

Stanford



Anthony Cesnik

Postdoctoral Scholar, Bioengineering

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BIO

I am advancing the vision of enabling an understanding of biology at the proteoform level, peering into the cellular machinery in a way that reveals precisely which molecule is acting in the biological system. Recently, I have been working in Emma Lundberg's lab on understanding how the expression of these molecules varies between individual cells in space and time. Emma Lundberg's group has a wealth of experience in using microscopy to yield biological images that paint a picture of this cell-to-cell heterogeneity of protein expression information, and joining her lab has deepened my expertise in integrating datasets to perform innovative analyses of single-cell protein expression. I hope to extend this towards analyzing single-cell proteoform expression, understanding the heterogeneity and flux between these proteoforms in space and time, and digging into the fundamental insights about human biology these data may reveal.

HONORS AND AWARDS

- Gary Parr Memorial Award, University of Wisconsin - Madison (2018)
- Richard and Joan Hartl Award for Research Excellence in Analytical Chemistry, University of Wisconsin - Madison (2017)
- Computation and Informatics in Biology and Medicine, Predoctoral Trainee, University of Wisconsin - Madison (2014-2017)
- Stephen Morton Research Award, University of Wisconsin - Madison (2015)
- Gerhard T. Alexis Scholarship, Gustavus Adolphus College (2011)

STANFORD ADVISORS

- Emma Lundberg, Postdoctoral Faculty Sponsor

Publications

PUBLICATIONS

- **The Blood Proteoform Atlas: A reference map of proteoforms in human hematopoietic cells.** *Science (New York, N.Y.)*
Melani, R. D., Gerbasi, V. R., Anderson, L. C., Sikora, J. W., Toby, T. K., Hutton, J. E., Butcher, D. S., Negrao, F., Seckler, H. S., Srzentic, K., Fornelli, L., Camarillo, J. M., LeDuc, et al
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- **MetaNetwork Enhances Biological Insights from Quantitative Proteomics Differences by Combining Clustering and Enrichment Analyses.** *Journal of proteome research*
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- **Proteomics Standards Initiative's ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms.** *Journal of proteome research*
LeDuc, R. D., Deutsch, E. W., Binz, P. A., Fellers, R. T., Cesnik, A. J., Klein, J. A., Van Den Bossche, T., Gabriels, R., Yalavarthi, A., Perez-Riverol, Y., Carver, J., Bittremieux, W., Kawano, et al
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- **Spatiotemporal dissection of the cell cycle with single-cell proteogenomics.** *Nature*
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- **Illuminating nongenetic cellular heterogeneity with spatial proteomics** *Trends in Cancer*
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- **Mapping the nucleolar proteome reveals a spatiotemporal organization related to intrinsic protein disorder.** *Molecular systems biology*
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2020; 16 (8): e9469
- **Comprehensive Detection of Single Amino Acid Variants and Evaluation of Their Deleterious Potential in a PANC-1 Cell Line.** *Journal of proteome research*
Tan, Z. n., Zhu, J. n., Stemmer, P. M., Sun, L. n., Yang, Z. n., Schultz, K. n., Gaffrey, M. J., Cesnik, A. J., Yi, X. n., Hao, X. n., Shortreed, M. R., Shi, T. n., Lubman, et al
2020
- **Spritz: A Proteogenomic Database Engine.** *Journal of proteome research*
Cesnik, A. J., Miller, R. M., Ibrahim, K. n., Lu, L. n., Millikin, R. J., Shortreed, M. R., Frey, B. L., Smith, L. M.
2020
- **Analysis of the Human Protein Atlas Image Classification competition.** *Nature methods*
Ouyang, W. n., Winsnes, C. F., Hjelmare, M. n., Cesnik, A. J., Åkesson, L. n., Xu, H. n., Sullivan, D. P., Dai, S. n., Lan, J. n., Jinmo, P. n., Galib, S. M., Henkel, C. n., Hwang, et al
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- **Comprehensive in vivo identification of the cMyc mRNA protein interactome using HyPR-MS RNA**
Spiniello, M., Steinbrink, M. I., Cesnik, A. J., Miller, R. M., Scalf, M., Shortreed, M. R., Smith, L. M.
2019; 25: 1337–1352
- **HyPR-MS for Multiplexed Discovery of MALAT1, NEAT1, and NORAD lncRNA Protein Interactomes** *JOURNAL OF PROTEOME RESEARCH*
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- **ProForma: A Standard Proteoform Notation** *JOURNAL OF PROTEOME RESEARCH*
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2018; 17 (3): 1321-1325
- **Expanding Proteoform Identifications in Top-Down Proteomic Analyses by Constructing Proteoform Families** *ANALYTICAL CHEMISTRY*
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- **Identification and Quantification of Murine Mitochondrial Proteoforms Using an Integrated TopDown and IntactMass Strategy** *Journal of Proteome Research*
Schaffer, L. V., Rensvold, J. W., Shortreed, M. R., Cesnik, A. J., Jochem, A., Scalf, M., Frey, B. L., Pagliarini, D. J., Smith, L. M.
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- **Proteoform Suite: Software for Constructing, Quantifying, and Visualizing Proteoform Families** *JOURNAL OF PROTEOME RESEARCH*
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- **Proteomics in non-human primates: utilizing RNA-Seq data to improve protein identification by mass spectrometry in rhesus monkeys** *BMC GENOMICS*
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- **Elucidating Escherichia coli Proteoform Families Using Intact-Mass Proteomics and a Global PTM Discovery Database** *JOURNAL OF PROTEOME RESEARCH*

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- **HyCCAPP as a tool to characterize promoter DNA-protein interactions in Saccharomyces cerevisiae** *GENOMICS*

Guillen-Ahlers, H., Rao, P. K., Levenstein, M. E., Kennedy-Darling, J., Perumalla, D. S., Jadhav, A. L., Glenn, J. P., Ludwig-Kubinski, A., Drigalenko, E., Montoya, M. J., Goring, H. H., Anderson, C. D., Scalf, et al

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- **Elucidating Proteoform Families from Proteoform Intact-Mass and Lysine-Count Measurements** *JOURNAL OF PROTEOME RESEARCH*

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- **Human Proteomic Variation Revealed by Combining RNA-Seq Proteogenomics and Global Post-Translational Modification (G-PTM) Search Strategy** *JOURNAL OF PROTEOME RESEARCH*

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- **Electrochemical Synthesis of Binary and Ternary Niobium-Containing Oxide Electrodes Using the p-Benzoquinone/Hydroquinone Redox Couple** *LANGMUIR*

Papa, C. M., Cesnik, A. J., Evans, T. C., Choi, K.

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