

BIOGRAPHICAL SKETCH

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NAME: Cendron, Laura

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Member of the school board of PhD program in Bioscience

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
University of Padova, Padova	OTH	07/2001	Degree in Chemistry, 110/110 and laude
University of Padova and VIMM Institute, Padova	PHD	04/2005	Chemical Sciences
ESRF, European Synchrotron Radiation Facility, Grenoble	Other training	present	2003 European specialized course, HERCULES

A. Personal Statement

I am a protein biochemist and structural biologist with extensive experience in protein engineering, production, X-Ray crystallography and functional studies. In my lab, we apply structure-based integrated approaches to investigate the molecular details of biological processes that occur at the cellular level. Our goal is to understand their mechanism of action and how that can lead to new biomarkers and therapeutics. The main broad context I've applied such approach is the bacterial one: throughout my carrier I spent many years in characterizing novel targets such as virulence factors, key enzymes and protein components involved in signaling and enzymatic processes. Starting from *Helicobacter pylori* secretome targets I was studying at the beginning of my carrier, I moved to other Gram Negative pathogens such as *Pseudomonas aeruginosa*, *Klebsiella pneumoniae* applying classical approaches where we target both serine and metallo β -lactamases, able to hydrolyze even the last resort antibiotics, by the development of small-molecule lead inhibitors combining in silico and in vitro studies. In the last ten years, to tackle the serious threat represented by bacterial resistance (AMR) by novel strategies, I'm exploiting the mechanisms according to which bacteria acquire resistance to develop tools and control superbugs spreading or even resensitize them toward standard treatments. In particular, we are taking advantage of nanobodies as versatile tools to target those mechanisms and validate the possibility of acting with efficacy against such processes. More in general, in collaboration with the VUB Institute in Brussel (Belgium) and Bonn Nanobodies Core Facility (Germany), I'm exploring the properties of nanobodies libraries both as research tools, diagnostic purposes and future therapeutics against multiple targets of interest.

Another investigation field concerns the study of drugs-target interactions. Indeed, I've been part of projects to develop novel approaches and promising lead molecules. The accurate description of complexes structures has been an important contribution to the characterization of bicyclic and macrocyclic inhibitors, selected by phage and yeast display technologies (bicyclics) and more recently by in vitro HT-synthesis and screening (macrocyclics), targeting Thrombin, human Urokinase Plasminogen Activator and more recently Chymotrypsin or β -lactamases. More recently, similar approaches have been investigated with national and international collaborators to discover novel strategies for tuning drug binders' properties and drugs' half-life in the serum. While as a Postdoc, I focused my attention on Transthyretin and its binders and mutants, in recent years, I've been carrying out projects more focused on albumin properties as a deliverer and detoxifying agent.

1. Chinellato M, Perin S, Carli A, Lastella L, Biondi B, Borsato G, Di Giorgio E, Brancolini C, Cendron L, Angelini A. Folding of Class IIa HDAC Derived Peptides into α -helices Upon Binding to Myocyte Enhancer Factor-2 in Complex with DNA. *J Mol Biol.* 2024 May 1;436(9):168541. PubMed PMID: 38492719.
2. De Felice S, Romanyuk Z, Chinellato M, Zoia G, Linciano S, Kumada Y, Pardon E, Steyaert J, Angelini A, Cendron L. Crystal structure of human serum albumin in complex with megabody reveals unique human and murine cross-reactive binding site. *Protein Sci.* 2024 Feb;33(2):e4887. PubMed Central PMCID: PMC10804666.
3. Maso L, Vascon F, Chinellato M, Goormaghtigh F, Bellio P, Campagnaro E, Van Melderen L, Ruzzene M, Pardon E, Angelini A, Celenza G, Steyaert J, Tondi D, Cendron L. Nanobodies targeting LexA autocleavage disclose a novel suppression strategy of SOS-response pathway. *Structure.* 2022 Nov 3;30(11):1479-1493.e9. PubMed PMID: 36240773.
4. Maso L, Trande M, Liberi S, Moro G, Daems E, Linciano S, Sobott F, Covaceuszach S, Cassetta A, Fasolato S, Moretto LM, De Wael K, Cendron L, Angelini A. Unveiling the binding mode of perfluorooctanoic acid to human serum albumin. *Protein Sci.* 2021 Apr;30(4):830-841. PubMed Central PMCID: PMC7980502.

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2024 - 2024	member of the International Selection Committee of COFUND ArchiFun 2024 (European International Doctoral Programme), COFUND ArchiFun 2024, Arqus Initiative
2023 - 2024	Member of the organizing committee and Session Chair at the ECM34 "34th European Crystallographic Meeting," University of Padova, Padova
2021 -	Associate Professor in Biochemistry, Dept. of Biology, University of Padova, Padova
2016 -	Member of the Teaching Committee for the Bachelor and Master Degree Courses in Molecular Biology, University of Padova
2013 -	Member of the school board of PhD program in Bioscience, University of Padova
2012 - 2021	Assistant professor in Biochemistry, Dept. of Biology, Univ. of Padova, Padova
2011 - 2012	Senior Fellow "Bando Giovani Studiosi", University of Padova, Padova
2009 - 2011	Post-graduate fellow, Dept of Biomedical Sciences, University of Padova, Padova
2005 - 2009	4 years Post-graduate fellow, Dept. of Chemical Sciences, University of Padova, Padova

Honors

2013 - 2013	Premio Nardelli for Young Italian Crystallographers, AIC, Italian Member of IUCr (International Union of Crystallography)
2011 - 2012	Young Investigators Award "Giovani Studiosi 2011", University of Padova

C. Contribution to Science

1. Scientific publications on peer-reviewed international journals: 112 (Wos); 4 book chapters; 2 patents; h-index: 29 (Wos); citations: 2346 (Wos). Laura Cendron is author of 119 structures deposited in the Protein Data Bank archive.
 - a. Chinellato M, Perin S, Carli A, Lastella L, Biondi B, Borsato G, Di Giorgio E, Brancolini C, Cendron L, Angelini A. Folding of Class IIa HDAC Derived Peptides into α -helices Upon Binding to Myocyte Enhancer Factor-2 in Complex with DNA. *J Mol Biol.* 2024 May 1;436(9):168541. PubMed PMID: 38492719.
 - b. De Felice S, Romanyuk Z, Chinellato M, Zoia G, Linciano S, Kumada Y, Pardon E, Steyaert J, Angelini A, Cendron L. Crystal structure of human serum albumin in complex with megabody

reveals unique human and murine cross-reactive binding site. *Protein Sci.* 2024 Feb;33(2):e4887. PubMed Central PMCID: PMC10804666.

- c. Maso L, Vascon F, Chinellato M, Goormaghtigh F, Bellio P, Campagnaro E, Van Melderen L, Ruzzene M, Pardon E, Angelini A, Celenza G, Steyaert J, Tondi D, Cendron L. Nanobodies targeting LexA autocleavage disclose a novel suppression strategy of SOS-response pathway. *Structure.* 2022 Nov 3;30(11):1479-1493.e9. PubMed PMID: 36240773.
- d. Maso L, Trande M, Liberi S, Moro G, Daems E, Linciano S, Sobott F, Covaceuszach S, Cassetta A, Fasolato S, Moretto LM, De Wael K, Cendron L, Angelini A. Unveiling the binding mode of perfluorooctanoic acid to human serum albumin. *Protein Sci.* 2021 Apr;30(4):830-841. PubMed Central PMCID: PMC7980502.