JENIFFER QUIJADA, Ph.D.

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SUMMARY OF QUALIFICATIONS

Trained researcher with extensive knowledge in bio-analytical techniques for protein analysis; in vivo and in vitro modeling for complex sample analysis; assay development for sample analysis in LC-MS with the following experience:

- 5 years Ph.D. graduate project focusing on proteins/peptides sample preparation and LC-MS
- 10 years of experience working on multidisciplinary research projects in experimental biochemistry, biophysics, molecular biology in the U.S.A.
- Experience in protein purification, data analysis for LC-MS, and familiarity with Matlab and LabVIEW programming
- Excellent verbal and written skills; strong interpersonal, organizational, and team oriented skills

EDUCATION

Northeastern University
PhD, Chemistry and Chemical Biology, May 2017
Protein analysis using LC-MS

Relevant Coursework: Analytical Separation, Principles of Mass Spectrometry, Optical Methods, Protein Chemistry, Foundation of Spectroscopy, Analytical Biochemistry, Research Skills and Ethics, Advanced Laboratory Methods, Advanced Problem Solving

Thesis: Method development of intact protein quantitation and protein half-life using metabolic labeling and LC-MS

Universidad Simon Bolivar, Venezuela
BS, Chemistry, May 2004

EXPERIENCE

Stanford University, Stanford, CA
Aug 2017 – Present
Postdoctoral research fellow, Department of Genetic
Research Project :

- Developed analytical methods by using multi-omics approach to analyze proteins, metabolites and lipids for understanding the human variation and health state in personalized medicine.

Northeastern University, Boston, MA
Sept 2011 – Jul 2017
PhD student researcher, Department of Chemistry and Chemical Biology
Research Project 1 (2015-2017):

- Developed a method for determination of intact protein half-life using metabolic incorporation of stable isotope labeling for LC-MS analysis. This technique has been tested in adult fruit fly heads
- Used the developed platform from global intact protein quantitation using LC-MS, project 2
- Manuscript in progress

Research Project 2 (2013-2016):

- Developed a quantitative technique for intact protein analysis using metabolic incorporation of stable isotope labeling for LC-MS analysis. This technique is inexpensive, can be multiplexed, and it has been tested in different organisms, such as bacteria, yeast, and fruit flies
- Developed platform for a global intact protein purification suitable for LC-MS analysis using a combination of instruments: Waters UPLC, Eksigent HPLCs coupled to Bruker Impact, Bruker SolariX FT-ICR
- Authored in Analytical Chemistry peer-reviewed publications

Research Project 3 (2012-2013):

- Developed a rapid workflow for neuropeptidome analysis in adult brains of *Drosophila Melanogaster* by MALDI-TOF –MS and data analysis for statistical differences in expression of a specific neuropeptide without isotopic labeling
- Performed dissection of adult brains of *Drosophila Melanogaster* and sample preparation for MALDI-MS
- Performed MALDI-MS data acquisition and pre-analysis
- Co-authored in Molecular Brain journal peer-reviewed publication

Teaching Biopharmaceutical Analysis Training Lab BATL (2013-2016)**:**

- Universal sample preparation, In-gel digest and LC-MS/MS, Filter-aided sample preparation, and native protein cleanup
- Trained graduate students, undergraduates, and volunteer in protein analysis and mass spectrometry

ICANH School of Medicine at Mount Sinai, New York, NY
2007 – 2011
Associate Researcher II, Department of Neuroscience

- Characterized human sweet tastes receptor GPCR with different sweeteners using calcium mobilization assay and molecular biology techniques
- **Project 1:** Characterized binding site of aspartame and human sweet taste receptor
- **Project 2:** Characterized binding site of brazzein and human sweet taste receptor
- Co-Authored two peer-review publications

The City College of New York, CUNY, NY
2006 – 2007
Research Assistant, Department of Biochemistry

- Evaluated redox protein Thioredoxin folding/unfolding states using NMR technique
- Authored a peer-review publication

LEADERSHIP

- Facilitated group discussions for 5 people to present current scientific publications
- Motivated collaboration between 3 graduate students to complete projects
- Taught and evaluated laboratory skills for classes of 15-20 students

- Managed two projects from the beginning to the end in graduate school
- Identified goals and tasks to be accomplished considering realistic timeline for completion
- Prioritized tasks while anticipating potential problems
- Maintained flexibility to maximize the outcome in the case of changing circumstances

ONGOING MEMBERSHIP IN PROFESSIONAL SOCIETIES

- American Chemistry Society (ACS) 2011
- Greater Boston Mass Spectrometry Discussion Group (GBMSDG) 2012
- Human Proteome Organization (HUPO) 2014

HONORS & AWARDS

- HUPO Travel Award, 16th Annual Meeting, Precision Proteomics for Discovery and Health, talk presentation, San Diego, CA, March 2017
- Honored for poster presentation at Janssen Research and Development, Spring House, PA and Johnson and Johnson Consumer, Skillman, New Jersey Open House, September 2016
- Scientist Mentoring & Diversity Program (SMDP) Biotech Scholar 2016
- American Society for Mass Spectrometry Travel Award 2015 from the Greater Boston Mass Spectrometry Discussion Group
- Cold Spring Harbor Laboratory Scholarship for Proteomics course, 2015
- Cold Spring Harbor Laboratory Scholarship for Protein Purification and Characterization course, 2013
- Northeastern University Assistantship, Department of Chemistry, 2011-2015

SKILLS AND TECHNIQUES

- **Mass Spectrometry:** Bruker Instruments and software, Compass Data Analysis, MALDI-TOF and flexanalysis, QTOF IMPACT I and otofControl, FT-ICR-MS and Control FTMS (Processing FTMS), Water instrument and software as QTOF Xevo G2 and UNIFI
- **Biochemistry:** HPLC/UPLC (Water, Eksigent), reverse phase (RP), size exclusion (SEC), ion-exchange (EIC), SDS-PAGE, ELISA, protein purification and sample preparation for MS
- **Molecular Biology:** DNA, DNA cloning and purification, primer design, PCR, in-vitro mutagenesis, sequencing, agarose gel electrophoresis.
- **Immunology:** fluorescence immunoassay, ELISA.
- **Microscopy:** light, dissecting, fluorescent, transmission electron microscopy (TEM), scanning electron microscopy (SEM)
- **Biological Cultures:** Cell culture, bacteria, yeast and fruit flies, sterile techniques, tissue culture.
- **Instrumentation:** UV-Visible and Infrared (FTIR) spectroscopy, nuclear magnetic resonance (NMR).
- **Software:** Illustrator, GraphPad Prism, Endnote, OriginLab, MATLAB, LabVIEW
- **Lab Management:** Chemical orders, instrumental maintenance, assist and train new users on instruments
- **Languages:** Spanish (native speaker), English (full professional proficiency)

PUBLICATIONS

- **Quijada JV**, Schmitt ND, Salisbury JP, Auclair JR, Agar JN. Heavy Sugar and Heavy Water Create Tunable Intact Protein Mass Increases for Quantitative MS in any Feed and Organism. Anal. Chem. (2016), 88 (22), pp 11139–11146.

- Salisbury J., Boggio K., Hsu Y., **Quijada J.**, Sivachenko A., Gloeckner G., Kowalski P., Easterling M., Rosbash M., Agar J. A rapid MALDI-TOF mass spectrometry workflow for Drosophila melanogaster differential neuropeptidomics. Mol Brain. (2013) 6 (1): 3-32.
- Assadi-Porter F., Maillet E., Radek J., **Quijada J.**, Markley J., and Max M. Key amino acid residues involved in multi-point binding interactions between brazzein, a sweet protein, and the T1R2–T1R3 human sweet receptor. Mol. Biol. (2010) 398(4): 584-99.
- Dittli S., Rao H., Tonelli M., **Quijada J.**, Markley J., Max M., and Assadi-Porter F. Structural role of the terminal disulfide bond in the sweetness of brazzein. Chem. Senses (2011) 36 (9): 821-830.
- Maillet E., Cui M., Jiang P., Mezei M., Hecht E., **Quijada J.**, Margolskee R., Osman R., and Max M. Characterization of the binding site of aspartame in the human sweet taste receptor. Chem. Senses (2015) 40 (8): 577-86.
- **Quijada J.**, Lopez G., Versace R., Ramirez L., Tasayco M. On the NMR analysis of pKa values in the unfolded state of proteins by extrapolation to zero denaturant. Biophysical Chemistry, (2007) 129(2-3): 242-250.

PRESENTATIONS

- Human Proteome Organization (HUPO) 16th Annual Meeting, Precision Proteomics for Discovery and Health, San Diego, CA, March 2017

  Jeniffer Quijada (Oral Presenter), and Jeffrey Agar. "Measuring Intact Protein Turnover on Drosophila Melanogaster Heads using Tunable Intact Protein Mass Increases Method (TIPMI)"

- Janssen Research and Development, Spring House, PA and Johnson and Johnson Consumer, Skillman, New Jersey Open House, September 2016

  Jeniffer Quijada (Poster Presenter), Nicholas Schmitt, Joseph Salisbury, Jared Auclair, and Jeffrey Agar. "TIPMI: Tunable Intact Protein Mass Increases for Quantitative MS in any Feed and Organism"

- 64th Annual Conference of the American Society for Mass Spectrometry, San Antonio, TX, June 2016

  Nicholas D Schmitt, **Jeniffer Quijada,** Jeffrey Agar (Oral Presenter), Christopher Thompson, Michael Easterling, Jeffrey Agar. "Just Add Water and Resolving Power: Metabolic Labeling and MS Techniques for Lipid and Intact Protein Quantitation in Any Organism"

- 63rd Annual Conference of the American Society for Mass Spectrometry, St. Louis, MO, June 2015

  Jeniffer Quijada (Oral Presenter), Jared Auclair, Joseph Salisbury, Jeffrey Agar. "Stochastic SILAC for Intact Protein Quantitation in Any Organism Using Any Growth Medium or Feed"