BIOGRAPHICAL SKETCH

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NAME	POSITION TITLE
Jessica Liberles	Assistant Professor
eRA COMMONS USER NAME (credential, e.g., agency login) LIBERLESJ	

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

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
Stockholm University, Sweden	M.S.	04/03	Biochemistry and Bioinformatics
University of Bergen, Norway	Ph.D.	11/08	Molecular evolution and structural bioinformatics
University of Wyoming, Wyoming, USA	Postdoc	05/09	Bioinformatics/Protein engineering

A. Personal Statement

We perform research in different areas of computational biology, in a comparative, evolutionary fashion. With an emphasis on understanding how protein structure and function have shaped the genomic sequence library of today, we pursue projects aimed at elucidating novel mechanisms of molecular evolution that contribute to biological divergence among and within a species. Thus, we travel back in time reconstructing the evolutionary history of protein families. As we gain insights from the past, we look to the future.

Currently, we are investigating what proteome characteristics allowed Metazoans to rapidly diversify during, and following, the Cambrian explosion. We are studying how the genomes of Corona viruses, such as SARS and MERS virus, Ebola virus, and of Flavivirus, such as Dengue and West Nile Virus, evolve on the proteome level in order to inform the development of broadly neutralizing antibodies and antivirals for present day and emerging viral strains.

We are also developing novel applications for analysis of whole exome data, on a systems biology level, targeted to the non-bioinformatician user. Integrating and interpreting the exome using a multitude of state-of-the art bioinformatics methods, this tool intends to identify functionally affected pathways in e.g. a tumor exome.

B. Positions and Honors

Positions and Employment

2013- Assistant Professor, Florida International University, Department of Biological Sciences, Miami, FL

2009-2013 Research scientist, Sr., University of Wyoming, Laramie, WY

(My position at University of Wyoming was equally divided between directing a Bioinformatics service core and developing my own independent research program in bioinformatics.)

Other Experience and Professional Memberships

2009 NSF ad-hoc reviewer
2010 NSF review panelist

C. Peer-reviewed Publications (in chronological order)

(Jessica Liberles has published as Siltberg J., Liberles J.S., and Siltberg-Liberles J.)

1. Ryu M.H., Kang I.H., Nelson M.D., Jensen T.M., Lyuksyutova A.I., Siltberg-Liberles J., Raizen D.M., & Gomelsky M. (2014). Engineering adenylate cyclases regulated by near-infrared window light. PNAS, 111(28):10167-10172.

2. Richmond K., *Masterson P., Ortiz J.F., & Siltberg-Liberles J. (2014). Did the prion protein become vulnerable to misfolding after an evolutionary divide and conquer event? J Biomol Struct Dyn, 32(7):1074-1084.

3. *Kutchko K.M., & Siltberg-Liberles J. (2013). Metazoan innovation: from aromatic amino acids to extracellular signaling. Amino Acids, 45(2):359-67.

4. Ortiz J.F., *MacDonald M.L., *Masterson P., Uversky V.N., & Siltberg-Liberles J. (2013). Rapid evolutionary dynamics of structural disorder as a potential driving force for biological divergence in flaviviruses. Genome Biol Evol, 5(3):504-13.

5. Siltberg-Liberles J., Grahnen J.A., & Liberles D.A. (2011). The evolution of protein structures and structural ensembles under functional constraint. Genes (Basel), 2(4):748-62.

6. Siltberg-Liberles J. (2011). Evolution of structurally disordered proteins promotes neostructuralization. Mol Biol Evol, 28(1):59-62.

7. Ryu M.H., Moskvin O.V., Siltberg-Liberles J., & Gomelsky M. (2010). Natural and engineered photoactivated nucleotidyl cyclases for optogenetic applications. J Biol Chem, 285(53):41501-8.

8. Perry D.J., Bittencourt D., Siltberg-Liberles J., Rech E.L., & Lewis R.V. (2010). Piriform Spider Silk Sequences Reveal Unique Repetitive Elements. Biomacromolecules, 11(11):3000-06.

9. Flydal M.I., Mohn T.C., Pey A.L., Siltberg-Liberles J., Teigen K., & Martinez A. (2010). Superstoichiometric binding of L-Phe to phenylalanine hydroxylase from Caenorhabditis elegans: evolutionary implications. Amino Acids, 39(5):1463-75.

10. Liberles S.D., Horowitz L.F., Kuang D., Contos J.J., Wilson K.L., Siltberg-Liberles J., Liberles D.A., & Buck L.B. (2009). Formyl peptide receptors are candidate chemosensory receptors in the vomeronasal organ. PNAS, 106(24):9842-7.

11. Siltberg-Liberles J., Steen I.H., Svebak R.M., & Martinez A. (2008). The phylogeny of the aromatic amino acid hydroxylases revisited by characterizing phenylalanine hydroxylase from Dictyostelium discoideum. Gene, 427(1-2):86-92.

12. Siltberg-Liberles J., & Martinez A. (2009). Searching distant homologs of the regulatory ACT domain in phenylalanine hydroxylase. Amino Acids, (2):235-49.

13. Liberles J.S., Thórólfsson M., & Martínez A. (2005). Allosteric mechanisms in ACT domain containing enzymes involved in amino acid metabolism. Amino Acids, 28(1):1-12.

14. Siltberg J. & Liberles D.A. (2001). A simple covarion-based approach to analyse nucleotide substitution rates J. Evol. Biol, 15(4) :588-94.

D. Research Support