

Stanford



Parag Mallick

Associate Professor (Research) of Radiology (Diagnostic Sciences Laboratory)

CONTACT INFORMATION

- **Administrative Contact**

Jamie Anderson - Research Administrator

Email jamie5@stanford.edu

Bio

ACADEMIC APPOINTMENTS

- Associate Professor (Research), Radiology
- Member, Bio-X
- Member, Stanford Cancer Institute

PROFESSIONAL EDUCATION

- PostDoc, Institute for Systems Biology , Proteomics & Systems Biology Mentor: Ruedi Aebersold
- Ph.D., University of California, Los Angeles , Chemistry & Biochemistry Mentor: David Eisenberg
- B.S., Washington University in St. Louis , Computer Science & Biochemistry

LINKS

- My Lab's Website: <http://mallicklab.stanford.edu>
- ProteoWizard: <http://proteowizard.sourceforge.net>
- ImmunoGlobe: <http://www.immunoglobe.org>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

The Mallick lab focuses on translating multi-omic discovery into precision diagnostics. In particular we use tightly integrated computational and experimental, multi-omic approaches to discover the processes underlying how cells behave (or misbehave) and accordingly how cancers develop and grow. We hope that by exploring these processes, and by formalizing our knowledge in predictive mathematical models that we will be able to better identify biomarkers that can be used to detect cancers earlier and describe how they are likely to behave (e.g. aggressive vs indolent, drug sensitive vs responsive).

More specifically, we are working in three focus areas: Cancer Systems Biology, Multi-scale Biomarker Biology and Technology Development. Notably, many of the studies in our group are investigating fundamental physiological processes and thus are generally applicable to a range of cell-types and diseases.

Our group has also been leading the development of ProteoWizard, an open source set of libraries and tools to simplify the process of developing proteomics tools. They read and write the HUPO-PSI mzML standard and have been incorporated into the ISB's transproteomicpipeline!

For more information see <http://mallicklab.stanford.edu>

Teaching

COURSES

2023-24

- Mass Spectrometry and Proteomics: Opening the Black Box: BIOS 227 (Win)

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Data Science (Phd Program)
- Cancer Biology (Phd Program)
- Immunology (Phd Program)

Publications

PUBLICATIONS

- **Prospector Heads: Generalized Feature Attribution for Large Models & Data.** *ArXiv*
Machiraju, G., Derry, A., Desai, A., Guha, N., Karimi, A. H., Zou, J., Altman, R. B., Ré, C., Mallick, P.
2024
- **Deep learning-based automated pipeline for blood vessel detection and distribution analysis in multiplexed prostate cancer images.** *Frontiers in bioinformatics*
Karageorgos, G. M., Cho, S., McDonough, E., Chadwick, C., Ghose, S., Owens, J., Jung, K. J., Machiraju, R., West, R., Brooks, J. D., Mallick, P., Ginty, F.
2023; 3: 1296667
- **Geostatistical visualization of ecological interactions in tumors.** *Proceedings. IEEE International Conference on Bioinformatics and Biomedicine*
Boyce, H. B., Mallick, P.
2019; 2019: 2741–49
- **Simulation of the Protein-Shedding Kinetics of a Fully Vascularized Tumor.** *Cancer informatics*
Frieboes, H. B., Curtis, L. T., Wu, M., Kani, K., Mallick, P.
2015; 14: 163-175
- **A cross-platform toolkit for mass spectrometry and proteomics** *NATURE BIOTECHNOLOGY*
Chambers, M. C., MacLean, B., Burke, R., Amodei, D., Ruderman, D. L., Neumann, S., Gatto, L., Fischer, B., Pratt, B., Egertson, J., Hoff, K., Kessner, D., Tasman, et al
2012; 30 (10): 918-920
- **Towards Continuous Scientific Data Analysis and Hypothesis Evolution** *Thirty-First AAAI Conference on Artificial Intelligence*
Gil, Y., Garijo, D., Ratnakar, V., Mayani, R., Adusumilli, R., Boyce, H., Srivastava, A., Mallick, P.
2017
- **Annotation-Free Prediction of Cancer Cells and Glands and Spatial Analysis of Immune Cells.** *bioRxiv : the preprint server for biology*
Jung, K. J., Ghose, S., Cho, S., McDonough, E., Chadwick, C., West, R., Brooks, J. D., Chung, D., Ginty, F., Machiraju, R., Mallick, P.
2025
- **A needed nomenclature for nucleosomes.** *Molecular cell*
Keogh, M. C., Almouzni, G., Andrews, A. J., Armache, K. J., Arrowsmith, C. H., Baek, S. H., Bedford, M. T., Bernstein, E., Côté, J., David, Y., Denu, J. M., Fierz, B., Garcia, et al

2025; 85 (19): 3554-3561

- **Integrated Plasma and Tumor Proteomics of Nasopharyngeal Carcinoma in a Moroccan Cohort.** *International journal of molecular sciences*
Reffai, A., Hori, M., Adusumilli, R., Bermudez, A., Haddad, H., Tawfiq, N., Pitteri, S., Bennani Mechita, M., Mallick, P.
2025; 26 (12)
- **A Proteomic Analysis of Nasopharyngeal Carcinoma in a Moroccan Subpopulation.** *Cancers*
Reffai, A., Hori, M., Adusumilli, R., Bermudez, A., Bouzoubaa, A., Pitteri, S., Bennani Mechita, M., Mallick, P.
2024; 16 (19)
- **AZGP1 deficiency promotes angiogenesis in prostate cancer.** *Journal of translational medicine*
Wen, R. M., Qiu, Z., Marti, G. E., Peterson, E. E., Marques, F. J., Bermudez, A., Wei, Y., Nolley, R., Lam, N., Polasko, A. L., Chiu, C. L., Zhang, D., Cho, et al
2024; 22 (1): 383
- **Examination of the role of mutualism in immune evasion.** *Frontiers in oncology*
Gourmet, L., Walker-Samuel, S., Mallick, P.
2024; 14: 1406744
- **An Inflection Point in Cancer Protein Biomarkers: What Was and What's Next.** *Molecular & cellular proteomics : MCP*
Barker, A. D., Alba, M. M., Mallick, P., Agus, D. B., Lee, J. S.
2023: 100569
- **A flexible electronic strain sensor for the real-time monitoring of tumor regression.** *Science advances*
Abramson, A., Chan, C. T., Khan, Y., Mermin-Bunnell, A., Matsuhisa, N., Fong, R., Shad, R., Hiesinger, W., Mallick, P., Gambhir, S. S., Bao, Z.
2022; 8 (37): eabn6550
- **Nano-omics: nanotechnology-based multidimensional harvesting of the blood-circulating cancerome.** *Nature reviews. Clinical oncology*
Gardner, L., Kostarelos, K., Mallick, P., Dive, C., Hadjidemetriou, M.
2022
- **A Dataset Generation Framework for Evaluating Megapixel Image Classifiers and Their Explanations**
Machiraju, G., Plevritis, S., Mallick, P.
edited by Avidan, S., Brostow, G., Cisse, M., Farinella, G. M., Hassner, T.
SPRINGER INTERNATIONAL PUBLISHING AG.2022: 422-442
- **Transcriptome and genome evolution during HER2-amplified breast neoplasia.** *Breast cancer research : BCR*
Lu, P., Foley, J., Zhu, C., McNamara, K., Sirinukunwattana, K., Vennam, S., Varma, S., Fehri, H., Srivastava, A., Zhu, S., Rittscher, J., Mallick, P., Curtis, et al
2021; 23 (1): 73
- **Epidemiological Profile and Clinicopathological, Therapeutic, and Prognostic Characteristics of Nasopharyngeal Carcinoma in Northern Morocco.** *Cancer control : journal of the Moffitt Cancer Center*
Reffai, A., Mesmoudi, M., Derkaoui, T., Ghailani Nourouti, N., Barakat, A., Sellal, N., Mallick, P., Bennani Mechita, M.
2021; 28: 10732748211050587
- **Sanjiv 'Sam' Gambhir (1962-2020).** *Nature nanotechnology*
Zavaleta, C., Mallick, P.
2020
- **ImmunoGlobe: enabling systems immunology with a manually curated intercellular immune interaction network.** *BMC bioinformatics*
Atallah, M. B., Tandon, V., Hiam, K. J., Boyce, H., Hori, M., Atallah, W., Spitzer, M. H., Engleman, E., Mallick, P.
2020; 21 (1): 346
- **Multicompartment modeling of protein shedding kinetics during vascularized tumor growth.** *Scientific reports*
Machiraju, G. B., Mallick, P. n., Frieboes, H. B.
2020; 10 (1): 16709
- **PTR Explorer: An approach to identify and explore Post Transcriptional Regulatory mechanisms using proteogenomics**
Srivastava, A., Sharpnack, M., Huang, K., Mallick, P., Machiraju, R.
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.

WORLD SCIENTIFIC PUBL CO PTE LTD.2020: 475-486

- **Physical, genomic, and proteomic characterization of a cancer cell line panel in an integrated dataset**
Nikolov, M., White, B., Pegoraro, A., Hope, D., Eljanne, M., Eddy, J., Janmey, P., Mallick, P., Dang, K.
AMER ASSOC CANCER RESEARCH.2019
- **Loss of ER retention motif of AGR2 can impact mTORC signaling and promote cancer metastasis** *ONCOGENE*
Tiemann, K., Garri, C., Lee, S., Malihi, P. D., Park, M., Alvarez, R. M., Yap, L., Ma, P., Katz, J. E., Gross, M. E., Kani, K.
2019; 38 (16): 3003–18
- **Improving Precursor Selectivity in Data-Independent Acquisition Using Overlapping Windows.** *Journal of the American Society for Mass Spectrometry*
Amodei, D., Egertson, J., MacLean, B. X., Johnson, R., Merrihew, G. E., Keller, A., Marsh, D., Vitek, O., Mallick, P., MacCoss, M. J.
2019
- **Semantic workflows for benchmark challenges: Enhancing comparability, reusability and reproducibility**
Srivastava, A., Adusumilli, R., Boyce, H., Garjjo, D., Ratnakar, V., Mayani, R., Yu, T., Machiraju, R., Gil, Y., Mallick, P.
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.
WORLD SCIENTIFIC PUBL CO PTE LTD.2019: 208–19
- **Geostatistical visualization of ecological interactions in tumors**
Boyce, H., Mallick, P.
edited by Yoo, I. H., Bi, J. B., Hu
IEEE.2019: 2741–49
- **Loss of ER retention motif of AGR2 can impact mTORC signaling and promote cancer metastasis.** *Oncogene*
Tiemann, K., Garri, C., Lee, S. B., Malihi, P. D., Park, M., Alvarez, R. M., Yap, L. P., Mallick, P., Katz, J. E., Gross, M. E., Kani, K.
2018
- **Proteogenomic Analysis of Surgically Resected Lung Adenocarcinoma** *JOURNAL OF THORACIC ONCOLOGY*
Sharpnack, M. F., Ranbaduge, N., Srivastava, A., Cerciello, F., Codreanu, S. G., Liebler, D. C., Mascaux, C., Miles, W. O., Morris, R., McDermott, J. E., Sharpnack, J. L., Amann, J., Maher, et al
2018; 13 (10): 1519–29
- **A Bayesian Active Learning Experimental Design for Inferring Signaling Networks** *JOURNAL OF COMPUTATIONAL BIOLOGY*
Ness, R. O., Sachs, K., Mallick, P., Vitek, O.
2018
- **A blood biomarker for monitoring response to anti-EGFR therapy.** *Cancer biomarkers : section A of Disease markers*
Hughes, N. P., Xu, L., Nielsen, C. H., Chang, E., Hori, S. S., Natarajan, A., Lee, S., Kjar, A., Kani, K., Wang, S. X., Mallick, P., Gambhir, S. S.
2018
- **The Predictive Value of Inflammation-Related Peripheral Blood Measurements in Cancer Staging and Prognosis** *FRONTIERS IN ONCOLOGY*
Sylman, J. L., Mitrugno, A., Atallah, M., Tormoen, G. W., Shatzel, J. J., Yunga, S., Wagner, T. H., Leppert, J. T., Mallick, P., McCarty, O. J. T.
2018; 8: 78
- **Longitudinal Multiplexed Measurement of Quantitative Proteomic Signatures in Mouse Lymphoma Models Using Magneto-Nanosensors.** *Theranostics*
Lee, J. R., Appelmann, I. n., Miething, C. n., Shultz, T. O., Ruderman, D. n., Kim, D. n., Mallick, P. n., Lowe, S. W., Wang, S. X.
2018; 8 (5): 1389–98
- **Imitating Pathologist Based Assessment With Interpretable and Context Based Neural Network Modeling of Histology Images.** *Biomedical informatics insights*
Srivastava, A., Kulkarni, C., Huang, K., Parwani, A., Mallick, P., Machiraju, R.
2018; 10: 1178222618807481
- **A Temporal Examination of Platelet Counts as a Predictor of Prognosis in Lung, Prostate, and Colon Cancer Patients.** *Scientific reports*
Sylman, J. L., Boyce, H. B., Mitrugno, A. n., Tormoen, G. W., Thomas, I. C., Wagner, T. H., Lee, J. S., Leppert, J. T., McCarty, O. J., Mallick, P. n.
2018; 8 (1): 6564

- **Multi-lectin Affinity Chromatography and Quantitative Proteomic Analysis Reveal Differential Glycoform Levels between Prostate Cancer and Benign Prostatic Hyperplasia Sera.** *Scientific reports*
Totten, S. M., Adusumilli, R. n., Kullolli, M. n., Tanimoto, C. n., Brooks, J. D., Mallick, P. n., Pitteri, S. J.
2018; 8 (1): 6509
- **Building trans-omics evidence: using imaging and 'omics' to characterize cancer profiles.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
Srivastava, A. n., Kulkarni, C. n., Mallick, P. n., Huang, K. n., Machiraju, R. n.
2018; 23: 377–87
- **Global Transcriptome Analysis of RNA Abundance Regulation by ADAR in Lung Adenocarcinoma.** *EBioMedicine*
Sharpnack, M. F., Chen, B. n., Aran, D. n., Kosti, I. n., Sharpnack, D. D., Carbone, D. P., Mallick, P. n., Huang, K. n.
2018; 27: 167–75
- **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
- **Assessing biological and technological variability in protein levels measured in pre-diagnostic plasma samples of women with breast cancer.** *Biomarker research*
Yeh, C. Y., Adusumilli, R., Kullolli, M., Mallick, P., John, E. M., Pitteri, S. J.
2017; 5: 30
- **Platelet count as a predictor of metastasis and venous thromboembolism in patients with cancer.** *Convergent science physical oncology*
Sylman, J. L., Mitrugno, A., Tormoen, G. W., Wagner, T. H., Mallick, P., McCarty, O. J.
2017; 3 (2)
- **JUN-Mediated downregulation of EGFR signaling is associated with resistance to gefitinib in EGFR-mutant NSCLC cell lines.** *Molecular cancer therapeutics*
Kani, K., Garri, C., Tiemann, K., Malihi, P. D., Punj, V., Nguyen, A. L., Lee, J., Hughes, L. D., Alvarez, R. M., Wood, D. M., Joo, A. Y., Katz, J. E., Agus, et al
2017
- **Data Conversion with ProteoWizard msConvert.** *Methods in molecular biology (Clifton, N.J.)*
Adusumilli, R., Mallick, P.
2017; 1550: 339-368
- **Cellular localization of ER chaperones may predict cancer patient prognosis.**
Tiemann, K., Garri, C., Lee, S., Malihi, P. D., Park, M., Alvarez, R., Yap, L., Conti, P. S., Mallick, P., Katz, J. E., Agus, D., Gross, M. E., Kani, et al
AMER SOC CELL BIOLOGY.2017
- **A Bayesian Active Learning Experimental Design for Inferring Signaling Networks**
Ness, R., Sachs, K., Mallick, P., Vitek, O.
edited by Sahinalp, S. C.
SPRINGER-VERLAG BERLIN.2017: 134–56
- **Assessing biological and technological variability in protein levels measured in pre-diagnostic plasma samples of women with breast cancer** *Biomarker Research*
Yeh, C. Y., Adusumilli, R., Kullolli, M., Mallick, P., John, E. M., Pitteri, S. J.
2017; 5: 30
- **Longitudinal Monitoring of Antibody Responses against Tumor Cells Using Magneto-nanosensors with a Nanoliter of Blood.** *Nano letters*
Lee, J. R., Chan, C. T., Ruderman, D. n., Chuang, H. Y., Gaster, R. S., Atallah, M. n., Mallick, P. n., Lowe, S. W., Gambhir, S. S., Wang, S. X.
2017; 17 (11): 6644–52
- **A Robust Protocol for Protein Extraction and Digestion.** *Methods in molecular biology (Clifton, N.J.)*
Atallah, M., Flory, M. R., Mallick, P.
2017; 1550: 1-10

- **Dual transcript and protein quantification in a massive single cell array.** *Lab on a chip*
Park, S., Lee, J. Y., Hong, S., Lee, S. H., Dimov, I. K., Lee, H., Suh, S., Pan, Q., Li, K., Wu, A. M., Mumenthaler, S. M., Mallick, P., Lee, et al
2016; 16 (19): 3682-3688
- **Single cell dynamic phenotyping** *SCIENTIFIC REPORTS*
Patsch, K., Chiu, C., Engeln, M., Agus, D. B., Mallick, P., Mumenthaler, S. M., Ruderman, D.
2016; 6
- **Protein biomarkers on tissue as imaged via MALDI mass spectrometry: A systematic approach to study the limits of detection** *PROTEOMICS*
van de Ven, S. M., Bemis, K. D., Lau, K., Adusumilli, R., Kota, U., Stolowitz, M., Vitek, O., Mallick, P., Gambhir, S. S.
2016; 16 (11-12): 1660-1669
- **Epigenetic changes mediated by polycomb repressive complex 2 and E2a are associated with drug resistance in a mouse model of lymphoma** *GENOME MEDICINE*
Flinders, C., Lam, L., Rubbi, L., Ferrari, R., Fitz-Gibbon, S., Chen, P., Thompson, M., Christofk, H., Agus, D. B., Ruderman, D., Mallick, P., Pellegrini, M.
2016; 8
- **Probabilistic Segmentation of Mass Spectrometry (MS) Images Helps Select Important Ions and Characterize Confidence in the Resulting Segments** *MOLECULAR & CELLULAR PROTEOMICS*
Bemis, K. D., Harry, A., Eberlin, L. S., Ferreira, C. R., van de Ven, S. M., Mallick, P., Stolowitz, M., Vitek, O.
2016; 15 (5): 1761-1772
- **AshwaMAX and Withaferin A inhibits gliomas in cellular and murine orthotopic models** *JOURNAL OF NEURO-ONCOLOGY*
Chang, E., Pohling, C., Natarajan, A., Witney, T. H., Kaur, J., Xu, L., Gowrishankar, G., D'Souza, A. L., Murty, S., Schick, S., Chen, L., Wu, N., Khaw, et al
2016; 126 (2): 253-264
- **AshwaMAX and Withaferin A inhibits gliomas in cellular and murine orthotopic models.** *Journal of neuro-oncology*
Chang, E., Pohling, C., Natarajan, A., Witney, T. H., Kaur, J., Xu, L., Gowrishankar, G., D'Souza, A. L., Murty, S., Schick, S., Chen, L., Wu, N., Khaw, et al
2016; 126 (2): 253-64
- **A high-content image-based method for quantitatively studying context-dependent cell population dynamics.** *Scientific reports*
Garvey, C. M., Spiller, E., Lindsay, D., Chiang, C., Choi, N. C., Agus, D. B., Mallick, P., Foo, J., Mumenthaler, S. M.
2016; 6: 29752-?
- **NEW HORIZONS IN INTACT PROTEIN ANALYSIS: OPTIMIZATION OF TOP-DOWN PROTEIN ANALYSIS** *CHEMICAL & ENGINEERING NEWS*
Sharma, S., Mallick, P., Stoyanova, T., Mullen, C., Weisbrod, C., Canterbury, J., Horn, D., Zabrouskov, V.
2015: 12-14
- **A fully human scFv phage display library for rapid antibody fragment reformatting** *PROTEIN ENGINEERING DESIGN & SELECTION*
Li, K., Zettlitz, K. A., Lipianskaya, J., Zhou, Y., Marks, J. D., Mallick, P., Reiter, R. E., Wu, A. M.
2015; 28 (10): 307-315
- **Cardinal: an R package for statistical analysis of mass spectrometry-based imaging experiments** *BIOINFORMATICS*
Bemis, K. D., Harry, A., Eberlin, L. S., Ferreira, C., van de Ven, S. M., Mallick, P., Stolowitz, M., Vitek, O.
2015; 31 (14): 2418-2420
- **Cardinal: an R package for statistical analysis of mass spectrometry-based imaging experiments.** *Bioinformatics*
Bemis, K. D., Harry, A., Eberlin, L. S., Ferreira, C., van de Ven, S. M., Mallick, P., Stolowitz, M., Vitek, O.
2015; 31 (14): 2418-2420
- **Predictive Modeling of Drug Response in Non-Hodgkin's Lymphoma** *PLOS ONE*
Frieboes, H. B., Smith, B. R., Wang, Z., Kotsuma, M., Ito, K., Day, A., Cahill, B., Flinders, C., Mumenthaler, S. M., Mallick, P., Simbawa, E., Al-Fhaid, A. S., Mahmoud, et al
2015; 10 (6)
- **Neuronal Activity Promotes Glioma Growth through Neuroligin-3 Secretion** *CELL*

- Venkatesh, H. S., Johung, T. B., Caretti, V., Noll, A., Tang, Y., Nagaraja, S., Gibson, E. M., Mount, C. W., Polepalli, J., Mitra, S. S., Woo, P. J., Malenka, R. C., Vogel, et al
2015; 161 (4): 803-816
- **Building high-quality assay libraries for targeted analysis of SWATH MS data.** *Nature protocols*
Schubert, O. T., Gillet, L. C., Collins, B. C., Navarro, P., Rosenberger, G., Wolski, W. E., Lam, H., Amodei, D., Mallick, P., MacLean, B., Aebersold, R.
2015; 10 (3): 426-441
 - **The Impact of Microenvironmental Heterogeneity on the Evolution of Drug Resistance in Cancer Cells.** *Cancer informatics*
Mumenthaler, S. M., Foo, J., Choi, N. C., Heise, N., Leder, K., Agus, D. B., Pao, W., Michor, F., Mallick, P.
2015; 14: 19-31
 - **Predictive Modeling of Drug Response in Non-Hodgkin's Lymphoma.** *PloS one*
Frieboes, H. B., Smith, B. R., Wang, Z., Kotsuma, M., Ito, K., Day, A., Cahill, B., Flinders, C., Mumenthaler, S. M., Mallick, P., Simbawa, E., Al-Fhaid, A. S., Mahmoud, et al
2015; 10 (6)
 - **Anti-MET ImmunoPET for Non-Small Cell Lung Cancer Using Novel Fully Human Antibody Fragments** *MOLECULAR CANCER THERAPEUTICS*
Li, K., Tavaré, R., Zettlitz, K. A., Mumenthaler, S. M., Mallick, P., Zhou, Y., Marks, J. D., Wu, A. M.
2014; 13 (11): 2607-2617
 - **Anti-MET immunoPET for non-small cell lung cancer using novel fully human antibody fragments.** *Molecular cancer therapeutics*
Li, K., Tavaré, R., Zettlitz, K. A., Mumenthaler, S. M., Mallick, P., Zhou, Y., Marks, J. D., Wu, A. M.
2014; 13 (11): 2607-2617
 - **Employing ProteoWizard to Convert Raw Mass Spectrometry Data.** *Current protocols in bioinformatics / editorial board, Andreas D. Baxevanis ... [et al.]*
Holman, J. D., Tabb, D. L., Mallick, P.
2014; 46: 13 24 1-9
 - **Characterizing deformability and surface friction of cancer cells.** *Proceedings of the National Academy of Sciences of the United States of America*
Byun, S., Son, S., Amodei, D., Cermak, N., Shaw, J., Kang, J. H., Hecht, V. C., Winslow, M. M., Jacks, T., Mallick, P., Manalis, S. R.
2013; 110 (19): 7580-7585
 - **A physical sciences network characterization of non-tumorigenic and metastatic cells** *SCIENTIFIC REPORTS*
Agus, D. B., Alexander, J. F., Arap, W., Ashili, S., Aslan, J. E., Austin, R. H., Backman, V., Bethel, K. J., Bonneau, R., Chen, W., Chen-Tanyolac, C., Choi, N. C., Curley, et al
2013; 3
 - **Anterior gradient 2 (AGR2): Blood-based biomarker elevated in metastatic prostate cancer associated with the neuroendocrine phenotype** *PROSTATE*
Kani, K., Malihi, P. D., Jiang, Y., Wang, H., Wang, Y., Ruderman, D. L., Agus, D. B., Mallick, P., Gross, M. E.
2013; 73 (3): 306-315
 - **Concurrent Transcript and Protein Quantification in a Massive Single Cell Array Enables Population-Wide Observation of Oncogene Escape** *57th Annual Meeting of the Biophysical-Society*
Park, S., Lee, J. Y., Hong, S., Dimov, I. K., Li, K., Wu, A. M., Mumenthaler, S., Mallick, P., Lee, L. P.
CELL PRESS.2013: 686A-686A
 - **Unexpected Dissemination Patterns in Lymphoma Progression Revealed by Serial Imaging within a Murine Lymph Node** *CANCER RESEARCH*
Ito, K., Smith, B. R., Parashurama, N., Yoon, J., Song, S. Y., Miething, C., Mallick, P., Lowe, S., Gambhir, S. S.
2012; 72 (23): 6111-6118
 - **Quantitative Proteomic Profiling Identifies Protein Correlates to EGFR Kinase Inhibition** *MOLECULAR CANCER THERAPEUTICS*
Kani, K., Faca, V. M., Hughes, L. D., Zhang, W., Fang, Q., Shahbaba, B., Luethy, R., Erde, J., Schmidt, J., Pitteri, S. J., Zhang, Q., Katz, J. E., Gross, et al
2012; 11 (5): 1071-1081

- **Investigation of acquired resistance to EGFR-targeted therapies in lung cancer using cDNA microarrays.** *Methods in molecular biology (Clifton, N.J.)*
Kani, K., Sordella, R., Mallick, P.
2012; 795: 233-253
- **Cancer as a Multi-scale Complex Adaptive System** *Assessment Of Physical Sciences And Engineering Advances In Life Sciences And Oncology (Aphelion) In Europe*
Parag Mallick
2012: 4-21
- **Installation and use of LabKey Server for proteomics.** *Current protocols in bioinformatics / editorial board, Andreas D. Baxevanis ... [et al.]*
Eckels, J., Hussey, P., Nelson, E. K., Myers, T., Rauch, A., Bellew, M., Connolly, B., Law, W., Eng, J. K., Katz, J., McIntosh, M., Mallick, P., Igra, et al
2011; Chapter 13: Unit 13 5-?
- **Evolutionary Modeling of Combination Treatment Strategies To Overcome Resistance to Tyrosine Kinase Inhibitors in Non-Small Cell Lung Cancer** *MOLECULAR PHARMACEUTICS*
Mumenthaler, S. M., Foo, J., Leder, K., Choi, N. C., Agus, D. B., Pao, W., Mallick, P., Michor, F.
2011; 8 (6): 2069-2079
- **A High-Confidence Human Plasma Proteome Reference Set with Estimated Concentrations in PeptideAtlas** *MOLECULAR & CELLULAR PROTEOMICS*
Farrah, T., Deutsch, E. W., Omenn, G. S., Campbell, D. S., Sun, Z., Bletz, J. A., Mallick, P., Katz, J. E., Malmstroem, J., Ossola, R., Watts, J. D., Lin, B., Zhang, et al
2011; 10 (9)
- **Impact of Protein Stability, Cellular Localization, and Abundance on Proteomic Detection of Tumor-Derived Proteins in Plasma** *PLOS ONE*
Fang, Q., Kani, K., Faca, V. M., Zhang, W., Zhang, Q., Jain, A., Hanash, S., Agus, D. B., McIntosh, M. W., Mallick, P.
2011; 6 (7)
- **Applying Multi-Agent Techniques to Cancer Modeling** *Proceedings of the Sixth Workshop on Multiagent Sequential Decision Making in Uncertain Domains*
Brown M, Bowring Epstein S, Maheswaran R, Mallick P, Tambe M.
2011
- **Interactively Mapping Data Sources into the Semantic Web** *Proceedings of The First International Symposium on Linked Science*
Knoblock C, , Szekely P, Ambite JL, Gupta S, Aman Goel, Muslea M, Lerman K, Mallick P
2011; 783
- **Model-based discovery of circulating biomarkers.** *Methods in molecular biology (Clifton, N.J.)*
Vogelsang, M. S., Kani, K., Katz, J. E., Mallick, P.
2011; 728: 87-107
- **Peptide Identification from Mixture Tandem Mass Spectra** *MOLECULAR & CELLULAR PROTEOMICS*
Wang, J., Perez-Santiago, J., Katz, J. E., Mallick, P., Bandeira, N.
2010; 9 (7): 1476-1485
- **Proteomics: a pragmatic perspective** *NATURE BIOTECHNOLOGY*
Mallick, P., Kuster, B.
2010; 28 (7): 695-709
- **Mass spectrometry based proteomics in cancer research** *Modern Molecular Biology: Approaches for Unbiased Discovery in Cancer Research*
Abbani M, Mallick P, Vogelsang M
2010: 117-156
- **Recommendations from the 2008 International Summit on Proteomics Data Release and Sharing Policy: The Amsterdam Principles** *JOURNAL OF PROTEOME RESEARCH*
Rodriguez, H., Snyder, M., Uhlen, M., Andrews, P., Beavis, R., Borchers, C., Chalkley, R. J., Cho, S. Y., Cottingham, K., Dunn, M., Dylag, T., Edgar, R., Hare, et al
2009; 8 (7): 3689-3692
- **ProteoWizard: open source software for rapid proteomics tools development** *BIOINFORMATICS*

Kessner, D., Chambers, M., Burke, R., Agusand, D., Mallick, P.
2008; 24 (21): 2534-2536

- **Halobacterium salinarum NRC-1 PeptideAtlas: Toward strategies for targeted proteomics and improved proteome coverage** *JOURNAL OF PROTEOME RESEARCH*
Van, P. T., Schmid, A. K., King, N. L., Kaur, A., Pan, M., Whitehead, K., Koide, T., Facciotti, M. T., Goo, Y. A., Deutsch, E. W., Reiss, D. J., Mallick, P., Baliga, et al
2008; 7 (9): 3755-3764
- **Precursor-ion mass re-estimation improves peptide identification on hybrid instruments** *JOURNAL OF PROTEOME RESEARCH*
Luethy, R., Kessner, D. E., Katz, J. E., McLean, B., Grothe, R., Kani, K., Faca, V., Pitteri, S., Hanash, S., Agus, D. B., Mallick, P.
2008; 7 (9): 4031-4039
- **The standard protein mix database: A diverse data set to assist in the production of improved peptide and protein identification software tools** *JOURNAL OF PROTEOME RESEARCH*
Klimek, J., Eddes, J. S., Hohmann, L., Jackson, J., Peterson, A., Letarte, S., Gafken, P. R., Katz, J. E., Mallick, P., Lee, H., Schmidt, A., Ossola, R., Eng, et al
2008; 7 (1): 96-103
- **Computational prediction of proteotypic peptides for quantitative proteomics.** *Nature biotechnology*
Mallick, P., Schirle, M., Chen, S. S., Flory, M. R., Lee, H., Martin, D., Ranish, J., Raught, B., Schmitt, R., Werner, T., Kuster, B., Aebersold, R.
2007; 25 (1): 125-131
- **eComputational prediction of proteotypic peptides for quantitative proteomics** *NATURE BIOTECHNOLOGY*
Mallick, P., Schirle, M., Chen, S. S., Flory, M. R., Lee, H., Martin, D., Raught, B., Schmitt, R., Werner, T., Kuster, B., Aebersold, R.
2007; 25 (1): 125-131
- **Quantitative proteomic analysis of the budding yeast cell cycle using acid-cleavable isotope-coded affinity tag reagents** *PROTEOMICS*
Flory, M. R., Lee, H., Bonneau, R., Mallick, P., Serikawa, K., Morris, D. R., Aebersold, R.
2006; 6 (23): 6146-6157
- **Protein cross-linking analysis using mass spectrometry, isotope-coded cross-linkers, and integrated computational data processing** *JOURNAL OF PROTEOME RESEARCH*
Seebacher, J., Mallick, P., Zhang, N., Eddes, J. S., Aebersold, R., Gelb, M. H.
2006; 5 (9): 2270-2282
- **Mutagenesis of putative serine-threonine phosphorylation sites proximal to Arg255 of human cytochrome P450c17 does not selectively promote its 17,20-lyase activity** *FERTILITY AND STERILITY*
Souter, I., Munir, I., Mallick, P., Weitsman, S. R., Geller, D. H., Magoffin, D. A.
2006; 85: 1290-1299
- **Signal maps for mass spectrometry-based comparative proteomics** *MOLECULAR & CELLULAR PROTEOMICS*
Prakash, A., Mallick, P., Whiteaker, J., Zhang, H. D., Paulovich, A., Flory, M., LEE, H., Aebersold, R., Schwikowski, B.
2006; 5 (3): 423-432
- **Analysis of the Saccharomyces cerevisiae proteome with PeptideAtlas** *GENOME BIOLOGY*
King, N. L., Deutsch, E. W., Ranish, J. A., Nesvizhskii, A. I., Eddes, J. S., Mallick, P., Eng, J., Desiere, F., Flory, M., Martin, D. B., Kim, B., Lee, H., Raught, et al
2006; 7 (11)
- **The PeptideAtlas project** *NUCLEIC ACIDS RESEARCH*
Desiere, F., Deutsch, E. W., King, N. L., Nesvizhskii, A. I., Mallick, P., Eng, J., Chen, S., Eddes, J., Loevenich, S. N., Aebersold, R.
2006; 34: D655-D658
- **A perspective on protein profiling of blood** *BJU INTERNATIONAL*
Katz, J. E., Mallick, P., Agus, D. B.
2005; 96 (4): 477-482
- **Scoring proteomes with proteotypic peptide probes** *NATURE REVIEWS MOLECULAR CELL BIOLOGY*
Kuster, B., Schirle, M., Mallick, P., Aebersold, R.
2005; 6 (7): 577-583

- **High throughput quantitative analysis of serum proteins using glycopeptide capture and liquid chromatography mass spectrometry** *MOLECULAR & CELLULAR PROTEOMICS*
Zhang, H., Yi, E. C., Li, X. J., Mallick, P., Kelly-Spratt, K. S., Masselon, C. D., Camp, D. G., Smith, R. D., Kemp, C. J., Aebersold, R.
2005; 4 (2): 144-155
- **Finding protein domain boundaries: an automated, non-homology-based method** *IEEE Intelligent Systems*
Gurbaxani BM, Mallick P
2005; Nov-Dec (6): 26-33
- **Integration with the human genome of peptide sequences obtained by high-throughput mass spectrometry** *GENOME BIOLOGY*
Desiere, F., Deutsch, E. W., Nesvizhskii, A. I., Mallick, P., King, N. L., Eng, J. K., Aderem, A., Boyle, R., Brunner, E., Donohoe, S., Fausto, N., Hafen, E., Hood, et al
2005; 6 (1)
- **PFIT and PFRIT: Bioinformatic algorithms for detecting glycosidase function from structure and sequence** *PROTEIN SCIENCE*
Kleiger, G., Panina, E. M., Mallick, P., Eisenberg, D.
2004; 13 (1): 221-229
- **Inference of protein function and protein linkages in Mycobacterium tuberculosis based on prokaryotic genome organization: a combined computational approach** *GENOME BIOLOGY*
Strong, M., Mallick, P., Pellegrini, M., Thompson, M. J., Eisenberg, D.
2003; 4 (9)
- **The directional atomic solvation energy: An atom-based potential for the assignment of protein sequences to known folds** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Mallick, P., Weiss, R., Eisenberg, D.
2002; 99 (25): 16041-16046
- **Genomic evidence that the intracellular proteins of archaeal microbes contain disulfide bonds** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Mallick, P., Boutz, D. R., Eisenberg, D., Yeates, T. O.
2002; 99 (15): 9679-9684
- **A modeled hydrophobic domain on the TCL1 oncoprotein mediates association with AKT at the cytoplasmic membrane** *BIOCHEMISTRY*
French, S. W., Shen, R. R., Koh, P. J., Malone, C. S., Mallick, P., Teitell, M. A.
2002; 41 (20): 6376-6382
- **GXXXG and AXXXA: Common alpha-helical interaction motifs in proteins, particularly in extremophiles** *BIOCHEMISTRY*
Kleiger, G., Grothe, R., Mallick, P., Eisenberg, D.
2002; 41 (19): 5990-5997
- **Making sense of proteomics: Using bioinformatics to discover a protein's structure, functions and interactions.** *Proteins and Proteomics: A Laboratory Manual. Cold Spring Harbor Laboratory Press:*
Parag Mallick, Edward Marcotte
2002: Chapter 11
- **The 1.7 angstrom crystal structure of BPI: A study of how two dissimilar amino acid sequences can adopt the same fold** *JOURNAL OF MOLECULAR BIOLOGY*
Kleiger, G., Beamer, L. J., Grothe, R., Mallick, P., Eisenberg, D.
2000; 299 (4): 1019-1034
- **The 1.7 Å crystal structure of BPI: A study of how two dissimilar amino acid sequences can adopt the same fold** *JOURNAL OF MOLECULAR BIOLOGY*
Kleiger, G., Beamer, L. J., Grothe, R., Mallick, P., Eisenberg, D.
2000; 299 (4): 1019-1034
- **Selecting protein targets for structural genomics of Pyrobaculum aerophilum: Validating automated fold assignment methods by using binary hypothesis testing** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Mallick, P., Goodwill, K. E., Fitz-Gibbon, S., Miller, J. H., Eisenberg, D.
2000; 97 (6): 2450-2455

- **The accidental bioinformaticist** *JOURNAL OF CELLULAR BIOCHEMISTRY*
Mallick, P.
2000; 80 (2): 208-209
- **A Bayesian Active Learning Experimental Design for Inferring Signaling Networks** *International Conference on Research in Computational Molecular Biology*
Ness, R., Sachs, K., Mallick, P., Vitek, O.
- **Automated Hypothesis Testing with Large Scientific Data Repositories** *Annual Conference on Advances in Cognitive Systems*
Gil, Y., Garijo, D., Ratnakar, V., Mayani, R., Adusumilli, R., Boyce, H., Mallick, P.
2016
- **Improving Publication and Reproducibility of Computational Experiments through Workflow Abstractions.** *Workshop on Capturing Scientific Knowledge (SciKnow), held in conjunction with the ACM International Conference on Knowledge Capture (K-CAP)*
Gil, Y., Garijo, D., Knoblock, M., Deng, A., Adusumilli, R., Ratnakar, V., Mallick, P.
2017