

Karl A.T. Makepeace

Structural Proteomics Scientist
Victoria, British Columbia, Canada
Citizenship: Canada

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I hold a Ph.D. in biochemistry from the University of Victoria, and I have accumulated over 12 years of research experience specializing in mass spectrometry-based techniques, structural proteomics, and bioinformatics. I am an expert in cross-linking mass spectrometry (XL-MS), having developed and applied innovative methods for studying protein structure, dynamics, and interactions in various biological contexts, such as mitochondria, prions, viral and intrinsically disordered proteins. I have cultivated a strong affinity for programming and software development, recognizing their capacity to enhance and accelerate analyses in my field. My recent focus on bioinformatics has involved the creation of R-based tools for proteogenomic applications which have not only deepened my understanding of genomics but also broadened my perspective to encompass a wider range of multiomic investigations in biological inquiries. Moving forward, I am driven to leverage my skills and experience in structural proteomic analyses and bioinformatics to contribute to the advancement of novel technologies and therapeutic solutions.

Research Experience

University of Victoria

Victoria, BC, Canada
Nov 2020 – Dec 2022

BIOINFORMATICIAN, DEPT OF BIOCHEMISTRY & MICROBIOLOGY

- Designed and implemented R-based software tools, including a package and a `shiny` web application, to access gene variant information from public databases, interpret Human Genome Variation Society (HGVS) nomenclature, and analyze resulting protein/peptide sequences for LCMS suitability and proteogenotypic status across various proteases.
- Developed an intuitive `shiny` web application enabling interactive access to gene variant information from prominent online databases such as Ensembl, COSMIC, and NCI Genomic Data Commons. This application empowers users to generate proteogenomically-informed peptide lists for genes of interest, accompanied by visualizations depicting predicted variant coverage based on LCMS suitability, proteogenotypic status, and chosen proteolysis agents.
- Integrated Git (GitHub) and issue-tracking methodologies into the software development workflow, enhancing collaboration, version control, and efficient issue resolution.
- Fostered a strong familiarity with the `tidyverse` style and strived to adhere to its principles and conventions in data analysis and code development.

University of Victoria

Sept 2015 – Aug 2022

GRADUATE RESEARCH ASSISTANT & PHD CANDIDATE, DEPT OF BIOCHEMISTRY & MICROBIOLOGY

- Developed and applied an experimental and computational approach for improved spectral match confidence and coverage of protein-protein interactions by *ex vivo* chemical crosslinking and mass spectrometry.
- Developed a crosslinker-specific data-dependent acquisition strategy that led to a >40% increase in crosslinker-modified precursor acquisition.

- Co-implemented a software pipeline to integrate crosslinker-specific mass spectral feature information into machine learning-based peptide-spectrum match (PSM) validation leading to a >20% improvement in crosslink identification rates.
- Developed and applied PyMOL scripts to validate identified crosslinks by mapping them to existing structural models.
- Developed and executed analyses to characterize structural changes in disordered proteins and protein chaperones resulting from ligand binding using differential structural proteomics techniques including crosslinking, top-down hydrogen-deuterium exchange (HDX), and covalent surface modification.
- Generated experimental distance constraints using a suite of chemically and structurally distinct crosslinking reagents which served as input for guidance of a *de novo* protein structure prediction method based on discrete molecular dynamics simulations.
- Implemented machine-learning based false-discovery rate control (Percolator) into our crosslinking data analysis pipeline.
- Used Mascot, PEAKS, Trans-Proteomic Pipeline, Crux, ProteoWizard, Proteome Discoverer, Protein Prospector, Xcalibur, RawMeat, and various crosslinking analysis softwares (e.g., Kojak, XlinkX/Slinks, StavroX/MeroX, XQuest) in addition to in-house software tools for evaluation and analysis of mass spectral data.
- Produced recombinant proteins in bacterial expression systems and performed protein purification using affinity, size exclusion, ion exchange chromatography techniques.
- Operated and acquired data with various mass spectrometers: Orbitrap Fusion (Thermo Scientific) (in addition to instruments listed in prior experience).
- Maintained and contributed to multiple academic collaborations from Canada, United States, and Europe.
- Supervised honors and co-op students in conducting experiments, gathering data, and analyzing results.
- Performed peer review of manuscripts involving crosslinking mass spectrometry for various publications.
- Presented research at multiple international conferences and symposia.
- Co-organized graduate research symposia over multiple years.
- Completed graduate-level coursework: practical crystallography and directed studies incl. attendance of MaxQuant Summer School in Berlin, Germany.
- Submitted experimental data from published works to public data repositories (e.g., PRIDE).
- Proposed use of structural proteomic methods in strain-typing and structural characterization of prions and prion-like proteins leveraging previously developed ¹⁴N/¹⁵N metabolically labelled homomeric intra/inter protein crosslink determination approach.
- Developed proficiency in LaTeX during the composition of my dissertation.

University of Victoria

Sept 2012 – Aug 2015

RESEARCH TECHNICIAN, GENOME BRITISH COLUMBIA PROTEOMICS CENTRE

- Contributed to and facilitated numerous intra and inter-institutional collaborations, providing expert guidance to investigators in the application of crosslinking methods and utilizing reagents developed within the Borchers laboratory.
- Supported Post-docs, Ph.D. students, and Co-op students with lab orientation, training, performing experiments, and data analysis.

- Developed a methodology utilizing mass spectrometry, non-specific proteinase K digestion and higher-order crosslink analysis (three-interlinked peptides) to improve disulfide bond identification in proteins.
- Contributed to the development of automated data analysis for mass spectral data of homomeric protein complexes, enabling differentiation between intra- and inter-protein crosslinks from mixed ¹⁵N metabolically labeled proteins and natural isotopic abundance proteins.
- Proficiently operated and obtained data using various mass spectrometers, including the Orbitrap Velos Pro (Thermo Scientific), alongside prior instrument experience.
- Devised and produced evaluation methods for crosslinking distance constraints on molecular models using PyMOL and I-TASSER.
- Employed PyMOL and UCSF Chimera to script molecular animations showcasing prion protein conformational changes and crosslinking distance constraints in molecular modeling for conference presentations.
- Proposed and implemented target-decoy based false-discovery rate control within the crosslinking data analysis pipeline.
- Introduced and demonstrated use of crosslinking constraints in interactive molecular modelling software (Foldit), which served as an initial *in silico* utilization of our structural proteomics data in molecular modelling efforts.
- Developed software to perform relative quantification of the extent of modification of methionine and tryptophan residues between two conformational states of prion protein using isotopically-coded hydrogen peroxide oxidation and mass spectrometry.
- Published protocols with troubleshooting guidelines for the analysis of protein structure by cross-linking combined with mass spectrometry.

University of Victoria

Sept 2011 – Aug 2012

RESEARCH CO-OP STUDENT, BORCHERS LAB

- Assisted in preparation and analysis of prion and malarial protein samples for GeLC-MS analysis.
- Operated and acquired data with various mass spectrometers: Voyager STR-DE MALDI-TOF-MS (Applied Biosystems); 4800 MALDI-TOF/TOF (Applied Biosystem-MDS SCIEX); LTQ Orbitrap Velos (Thermo Scientific); Bruker 12 T Apex-Qe hybrid Fourier transform mass spectrometer, equipped with an Apollo II electrospray source.

Education

University of Victoria

Victoria, BC, Canada
2022

PH.D. BIOCHEMISTRY

- Dissertation: *“The Development and Application of Mass Spectrometry-based Structural Proteomic Approaches to Study Protein Structure and Interactions”*
- Received British Columbia Proteomics Network Travel Award for MaxQuant Summer School (2017)
- Received University of Victoria Fellowship (2016-2018) (\$10,000)
- Received University of Victoria Graduate Awards (4) (2016-2018) (\$13313)

BSC BIOCHEMISTRY WITH CO-OP

2014

- Received Canadian National Proteomics Network Young Investigator Travel Award (2013) (\$500)

BSC BIOLOGY & PSYCHOLOGY

2009

Teaching Experience

University of Victoria

May 2016 – Oct 2019

TEACHING Assistant, DEPT OF BIOCHEMISTRY & MICROBIOLOGY

- Assisted students in 400-level Applied Research Techniques laboratory courses (BCMB 406A & 406B).
- Explained and demonstrated MALDI-TOF\TOF mass spectrometric data acquisition and data processing to groups of students.
- Individually supervised student acquisition of data using a MALDI-TOF mass spectrometer.
- Analyzed student-generated mass spectral data with Mascot for peptide fingerprinting (MS¹) and bottom-up GeLC-MS\MS (MS²) analyses.

Publications

* These authors contributed equally

2020

Ligand-induced disorder-to-order transitions characterized by structural proteomics and molecular dynamics simulations

Journal Proteomics January 2020

[Karl A.T. Makepeace*](#), Nicholas I. Brodie*, Konstantin I. Popov*, Geoff Gudavicius, Christopher J Nelson, Evgeniy V. Petrotchenko, Nikolay V. Dokholyan, Christoph H. Borchers

Improving identification of *in-organello* protein-protein interactions using an affinity-enrichable, isotopically-coded, and mass spectrometry-cleavable chemical crosslinker

Molecular & Cellular Proteomics January 2020

[Karl A.T. Makepeace*](#), Yassene Mohammed*, Elena L. Rudashevskaya*, Evgeniy V. Petrotchenko, F-Nora Vögtle, Christof Meisinger, Albert Sickmann, Christoph H. Borchers

2019

Insight into the structure of the “unstructured” tau protein

Structure November 2019

Konstantin I. Popov*, [Karl A.T. Makepeace*](#), Evgeniy V. Petrotchenko, Nikolay V. Dokholyan, Christoph H. Borchers

Chaperone activation and client binding of a 2-cysteine peroxiredoxin

Nature Communications February 2019

Filipa Teixeira, Eric Tse, Helena Castro, [Karl A.T. Makepeace](#), Ben A. Meinen, Christoph H. Borchers, Leslie B. Poole, James C.A. Bardwell, Ana M. Tomás, Daniel R. Southworth, Ursula Jakob

2016

Protein unfolding as a switch from self-recognition to high-affinity client binding

Nature Communications January 2016

Bastian Groitl, Scott Horowitz, [Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, Christoph H. Borchers, Dana Reichmann, James C.A. Bardwell, Ursula Jakob

2015

Comprehensive identification of disulfide bonds using non-specific proteinase K digestion and CID-cleavable crosslinking analysis methodology for Orbitrap LC/ESI-MS/MS data

Methods March 2015

[Karl A.T. Makepeace](#), Jason J. Serpa, Evgeniy V. Petrotchenko, Christoph H. Borchers

Structure of EspB from the ESX-1 Type VII Secretion System and Insights into its Export Mechanism

Structure February 2015

Matthew Solomonson, Dheva Setiাপutra, [Karl A.T. Makepeace](#), Emilie Lameignere, Evgeniy V. Petrotchenko, Deborah G. Conrady, Julien R. Bergeron, Marija Vuckovic, Frank DiMaio, Christoph H. Borchers, Calvin K. Yip, Natalie C.J. Strynadka

2014

DXMSMS Match program for the automated analysis of LC-MS/MS data obtained using isotopically-coded CID-cleavable crosslinking reagents.

Current Protocols in Bioinformatics December 2014

Evgeniy V. Petrotchenko, [Karl A.T. Makepeace](#), Christoph H. Borchers

Isotopically-coded short-range hetero-bifunctional photo-reactive crosslinkers for studying protein structure

Journal of Proteomics September 2014

Nick I. Brodie, [Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, Christoph H. Borchers

¹⁴N¹⁵N DXMSMS Match program for the automated analysis of LC/ESI-MS/MS crosslinking data from experiments using ¹⁵N metabolically labeled proteins

Journal of Proteomics June 2014

Evgeniy V. Petrotchenko, Jason J. Serpa, [Karl A.T. Makepeace](#), Nick I. Brodie, Christoph H. Borchers

Analysis of Protein Structure by Cross-Linking Combined with Mass Spectrometry

Methods in Molecular Biology: Shotgun Proteomics April 2014

Evgeniy V. Petrotchenko, [Karl A.T. Makepeace](#), Jason J. Serpa, Christoph H. Borchers

Super Spy variants implicate flexibility in chaperone action

eLife February 2014

Shu Quan, Lili Wang, Evgeniy V. Petrotchenko, [Karl A.T. Makepeace](#), Scott Horowitz, Jianyi Yang, Yang Zhang, Christoph H. Borchers, James C.A. Bardwell

2013

Using isotopically-coded hydrogen peroxide as a surface modification reagent for the structural characterization of prion protein aggregates

Journal of Proteomics December 2013

Jason J. Serpa, [Karl A.T. Makepeace](#), Tristan H. Borchers, David S. Wishart, Evgeniy V. Petrotchenko, Christoph H. Borchers

Structural and biochemical characterization of *Plasmodium falciparum* 12 (Pf12) reveals a unique interdomain organization and the potential for an antiparallel arrangement with Pf41

Journal of Biological Chemistry March 2013

Michelle L. Tonkin, Silvia A. Arredondo, Bianca C. Loveless, Jason J. Serpa, [Karl A.T. Makepeace](#), Natharajan Sundar, Evgeniy V. Petrotchenko, Louis H. Miller, Michael E. Grigg, Martin J. Boulanger

Working Papers

*n.b. order and extent of authors not yet fully determined.

*2023

The {hgvsr} R package for proteogenomics in R

Working title / In progress

[Karl A.T. Makepeace](#), Pallab Bhowmick, Christoph H. Borchers, Yassene Mohammed

PIGQpipe: An online tool for predicting variant peptide coverage in bottom-up proteomics experiments using a variety of proteases

Working title / In progress

[Karl A.T. Makepeace](#), Pallab Bhowmick, Christoph H. Borchers, Yassene Mohammed

Developing differential absolute quantification assays for targeted cancer proteogenomics

Abstract submitted for 71st ASMS Conference, Houston, TX, USA

Yassene Mohammed (presenting), Constantinos Blidjios, [Karl A.T. Makepeace](#), Pallab Bhowmick, Vincent R. Richard, Christoph H. Borchers

Presentations

Presenters are underlined.

2018

Oral Presentation: Improving crosslink identification with affinity-enrichment, isotopic-coding, and MS-cleavability

July 2018 Cascadia Proteomics Symposium, Seattle, WA, USA

[Karl A.T. Makepeace](#), Yassene Mohammed, Elena L. Rudashevskaya, Evgeniy V. Petrotchenko, Albert Sickmann, Christoph H. Borchers

Oral Presentation: Integrated experimental and computational pipeline for proteome-wide in tissue crosslinking analysis

June 2018 66th ASMS Conference on Mass Spectrometry and Allied Topics, San Diego, CA, USA

Karl A.T. Makepeace, Yassene Mohammed, Elena L. Rudashevskaya, Rachael D. Brown, Evgeniy V. Petrotchenko, Albert Sickmann, [Christoph H. Borchers](#)

Poster Presentation: Including target crosslink-peptide spectrum matches that lack crosslinker-cleavage fragment ions with decoy-based negative examples for classifier training improves crosslink identification

June 2018 66th ASMS Conference on Mass Spectrometry and Allied Topics, San Diego, CA, USA

[Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, Christoph H. Borchers

Poster Presentation: Native tau protein structure in solution as determined by short-distance crosslinking constraint-guided discrete molecular dynamics simulations

June 2018 66th ASMS Conference on Mass Spectrometry and Allied Topics, San Diego, CA, USA

Karl A.T. Makepeace, Konstantin I. Popov, [Evgeniy V. Petrotchenko](#), Nikolay V. Dokholyan, Christoph H. Borchers

Poster Presentation: Proteome-wide identification of protein-protein interactions by *in vivo* chemical crosslinking and mass spectrometry*

Feb 2018 UVic 23rd Annual BCMB Graduate Student Research Symposium, Victoria, BC, Canada

[Karl A.T. Makepeace](#), Yassene Mohammed, Elena L. Rudashevskaya, Evgeniy V. Petrotchenko, Albert Sickmann, Christoph H. Borchers

*awarded 2nd place poster prize at symposium

2017

Poster Presentation: Analysis of mitochondrial protein interactome by in organello crosslinking and mass spectrometry

Sept 2017 16th Human Proteome Organization World Congress, Dublin, Ireland

[Elena L. Rudashevskaya](#), Karl A.T. Makepeace, Yassene Mohammed, Jason J. Serpa, Evgeniy V. Petrotchenko, Chris Meisinger, Rene Zahedi, Albert Sickman, Christoph H. Borchers

Poster Presentation: Proteome-wide identification of protein-protein interactions by *in vivo* chemical crosslinking and mass spectrometry

June 2017 65th ASMS Conference on Mass Spectrometry and Allied Topics, Indianapolis, IN, USA

[Elena L. Rudashevskaya](#), Tomáš Ječmen, Karl A.T. Makepeace, Jason J. Serpa, Yassene Mohammed, Evgeniy V. Petrotchenko, Chris Meisinger, Rene Zahedi, Albert Sickman, Christoph H. Borchers

Poster Presentation: Quantitative crosslinking and quantitative surface modification for the structural characterization of disorder-to-order transitions

June 2017 65th ASMS Conference on Mass Spectrometry and Allied Topics, Indianapolis, IN, USA

[Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, Christoph H. Borchers

Poster Presentation: Proteome-wide identification of protein-protein interactions by *in vivo* chemical crosslinking and mass spectrometry

April 2017 Proteomic Forum 2017, Potsdam, Germany

[Elena L. Rudashevskaya](#), Tomáš Ječmen, Karl A.T. Makepeace, Evgeniy V. Petrotchenko, Kerstin Jurk, Chris Meisinger, Rene Zahedi, Albert Sickman, Christoph H. Borchers

Poster Presentation: Disorder-to-order conformational change determined by a combination of quantitative crosslinking, quantitative surface modification, and hydrogen-deuterium exchange

Feb 2017 UVic 22nd Annual BCMB Graduate Student Research Symposium, Victoria, BC, Canada

[Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, Christoph H. Borchers

Oral Presentation: Multiple structural proteomic techniques for the structural elucidation of tau protein oligomerization

Feb 2017 UVic BCMB Graduate Student Research Seminar (BCMB 580), Victoria, BC, Canada

[Karl A.T. Makepeace](#)

2016

Poster Presentation: Crosslinkers with Isotope-Coding and Cleavable Spacers Improve Peptide Crosslink Identification by a Semi-Supervised Machine Learning Algorithm

June 2016 64th ASMS Conference on Mass Spectrometry and Allied Topics, San Antonio, TX, USA

Karl A.T. Makepeace, Evgeniy V. Petrotchenko, [Christoph H. Borchers](#)

Poster Presentation: Structural Proteomics Analysis of the Native Tau Protein

June 2016 64th ASMS Conference on Mass Spectrometry and Allied Topics, San Antonio, TX, USA

[Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, Nicole Sessler, Christoph H. Borchers

Poster Presentation: Crosslinker specific features for the improvement of peptide cross-link identification by a semi-supervised machine learning algorithm

Feb 2016 UVic 21st Annual BCMB Graduate Student Research Symposium, Victoria, BC, Canada

[Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, Christoph H. Borchers

2015

Poster Presentation: Crosslinking Analysis of Fibrin Polymerization

Sept 2015 14th Human Proteome Organization World Congress, Vancouver, BC, Canada
[Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, Nicole Sessler, Christoph H. Borchers

Poster Presentation: Crosslinking Analysis of the Tau-Protein-Microtubules Interaction

June 2015 63rd ASMS Conference on Mass Spectrometry and Allied Topics, St. Louis, MO, USA
[Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, Nicole Sessler, Christoph H. Borchers

Poster Presentation: Crosslinking Analysis of Fibrin Polymerization

June 2015 63rd ASMS Conference on Mass Spectrometry and Allied Topics, St. Louis, MO, USA
[Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, Christoph H. Borchers

2014

Poster Presentation: Comprehensive identification of disulfide bonds using proteinase K digestion and second-order crosslinking analysis

June 2014 62nd ASMS Conference on Mass Spectrometry and Allied Topics, Baltimore, MD, USA
[Karl A.T. Makepeace](#), Jason J. Serpa, Evgeniy V. Petrotchenko, Christoph H. Borchers

2013

Oral Presentation: Identification of the binding site of the Spy chaperone by Cross-linking and Hydrogen-Deuterium Exchange Mass Spectrometry

Dec 2013 26th Annual Tandem Mass Spectrometry Workshop, Lake Louise, AB, Canada
Karl A.T. Makepeace, Shu Quan, Lily Wang, Evgeniy V. Petrotchenko, Scott Horowitz, Jianyi Yang, Yang Zhang, [Christoph H. Borchers](#), James C.A. Bardwell

Oral Presentation: Identification of the binding site of the Spy chaperone by Cross-linking and Hydrogen-Deuterium Exchange Mass Spectrometry

Nov 2013 3rd Symposium on Structural Proteomics, Prague, Czech Republic
[Karl A.T. Makepeace](#), Shu Quan, Lily Wang, Evgeniy V. Petrotchenko, Scott Horowitz, Jianyi Yang, Yang Zhang, Christoph H. Borchers, James C.A. Bardwell

Oral Presentation: Novel isotopically-coded photo-reactive hetero-bifunctional short-range crosslinkers for studying protein structure

July 2013 Cascadia Proteomics Symposium, Seattle, WA, USA
[Nicholas I. Brodie](#), Karl A.T. Makepeace, Evgeniy V. Petrotchenko, Christoph H. Borchers

Poster Presentation: Using isotopically-coded hydrogen peroxide as a surface modification reagent for the structural characterization of prion-protein aggregates

July 2013 Cascadia Proteomics Symposium, Seattle, WA, USA
[Jason J. Serpa](#), Karl A.T. Makepeace, Tristan H. Borchers, David S. Wishart, Evgeniy V. Petrotchenko, Christoph H. Borchers

Poster Presentation: Zero-length crosslinking of protein heterodimers using ¹⁵N-metabolically labelled monomers

July 2013 Cascadia Proteomics Symposium, Seattle, WA, USA
[Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, Shu Quan, James C.A. Bardwell, Christoph H. Borchers

Poster Presentation: Crosslinking Study of the Malaria Pathogen Surface Protein Complex Pf12-Pf41

June 2013 61st ASMS Conference on Mass Spectrometry and Allied Topics, Minneapolis, MN, USA
Michelle L. Tonkin, [Karl A.T. Makepeace](#), Jason J. Serpa, Evgeniy V. Petrotchenko, Martin J. Boulanger, Carol Parker, Christoph H. Borchers

Poster Presentation: Zero-length crosslinking of protein heterodimers using ¹⁵N-metabolically labelled monomers

June 2013 61st ASMS Conference on Mass Spectrometry and Allied Topics, Minneapolis, MN, USA
[Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, James C.A. Bardwell, Shu Quan, Christoph H. Borchers

Poster Presentation: Novel isotopically-coded photo-reactive hetero-bifunctional short-range crosslinkers for studying protein structure

June 2013 61st ASMS Conference on Mass Spectrometry and Allied Topics, Minneapolis, MN, USA
Karl A.T. Makepeace, [Nicholas I. Brodie](#), Evgeniy V. Petrotchenko, Christoph H. Borchers

Poster Presentation: Zero-length crosslinking of protein heterodimers using ¹⁵N-metabolically labelled monomers

April 2013 5th Annual Canadian National Proteomics Network Symposium, Vancouver, BC, Canada
[Karl A.T. Makepeace](#), Evgeniy V. Petrotchenko, James C.A. Bardwell, Shu Quan, Christoph H. Borchers

2012

Poster Presentation: Novel photo-reactive reagents for structural proteomics

Dec 2012 25th Annual Tandem Mass Spectrometry Workshop, Lake Louise, AB, Canada
[Evgeniy V. Petrotchenko](#), Karl A.T. Makepeace, Nick I. Brodie, Christoph H. Borchers

Acknowledgements

Article: Solving protein structures using short-distance crosslinking constraints as a guide for discrete molecular dynamics simulations

July 2017

Science Advances

Nicholas I. Brodie, Konstantin I. Popov, Evgeniy V. Petrotchenko, Nikolay V. Dokholyan, Christoph H. Borchers

Acknowledgement for: Supplying data used for the myoglobin crosslinking analysis. I designed experiments, performed experiments, and acquired the mass spectrometry data for all myoglobin crosslinking related analyses described in the paper.

Article: Architecture of the RNA polymerase II-Mediator core initiation complex

February 2015

Nature

Clemens Plaschka, Laurent Larivière, Larissa Wenzek, Martin Seizl, Matthias Hemann, Dmitry Tegunov, Evgeniy V.

Petrotchenko, Christoph H. Borchers, Wolfgang Baumeister, Franz Herzog, Elizabeth Villa, Patrick Cramer

Acknowledgement for: "help with mass spectrometry measurements." I designed the mass spectrometry data acquisition methods and operated the mass spectrometer for collection of data for the core Mediator complex crosslinking experiments and assisted in initial interpretation of the resulting data.

Article: Model of the Mediator middle module based on protein cross-linking

August 2013

Nucleic Acids Research

Laurent Larivière, Clemens Plaschka, Martin Seizl, Evgeniy V. Petrotchenko, Larissa Wenzek, Christoph H. Borchers, Patrick Cramer

Acknowledgement for: "help with mass spectrometry measurements." I designed the mass spectrometry data acquisition methods and operated the mass spectrometer for collection of data for the protein cross-linking experiments and assisted in initial interpretation of the resulting data.