

Stefano Grasso



4 Rue Copernic,
Marcq-en-Baroeul, FR



+33 7 513 776 36



stefano@2000e.it



in/stefano-grasso-
biotech



ResearchGate
Personal Website

Professional skills

Molecular Biology



Microbiology



Functional analyses
and predictions



Project and people
management



Python



Bash



HPC



Automation



NGS-workflow
(design, execution,
data analysis)



git



Biochemistry



IPR



Experience

- 07/22 - now **Multiplex Synthetic Biology Scientist** [Lesaffre International, Lille, FR](#)
High-throughput scientist in the newly established Biofundry. Implementing NGS approaches (transcriptomics, genome and plasmid sequencing), LIMS (Benchling) and related integrations with manual and automated instruments. Working on *S. cerevisiae*.
- 03/21 - 05/22 **Post-Doctoral fellow** [CBGP, UPM, Madrid, ES](#)
Lab manager and tech specialist at the Biocomputation Lab. I set-up a new synthetic biology laboratory, complemented with an automated liquid handler and a 3D printer for smart and innovative solutions. Using SynBio to study and exploit spatial transcriptomics in *P. putida*. I also supervised one Master's student. Group leader: Dr. Angel Goñi Moreno.
- 09/15 - 12/20 **PhD candidate** [University medical center Groningen \(UMCG\), Groningen, NL](#)
MSCA-ITN fellowship within ProteinFactory (proteinfactory-msca-itn.eu). I spent approximately half of my PhD in an academic context: here I have mainly learned and worked on cloning and transformation for *B. subtilis* and *E. coli*, at the same time I have been working on a prediction tool, I started a number of collaborations providing mainly bioinformatic support and knowledge, and supervised one Master's student.
- 04/17 - 12/19 **PhD candidate** [DSM B.V., Delft, NL](#)
MSCA-ITN fellowship within ProteinFactory (proteinfactory-msca-itn.eu). I spent the second half of my PhD in an industrial context: here I designed, cloned and transformed a 13k elements DNA library in *B. subtilis*, generated a ML predictive model which was then studied with SHAP to provide an interpretation, and experimentally validated the model. Additionally, I kept working on other projects (both *in vitro* and *in silico*) and on a number of collaborations, and also supervised one Master's student.
- 07/17 - 08/17 **Visiting PhD candidate** [FGen GmbH, Basel, CH](#)
Short period where combining the usage of a specific proprietary technology (NLR) with particle sorting (COPAS), I was able to screen a 13k elements DNA library for different protein secretion levels.
- 02/16 - 04/16 **Visiting PhD candidate** [SciLifeLab, Stockholm, SE](#)
Short period where I worked and collaborated with a group bioinformaticians in order to improve my programming skills and gain knowledge about predictions in a biological context.
- 02/15 - 05/15 **Erasmus+ traineeship** [Leibniz Institute of Plant Genetics and Crop Plant Research \(IPK\), Gatersleben, DE](#)
Optimization of Hi-C library preparation in different tissues of barley; Hi-C and TCC library preparation procedures for green and etiolated barley seedling leaf tissue; Hi-Seq 2000 sequencing.
- 02/14 - 12/14 **Academic tutor** [Udine University, Udine \(UD\), IT](#)
Assistance and support to students, both on didactic and administrative duties and issues. Organization of "Nursing café" and a job fair for nursery students.
- 09/12 - 03/13 **Erasmus Project** [Gothenburg University, Gothenburg, SE](#)
During Erasmus I have been following various courses and working on production and purification of hAQP10 in yeast.

Languages

Italian ★★★★★

English ★★★★★

French ★★★★★

Soft Skills



01/12 - 07/12 **IT support**

[Udine University, Udine \(UD\), IT](#)

Assistant of the IT helpdesk, dealing with public in order to solve customer and system problems.

Education

2015 - 2020 **PhD in Medical Microbiology**

[Rijksuniversiteit Groningen, Groningen, NL](#)

MSCA-ITN fellowship within ProteinFactory ([proteinfactory-msca-itn.eu](#)). Supervisors: Prof. Jan Maarten van Dijl (UMCG), Dr. Tjeerd van Rij (DSM B.V). Main research topic: protein secretion in *Bacillus subtilis*. Thesis: "Bacterial protein sorting: experimental and computational approaches" doi: 10.33612/diss.150510580.

2010 - 2015 **Diploma di Licenza della Scuola Superiore**

[Scuola Superiore dell'Università degli Studi di Udine, Udine \(UD\), IT](#)

Grade: 110 *cum laude*/110. Institute of excellence providing a scholarship covering living expenses and tuition fees. Additionally, it integrates the normal university courses with both interdisciplinary and more advanced ones. For more info: [scuolasuperiore.uniud.it](#)

2013 - 2015 **Master of Science in Plant and Animal Biotechnology**

[Udine University, Udine \(UD\), IT](#)

Grade: 110 *cum laude*/110. All the courses were taught in English. Thesis: "Production and optimization of next generation sequencing libraries for contact genomics analysis in *Hordeum vulgare* and *Vitis vinifera*"; supervisor: Prof. Michele Morgante. EQF level 7.

2010 - 2013 **Bachelor of Science in Biotechnology**

[Udine University, Udine \(UD\), IT](#)

Grade: 110 *cum laude*/110. Thesis: "Effects of nutraceuticals on human visceral preadipocytes and adipocytes: preliminary results"; supervisor: Prof. Monica Colitti. EQF level 6.

2005 - 2010 **Scientific High School Diploma**

[ITIS G.C. Faccio, Vercelli \(VC\), IT](#)

Grade: 100 *cum laude*/100. EQF level 4.

Other positions held

2/22 - Now **Steering Committee Member**

[EUSynBioS, Paris, France](#)

The European Synthetic Biology Society is an association dedicated to bringing together synthetic biologists from across Europe and beyond. EUSynBioS strives to support synthetic biology researchers in Europe, promote European synthetic biology in our conferences, collect and distribute up-to-date news on the field, and build a network of investigators, academics, and industry representatives. Some activities I was involved in: organizing the first talk about Biofoundry in Italian, publication and poster about synthetic biology in Europe, organizing event, interviewing and recruiting.

- 12/20 - Now **Board Member** [Alumni of the Scuola Superiore Association, Udine \(UD\), IT](#)
 Association grouping the Alumni of the Scuola Superiore of the University of Udine. Association goals are to promote culture and knowledge within the general public, to orient talented high school students toward institutes of excellence, to orient and support students of the Scuola Superiore toward academic and industrial careers. Some activities I was involved in: organizing 'Meet the Alumni' sessions, 'Scintillae', a daily in-presence event for Alumni, and fostering a network of Alumni from the various Excellence Institutes.
- 01/14 - 02/15 **Member of the Academic Quality Board** [Udine University, Udine \(UD\), IT](#)
 Board in charge for evaluating and promoting quality at both didactic and research levels.
- 05/12 - 11/14 **Elected member in the Academic Senate as student representative** [Udine University, Udine \(UD\), IT](#)
 Highest steering body within universities. I worked toward rationalizing didactic laboratories expenses proposing a project based approach; defined rules for meritocratic student awards assignment; promoted realistic internationalization of the university; counseled university staff during redefinition of tuition fees; promoted quality and rationalization both throughout courses and research activities; advocated for student rights and fair treatment.
- 01/12 - 08/12 **Vice-president** [Student association "Neoateneo", Udine \(UD\), IT](#)
 Coordination and execution of association activities such as: fundraising, projects proposal, task assignment, verification of financial statements.
- 05/12 - 11/14 **Elected member of Scuola Superiore in the Governing Council** [Rete Italiana degli Allievi delle Scuole e degli Istituti di Studi Superiori Universitari](#)
 Represented Scuola Superiore at the Network of the Excellence Institutes and Schools in Italy. Promoted the transformation of the Network into an official association, achieved in 2016. Reformed the "Rete di Idee" contest introducing peer-review and double-blind, standardizing procedures and evaluation. Organized the 2014 edition of the "Rete di Idee" held in Udine. Advocated and paved the way for openness of the Network toward newly established Institution and Schools, based on high standard of excellence, and for respect toward the different approaches (fully achieved with the following Council).
- 05/11 - 11/14 **Member of the University Student Council** [Udine University, Udine \(UD\), IT](#)
 Highest student representative body within universities.
- 05/11 - 05/12 **Elected member in the Veterinary Faculty Council** [Udine University, Udine \(UD\), IT](#)
 Proposed the creation of a M.Sc. in Molecular Biotechnology in order to rationalize courses and exploit University excellence in the field; it has been created in 2016. Counseled to optimize and improve courses for future students in B.Sc. Biotechnology.

Professional skills

Main laboratory techniques: PCR, RT-PCR, qPCR, electrophoresis, design and perform molecular cloning (Gibson, GoldenGate, OE-PCR...), biobricks-oriented approaches, transformation (mainly *E. coli*, *B. subtilis*, *P. putida*), DNA/RNA extraction and purification, **DNA quantification** (UV, Nanodrop, Qbit, Bioanalyzer/capillary electrophoresis), variant library design and construction, **NGS**-library preparation, sequencer usage (iSeq, NextSeq2000, MinION), **Hi-C**. Enzymatic assays, protein extraction, PAGE, western blotting, mass-spectrometry proteomics-data analysis. Cultures of bacteria and yeast, replica plating, bacterial growth assays, **large particle flow cytometry (COPAS)**, **flow cytometry**.

Usage of **automated liquid handlers** (TECAN EVO) and their programming (OT-2).

Main bioinformatics skills: **Python** (including scikit-learn and shap) and **BioPython**, **bash**, git, \LaTeX , high-performance computing (**HPC**)/cluster computing (e.g. SLURM). Advanced usage of gene and protein data-bases, understanding of algorithms for biological purposes (e.g. local and global alignment, HMMs), command-line and API bioinformatic tools for molecular biology, functional annotation of proteins, **development of prediction tools and pipelines**, NGS classical workflow. Basic knowledge of **AWS**, C/C++, Ruby and Java. Ability to understand code from other languages for bug-fixing or small customization. Ability to prepare cartoons and data-figures for articles.

Management skills: I have been involved in coordinating and contributing to association activities since I started university, and I have been (co-)organizing events (both professional and leisure) since high school (up to 500 participants). I further developed **project management** skills during the PhD *via* multiple courses and learning by doing, as well as during the establishment of the Biocomputation lab. Timing of projects through Gantt charts, setting goals, KPI, and checkpoints through working packages, milestones, and deliverables. Skilled in both scientific communication, in particular **cross-communication** between different areas, and diplomatic communication, due to institutional positions held. Advanced **people management** skills developed by supervising students during my academic career (3 graduated master students) and by coordinating consultants and technicians at Lesafre. Thanks to my broad international and diverse experience, and an innate empathy, I can easily relate to people, make them comfortable, and motivate them to reach personal and professional milestones. Good organizational, decision-making, team-player, and leading skills, and capacity to form long-lasting professional networks, initially developed while holding institutional positions at Udine University.

Transferable skills: Eager learner, flexible, innovator. Great research and analytical skills also in other fields (understanding norms, laws and rules about both scientific and academic topics), **problem solving and rationalization**. **3D printing** (printer assembly, design, printing) with Prusa and **basic 3D design** (Fusion360/Autocad Inventor).

Publications

Signal Peptide Efficiency: From High-Throughput Data to Prediction and Explanation.

S. Grasso, V. Dabene, M. M. W. B. Hendriks, P. Zwartjens, R. Pellaux, M. Held, S. Panke, J. M. van Dijk, A. Meyer, and T. van Rijk

ACS synthetic biology (Jan. 2023). *American Chemical Society (ACS)*, 2023, doi: [10.1021/acssynbio.2c00328](https://doi.org/10.1021/acssynbio.2c00328)

Synthetic biology in Europe: current community landscape and future perspectives

S. Donati, I. Barbier, D. A. García-Soriano, **S. Grasso**, P. Handal-Marquez, K. Malci, L. Marlow, C. Westmann, and A. Amara

Biotechnology Notes 3 (2022) pp. 54–61. Elsevier BV, 2022, doi: <https://doi.org/10.1016/j.biotno.2022.07.003>

Proteomic Charting of Imipenem Adaptive Responses in a Highly Carbapenem Resistant Clinical *Enterobacter roggkampii* Isolate

S. Nepal, S. Maaß, **S. Grasso**, F. M. Cavallo, J. Bartel, D. Becher, E. Bathoorn, and J. M. van Dijk

Antibiotics 10.5 (5 Apr. 2021) p. 501. MDPI AG, 2021, doi: [10.3390/antibiotics10050501](https://doi.org/10.3390/antibiotics10050501)

GP4: an integrated Gram-Positive Protein Prediction Pipeline for subcellular localization mimicking bacterial sorting.

S. Grasso, T. van Rijk, and J. M. van Dijk

Briefings in bioinformatics 22.4 (Nov. 2020). Oxford University Press (OUP), 2020, doi: [10.1093/bib/bbaa302](https://doi.org/10.1093/bib/bbaa302)

Gingimaps: Protein Localization in the Oral Pathogen *Porphyromonas gingivalis*

G. Gabarrini, **S. Grasso**, A. J. van Winkelhoff, and J. M. van Dijk

Microbiology and molecular biology reviews : MMBR 84.1 (1 Feb. 2020). American Society for Microbiology, 2020, doi: 10.1128/MMBR.00032-19

An ancient family of mobile genomic islands introducing cephalosporinase and carbapenemase genes in *Enterobacteriaceae*.

S. Nepal, F. Bonn, **S. Grasso**, T. Stobernack, A. de Jong, K. Zhou, R. Wedema, S. Rosema, D. Becher, A. Otto, J. W. Rossen, J. M. van Dijl, and E. Bathoorn

Virulence 9.1 (1 Aug. 2018) pp. 1377–1389. Informa UK Limited, 2018, doi: 10.1080/21505594.2018.1509666

Signatures of cytoplasmic proteins in the exoproteome distinguish community- and hospital-associated methicillin-resistant *Staphylococcus aureus* USA300 lineages.

S. A. Mekonnen, L. M. Palma Medina, C. Glasner, E. Tsompanidou, A. de Jong, **S. Grasso**, M. Schaffer, U. Mäder, A. R. Larsen, H. Gumpert, H. Westh, U. Völker, A. Otto, D. Becher, and J. M. van Dijl

Virulence 8.6 (6 Aug. 2017) pp. 891–907. Informa UK Limited, 2017, doi: 10.1080/21505594.2017.1325064

Construction of a map-based reference genome sequence for barley, *Hordeum vulgare* L.

S. Beier, A. Himmelbach, C. Colmsee, X.-Q. Zhang, R. A. Barrero, Q. Zhang, L. Li, M. Bayer, D. Bolser, S. Taudien, M. Groth, M. Felder, A. Hastie, H. Šimková, H. Staňková, J. Vrána, S. Chan, M. Muñoz-Amatriaín, R. Ounit, S. Wanamaker, T. Schmutzer, L. Aliyeva-Schnorr, **S. Grasso**, J. Tanskanen, D. Sampath, D. Heavens, S. Cao, B. Chapman, F. Dai, Y. Han, H. Li, X. Li, C. Lin, J. K. McCooke, et al.

Scientific data 4.1 (Apr. 2017) p. 170044. Springer Science and Business Media LLC, 2017, doi: 10.1038/sdata.2017.44

A chromosome conformation capture ordered sequence of the barley genome.

M. Mascher, H. Gundlach, A. Himmelbach, S. Beier, S. O. Twardziok, T. Wicker, V. Radchuk, C. Dockter, P. E. Hedley, J. Russell, M. Bayer, L. Ramsay, H. Liu, G. Haberer, X.-Q. Zhang, Q. Zhang, R. A. Barrero, L. Li, S. Taudien, M. Groth, M. Felder, A. Hastie, H. Šimková, H. Staňková, J. Vrána, S. Chan, M. Muñoz-Amatriaín, R. Ounit, S. Wanamaker, D. Bolser, C. Colmsee, T. Schmutzer, L. Aliyeva-Schnorr, **S. Grasso**, et al.

Nature 544.7651 (7651 Apr. 2017) pp. 427–433. Springer Science and Business Media LLC, 2017, doi: 10.1038/nature22043

Base excision repair in Archaea: back to the future in DNA repair.

S. Grasso and G. Tell

DNA repair 21 (Sept. 2014) pp. 148–157. Elsevier BV, 2014, doi: 10.1016/j.dnarep.2014.05.006

Nutraceuticals and regulation of adipocyte life: premises or promises.

M. Colitti and **S. Grasso**

BioFactors (Oxford, England) 40.4 (4 Apr. 2014) pp. 398–418. Wiley, 2014, doi: 10.1002/biof.1164

Conferences

- 2022 **ASBE VI (6th Applied Synthetic Biology in Europe)** Edinburgh, UK
Oral presentation: “Signal peptide efficiency: from high-throughput data to prediction and explanation”
- 2022 **SEED (Synthetic Biology: Engineering, Evolution & Design)** Arlington, VA, USA
Poster presentation: “Modulating intracellular space-filling to fine-tune gene regulatory interactions”
- 2021 **KNVM (Royal Dutch Society of Microbiology)** Virtually held
Poster presentation: “Signal-based, tailored, and (re-)interpretable protein sub-cellular localization predictions in Gram-positive bacteria through a novel meta-predictor”

- 2019 **GIM (Genetics of Industrial Microorganisms)** [Pisa, IT](#)
Oral presentation: "Homology-independent prediction of subcellular protein localization in beneficial and engineered microbes"
- 2018 **SDD (Supranational Democracy Dialogue)** [Lecce, IT](#)
Oral presentation: "Educated Democracy: Creating the Tools for an Aware Democratic System"

Additional information, courses, certificates and copies of publications and thesis are available upon request.

Stefano Grasso