

Luigi D'Ascenzo, Ph.D.

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San Diego (CA)

Summary of Qualifications

- Computational scientist with **8** years of experience in software development for data analysis and data mining of structural biology databases with a focus on RNA.
- International scientific impact through **9** peer-reviewed publications (**5** first author), with **150** citations (h-index **6**, Google Scholar data).
- Experienced in written and oral communication with **5** invited talks and seminars, **2** oral presentations and **14** posters at national and international scientific conferences.
- Demonstrated collaborative and leadership abilities through team and project management.

Current Position

The Scripps Research Institute,

Department of Integrative Computational and Structural Biology (La Jolla, CA)

Apr 2017-Present

Postdoctoral Fellow, Prof. James Williamson Lab

- Leader of the development of **Pytheas**, a novel software workflow for the analysis of LC-MS/MS data on RNA. It focuses on the modification and flexible isotopic labelling schemes, with incorporated statistical analysis.
- Performed **quantitative proteomics** analysis on samples from marine bacteria *Vibrio splendidus*, employing a pipeline based on the Trans Proteomic Pipeline (TPP) integrated with custom Python and R scripts.
- Grown *E. coli* cells with selective genetic deletion for proteomics studies on proteins degradation.
- Elaborated a model to generate a movie of the **bacterial ribosome transcription and folding**. This model is based on coarse-grained Molecular Dynamics simulations coupled with 3D modelling.
- Prepared **3D-printed models** of several simulation snapshots of the ribosome assembly, in order to build a real-life model of the fundamental cellular process of ribosome biogenesis.
- Managed and improved the laboratory website; supervised two laboratory servers, used by multiple users for various scientific applications.

Previous Research Experience

University of Strasbourg, Institute of Molecular and Cellular Biology (Strasbourg, France) **Sep 2013-Dec 2016**

Graduate Researcher, Prof. Pascal Auffinger Lab

Ph.D. Thesis: “Atomic-scale investigation of recognition networks in RNA and RNA/protein systems”

- Analyzed **RNA** and **RNA-protein interactions** at the atomic scale through data mining studies of available structural data from the Protein Data Bank (PDB).
- Established and maintained a **MySQL database** with more than 1 million entries of structural RNA data (at the atomic-level definition), from the PDB X-ray structures.
- Studied the binding of **metal ions (Mg²⁺, Na⁺, K⁺)** to RNA within crystallographic structures and the pitfalls associated with their structural determination.
- Developed and implemented automated pipelines for **PDB data mining** via custom Python and Perl scripts.
- Performed **Molecular Dynamics** (MD) simulations on RNA hairpin loops and transfer RNA (tRNA), focusing on solvent and chemical modification stabilization effects.
- Developed Python scripts for the analysis of MD results.
- Completed sequence alignment on ribosomal RNAs from all life domains. These molecules vary in size between one and four thousand bases.
- **Mentored** a Master Student for 6 months, focusing on MD of tRNAs.

University of Strasbourg, Institute of Molecular and Cellular Biology (Strasbourg, France)

Jan-Jul 2013

Undergraduate Research Intern, Prof. Pascal Auffinger Lab

- Collaborated to the development of a **web server** of RNA structural data.
- Analyzed the protonated and tautomeric forms of RNA nucleic acids, via data mining from PDB crystallographic structures.

University Tor Vergata, Department of Chemistry (Rome, Italy)

Mar-Jun 2011

Undergraduate Training Fellow, Prof. Barbara Floris Lab

- Optimized the **total synthesis of compounds of the quinone class**, by studying different reaction conditions.
- Purified the products with **chromatographic techniques**: silica column chromatography, analytical and preparative thin-layer chromatography (TLC), analytical and preparative high-performance liquid chromatography (HPLC).
- Characterized the physico-chemical properties of the quinones via Nuclear Magnetic Resonance (NMR) and Cyclic Voltammetry.
- Elaborated models of the quinone synthesis reaction mechanism.

Education

University of Strasbourg, France

- **Ph.D. in biochemistry and biophysics**, Institute of Molecular and Cellular Biology (September 2016).
- **M.Sc. with first class honor in chemistry and biology**, specialization: pharmaceutical chemical biology, Department of Chemistry (June 2013).

University of Tor Vergata, Rome, Italy

- **B.Sc. cum laude in chemistry**, specialization: organic chemistry (June 2011).

Skills

- **Programming Languages**: Python, HTML, JavaScript, CSS, XPLOR-NIH, R, SQL, Bash/Shell script.
- **3D visualization/modelling software**: PyMol, Chimera, VMD.
- **Other Scientific Software**: ChemDraw, MySQL, UniPro UGENE, EndNote, Evernote, Adobe Illustrator.
- **Statistical analysis tools**: R, StatCrunch and Microsoft Excel.
- **Quantitative Proteomics**.
- **Mass Spectrometry**: QTOF MS/MS, Triple TOF MS/MS.
- Data analysis and model building for **X-ray crystallography**.
- Writing scientific manuscripts and reports and presenting the outcome of research.
- Excellent communication skills, ability to work in a team or independently with minimal supervision.
- Ability to multitask, very good planning and organizational skills.
- Flexibility, ability to adapt easily to the new situations, creativity in solving issues.

Languages: Italian (Native), English and French (Proficient), Spanish and German (Basic user).

Leadership and Scientific Activities

Scientific Service

- Ad hoc reviewer for *Nucleic Acids Research*, *RNA*, *Journal of Proteome Research*, *PeerJ*.

Courses

- Torrey Pines Leadership Development Program (La Jolla, CA, Aug 2019 – Jun 2020)
- The theory and practice of small molecules drug discovery – Vertex lecture series (San Diego, CA, Jul-Aug 2019).
- Statistics for Data Analysis (University of California San Diego Extension – Apr-Jun 2019).
- Effective scientific writing (Strasbourg, France. October 5-7, 2015).
- Data analysis with Python (Online course, Coursera – Apr-May 2020).
- Python jumpstart by building 10 Apps (Online course, TalkPython – Apr-Jun 2020)

Workshops and Training

- Case studies in Quantitative Proteomics (ASMS – Atlanta, GA. June 1-2, 2019).
- The Role of Data Resources in Biophysics (Biophysical Society Conference – Baltimore, MD. March 5, 2019).
- Using R for Mass Spectrometry Data Analysis and Workflows (ASMS – San Diego, CA. June 6, 2018).

- Bioinformatics for Protein Identification – (ASMS – San Diego, CA. June 1-2, 2018).

Volunteering

- **Scripps Research Society of Fellows** (SoF, the oldest postdoctoral association in the US, founded in 1962):
 - **President** (since Jan 2020): representing the organization, managing all the SoF Chairs and Executive Committee members, organizing and running the monthly meetings.
 - **Career development chair** (2018-2019): organization of events for up to 200 postdocs and students, providing lectures from industry and academic professionals, happy hours with representative from local biopharmaceutical companies and scientific presentation competitions for peers.
 - **Industry Bridge Program chair** (2019): collaboration with biotech and pharmaceutical companies in San Diego (CA) to organize site visits for groups of postdocs and students. Coordinated site visits: **Vertex Pharmaceuticals, Eli Lilly, The Genomics Institute of the Novartis Research Foundation (GNF), Takeda California, BASF, Pfizer and Janssen.**
- **Scripps Outstanding Speakers (SOS) Toastmasters** (Since 2019): member of an organization dedicated to improving public speaking and leadership skills, over weekly meetings focusing on preparing and delivering talks to an audience that will evaluate the speaker.

Professional Associations

- The RNA Society, since 2016.
- American Society for Mass Spectrometry (ASMS), since 2018.
- The Biophysical Society, since 2019.
- American Association for the Advancement of Science (AAAS), since 2015.
- National Postdoctoral Association (NPA), since 2017.

Honors and Awards

- Simons Foundation Life Sciences – Postdoctoral Fellowship (since 2019).
- Society of friends of the Strasbourg Universities Academy, Ph.D. thesis prize (2017).
- Biochemical and Molecular Biology French Society (SFBBM), “Article du mois” (Article of the month) for the paper “Z-DNA like” fragments in RNA: a novel structural motif with implications for folding and RNA/protein recognition and immunology. *Nucleic Acid Res.* (August 2016).
- Biochemical and Molecular Biology French Society (SFBBM), Travel Grant “Jean-Pierre EBEL” (June 2016).
- 12th European Biological Inorganic Chemistry Conference (Zurich, Switzerland), Selected Poster for Flash Oral presentation (August 2014) .
- ACLS International Summer School – Purdue University (West Lafayette, IN), Best Research Award – Protein Structure (August 2014).
- French Ministry of National Education – Doctoral Fellowship (2013-2016).

Publications

1. Leonarski F., **D’Ascenzo L.**, and Auffinger P. (2019) Nucleobase carbonyl groups are poor Mg²⁺ inner-sphere binders but excellent monovalent ion binders—a critical PDB survey. *RNA* 25, 173-192.
2. **D’Ascenzo L.**, Vicens Q., and Auffinger P. (2018) Identification of receptors for UNCG and GNRA Z-turns and their occurrence in rRNA. *Nucleic Acids Res.*, 46, 7989-7997.
3. **D’Ascenzo L.**, Leonarski F., Vicens Q., and Auffinger P. (2017) Revisiting GNRA and UNCG folds: U-turns versus Z-turns in RNA hairpin loops. *RNA*, 23, 259–69.
4. Leonarski F., **D’Ascenzo L.**, and Auffinger P. (2017) Mg²⁺ ions: do they bind to nucleobase nitrogens? *Nucleic Acids Res.*, 45, 987-1004.
5. **D’Ascenzo L.**, Leonarski F., Vicens Q. and Auffinger P. (2016) “Z-DNA like” fragments in RNA: a novel structural motif with implications for folding and RNA/protein recognition and immunology. *Nucleic Acids Res.*, 44, 5944-56.
6. Leonarski F., **D’Ascenzo L.**, and Auffinger P. (2016) Binding of metals to purine N7 nitrogen atoms and implications for nucleic acids: a CSD survey. *Inorg. Chim. Acta*, 452, 82-9.
7. **D’Ascenzo L.** and Auffinger P. (2016) Anions in nucleic acid crystallography. *Methods Mol. Biol.*, 1320, 337-51.
8. Auffinger P., **D’Ascenzo L.**, and Ennifar E. (2016) Sodium and potassium interactions with nucleic acids. *Met.*

Ions Life Sci., 16, 167-201.

9. **D'Ascenzo L.** and Auffinger P. (2015) A comprehensive classification and nomenclature of carboxyl-carboxyl(ate) supramolecular motifs and related catemers: implications for biomolecular systems. *Acta Cryst.*, B71, 164-75.

Upcoming publications

1. **D'Ascenzo L.**, Popova A., and Williamson J. – Pytheas: a software to map RNA modifications via tandem Mass Spectrometry. *In preparation.*
2. Kruse H., Mrazikova K., **D'Ascenzo L.**, Sponer J., and Auffinger P. – Short but weak! The Z-DNA lone-pair- π conundrum challenges standard carbon vdW radii. *In review in Angewandte Chemie* (submitted March 2020).
3. Auffinger P., Ennifar E., **D'Ascenzo L.** – Deflating the RNA Mg^{2+} bubble. Stereochemistry to the rescue! *In review in RNA* (submitted April 2020).

Presentations

- Presented **15** posters, **8** oral presentations and **1** invited talk at scientific conferences and workshops.
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References

James R. Williamson, Ph.D.

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and Academic Affairs
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