013

## Relevant publications

Ricart, Emma, Maude Pupin, Markus Muller, and Frédérique Lisacek. Automatic annotation and dereplication of tandem mass spectra of peptidic natural products. *Analytical Chemistry*, 92(24):15862–15871, 2020.

Ricart, Emma, Valérie Leclère, Areski Flissi, Markus Mueller, Maude Pupin, and Frédérique Lisacek. rban: retro-biosynthetic analysis of nonribosomal peptides. *Journal of cheminformatics*, 11(1):1–14, 2019.

Areski Flissi, Ricart, Emma, Clémentine Campart, Mickael Chevalier, Yoann Dufresne, Juraj Michalik, Philippe Jacques, Christophe Flahaut, Frédérique Lisacek, Valérie Leclère, et al. Norine: update of the nonribosomal peptide resource. *Nucleic acids research*, 48(D1):D465–D469, 2020.

Markus Müller, Florian Huber, Marion Arnaud, Anne Kraemer, Altimiras, Emma Ricart, Justine Michaux, Marie Taillandier-Coindard, Johanna Chiffelle, Baptiste Murgues, Talita Gehret, et al. Machine learning methods and harmonized datasets improve immunogenic neoantigen prediction. *Immunity*, 56(11):2650–2663, 2023.

Anne Kraemer, Chloe Chong, Florian Huber, HuiSong Pak, Brian J Stevenson, Markus Müller, Justine Michaux, Altimiras, Emma Ricart, Sylvie Rusakiewicz, Laia Simó-Riudalbas, et al. The immunopeptidome landscape associated with t cell infiltration, inflammation and immune editing in lung cancer. *Nature Cancer*, pages 1–21, 2023.