



Emma Lundberg

Associate Professor of Bioengineering and of Pathology

CONTACT INFORMATION

- **Alternate Contact**

Devyn James - Administrative Assistant

Email devynj@stanford.edu

Bio

BIO

Dr. Emma Lundberg is an Associate Professor of Bioengineering and Pathology at Stanford University and serves at the Director of the Cell Atlas of the Human Protein Atlas initiative in Sweden, where she is also Professor at KTH Royal Institute of Technology. At the intersection of bioimaging, proteomics, and artificial intelligence, her research aims to define the spatiotemporal organization of the human proteome at both cellular and subcellular level. Dr. Lundberg aims to develop integrated models of human cells to elucidate how variations in protein localization patterns influence cellular function, ultimately enabling the simulation of cell behavior and a systems-level understanding of how biological information is spatially encoded. The Lundberg Lab is responsible for creating the Subcellular Atlas of the Human Protein Atlas database (<https://www.proteinatlas.org/>). Dr. Lundberg is dedicated to building virtual cell models to simulate cell behavior, and is passionate about engaging the public in her work through citizen science games and computational challenges.

Dr. Lundberg holds a Master's degree in Bioengineering and a PhD in Biotechnology from KTH Royal Institute of Technology in Sweden. She has served as Secretary General of the Human Proteome Organization, and is actively involved in advisory roles for numerous open-access databases and cell mapping efforts such as the CZI AI Virtual Cell, Human Cell Atlas consortium, UniProt db, Reactome db, Human Proteome Project and various pharma and biotech companies. As a token of her leadership skills and advocate for open science, she was twice recognized as top 10 under 40 for future leaders in biopharma and omics.

ACADEMIC APPOINTMENTS

- Associate Professor, Bioengineering
- Associate Professor, Pathology
- Member, Bio-X
- Member, Wu Tsai Human Performance Alliance
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Chan Zuckerberg Biohub Investigator, Chan Zuckerberg Biohub, (2022- present)
- Director of Graduate Studies, Stanford Bioengineering, (2022- present)

- Steering Committee of Knight Initiative for Brain Resilience, Stanford University, (2022- present)
- Head of Department of Clinical and Cell Proteomics, KTH Royal Institute of Technology, (2020-2021)
- Director of Spatial Proteomics facility, Science for Life Laboratory, (2017-2022)
- Secretary General, Human Proteome Organization, (2017-2018)
- Co-Director, Human Protein Atlas, (2008- present)

HONORS AND AWARDS

- McCormick and Gabilan Award, Stanford University (2022)
- Göran Gustafsson Award, Göran Gustafsson Foundation (2022)
- Royal Microscopy Society Scientific Achievement Award, Royal Microscopy Society (2021)
- Anne Heidenthal prize for fluorescent research, Chroma Technology Group (2019)
- Ken Standing award for technology development in Life Science, University of Manitoba (2019)
- Swedish national association of chemical engineers' annual prize, Swedish national association of chemical engineers (2017)
- Wallenberg Academy Fellow Award, Knut and Alice Wallenberg Foundation (2016)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- AI Advisory Board Member, Chan Zuckerberg Initiative (2024 - present)
- Chair of Scientific Advisory Board, Max Planck Institute of Biochemistry (2024 - present)
- Scientific Advisory Board, EMBL-EBI Biomaging (2022 - present)
- Scientific Advisory Board, AI for science, AISSAI, CNRS, France (2022 - 2024)
- Scientific Advisory Board, Center for Open Bioimage Analysis (NIH P41 center) (2020 - 2024)
- Scientific Advisory Board, Wellcome Genome Center Oxford (2020 - 2022)
- Scientific Advisory Board, UniProt db (2018 - present)
- Standards and Technologies Working Group, Human Cell Atlas (2018 - present)
- Scientific Advisory Board, Reactome (2018 - 2023)

PROFESSIONAL EDUCATION

- Ph.D., KTH Royal Institute of Technology , Biotechnology (2008)
- M.S, KTH Royal Institute of Technology , Bioengineering (2004)

LINKS

- Lab website: <https://lundberglab.stanford.edu/>
- Human Protein Atlas: <https://www.proteinatlas.org>

Teaching

COURSES

2025-26

- Senior Capstone Design I: BIOE 141A (Aut)
- Senior Capstone Design II: BIOE 141B (Win)

2024-25

- Senior Capstone Design I: BIOE 141A (Aut)
- Senior Capstone Design II: BIOE 141B (Win)

2023-24

- Senior Capstone Design I: BIOE 141A (Aut)
- Senior Capstone Design II: BIOE 141B (Win)

2022-23

- Senior Capstone Design I: BIOE 141A (Aut)
- Senior Capstone Design II: BIOE 141B (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

James Burgess, George Crowley, Jeremy D'Silva, Maylin Fu, Maiko Hermsmeier, Cyrus Knudsen, Eduardo Lozano Garcia, Nicholas Manfred, Gowri Nayar, Janella Schwab Lizárraga, Christine Yiwen Yeh

Postdoctoral Faculty Sponsor

Noorsher Ahmed, Ludvig Bergensträhle, Jan Niklas Hansen, Alissa Hummer, Konstantin Kahnert, William Leineweber, Viviana Macarelli, Mariya Mardamshina, Huangqingbo Sun

Doctoral Dissertation Advisor (AC)

Frida Bjoerklund, Rong Chi, Nicolai Dorka, Mohini Misra, Samantha Mutiti, Ernst Pulido, Anton Thieme

Doctoral (Program)

Janelle Kaneda, Zoe Wefers

Publications

PUBLICATIONS

- **Technologies to measure and modulate protein subcellular localization.** *Nature reviews. Molecular cell biology*
Leineweber, W., Tei, R., Mäkinen, A., Ting, A., Lundberg, E.
2026
- **Subcellular localization as a driver of protein function.** *Nature reviews. Molecular cell biology*
Sigaeva, A., Hutchings, C., Cesnik, A., Lilley, K. S., Lundberg, E.
2026
- **Intrinsic heterogeneity of primary cilia revealed through spatial proteomics.** *Cell*
Hansen, J. N., Sun, H., Kahnert, K., Westenius, E., Johannesson, A., Villegas, C., Le, T., Tzavlaki, K., Winsnes, C., Pohjanen, E., Mäkinen, A., Fall, J., Ballillosera Navarro, et al
2025
- **Multimodal cell maps as a foundation for structural and functional genomics.** *Nature*
Schaffer, L. V., Hu, M., Qian, G., Moon, K. M., Pal, A., Soni, N., Latham, A. P., Pontano Vaites, L., Tsai, D., Mattson, N. M., Licon, K., Bachelder, R., Cesnik, et al
2025
- **How to build the virtual cell with artificial intelligence: Priorities and opportunities.** *Cell*
Bunne, C., Roohani, Y., Rosen, Y., Gupta, A., Zhang, X., Roed, M., Alexandrov, T., AlQuraishi, M., Brennan, P., Burkhardt, D. B., Califano, A., Cool, J., Dernburg, et al
2024; 187 (25): 7045-7063
- **Spatiotemporal dissection of the cell cycle with single-cell proteogenomics.** *Nature*
Mahdessian, D., Cesnik, A. J., Gnann, C., Danielsson, F., Stenstrom, L., Arif, M., Zhang, C., Le, T., Johansson, F., Shutten, R., Backstrom, A., Axelsson, U., Thul, et al
2021; 590 (7847): 649–54

- **A multi-scale map of cell structure fusing protein images and interactions.** *Nature*
Qin, Y., Huttlin, E. L., Winsnes, C. F., Gosztyla, M. L., Wacheul, L., Kelly, M. R., Blue, S. M., Zheng, F., Chen, M., Schaffer, L. V., Licon, K., Bäckström, A., Vaites, et al
2021
- **Spatial proteomics: a powerful discovery tool for cell biology** *NATURE REVIEWS MOLECULAR CELL BIOLOGY*
Lundberg, E., Borner, G. H. H.
2019; 20 (5): 285–302
- **Deep learning is combined with massive-scale citizen science to improve large-scale image classification** *NATURE BIOTECHNOLOGY*
Sullivan, D. P., Winsnes, C. F., Akesson, L., Hjelmare, M., Wiking, M., Schutten, R., Campbell, L., Leifsson, H., Rhodes, S., Nordgren, A., Smith, K., Revaz, B., Finnbogason, et al
2018; 36 (9): 820+
- **A subcellular map of the human proteome.** *Science (New York, N.Y.)*
Thul, P. J., Åkesson, L., Wiking, M., Mahdessian, D., Geladaki, A., Ait Blal, H., Alm, T., Asplund, A., Björk, L., Breckels, L. M., Bäckström, A., Danielsson, F., Fagerberg, et al
2017; 356 (6340)
- **Proteomics. Tissue-based map of the human proteome.** *Science (New York, N.Y.)*
Uhlén, M., Fagerberg, L., Hallström, B. M., Lindskog, C., Oksvold, P., Mardinoglu, A., Sivertsson, Å., Kampf, C., Sjöstedt, E., Asplund, A., Olsson, I., Edlund, K., Lundberg, et al
2015; 347 (6220): 1260419
- **A framework for the exploration of subcellular compartmentalization of RNA-binding proteins.** *Nature communications*
Guo, X., Hu, J., Kanwal, S., Yuan, J., Tariq, M., Zheng, J., Sun, M., Lu, Y., Wang, J., Jiang, M., Wang, A., Castells-Garcia, A., Zheng, et al
2026
- **A high-resolution spatial map of cilia-associated proteins in the human fallopian tube.** *Nature communications*
Hikmet, F., Digre, A., Hansen, J. N., Schon, S. B., Lundberg, E., Olovsson, M., Uhlén, M., Méar, L., Lindskog, C.
2026; 17 (1)
- **Cell shapes decode molecular phenotypes in image-based spatial proteomics.** *Cell systems*
Le, T., Leineweber, W. D., Viana, M. P., Cesnik, A., Hansen, J. N., Ouyang, W., Rafelski, S. M., Lundberg, E.
2026: 101589
- **Generative machine learning unlocks the first proteome-wide image of human cells.** *bioRxiv : the preprint server for biology*
Sun, H., Kahnert, K., Hansen, J. N., Leineweber, W., Li, M., Feng, W., Ballllosera, F., Axelsson, U., Ouyang, W., Lundberg, E.
2026
- **Large-scale mapping of environmental-genetic interactions illustrates the dynamic nature of cell-cycle and DNA repair regulation.** *Molecular cell*
Herken, B. W., Wong, G. T., Mäkinen, A., Lundberg, E., Norman, T. M., Gilbert, L. A.
2026; 86 (4): 757-773.e5
- **RNA origin of sex-biased immunity** *MOLECULAR THERAPY NUCLEIC ACIDS*
Chang, H. Y., Chung, L., Davis, M. M., Fiorentino, D., Lee, J., Lundberg, E., Utz, P. J.
2026; 37 (1)
- **Molecular pixelation of the CAR T cell surface proteome.** *bioRxiv : the preprint server for biology*
Cesnik, A., Takacs-Nagy, O., Le, T., Roth, T. L., Satpathy, A. T., Lundberg, E.
2026
- **Ageing promotes microglial accumulation of slow-degrading synaptic proteins.** *Nature*
Guldner, I. H., Wagner, V. P., Moran-Losada, P., Shi, S. M., Golub, S. W., Hevler, J. F., Chen, K., Meese, B. T., Ghoochani, A., Pulido, E., Oh, H. S., Le Guen, Y., Lu, et al
2026
- **Engineered calcium-regulated affinity protein for efficient internalization and lysosomal toxin delivery.** *Proceedings of the National Academy of Sciences of the United States of America*
Jonsson, M., Moller, M., Schierholz, L., Dorka, N., Tegel, H., Lundberg, E., Uhlen, M., Wolf-Watz, M., Brismar, H., Hober, S.

2025; 122 (48): e2509081122

- **SubCell: Proteome-aware vision foundation models for microscopy capture single-cell biology.** *bioRxiv : the preprint server for biology*
Gupta, A., Wefers, Z., Kahnert, K., Hansen, J. N., Misra, M. K., Leineweber, W., Cesnik, A., Lu, D., Axelsson, U., Baillouera, F., Altman, R. B., Karaletsos, T., Lundberg, et al
2025
- **Spatiotemporal gene expression and cellular dynamics of the developing human heart.** *Nature genetics*
Lázár, E., Mauron, R., Andrusivová, Ž., Foyer, J., He, M., Larsson, L., Shakari, N., Salas, S. M., Avenel, C., Sariyar, S., Hansen, J. N., Vicari, M., Czarnecki, et al
2025
- **Latent plasticity of the human pancreas across development, health, and disease.** *bioRxiv : the preprint server for biology*
Mereu, E., Balboa, D., Liebig, J., Gonzalez-Herrero, A., Martinez-Casals, A., Mardamshina, M., Mollandin, F., Schickanz, F., Tosti, L., Vandenbempt, V., Avrahami, D., Bernardo, E., Björklund, et al
2025
- **Flexible and robust cell-type annotation for highly multiplexed tissue images.** *Cell systems*
Sun, H., Yu, S., Casals, A. M., Bäckström, A., Lu, Y., Lindskog, C., Ruffalo, M., Lundberg, E., Murphy, R. F.
2025: 101374
- **Image based subcellular mapping of the protein landscape of SARS-CoV-2 infected cells for target-centric drug repurposing.** *Biomedicine & pharmacotherapy = Biomedecine & pharmacotherapie*
Tampere, M., H Le, T., Asp, E., Kalman, A., Kaimal, J. M., Njenda, D., Backstrom, A., Axelsson, U., Xu, H., Ouyang, W., Axelsson, H., Marabita, F., Moussaud-Lamodiere, et al
2025; 191: 118447
- **Cell shapes decode molecular phenotypes in image-based spatial proteomics.** *bioRxiv : the preprint server for biology*
Le, T., Leineweber, W. D., Viana, M. P., Cesnik, A., Hansen, J. N., Ouyang, W., Rafelski, S. M., Lundberg, E.
2025
- **Streamlining Multiplexed Tissue Image Analysis with PIPSigmaX: An Integrated Automated Pipeline for Image Processing and EXploration for Diverse Tissue Types.** *bioRxiv : the preprint server for biology*
Mardamshina, M., Navarro, F. B., Casals, A. M., Avenel, C., Wahlby, C., Lundberg, E.
2025
- **Enabling global image data sharing in the life sciences.** *Nature methods*
Bajcsy, P., Bhattacharya, S., Börner, K., Cimini, B. A., Collinson, L., Ellenberg, J., Fiolka, R., Giger, M., Goscinski, W., Hartley, M., Hotaling, N., Horwitz, R., Jug, et al
2025
- **MicroVQA: A Multimodal Reasoning Benchmark for Microscopy-Based Scientific Research.** *ArXiv*
Burgess, J., Nirschl, J. J., Bravo-Sánchez, L., Lozano, A., Gupte, S. R., Galaz-Montoya, J. G., Zhang, Y., Su, Y., Bhowmik, D., Coman, Z., Hasan, S. M., Johannesson, A., Leineweber, et al
2025
- **Human BioMolecular Atlas Program (HuBMAP): 3D Human Reference Atlas construction and usage.** *Nature methods*
Börner, K., Blood, P. D., Silverstein, J. C., Ruffalo, M., Satija, R., Teichmann, S. A., Pryhuber, G. J., Misra, R. S., Purkerson, J. M., Fan, J., Hickey, J. W., Molla, G., Xu, et al
2025
- **MicroVQA: A Multimodal Reasoning Benchmark for Microscopy-Based Scientific Research**
Burgess, J., Nirschl, J. J., Bravo-Sanchez, L., Lozano, A., Gupte, S., Galaz-Montoya, J. G., Zhang, Y., Su, Y., Bhowmik, D., Coman, Z., Hasan, S. M., Johannesson, A., Leineweber, et al
IEEE COMPUTER SOC.2025: 19552-19564
- **A PERTURBATION CELL ATLAS OF HUMAN INDUCED PLURIPOTENT STEM CELLS.** *bioRxiv : the preprint server for biology*
Nourredine, S., Doctor, Y., Dailamy, A., Forget, A., Lee, Y. H., Chinn, B., Khaliq, H., Polacco, B., Muralidharan, M., Pan, E., Zhang, Y., Sigaeva, A., Hansen, et al
2024

- **High-parametric protein maps reveal the spatial organization in early-developing human lung.** *Nature communications*
Sariyar, S., Sountoulidis, A., Hansen, J. N., Marco Salas, S., Mardamshina, M., Martinez Casals, A., Ballllosera Navarro, F., Andrusivova, Z., Li, X., Czarnewski, P., Lundberg, J., Linnarsson, S., Nilsson, et al
2024; 15 (1): 9381
- **How to Build the Virtual Cell with Artificial Intelligence: Priorities and Opportunities.** *ArXiv*
Bunne, C., Roohani, Y., Rosen, Y., Gupta, A., Zhang, X., Roed, M., Alexandrov, T., AlQuraishi, M., Brennan, P., Burkhardt, D. B., Califano, A., Cool, J., Dernburg, et al
2024
- **Flexible and robust cell type annotation for highly multiplexed tissue images.** *bioRxiv : the preprint server for biology*
Sun, H., Yu, S., Casals, A. M., Bäckström, A., Lu, Y., Lindskog, C., Lundberg, E., Murphy, R. F.
2024
- **Early AI Lifecycle Co-Reasoning: Ethics Through Integrated and Diverse Team Science.** *The American journal of bioethics : AJOB*
Pacia, D. M., Ravitsky, V., Hansen, J. N., Lundberg, E., Schulz, W., Bélisle-Pipon, J. C.
2024; 24 (9): 86-88
- **Open-source, high-throughput targeted in-situ transcriptomics for developmental and tissue biology.** *Development (Cambridge, England)*
Lee, H., Mattsson Langseth, C., Marco Salas, S., Sariyar, S., Metousis, A., Rueda Alana, E., Bekiari, C., Lundberg, E., Garcia-Moreno, F., Grillo, M., Nilsson, M.
2024
- **Deconvolf enables high-performance deconvolution of widefield fluorescence microscopy images.** *Nature methods*
Wernersson, E., Gelali, E., Girelli, G., Wang, S., Castillo, D., Mattsson Langseth, C., Verron, Q., Nguyen, H. Q., Chattoraj, S., Martinez Casals, A., Blom, H., Lundberg, E., Nilsson, et al
2024
- **Decrypting lysine deacetylase inhibitor action and protein modifications by dose-resolved proteomics.** *Cell reports*
Chang, Y. C., Gnann, C., Steimbach, R. R., Bayer, F. P., Lechner, S., Sakhteman, A., Abele, M., Zecha, J., Trendel, J., The, M., Lundberg, E., Miller, A. K., Kuster, et al
2024; 43 (6): 114272
- **Cell Maps for Artificial Intelligence: AI-Ready Maps of Human Cell Architecture from Disease-Relevant Cell Lines.** *bioRxiv : the preprint server for biology*
Clark, T., Mohan, J., Schaffer, L., Obernier, K., Al Manir, S., Churas, C. P., Dailamy, A., Doctor, Y., Forget, A., Hansen, J. N., Hu, M., Lenkiewicz, J., Levinson, et al
2024
- **Mapping the Multiscale Proteomic Organization of Cellular and Disease Phenotypes.** *Annual review of biomedical data science*
Cesnik, A., Schaffer, L. V., Gaur, I., Jain, M., Ideker, T., Lundberg, E.
2024
- **Bento: a toolkit for subcellular analysis of spatial transcriptomics data.** *Genome biology*
Mah, C. K., Ahmed, N., Lopez, N. A., Lam, D. C., Pong, A., Monell, A., Kern, C., Han, Y., Prasad, G., Cesnik, A. J., Lundberg, E., Zhu, Q., Carter, et al
2024; 25 (1): 82
- **Macromolecular condensation organizes nucleolar sub-phases to set up a pH gradient.** *Cell*
King, M. R., Ruff, K. M., Lin, A. Z., Pant, A., Farag, M., Lalmansingh, J. M., Wu, T., Fossat, M. J., Ouyang, W., Lew, M. D., Lundberg, E., Vahey, M. D., Pappu, et al
2024
- **Harmonizing the Generation and Pre-publication Stewardship of FAIR Image data.** *ArXiv*
Bialy, N., Alber, F., Andrews, B., Angelo, M., Beliveau, B., Bintu, L., Boettiger, A., Boehm, U., Brown, C. M., Maina, M. B., Chambers, J. J., Cimini, B. A., Eliceiri, et al
2024
- **Xist ribonucleoproteins promote female sex-biased autoimmunity.** *Cell*
Dou, D. R., Zhao, Y., Belk, J. A., Zhao, Y., Casey, K. M., Chen, D. C., Li, R., Yu, B., Srinivasan, S., Abe, B. T., Kraft, K., Hellström, C., Sjöberg, et al
2024; 187 (3): 733-749.e16

- **Tools for assembling the cell: Towards the era of cell structural bioinformatics**
Hu, M., Zhang, X., Latham, A., Sali, A., Ideker, T., Lundberg, E.
edited by Hunter, L., Altman, R. B., Ritchie, M. D., Murray, T., Klein, T. E.
WORLD SCIENTIFIC PUBL CO PTE LTD.2024: 661-665
- **Single Cell Spatial Biology for Precision Cancer Medicine.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
Gentles, A. J., Nirmal, A. J., Heiser, L. M., Lundberg, E., Newman, A. M.
2023; 28: 549-553
- **Xist Ribonucleoproteins Promote Female Sex-biased Autoimmunity**
Dou, D., Zhao, Y., Belk, J., Zhao, Y., Casey, K., Chen, D., Li, R., Yu, B., Srinivasan, S., Abe, B., Kraft, K., Hellstroem, C., Sjoeborg, et al
WILEY.2023: 25-26
- **Segmenting functional tissue units across human organs using community-driven development of generalizable machine learning algorithms.** *Nature communications*
Jain, Y., Godwin, L. L., Joshi, S., Mandarapu, S., Le, T., Lindskog, C., Lundberg, E., Börner, K.
2023; 14 (1): 4656
- **Organ Mapping Antibody Panels: a community resource for standardized multiplexed tissue imaging.** *Nature methods*
Quardokus, E. M., Saunders, D. C., McDonough, E., Hickey, J. W., Werlein, C., Surette, C., Rajbhandari, P., Casals, A. M., Tian, H., Lowery, L., Neumann, E. K., Björklund, F., Neelakantan, et al
2023
- **Building the next generation of virtual cells to understand cellular biology.** *Biophysical journal*
Johnson, G. T., Agmon, E., Akamatsu, M., Lundberg, E., Lyons, B., Ouyang, W., Quintero-Carmona, O. A., Rafelski, S., Horwitz, R.
2023
- **A topographic atlas defines developmental origins of cell heterogeneity in the human embryonic lung.** *Nature cell biology*
Sountoulidis, A., Marco Salas, S., Braun, E., Avenel, C., Bergensträhle, J., Theelke, J., Vicari, M., Czarnewski, P., Lontos, A., Abalo, X., Andrusivová, Ž., Mirzazadeh, R., Asp, et al
2023
- **Segmenting functional tissue units across human organs using community-driven development of generalizable machine learning algorithms.** *bioRxiv : the preprint server for biology*
Jain, Y., Godwin, L. L., Joshi, S., Mandarapu, S., Le, T., Lindskog, C., Lundberg, E., Borner, K.
2023
- **Analysis of the Human Protein Atlas Weakly Supervised Single-Cell Classification competition.** *Nature methods*
Le, T., Winsnes, C. F., Axelsson, U., Xu, H., Mohanakrishnan Kaimal, J., Mahdessian, D., Dai, S., Makarov, I. S., Ostankovich, V., Xu, Y., Benhamou, E., Henkel, C., Solovyev, et al
2022
- **Imaging cell biology.** *Nature cell biology*
Andrews, B., Chang, J. B., Collinson, L., Li, D., Lundberg, E., Mahamid, J., Manley, S., Mhlanga, M., Nakano, A., Schöneberg, J., Van Valen, D., Wu, T. ', Zaritsky, et al
2022
- **The emerging landscape of spatial profiling technologies.** *Nature reviews. Genetics*
Moffitt, J. R., Lundberg, E., Heyn, H.
2022
- **New views of old proteins: clarifying the enigmatic proteome.** *Molecular & cellular proteomics : MCP*
Burnum-Johnson, K. E., Conrads, T. P., Drake, R. R., Herr, A. E., Iyengar, R., Kelly, R. T., Lundberg, E., MacCoss, M. J., Naba, A., Nolan, G. P., Pevzner, P. A., Rodland, K. D., Sechi, et al
2022: 100254
- **Deep Visual Proteomics defines single-cell identity and heterogeneity.** *Nature biotechnology*
Mund, A., Coscia, F., Kriston, A., Hollandi, R., Kovacs, F., Brunner, A., Migh, E., Schweizer, L., Santos, A., Bzorek, M., Naimy, S., Rahbek-Gjerdum, L. M., Dyring-Andersen, et al
2022

- **Understudied proteins: opportunities and challenges for functional proteomics.** *Nature methods*
Kustatscher, G., Collins, T., Gingras, A., Guo, T., Hermjakob, H., Ideker, T., Lilley, K. S., Lundberg, E., Marcotte, E. M., Ralser, M., Rappsilber, J.
2022
- **An open invitation to the Understudied Proteins Initiative.** *Nature biotechnology*
Kustatscher, G., Collins, T., Gingras, A., Guo, T., Hermjakob, H., Ideker, T., Lilley, K. S., Lundberg, E., Marcotte, E. M., Ralser, M., Rappsilber, J.
2022
- **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
1800; 375 (6579): 411-418
- **The new era of quantitative cell imaging-challenges and opportunities.** *Molecular cell*
Bagheri, N., Carpenter, A. E., Lundberg, E., Plant, A. L., Horwitz, R.
2022; 82 (2): 241-247
- **Spatial mapping of protein composition and tissue organization: a primer for multiplexed antibody-based imaging.** *Nature methods*
Hickey, J. W., Neumann, E. K., Radtke, A. J., Camarillo, J. M., Beuschel, R. T., Albanese, A., McDonough, E., Hatler, J., Wiblin, A. E., Fisher, J., Croteau, J., Small, E. C., Sood, et al
2021
- **DeepImageJ: A user-friendly environment to run deep learning models in ImageJ.** *Nature methods*
Gómez-de-Mariscal, E., García-López-de-Haro, C., Ouyang, W., Donati, L., Lundberg, E., Unser, M., Muñoz-Barrutia, A., Sage, D.
2021; 18 (10): 1192-1195
- **A roadmap for the Human Developmental Cell Atlas** *NATURE*
Haniffa, M., Taylor, D., Linnarsson, S., Aronow, B. J., Bader, G. D., Barker, R. A., Camara, P. G., Camp, J., Chedotal, A., Copp, A., Etchevers, H. C., Giacobini, P., Gottgens, et al
2021; 597 (7875): 196-205
- **Which image-based phenotypes are most promising for using AI to understand cellular functions and why?** *CELL SYSTEMS*
Lundberg, E., Funke, J., Bakal, C., Uhlmann, V., Gerlich, D., Walter, T., Carpenter, A., Coehlo, L.
2021; 12 (5): 384-387
- **Pycro-Manager: open-source software for customized and reproducible microscope control.** *Nature methods*
Pinkard, H., Stuurman, N., Ivanov, I. E., Anthony, N. M., Ouyang, W., Li, B., Yang, B., Tsuchida, M. A., Chhun, B., Zhang, G., Mei, R., Anderson, M., Shepherd, et al
2021
- **Building a high-quality Human Cell Atlas** *NATURE BIOTECHNOLOGY*
Rozenblatt-Rosen, O., Shin, J. W., Rood, J. E., Hupalowska, A., Regev, A., Heyn, H., Human Cell Atlas Stand Technology
2021; 39 (2): 149-153
- **Illuminating nongenetic cellular heterogeneity with spatial proteomics** *Trends in Cancer*
Gnann, C., Cesnik, A. J., Lundberg, E.
2021; 7 (4): 278-282
- **Illuminating Non-genetic Cellular Heterogeneity with Imaging-Based Spatial Proteomics.** *Trends in cancer*
Gnann, C., Cesnik, A. J., Lundberg, E.
2021
- **LifeTime and improving European healthcare through cell-based interceptive medicine** *NATURE*
Rajewsky, N., Almouzni, G., Gorski, S. A., Aerts, S., Amit, I., Bertero, M. G., Bock, C., Bredenoord, A. L., Cavalli, G., Chiocca, S., Clevers, H., De Strooper, B., Eggert, et al
2020; 587 (7834): 377-386
- **Mapping the nucleolar proteome reveals a spatiotemporal organization related to intrinsic protein disorder.** *Molecular systems biology*
Stenstrom, L., Mahdessian, D., Gnann, C., Cesnik, A. J., Ouyang, W., Leonetti, M. D., Uhlen, M., Cuylen-Haering, S., Thul, P. J., Lundberg, E.
2020; 16 (8): e9469

- **Mapping the nucleolar proteome reveals a spatiotemporal organization related to intrinsic protein disorder** *MOLECULAR SYSTEMS BIOLOGY*
Stenstrom, L., Mahdessian, D., Gnann, C., Cesnik, A. J., Ouyang, W., Leonetti, M. D., Uhlen, M., Cuylen-Haering, S., Thul, P. J., Lundberg, E.
2020; 16 (8)
- **A Sample Preparation Protocol for High Throughput Immunofluorescence of Suspension Cells on an Adherent Surface** *JOURNAL OF HISTOCHEMISTRY & CYTOCHEMISTRY*
Backstrom, A., Kugel, L., Gnann, C., Xu, H., Aslan, J. E., Lundberg, E., Stadler, C.
2020; 68 (7): 473-489
- **Analysis of the Human Protein Atlas Image Classification competition (vol 16, pg 1254, 2019)** *NATURE METHODS*
Ouyang, W., Winsnes, C. F., Hjelmare, M., Cesnik, A. J., Akesson, L., Xu, H., Sullivan, D. P., Dai, S., Lan, J., Jinmo, P., Galib, S. M., Henkel, C., Hwang, et al
2020; 17 (1): 115
- **A high-stringency blueprint of the human proteome.** *Nature communications*
Adhikari, S., Nice, E. C., Deutsch, E. W., Lane, L., Omenn, G. S., Pennington, S. R., Paik, Y., Overall, C. M., Corrales, F. J., Cristea, I. M., Van Eyk, J. E., Uhlen, M., Lindskog, et al
2020; 11 (1): 5301
- **Spatial Characterization of the Human Centrosome Proteome Opens up New Horizons for a Small but Versatile Organelle.** *Proteomics*
Danielsson, F. n., Mahdessian, D. n., Axelsson, U. n., Sullivan, D. n., Uhlén, M. n., Andersen, J. S., Thul, P. J., Lundberg, E. n.
2020: e1900361
- **Spatial proteomics: a powerful discovery tool for cell biology.** *Nature reviews. Molecular cell biology*
Lundberg, E., Borner, G. H.
2019
- **Voices in methods development.** *Nature methods*
Anikeeva, P. n., Boyden, E. n., Brangwynne, C. n., Cissé, I. I., Fiehn, O. n., Fromme, P. n., Gingras, A. C., Greene, C. S., Heard, E. n., Hell, S. W., Hillman, E. n., Jensen, G. J., Karchin, et al
2019; 16 (10): 945–51
- **ImJoy: an open-source computational platform for the deep learning era.** *Nature methods*
Ouyang, W. n., Mueller, F. n., Hjelmare, M. n., Lundberg, E. n., Zimmer, C. n.
2019; 16 (12): 1199–1200
- **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
2019; 16 (12): 1254–61
- **The human secretome.** *Science signaling*
Uhlén, M. n., Karlsson, M. J., Hober, A. n., Svensson, A. S., Scheffel, J. n., Kotol, D. n., Zhong, W. n., Tebani, A. n., Strandberg, L. n., Edfors, F. n., Sjöstedt, E. n., Mulder, J. n., Mardinoglu, et al
2019; 12 (609)
- **Experimental validation of predicted cancer genes using FRET.** *Methods and applications in fluorescence*
Guala, D., Bernhem, K., Blal, H. A., Jans, D., Lundberg, E., Brismar, H., Sonnhammer, E. L.
2018; 6 (3): 035007
- **Seeing More: A Future of Augmented Microscopy.** *Cell*
Sullivan, D. P., Lundberg, E.
2018; 173 (3): 546-548
- **Transcriptome profiling of the interconnection of pathways involved in malignant transformation and response to hypoxia.** *Oncotarget*
Danielsson, F., Fasterius, E., Sullivan, D., Hases, L., Sanli, K., Zhang, C., Mardinoglu, A., Al-Khalili, C., Huss, M., Uhlén, M., Williams, C., Lundberg, E.
2018; 9 (28): 19730-19744

- **CEP128 Localizes to the Subdistal Appendages of the Mother Centriole and Regulates TGF- β /BMP Signaling at the Primary Cilium.** *Cell reports*
Mönnich, M., Borgeskov, L., Breslin, L., Jakobsen, L., Rogowski, M., Doganli, C., Schröder, J. M., Mogensen, J. B., Blinkenkjær, L., Harder, L. M., Lundberg, E., Geimer, S., Christensen, et al
2018; 22 (10): 2584-2592
- **GeneGini: Assessment via the Gini Coefficient of Reference "Housekeeping" Genes and Diverse Human Transporter Expression Profiles.** *Cell systems*
O'Hagan, S., Wright Muelas, M., Day, P. J., Lundberg, E., Kell, D. B.
2018; 6 (2): 230-244.e1
- **How many human proteoforms are there?** *Nature chemical biology*
Aebersold, R. n., Agar, J. N., Amster, I. J., Baker, M. S., Bertozzi, C. R., Boja, E. S., Costello, C. E., Cravatt, B. F., Fenselau, C. n., Garcia, B. A., Ge, Y. n., Gunawardena, J. n., Hendrickson, et al
2018; 14 (3): 206-14
- **Comparative cell cycle transcriptomics reveals synchronization of developmental transcription factor networks in cancer cells.** *PLoS one*
Boström, J., Sramkova, Z., Salašová, A., Johard, H., Mahdessian, D., Fedr, R., Marks, C., Medalová, J., Souček, K., Lundberg, E., Linnarsson, S., Bryja, V., Sekyrova, et al
2017; 12 (12): e0188772
- **The Human Cell Atlas** *ELIFE*
Regev, A., Teichmann, S. A., Lander, E. S., Amt, I., Benoist, C., Birney, E., Bodenmiller, B., Campbell, P., Carninci, P., Clatworthy, M., Clevers, H., Deplancke, B., Dunham, et al
2017; 6
- **Progress on the HUPO Draft Human Proteome: 2017 Metrics of the Human Proteome Project.** *Journal of proteome research*
Omenn, G. S., Lane, L., Lundberg, E. K., Overall, C. M., Deutsch, E. W.
2017; 16 (12): 4281-4287
- **A comprehensive structural, biochemical and biological profiling of the human NUDIX hydrolase family** *NATURE COMMUNICATIONS*
Carreras-Puigvert, J., Zitnik, M., Jemth, A., Carter, M., Unterlass, J. E., Hallstrom, B., Loseva, O., Karem, Z., Calderon-Montano, J., Lindskog, C., Edqvist, P., Matuszewski, D. J., Blal, et al
2017; 8: 1541
- **Proteomic analysis of cell cycle progression in asynchronous cultures, including mitotic subphases, using PRIMMUS.** *eLife*
Ly, T., Whigham, A., Clarke, R., Brenes-Murillo, A. J., Estes, B., Madhessian, D., Lundberg, E., Wadsworth, P., Lamond, A. I.
2017; 6
- **A pathology atlas of the human cancer transcriptome.** *Science (New York, N.Y.)*
Uhlen, M., Zhang, C., Lee, S., Sjöstedt, E., Fagerberg, L., Bidkhori, G., Benfeitas, R., Arif, M., Liu, Z., Edfors, F., Sanli, K., von Feilitzen, K., Oksvold, et al
2017; 357 (6352)
- **RhoA knockout fibroblasts lose tumor-inhibitory capacity in vitro and promote tumor growth in vivo.** *Proceedings of the National Academy of Sciences of the United States of America*
Alkasalias, T., Alexeyenko, A., Hennig, K., Danielsson, F., Lebbink, R. J., Fielden, M., Turunen, S. P., Lehti, K., Kashuba, V., Madapura, H. S., Bozoky, B., Lundberg, E., Balland, et al
2017; 114 (8): E1413-E1421
- **Antibody Validation in Bioimaging Applications Based on Endogenous Expression of Tagged Proteins.** *Journal of proteome research*
Skogs, M., Stadler, C., Schutten, R., Hjelmare, M., Gnann, C., Björk, L., Poser, I., Hyman, A., Uhlén, M., Lundberg, E.
2017; 16 (1): 147-155
- **The endosomal transcriptional regulator RNF11 integrates degradation and transport of EGFR.** *The Journal of cell biology*
Scharaw, S., Iskar, M., Ori, A., Boncompain, G., Laketa, V., Poser, I., Lundberg, E., Perez, F., Beck, M., Bork, P., Pepperkok, R.
2016; 215 (4): 543-558
- **Metrics for the Human Proteome Project 2016: Progress on Identifying and Characterizing the Human Proteome, Including Post-Translational Modifications.** *Journal of proteome research*
Omenn, G. S., Lane, L., Lundberg, E. K., Beavis, R. C., Overall, C. M., Deutsch, E. W.

2016; 15 (11): 3951-3960

- **Gene-specific correlation of RNA and protein levels in human cells and tissues.** *Molecular systems biology*
Edfors, F., Danielsson, F., Hallström, B. M., Käll, L., Lundberg, E., Pontén, F., Forsström, B., Uhlén, M.
2016; 12 (10): 883
- **A proposal for validation of antibodies** *NATURE METHODS*
Uhlen, M., Bandrowski, A., Carr, S., Edwards, A., Ellenberg, J., Lundberg, E., Rimm, D. L., Rodriguez, H., Hiltke, T., Snyder, M., Yamamoto, T.
2016; 13 (10): 823-?
- **Voices of biotech.** *Nature biotechnology*
Amit, I., Baker, D., Barker, R., Berger, B., Bertozzi, C., Bhatia, S., Biffi, A., Demichelis, F., Doudna, J., Dowdy, S. F., Endy, D., Helmstaedter, M., Junca, et al
2016; 34 (3): 270-275
- **Introducing the Affinity Binder Knockdown Initiative#A public#private partnership for validation of affinity reagents.** *EuPA open proteomics*
Alm, T., Lundberg, E., Uhlén, M.
2016; 10: 56-58
- **Towards a functional definition of the mitochondrial human proteome.** *EuPA open proteomics*
Fasano, M., Alberio, T., Babu, M., Lundberg, E., Urbani, A.
2016; 10: 24-27
- **Systems Proteomics View of the Endogenous Human Claudin Protein Family** *JOURNAL OF PROTEOME RESEARCH*
Liu, F., Koval, M., Ranganathan, S., Fanayan, S., Hancock, W. S., Lundberg, E. K., Beavis, R. C., Lane, L., Duek, P., McQuade, L., Kelleher, N. L., Baker, M. S.
2016; 15 (2): 339-359
- **The folate-coupled enzyme MTHFD2 is a nuclear protein and promotes cell proliferation.** *Scientific reports*
Gustafsson Sheppard, N., Jarl, L., Mahadessian, D., Strittmatter, L., Schmidt, A., Madhusudan, N., Tegnér, J., Lundberg, E. K., Asplund, A., Jain, M., Nilsson, R.
2015; 5: 15029
- **Metrics for the Human Proteome Project 2015: Progress on the Human Proteome and Guidelines for High-Confidence Protein Identification.** *Journal of proteome research*
Omenn, G. S., Lane, L., Lundberg, E. K., Beavis, R. C., Nesvizhskii, A. I., Deutsch, E. W.
2015; 14 (9): 3452-60
- **Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project.** *Journal of proteome research*
Horvatovich, P., Lundberg, E. K., Chen, Y. J., Sung, T. Y., He, F., Nice, E. C., Goode, R. J., Yu, S., Ranganathan, S., Baker, M. S., Domont, G. B., Velasquez, E., Li, et al
2015; 14 (9): 3415-31
- **Analysis of the Human Prostate-Specific Proteome Defined by Transcriptomics and Antibody-Based Profiling Identifies TMEM79 and ACOXL as Two Putative, Diagnostic Markers in Prostate Cancer.** *PLoS one*
O'Hurley, G., Busch, C., Fagerberg, L., Hallström, B. M., Stadler, C., Tolf, A., Lundberg, E., Schwenk, J. M., Jirstrom, K., Bjartell, A., Gallagher, W. M., Uhlén, M., Pontén, et al
2015; 10 (8): e0133449
- **The human liver-specific proteome defined by transcriptomics and antibody-based profiling.** *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*
Kampf, C., Mardinoglu, A., Fagerberg, L., Hallström, B. M., Edlund, K., Lundberg, E., Pontén, F., Nielsen, J., Uhlen, M.
2014; 28 (7): 2901-14
- **Immunoproteomics using polyclonal antibodies and stable isotope-labeled affinity-purified recombinant proteins.** *Molecular & cellular proteomics : MCP*
Edfors, F., Boström, T., Forsström, B., Zeiler, M., Johansson, H., Lundberg, E., Hober, S., Lehtiö, J., Mann, M., Uhlen, M.
2014; 13 (6): 1611-24
- **RNA- and antibody-based profiling of the human proteome with focus on chromosome 19.** *Journal of proteome research*
Stadler, C., Fagerberg, L., Sivertsson, Å., Oksvold, P., Zwahlen, M., Hallström, B. M., Lundberg, E., Uhlén, M.

2014; 13 (4): 2019-27

- **A chromosome-centric analysis of antibodies directed toward the human proteome using Antibodypedia.** *Journal of proteome research*
Alm, T., von Feilitzen, K., Lundberg, E., Sivertsson, Å., Uhlén, M.
2014; 13 (3): 1669-76
- **Molecular- and Organelle-Based Predictive Paradigm Underlying Recovery by Left Ventricular Assist Device Support** *CIRCULATION-HEART FAILURE*
Liem, D. A., Nsair, A., Setty, S. P., Cadeiras, M., Wang, D., MacLellan, R., Lotz, C., Lin, A. J., Tabaraki, J., Li, H., Ge, J., Odeberg, J., Ponten, et al
2014; 7 (2): 359-366
- **Antibody performance in western blot applications is context-dependent.** *Biotechnology journal*
Algenäs, C., Agaton, C., Fagerberg, L., Asplund, A., Björling, L., Björling, E., Kampf, C., Lundberg, E., Nilsson, P., Persson, A., Wester, K., Pontén, F., Wernérus, et al
2014; 9 (3): 435-45
- **Analysis of the human tissue-specific expression by genome-wide integration of transcriptomics and antibody-based proteomics.** *Molecular & cellular proteomics : MCP*
Fagerberg, L., Hallström, B. M., Oksvold, P., Kampf, C., Djureinovic, D., Odeberg, J., Habuka, M., Tahmasebpour, S., Danielsson, A., Edlund, K., Asplund, A., Sjöstedt, E., Lundberg, et al
2014; 13 (2): 397-406
- **Analysis of the Human Tissue-specific Expression by Genome-wide Integration of Transcriptomics and Antibody-based Proteomics.** *Molecular & cellular proteomics : MCP*
Fagerberg, L., Hallström, B. M., Oksvold, P., Kampf, C., Djureinovic, D., Odeberg, J., Habuka, M., Tahmasebpour, S., Danielsson, A., Edlund, K., Asplund, A., Sjöstedt, E., Lundberg, et al
2014; 13 (2): 397-406
- **Metrics for the Human Proteome Project 2013-2014 and strategies for finding missing proteins.** *Journal of proteome research*
Lane, L., Bairoch, A., Beavis, R. C., Deutsch, E. W., Gaudet, P., Lundberg, E., Omenn, G. S.
2014; 13 (1): 15-20
- **Contribution of antibody-based protein profiling to the human Chromosome-centric Proteome Project (C-HPP).** *Journal of proteome research*
Fagerberg, L., Oksvold, P., Skogs, M., Algenäs, C., Lundberg, E., Pontén, F., Sivertsson, A., Odeberg, J., Klevebring, D., Kampf, C., Asplund, A., Sjöstedt, E., Al-Khalili Szigyar, et al
2013; 12 (6): 2439-48
- **Initial quantitative proteomic map of 28 mouse tissues using the SILAC mouse.** *Molecular & cellular proteomics : MCP*
Geiger, T., Velic, A., Macek, B., Lundberg, E., Kampf, C., Nagaraj, N., Uhlen, M., Cox, J., Mann, M.
2013; 12 (6): 1709-22
- **A texture based pattern recognition approach to distinguish melanoma from non-melanoma cells in histopathological tissue microarray sections.** *PloS one*
Rexhepaj, E., Agnarsdóttir, M., Bergman, J., Edqvist, P. H., Bergqvist, M., Uhlén, M., Gallagher, W. M., Lundberg, E., Ponten, F.
2013; 8 (5): e62070
- **Majority of differentially expressed genes are down-regulated during malignant transformation in a four-stage model.** *Proceedings of the National Academy of Sciences of the United States of America*
Danielsson, F., Skogs, M., Huss, M., Rexhepaj, E., O'Hurley, G., Klevebring, D., Pontén, F., Gad, A. K., Uhlén, M., Lundberg, E.
2013; 110 (17): 6853-8
- **Immunofluorescence and fluorescent-protein tagging show high correlation for protein localization in mammalian cells.** *Nature methods*
Stadler, C., Rexhepaj, E., Singan, V. R., Murphy, R. F., Pepperkok, R., Uhlén, M., Simpson, J. C., Lundberg, E.
2013; 10 (4): 315-23
- **Centrosome isolation and analysis by mass spectrometry-based proteomics.** *Methods in enzymology*
Jakobsen, L., Schrøder, J. M., Larsen, K. M., Lundberg, E., Andersen, J. S.
2013; 525: 371-93
- **RNA deep sequencing as a tool for selection of cell lines for systematic subcellular localization of all human proteins.** *Journal of proteome research*

- Danielsson, F., Wiking, M., Mahdessian, D., Skogs, M., Ait Blal, H., Hjelmare, M., Stadler, C., Uhlén, M., Lundberg, E.
2013; 12 (1): 299-307
- **A Chromosome-centric Human Proteome Project (C-HPP) to Characterize the Sets of Proteins Encoded in Chromosome 17** *JOURNAL OF PROTEOME RESEARCH*
Liu, S., Im, H., Bairoch, A., Cristofanilli, M., Chen, R., Deutsch, E. W., Dalton, S., Fenyo, D., Fanayan, S., Gates, C., Gaudet, P., Hincapie, M., Hanash, et al
2013; 12 (1): 45-57
 - **Automated analysis and reannotation of subcellular locations in confocal images from the Human Protein Atlas.** *PLoS one*
Li, J., Newberg, J. Y., Uhlén, M., Lundberg, E., Murphy, R. F.
2012; 7 (11): e50514
 - **Estimating microtubule distributions from 2D immunofluorescence microscopy images reveals differences among human cultured cell lines.** *PLoS one*
Li, J., Shariff, A., Wiking, M., Lundberg, E., Rohde, G. K., Murphy, R. F.
2012; 7 (11): e50292
 - **Comprehensive analysis of the genome transcriptome and proteome landscapes of three tumor cell lines.** *Genome medicine*
Akan, P., Alexeyenko, A., Costea, P. I., Hedberg, L., Solnestam, B. W., Lundin, S., Hällman, J., Lundberg, E., Uhlén, M., Lundeberg, J.
2012; 4 (11): 86
 - **Comparison of total and cytoplasmic mRNA reveals global regulation by nuclear retention and miRNAs.** *BMC genomics*
Solnestam, B. W., Stranneheim, H., Hällman, J., Källner, M., Lundberg, E., Lundeberg, J., Akan, P.
2012; 13: 574
 - **Proteomic Analysis Reveals Drug Accessible Cell Surface N-Glycoproteins of Primary and Established Glioblastoma Cell Lines** *JOURNAL OF PROTEOME RESEARCH*
Bock, T., Moest, H., Omasits, U., Dolski, S., Lundberg, E., Frei, A., Hofmann, A., Bausch-Fluck, D., Jacobs, A., Krayenbuehl, N., Uhlen, M., Aebersold, R., Frei, et al
2012; 11 (10): 4885-4893
 - **A tool to facilitate clinical biomarker studies--a tissue dictionary based on the Human Protein Atlas.** *BMC medicine*
Kampf, C., Bergman, J., Oksvold, P., Asplund, A., Navani, S., Wiking, M., Lundberg, E., Uhlén, M., Ponten, F.
2012; 10: 103
 - **Systematic validation of antibody binding and protein subcellular localization using siRNA and confocal microscopy.** *Journal of proteomics*
Stadler, C., Hjelmare, M., Neumann, B., Jonasson, K., Pepperkok, R., Uhlén, M., Lundberg, E.
2012; 75 (7): 2236-51
 - **Identification of autophagosome-associated proteins and regulators by quantitative proteomic analysis and genetic screens.** *Molecular & cellular proteomics : MCP*
Dengjel, J., Høyer-Hansen, M., Nielsen, M. O., Eisenberg, T., Harder, L. M., Schandorff, S., Farkas, T., Kirkegaard, T., Becker, A. C., Schroeder, S., Vanselow, K., Lundberg, E., Nielsen, et al
2012; 11 (3): M111.014035
 - **Antibody-based protein profiling of the human chromosome 21.** *Molecular & cellular proteomics : MCP*
Uhlén, M., Oksvold, P., Älgenäs, C., Hamsten, C., Fagerberg, L., Klevebring, D., Lundberg, E., Odeberg, J., Pontén, F., Kondo, T., Sivertsson, Å.
2012; 11 (3): M111.013458
 - **Characterization of MRFAP1 turnover and interactions downstream of the NEDD8 pathway.** *Molecular & cellular proteomics : MCP*
Larance, M., Kirkwood, K. J., Xirodimas, D. P., Lundberg, E., Uhlen, M., Lamond, A. I.
2012; 11 (3): M111.014407
 - **Systematic analysis of protein pools, isoforms, and modifications affecting turnover and subcellular localization.** *Molecular & cellular proteomics : MCP*
Ahmad, Y., Boisvert, F. M., Lundberg, E., Uhlen, M., Lamond, A. I.
2012; 11 (3): M111.013680
 - **A Protein Epitope Signature Tag (PrEST) library allows SILAC-based absolute quantification and multiplexed determination of protein copy numbers in cell lines.** *Molecular & cellular proteomics : MCP*

- Zeiler, M., Straube, W. L., Lundberg, E., Uhlen, M., Mann, M.
2012; 11 (3): O111.009613
- **Generation of monospecific antibodies based on affinity capture of polyclonal antibodies.** *Protein science : a publication of the Protein Society*
Hjelm, B., Forsström, B., Igel, U., Johannesson, H., Stadler, C., Lundberg, E., Ponten, F., Sjöberg, A., Rockberg, J., Schwenk, J. M., Nilsson, P., Johansson, C., Uhlén, et al
2011; 20 (11): 1824-35
 - **Mapping the subcellular protein distribution in three human cell lines.** *Journal of proteome research*
Fagerberg, L., Stadler, C., Skogs, M., Hjelmare, M., Jonasson, K., Wiking, M., Abergh, A., Uhlén, M., Lundberg, E.
2011; 10 (8): 3766-77
 - **SATB2 in combination with cytokeratin 20 identifies over 95% of all colorectal carcinomas.** *The American journal of surgical pathology*
Magnusson, K., de Wit, M., Brennan, D. J., Johnson, L. B., McGee, S. F., Lundberg, E., Naicker, K., Klinger, R., Kampf, C., Asplund, A., Wester, K., Gry, M., Bjartell, et al
2011; 35 (7): 937-48
 - **Novel asymmetrically localizing components of human centrosomes identified by complementary proteomics methods.** *The EMBO journal*
Jakobsen, L., Vanselow, K., Skogs, M., Toyoda, Y., Lundberg, E., Poser, I., Falkenby, L. G., Bennetzen, M., Westendorf, J., Nigg, E. A., Uhlen, M., Hyman, A. A., Andersen, et al
2011; 30 (8): 1520-35
 - **What determines specific cell functions? LAB ON A CHIP**
Lundberg, E., Svahn, H.
2011; 11 (12): 2039-2041
 - **Selection and characterisation of affibody molecules inhibiting the interaction between Ras and Raf in vitro.** *New biotechnology*
Grimm, S., Lundberg, E., Yu, F., Shibasaki, S., Vernet, E., Skogs, M., Nygren, P. Å., Gräslund, T.
2010; 27 (6): 766-73
 - **Defining the transcriptome and proteome in three functionally different human cell lines.** *Molecular systems biology*
Lundberg, E., Fagerberg, L., Klevebring, D., Matic, I., Geiger, T., Cox, J., Algenäs, C., Lundeberg, J., Mann, M., Uhlen, M.
2010; 6: 450
 - **Analysis of transcript and protein overlap in a human osteosarcoma cell line.** *BMC genomics*
Klevebring, D., Fagerberg, L., Lundberg, E., Emanuelsson, O., Uhlén, M., Lundeberg, J.
2010; 11: 684
 - **Towards a knowledge-based Human Protein Atlas.** *Nature biotechnology*
Uhlen, M., Oksvold, P., Fagerberg, L., Lundberg, E., Jonasson, K., Forsberg, M., Zwahlen, M., Kampf, C., Wester, K., Hober, S., Wernerus, H., Björling, L., Ponten, et al
2010; 28 (12): 1248-50
 - **Creation of an antibody-based subcellular protein atlas.** *Proteomics*
Lundberg, E., Uhlén, M.
2010; 10 (22): 3984-96
 - **Subcellular distribution and expression of prenylated Rab acceptor 1 domain family, member 2 (PRAF2) in malignant glioma: Influence on cell survival and migration.** *Cancer science*
Borsics, T., Lundberg, E., Geerts, D., Koomoa, D. T., Koster, J., Wester, K., Bachmann, A. S.
2010; 101 (7): 1624-31
 - **A single fixation protocol for proteome-wide immunofluorescence localization studies.** *Journal of proteomics*
Stadler, C., Skogs, M., Brismar, H., Uhlén, M., Lundberg, E.
2010; 73 (6): 1067-78
 - **Selection of affibody molecules to the ligand-binding site of the insulin-like growth factor-1 receptor.** *Biotechnology and applied biochemistry*
Li, J., Lundberg, E., Vernet, E., Larsson, B., Höidén-Guthenberg, I., Gräslund, T.
2010; 55 (2): 99-109

- **A global view of protein expression in human cells, tissues, and organs.** *Molecular systems biology*
Pontén, F., Gry, M., Fagerberg, L., Lundberg, E., Asplund, A., Berglund, L., Oksvold, P., Björling, E., Hober, S., Kampf, C., Navani, S., Nilsson, P., Ottosson, et al
2009; 5: 337
- **Affibody-mediated retention of the epidermal growth factor receptor in the secretory compartments leads to inhibition of phosphorylation in the kinase domain.** *New biotechnology*
Vernet, E., Lundberg, E., Friedman, M., Rigamonti, N., Klausning, S., Nygren, P. A., Gräslund, T.
2009; 25 (6): 417-23
- **Selective expression of Syntaxin-7 protein in benign melanocytes and malignant melanoma.** *Journal of proteome research*
Strömberg, S., Agnarsdóttir, M., Magnusson, K., Rexhepaj, E., Bolander, A., Lundberg, E., Asplund, A., Ryan, D., Rafferty, M., Gallagher, W. M., Uhlen, M., Bergqvist, M., Ponten, et al
2009; 8 (4): 1639-46
- **Automated Analysis of Human Protein Atlas Immunofluorescence Images.** *Proceedings. IEEE International Symposium on Biomedical Imaging*
Newberg, J. Y., Li, J., Rao, A., Pontén, F., Uhlén, M., Lundberg, E., Murphy, R. F.
2009; 5193229: 1023-1026
- **Selection and characterization of Affibody ligands to the transcription factor c-Jun.** *Biotechnology and applied biochemistry*
Lundberg, E., Brismar, H., Gräslund, T.
2009; 52 (Pt 1): 17-27
- **The correlation between cellular size and protein expression levels--normalization for global protein profiling.** *Journal of proteomics*
Lundberg, E., Gry, M., Oksvold, P., Kononen, J., Andersson-Svahn, H., Pontén, F., Uhlén, M., Asplund, A.
2008; 71 (4): 448-60
- **A genecentric Human Protein Atlas for expression profiles based on antibodies.** *Molecular & cellular proteomics : MCP*
Berglund, L., Björling, E., Oksvold, P., Fagerberg, L., Asplund, A., Szigartyo, C. A., Persson, A., Ottosson, J., Wernérus, H., Nilsson, P., Lundberg, E., Sivertsson, A., Navani, et al
2008; 7 (10): 2019-27
- **Affinity-based entrapment of the HER2 receptor in the endoplasmic reticulum using an affibody molecule.** *Journal of immunological methods*
Vernet, E., Konrad, A., Lundberg, E., Nygren, P. A., Gräslund, T.
2008; 338 (1-2): 1-6
- **Toward a confocal subcellular atlas of the human proteome.** *Molecular & cellular proteomics : MCP*
Barbe, L., Lundberg, E., Oksvold, P., Stenius, A., Lewin, E., Björling, E., Asplund, A., Pontén, F., Brismar, H., Uhlén, M., Andersson-Svahn, H.
2008; 7 (3): 499-508
- **A novel method for reproducible fluorescent labeling of small amounts of antibodies on solid phase.** *Journal of immunological methods*
Lundberg, E., Sundberg, M., Gräslund, T., Uhlén, M., Svahn, H. A.
2007; 322 (1-2): 40-9
- **Site-specifically conjugated anti-HER2 Affibody molecules as one-step reagents for target expression analyses on cells and xenograft samples.** *Journal of immunological methods*
Lundberg, E., Höidén-Guthenberg, I., Larsson, B., Uhlén, M., Gräslund, T.
2007; 319 (1-2): 53-63