



Ruth Huttenhain

Assistant Professor of Molecular and Cellular Physiology
Molecular & Cellular Physiology

Bio

BIO

Ruth obtained her Ph.D. in Systems Biology from ETH Zurich, Switzerland, where she worked with Ruedi Aebersold, Ph.D, to develop a targeted proteomics strategy for sensitive and reproducible quantification of proteins across large sample cohorts. Supported by the Swiss National Science and the Human Frontiers Science Foundation, Ruth performed her postdoctoral work with Nevan Krogan, Ph.D., at the University of California, San Francisco (UCSF). During her postdoc, Ruth studied protein network dynamics in the context of HIV infection. She also pioneered the first proteomics approach that can resolve protein interaction networks with temporal and spatial resolution. Applying this approach to study dynamics of protein networks engaged by ligand-activated GPCRs led to the discovery of a previously unrecognized ubiquitin network regulating opioid receptor function. After her postdoc Ruth continued at UCSF as an Assistant Adjunct Professor with a research focus on how GPCRs decode extracellular cues into dynamic and context-specific cellular signaling networks to elicit diverse physiologic responses, a research direction that she now further explores in her lab at Stanford. Her lab exploits quantitative proteomics to capture the spatiotemporal organization of GPCR signaling networks combined with functional genomics to study their impact on physiology. Ruth is the Chair of the Early Career Researcher Committee in the Human Proteome Organization. In this role Ruth advocates for the young generation of scientists in proteomics and has created numerous mentoring and training programs.

ACADEMIC APPOINTMENTS

- Assistant Professor, Molecular & Cellular Physiology
- Member, Bio-X
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Assistant Adjunct Professor, University of California San Francisco (UCSF), (2018-2023)

HONORS AND AWARDS

- Early Career Researcher Award, Human Proteome Organization (HUPO) (2018)
- Long-Term Postdoctoral Fellowship, Human Frontiers Science Program (HFSP) (2014)
- Advanced Postdoc Mobility Fellowship, Swiss National Science Foundation (SNSF) (2015)
- Long-Term Postdoctoral Fellowship, European Molecular Biology Organization (EMBO) (2014)
- Early Postdoc Mobility Fellowship, Swiss National Science Foundation (SNSF) (2013)
- ETH medal for outstanding dissertation, ETH Zurich, Switzerland (2012)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Executive Committee Member, Human Proteome Organization (HUPO) (2024 - present)
- Chair of Early Career Researcher (ECR) Committee, Human Proteome Organization (HUPO) (2021 - present)

PROFESSIONAL EDUCATION

- Postdoc, University of California San Francisco (UCSF), CA , Systems Biology, Protein interaction networks, GPCR signaling (2018)
- Postdoc, ETH Zurich, Switzerland , Mass spectrometry-based proteomics, Cancer biomarkers (2013)
- PhD, ETH Zurich, Switzerland , Mass spectrometry-based proteomics, Cancer biomarkers (2011)
- PharmD, University of Bonn, Germany , Pharmaceutical Sciences (2005)

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

My group deciphers how G protein-coupled receptors decode extracellular cues into dynamic and context-specific cellular signaling networks to elicit diverse physiologic responses. We exploit quantitative proteomics to capture the spatiotemporal organization of signaling networks combined with functional genomics to study their impact on physiology.

Teaching

STANFORD ADVISEES

Postdoctoral Faculty Sponsor

Alejandro Matia

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Molecular and Cellular Physiology (Phd Program)
- Neurosciences (Phd Program)

Publications

PUBLICATIONS

- **Profiling the proximal proteome of the activated μ -opioid receptor.** *Nature chemical biology*
Polacco, B. J., Lobingier, B. T., Blythe, E. E., Abreu, N., Khare, P., Howard, M. K., Gonzalez-Hernandez, A. J., Xu, J., Li, Q., Novy, B., Naing, Z. Z., Shoichet, B. K., Coyote-Maestas, et al
2024
- **A foundational atlas of autism protein interactions reveals molecular convergence.** *bioRxiv : the preprint server for biology*
Wang, B., Vartak, R., Zaltsman, Y., Naing, Z. Z., Hennick, K. M., Polacco, B. J., Bashir, A., Eckhardt, M., Bouhaddou, M., Xu, J., Sun, N., Lasser, M. C., Zhou, et al
2023
- **The multi-lineage transcription factor ISL1 controls cardiomyocyte cell fate through interaction with NKX2.5.** *Stem cell reports*
Maven, B. E., Gifford, C. A., Weilert, M., Gonzalez-Teran, B., Hüttenhain, R., Pelonero, A., Ivey, K. N., Samse-Knapp, K., Kwong, W., Gordon, D., McGregor, M., Nishino, T., Okorie, et al
2023
- **SARS-CoV-2 variants evolve convergent strategies to remodel the host response.** *Cell*
Bouhaddou, M., Reuschl, A., Polacco, B. J., Thorne, L. G., Ummadi, M. R., Ye, C., Rosales, R., Pelin, A., Batra, J., Jang, G. M., Xu, J., Moen, J. M., Richards, et al
2023
- **An automated proximity proteomics pipeline for subcellular proteome and protein interaction mapping.** *bioRxiv : the preprint server for biology*
Zhong, X., Li, Q., Polacco, B. J., Patil, T., DiBerto, J. F., Vartak, R., Xu, J., Marley, A., Foussard, H., Roth, B. L., Eckhardt, M., Zastrow, M. V., Krogan, et al
2023
- **Structure-function analysis of enterovirus protease 2A in complex with its essential host factor SETD3.** *Nature communications*
Peters, C. E., Schulze-Gahmen, U., Eckhardt, M., Jang, G. M., Xu, J., Pulido, E. H., Bardine, C., Craik, C. S., Ott, M., Gozani, O., Verba, K. A., Hüttenhain, R., Carette, et al

2022; 13 (1): 5282

- **Signaling snapshots of a serotonin receptor activated by the prototypical psychedelic LSD.** *Neuron*
Cao, C., Barros-Alvarez, X., Zhang, S., Kim, K., Damgen, M. A., Panova, O., Suomivuori, C., Fay, J. F., Zhong, X., Krumm, B. E., Gumpfer, R. H., Seven, A. B., Robertson, et al
2022
- **Transcription Factor GATA4 Regulates Cell Type-Specific Splicing Through Direct Interaction With RNA in Human Induced Pluripotent Stem Cell-Derived Cardiac Progenitors.** *Circulation*
Zhu, L., Choudhary, K., Gonzalez-Teran, B., Ang, Y., Thomas, R., Stone, N. R., Liu, L., Zhou, P., Zhu, C., Ruan, H., Huang, Y., Jin, S., Pelonero, et al
2022: CIRCULATIONAHA121057620
- **Global post-translational modification profiling of HIV-1-infected cells reveals mechanisms of host cellular pathway remodeling** *CELL REPORTS*
Johnson, J. R., Crosby, D. C., Hultquist, J. F., Kurland, A. P., Adhikary, P., Li, D., Marlett, J., Swann, J., Huttenhain, R., Verschueren, E., Johnson, T. L., Newton, B. W., Shales, et al
2022; 39 (2): 110690
- **Tau interactome maps synaptic and mitochondrial processes associated with neurodegeneration.** *Cell*
Tracy, T. E., Madero-Pérez, J., Swaney, D. L., Chang, T. S., Moritz, M., Konrad, C., Ward, M. E., Stevenson, E., Hüttenhain, R., Kauwe, G., Mercedes, M., Sweetland-Martin, L., Chen, et al
2022; 185 (4): 712-728.e14
- **Brahma safeguards canalization of cardiac mesoderm differentiation** *NATURE*
Hota, S. K., Rao, K. S., Blair, A. P., Khalilimeybodi, A., Hu, K. M., Thomas, R., So, K., Kameswaran, V., Xu, J., Polacco, B. J., Desai, R., Chatterjee, N., Hsu, et al
2022; 602 (7895): 129-+
- **Transcription factor protein interactomes reveal genetic determinants in heart disease.** *Cell*
Gonzalez-Teran, B., Pittman, M., Felix, F., Thomas, R., Richmond-Buccola, D., Hüttenhain, R., Choudhary, K., Moroni, E., Costa, M. W., Huang, Y., Padmanabhan, A., Alexanian, M., Lee, et al
2022
- **Proteomic Approaches to Study SARS-CoV-2 Biology and COVID-19 Pathology** *JOURNAL OF PROTEOME RESEARCH*
Haas, P., Muralidharan, M., Krogan, N. J., Kaake, R. M., Huttenhain, R.
2021; 20 (2): 1133-1152
- **Genetic interaction mapping informs integrative structure determination of protein complexes** *SCIENCE*
Braberg, H., Echeverria, I., Bohn, S., Cimermancic, P., Shiver, A., Alexander, R., Xu, J., Shales, M., Dronamraju, R., Jiang, S., Dwivedi, G., Bogdanoff, D., Chaung, et al
2020; 370 (6522): 1294-+
- **Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms** *SCIENCE*
Gordon, D. E., Hiatt, J., Bouhaddou, M., Rezeli, V. V., Ulferts, S., Braberg, H., Jureka, A. S., Obernier, K., Guo, J. Z., Batra, J., Kaake, R. M., Weckstein, A. R., Owens, et al
2020; 370 (6521): 1181-+
- **MassIVE.quant: a community resource of quantitative mass spectrometry-based proteomics datasets** *NATURE METHODS*
Choi, M., Carver, J., Chiva, C., Tzouros, M., Huang, T., Tsai, T., Pullman, B., Bernhardt, O. M., Huttenhain, R., Teo, G., Perez-Riverol, Y., Muntel, J., Mueller, et al
2020; 17 (10): 981-+
- **The Global Phosphorylation Landscape of SARS-CoV-2 Infection.** *Cell*
Bouhaddou, M., Memon, D., Meyer, B., White, K. M., Rezeli, V. V., Correa Marrero, M., Polacco, B. J., Melnyk, J. E., Ulferts, S., Kaake, R. M., Batra, J., Richards, A. L., Stevenson, et al
2020; 182 (3): 685-712.e19
- **A systems approach to infectious disease** *NATURE REVIEWS GENETICS*
Eckhardt, M., Hultquist, J. F., Kaake, R. M., Huttenhain, R., Krogan, N. J.
2020; 21 (6): 339-354
- **A SARS-CoV-2 protein interaction map reveals targets for drug repurposing.** *Nature*
Gordon, D. E., Jang, G. M., Bouhaddou, M., Xu, J., Obernier, K., White, K. M., O'Meara, M. J., Rezeli, V. V., Guo, J. Z., Swaney, D. L., Tummino, T. A., Hüttenhain, R., Kaake, et al

2020; 583 (7816): 459-468

- **A Targeted Mass Spectrometry Strategy for Developing Proteomic Biomarkers: A Case Study of Epithelial Ovarian Cancer.** *Molecular & cellular proteomics : MCP*
 Hüttenhain, R., Choi, M., Martin de la Fuente, L., Oehl, K., Chang, C. Y., Zimmermann, A. K., Malander, S., Olsson, H., Surinova, S., Clough, T., Heinzelmann-Schwarz, V., Wild, P. J., Dinulescu, et al
 2019; 18 (9): 1836-1850
- **ARIH2 Is a Vif-Dependent Regulator of CUL5-Mediated APOBEC3G Degradation in HIV Infection** *CELL HOST & MICROBE*
 Huttenhain, R., Xu, J., Burton, L. A., Gordon, D. E., Hultquist, J. F., Johnson, J. R., Satkamp, L., Hiatt, J., Rhee, D. Y., Baek, K., Crosby, D. C., Frankel, A. D., Marson, et al
 2019; 26 (1): 86-+
- **Enterovirus pathogenesis requires the host methyltransferase SETD3.** *Nature microbiology*
 Diep, J. n., Ooi, Y. S., Wilkinson, A. W., Peters, C. E., Foy, E. n., Johnson, J. R., Zengel, J. n., Ding, S. n., Weng, K. F., Laufman, O. n., Jang, G. n., Xu, J. n., Young, et al
 2019
- **Comparative Flavivirus-Host Protein Interaction Mapping Reveals Mechanisms of Dengue and Zika Virus Pathogenesis** *CELL*
 Shah, P. S., Link, N., Jang, G. M., Sharp, P. P., Zhu, T., Swaney, D. L., Johnson, J. R., Von Dollen, J., Ramage, H. R., Satkamp, L., Newton, B., Huttenhain, R., Petit, et al
 2018; 175 (7): 1931-+
- **CRL4(AMBRA1) targets Elongin C for ubiquitination and degradation to modulate CRL5 signaling** *EMBO JOURNAL*
 Chen, S., Jang, G. M., Huttenhain, R., Gordon, D. E., Du, D., Newton, B. W., Johnson, J. R., Hiatt, J., Hultquist, J. F., Johnson, T. L., Liu, Y., Burton, L. A., Ye, et al
 2018; 37 (18)
- **The Psychiatric Cell Map Initiative: A Convergent Systems Biological Approach to Illuminating Key Molecular Pathways in Neuropsychiatric Disorders** *CELL*
 Willsey, A., Morris, M. T., Wang, S., Willsey, H. R., Sun, N., Teerikorpi, N., Baum, T. B., Cagney, G., Bender, K. J., Desai, T. A., Srivastava, D., Davis, G. W., Doudna, et al
 2018; 174 (3): 505-520
- **Similarities and Differences of Blood N-Glycoproteins in Five Solid Carcinomas at Localized Clinical Stage Analyzed by SWATH-MS** *CELL REPORTS*
 Sajic, T., Liu, Y., Arvaniti, E., Surinova, S., Williams, E. G., Schiess, R., Huttenhain, R., Sethi, A., Pan, S., Brentnall, T. A., Chen, R., Blattmann, P., Friedrich, et al
 2018; 23 (9): 2819-+
- **An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells** *CELL*
 Lobingier, B. T., Huttenhain, R., Eichel, K., Miller, K. B., Ting, A. Y., von Zastrow, M., Krogan, N. J.
 2017; 169 (2): 350-360
- **Prediction of colorectal cancer diagnosis based on circulating plasma proteins** *EMBO MOLECULAR MEDICINE*
 Surinova, S., Choi, M., Tao, S., Schueffler, P. J., Chang, C., Clough, T., Vyslouzil, K., Khoylou, M., Srovnal, J., Liu, Y., Matondo, M., Huettenhain, R., Weisser, et al
 2015; 7 (9): 1166-1178
- **Targeted Peptide Measurements in Biology and Medicine: Best Practices for Mass Spectrometry- based Assay Development Using a Fit- for- Purpose Approach** *MOLECULAR & CELLULAR PROTEOMICS*
 Carr, S. A., Abbatiello, S. E., Ackermann, B. L., Borchers, C., Domon, B., Deutsch, E. W., Grant, R. P., Hoofnagle, A. N., Huettenhain, R., Koomen, J. M., Liebler, D. C., Liu, T., MacLean, et al
 2014; 13 (3): 907-917
- **Mass spectrometric protein maps for biomarker discovery and clinical research** *EXPERT REVIEW OF MOLECULAR DIAGNOSTICS*
 Liu, Y., Huettenhain, R., Collins, B., Aebersold, R.
 2013; 13 (8): 811-825
- **Automated selected reaction monitoring data analysis workflow for large-scale targeted proteomic studies** *NATURE PROTOCOLS*
 Surinova, S., Huettenhain, R., Chang, C., Espona, L., Vitek, O., Aebersold, R.
 2013; 8 (8): 1602-1619

- **N-Glycoprotein SRMAtlas A RESOURCE OF MASS SPECTROMETRIC ASSAYS FOR N-GLYCOSITES ENABLING CONSISTENT AND MULTIPLEXED PROTEIN QUANTIFICATION FOR CLINICAL APPLICATIONS** *MOLECULAR & CELLULAR PROTEOMICS*
Huettenhain, R., Surinova, S., Ossola, R., Sun, Z., Campbell, D., Cerciello, F., Schiess, R., Bausch-Fluck, D., Rosenberger, G., Chen, J., Rinner, O., Kusebauch, U., Hajduch, et al
2013; 12 (4): 1005-1016
- **Quantitative measurements of N-linked glycoproteins in human plasma by SWATH-MS** *PROTEOMICS*
Liu, Y., Huettenhain, R., Surinova, S., Gillet, L. J., Mouritsen, J., Brunner, R., Navarro, P., Aebersold, R.
2013; 13 (8): 1247-1256
- **Reproducible Quantification of Cancer-Associated Proteins in Body Fluids Using Targeted Proteomics** *SCIENCE TRANSLATIONAL MEDICINE*
Huttenhain, R., Soste, M., Selevsek, N., Roest, H., Sethi, A., Carapito, C., Farrah, T., Deutsch, E. W., Kusebauch, U., Moritz, R. L., Nimeus-Malmstroem, E., Rinner, O., Aebersold, et al
2012; 4 (142): 142ra94
- **Range of protein detection by selected/multiple reaction monitoring mass spectrometry in an unfractionated human cell culture lysate** *PROTEOMICS*
Ebhardt, H., Sabido, E., Huettenhain, R., Collins, B., Aebersold, R.
2012; 12 (8): 1185-1193
- **Protein Significance Analysis in Selected Reaction Monitoring (SRM) Measurements** *MOLECULAR & CELLULAR PROTEOMICS*
Chang, C., Picotti, P., Huettenhain, R., Heinzelmann-Schwarz, V., Jovanovic, M., Aebersold, R., Vitek, O.
2012; 11 (4): M111.014662
- **PASSEL: The PeptideAtlas SRM experiment library** *PROTEOMICS*
Farrah, T., Deutsch, E. W., Kreisberg, R., Sun, Z., Campbell, D. S., Mendoza, L., Kusebauch, U., Brusniak, M., Huettenhain, R., Schiess, R., Selevsek, N., Aebersold, R., Moritz, et al
2012; 12 (8): 1170-1175
- **mProphet: automated data processing and statistical validation for large-scale SRM experiments** *NATURE METHODS*
Reiter, L., Rinner, O., Picotti, P., Huettenhain, R., Beck, M., Brusniak, M., Hengartner, M. O., Aebersold, R.
2011; 8 (5): 430-U85
- **On the Development of Plasma Protein Biomarkers** *JOURNAL OF PROTEOME RESEARCH*
Surinova, S., Schiess, R., Huettenhain, R., Cerciello, F., Wollscheid, B., Aebersold, R.
2011; 10 (1): 5-16
- **A combined top-down and bottom-up MS approach for the characterization of hemoglobin variants in Rhesus monkeys** *PROTEOMICS*
Huettenhain, R., Hess, S.
2010; 10 (20): 3657-3668
- **Perspectives of targeted mass spectrometry for protein biomarker verification** *CURRENT OPINION IN CHEMICAL BIOLOGY*
Huettenhain, R., Malmstroem, J., Picotti, P., Aebersold, R.
2009; 13 (5-6): 518-525