

Runyu Hong

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ORCID: 0000-0002-0941-351X

SKILLS

Programming: Python (experienced), R (experienced), SQL (familiar), Matlab (familiar), SAS (basic), Java (basic)

Data and ML: Tensorflow/Keras (experienced), Pytorch (experienced), Shiny (experienced), pandas (experienced), Linux (experienced), scikit-learn (familiar), HPC/slurm (familiar), openCV (familiar), AWS (familiar), Database (familiar), LLM (familiar)

Biomedical Informatics: Omics Data Analysis (experienced), Spatial Transcriptomics Analysis (experienced), EHR (familiar)

EDUCATION

Ph.D., New York University Grossman School of Medicine 2017.08-2022.06

Systems and Computational Biomedicine Training Program

Dissertation: Linking Histopathology and Proteo-genomics with Deep Learning in Cancers

M.Phil., New York University Grossman School of Medicine 2017.08-2020.09

Systems and Computational Biomedicine Training Program

B.S. with Honors, University of Wisconsin Madison 2013.05-2017.05

Biochemistry/Mathematics

Thesis: Predicting and Interpreting the Hofmeister Effects of Different Salts with Nucleic Bases and Aromatic Compounds Using Solubility Assay

Certificates, Harvard Business School Online

Business Analytics (2018.04-2018.06), Credential of Readiness (2022.01-2022.04)

EXPERIENCE

Senior Scientist, Regeneron Pharmaceuticals 2023.02-present

- Led and supported the computational and statistical analysis of histological image-based omics data.
- Developed computational methods, predictive models, and analytical pipelines for biomarker discovery.
- Built quantitative analysis and visualization tools and managed data acquisition and storage and AI infrastructure.
- Communicated and collaborated with interdisciplinary and cross-functional teams.

Senior Data Scientist, Boston Consulting Group 2022.08-2023.02

- Engineered a recommendation system that boosted the quarterly revenue of a pharmaceutical company by 30%.
- Implemented a digital sales optimization strategy that cut the labor cost by 50% for a pharmaceutical company.
- Presented to client's senior management team and collaborated closely with client's IT and sales teams.

Graduate Assistant, New York University Grossman School of Medicine (PI: Dr. D. Fenyö) 2017.08-2022.07

- Developed and applied deep learning models in automating and improving image-based cancer prognosis.
- Analyzed proteo-genomics data using advanced bioinformatics tools to get insights with clinical outcomes.
- Discovered morphological features that link to molecular-level understandings in cancer histopathology.
- Multitasked with 5 ongoing computational projects in collaboration with researchers and clinicians around the world.

Data Scientist (Intern), Novartis 2021.06-2021.08

- Conducted HEOR research and built advanced machine learning models to characterize real world heterogeneity of KRAS-G12C mutant NSCLC patient population.
- Developed interactive apps to visualize potential prognostic features among NSCLC patient population.

Undergraduate Researcher (Part-time), University of Wisconsin Madison (PI: Dr. M.T. Record) 2014.01-2017.05

- Computationally predicted and experimentally validated nucleic acids and aromatic compounds interactions based on Hofmeister Series.
- Received 3 research scholarships and fellowships and the thesis was completed with honors.

Research Trainee (Intern), European Molecular Biology Laboratory (PI: Dr. E. Lemke) 2016.05-2016.08

- Designed and tested the feasibility of using hepatitis B virus capsids as artificial nuclear import carriers.

- Participated in a highly competitive and fully funded internship abroad program.

PUBLICATIONS

Published

Magdalena Kuras*, Lazaro Hiram Betancourt*, **Runyu Hong***, Leticia Szadai, Jimmy Rodriguez, Peter Horvatovich, Indira Pla, Jonatan Eriksson, Beáta Szeitz, Bartłomiej Deszcz, Charlotte Welinder, Yutaka Sugihara, Henrik Ekedahl, Bo Baldetorp, Christian Ingvar, Lotta Lundgren, Henrik Lindberg, Henriett Oskolas, Zsolt Horvath, Melinda Rezeli, Jeovanis Gil, Roger Appelqvist, Lajos V Kemeny, Johan Malm, Aniel Sanchez, A. Marcell Szasz, Krzysztof Pawłowski, Elisabet Wieslander, David Fenyő, Istvan Nemeth, György Marko-Varga. (2025) Proteogenomic Profiling of Treatment-Naïve Metastatic Malignant Melanoma. **Cancers**.

Joshua M. Wang*, **Runyu Hong***, Elizabeth G. Demicco, Jimin Tan, Rossana Lazcano, Andre L. Moreira, Yize Li, Anna Calinawan, Narges Razavian, Tobias Schraink, Michael A. Gillette, Gilbert S. Omenn, Eunkyung An, Henry Rodriguez, Aristotelis Tsirigos, Kelly V. Ruggles, Li Ding, Ana I. Robles, D.R. Mani, Karin D. Rodland, Alexander J. Lazar*, Wenke Liu*, David Fenyő*, and Clinical Proteomic Tumor Analysis Consortium. (2023) Deep Learning Integrates Histopathology and Proteogenomics at a Pan-cancer Level. **Cell Reports Medicine**.

Natália Pinto de Almeida, Ágnes Judit Jánosi, **Runyu Hong**, Ahmad Rajeh, Fábio Nogueira, Leticia Szadai, Beata Szeitz, Indira Pla Parada, Viktória Doma, Nicole Woldmar, Jéssica Guedes, Zsuzsanna Újfaludi, Aron Bartha, Yonghyo Kim, Charlotte Welinder, Bo Baldetorp, Lajos Vince Kemény, Zoltan Pahi, Guihong Wan, Nga Nguyen, Tibor Pankotai, Balázs Györfly, Krzysztof Pawłowski, Peter Horvatovich, Attila Marcell Szasz, Aniel Sanchez, Magdalena Kuras, Jimmy Rodriguez Murillo, Lazaro Betancourt, Gilberto B. Domont, Yevgeniy R. Semenov, Kun-Hsing Yu, Ho Jeong Kwon, István Balázs Németh, David Fenyő, Elisabet Wieslander, György Marko-Varga, Jeovanis Gil. (2024) Mitochondrial Dysfunction and Immune Suppression in BRAF V600E-mutated Metastatic Melanoma. **Clinical and Translational Medicine**.

Yongchao Dou*, Lizabeth Katsnelson*, Marina A. Gritsenko*, Yingwei Hu[†], Boris Reva[†], **Runyu Hong[†]**, Yi-Ting Wang[†], Iga Kolodziejczak[†], Rita Jui-Hsien Lu[†], Chia-Feng Tsai[†], Eunkyung An, Jasmin Bavara, Lijun Chen, Rosalie K. Chu, Andrzej Czekanski, Teresa Davoli, Deborah DeLair, Kelly Devereaux, Saravana M. Dhanasekaran, Peter Dottino, Thomas L. Fillmore, Catherine E. Hermann, Tara Hiltke, Galen Hostetter, Marcin Jędryka, Scott D. Jewell, Isabelle Johnson, Chandan Kumar-Sinha, Paweł Kurzawa, Jonathan T. Lei, Yuxing Liao, Tung-Shing M. Lih, Wenke Liu, John Martignetti, Ramya Masand, Rafał Matkowski, Wilson McKerrow, Mehdi Mesri, Matthew E. Monroe, Jamie Moon, Ronald J. Moore, Michael D. Nestor, Chelsea Newton, Tatiana Omelchenko, Gilbert Omenn, Samuel H. Payne, Vladislav A. Petyuk, Ana I. Robles, Henry Rodriguez, Kelly V. Ruggles, Dimitri Rykunov, Sara Savage, Athena A. Schepmoes, Tujin Shi, Zhiao Shi, Mason Taylor, Mathangi Thiagarajan, Joshua Wang, Karl K. Weitz, Bo Wen, C. M. Williams, Yige Wu, Matthew A. Wyczalkowski, Xinpei Yi, Xu Zhang, Rui Zhao, David Mutch, Arul M. Chinnaiyan, Richard D. Smith, Alexey I. Nesvizhskii, Pei Wang, Maciej Wiznerowicz, Li Ding, D. R. Mani, Hui Zhang, Matthew L. Anderson, Karin D. Rodland, Bing Zhang, Tao Liu, David Fenyő, Clinical Proteomic Tumor Analysis Consortium. (2023) Proteogenomic insights suggest druggable pathways in endometrial carcinoma. **Cancer Cell**.

Yize Li, Yongchao Dou, Felipe Da Veiga Leprevost, Yifat Geffen, Anna P. Calinawan, Francois Aguet, Yo Akiyama, Shankara Anand, Chet Birger, Song Cao, Rekha Chaudhary, Padmini Chilappagari, Marcin Cieslik, Antonio Colaprico, Daniel Cui Zhou, Corbin Day, Marcin J. Domagalski, Myvizhi Esai Selvan, David Fenyő, Steven M. Foltz, Alicia Francis, Tania Gonzalez-Robles, Zeynep H. Gumus, David Heiman, Michael Holck, **Runyu Hong**, Yingwei Hu, Eric J. Jaehnig, Jiayi Ji, Wen Jiang, Lizabeth Katsnelson, Karen A. Ketchum, Robert J. Klein, Jonathan T. Lei, Wen-Wei Liang, Yuxing Liao, Caleb M. Lindgren, Weiping Ma, Lei Ma, Michael J. MacCoss, Fernanda Martins Rodrigues, Wilson McKerrow, Ngoc Nguyen, Robert Oldroyd, Alexander Pillozzi, Pietro Pugliese, Boris Reva, Paul Rudnick, Kelly V. Ruggles, Dmitry Rykunov, Sara R. Savage, Michael Schnaubelt, Tobias Schraink, Zhiao Shi, Deepak Singhal, Xiaoyu Song, Erik Storrs, Nadezhda V. Terekhanova, Ratna R. Thangudu, Mathangi Thiagarajan, Liang-Bo Wang, Joshua M. Wang, Ying Wang, Bo Wen, Yige Wu, Matthew A. Wyczalkowski, Yi Xin, Lijun Yao, Xinpei Yi, Hui Zhang, Qing Zhang, Maya Zuhl, Gad Getz, Li Ding, Alexey I. Nesvizhskii, Pei Wang, Ana I. Robles*, Bing Zhang*, Samuel H. Payne*, and Clinical Proteomic Tumor Analysis Consortium. (2023) Proteogenomic data and resources for pan-cancer analysis. **Cancer Cell**.

Yize Li, Tung-Shing M. Lih, Saravana Mohan Dhanasekaran, Rahul Mannan, Lijun Chen, Marcin Cieslik, Yige Wu, Rita Jui-Hsien Lu, David J. Clark, **Runyu Hong**, Siqi Chen, Chelsea J. Newton, Karsten Krug, Iga Kolodziejczak, Yuanwei Xu, Kyung-Cho Cho, Yingwei Hu, Yuping Zhang, Chandan Kumar-Sinha, Nataly Naser Al Deen, Wagma Caravan, Noshad Hosseini, Weiping Ma, Anna Calinawan, Matthew A. Wyczalkowski, Michael C. Wendl, Yuefan Wang, Shenghao Guo, Cissy Zhang, Anne Le, Aniket Dagar, Alex Hopkins, Hanbyul Cho, Felipe da Veiga Leprevost, Xiaojun Jing, Seema Chugh, Guo Ci Teo, Wenke Liu, Melissa Reimers, Russell Pachynski, Feng Chen, Arul M. Chinnaiyan, Brian Van Tine, Bing Zhang, Karin D. Rodland, Gad Getz, DR Mani, Pei Wang, Maciej Wiznerowicz, Galen Hostetter, Mathangi Thiagarajan, W. Marston Linehan, David Fenyő, Scott D. Jewell, Gilbert S. Omenn, Rohit Mehra, Ana I. Robles, Mehdi Mesri, Tara Hiltke, Eunkyung An, Henry Rodriguez, Daniel W. Chan, Christopher J. Ricketts, Alexey I. Nesvizhskii, Hui Zhang, Li Ding. (2023) Histopathologic and proteogenomic heterogeneity reveals features of clear cell renal cell carcinoma aggressiveness.

Cancer Cell.

Katherine Klein, Sadia Sayeed, Elizabeth Miller, Jessica Kirshner, Jurriaan Brouwer-Visser, **Runyu Hong**, David Knorr, Nathalie Fiaschi, Michael Dobosz, Prachi Sharma, Thomas Uldrick, Leslie Randall. (2025) MUC16 as a novel therapeutic target for high-grade endometrial cancer. **Gynecologic Oncology**.

Aron Bartha, Boglárka Weltz, Lazaro Hiram Betancourt, Jeovanis Gil, Natália Almeida, Giampaolo Bianchini, Beáta Szeitz, Leticia Szadai, Indira Pla, Lajos V. Kemény, Ágnes Judit Jánosi, **Runyu Hong**, Ahmad Rajeh, Fábio Nogueira, Viktória Doma, Nicole Woldmar, Jéssica Guedes, Zsuzsanna Újfaludi, Yonghyo Kim, Tibor Szarvas, Zoltan Pahi, Tibor Pankotai, A. Marcell Szasz, Aniel Sanchez, Bo Baldetorp, József Tímár, István Balázs Németh, Sarolta Kárpáti, Roger Appelqvist, Gilberto Domont, Krzysztof Pawlowski, Elisabet Wieslander, Johan Malm, David Fenyő, Peter Horvatovich, György Marko-Varga. (2025) Melanoma Proteomics Unveiled: Integrating Diverse Datasets for Biomarker Discovery and Clinical Insights via MEL-PLOT. **Journal of Proteome Research**.

Fernanda Martins Rodrigues, Nadezhda V. Terekhanova, Kathleen J. Imbach, Karl R. Clauser, Myvizhi Esai Selvan, Isabel Mendizabal, Yifat Geffen et al. Clinical Proteomic Tumor Analysis Consortium (Contributors include **Runyu Hong**). (2025) Precision Proteogenomics Reveals Pan-cancer Impact of Germline Variants. **Cell**.

Iga Kołodziejczak-Guglas, Renan LS Simões, Emerson de Souza Santos, Elizabeth G. Demicco, Rossana N. Lazcano Segura, Weiping Ma, Pei Wang et al. Clinical Proteomic Tumor Analysis Consortium (Contributors include **Runyu Hong**). (2025) Proteomic-based stemness score measures oncogenic dedifferentiation and enables the identification of druggable targets. **Cell Genomics**.

Yonghyo Kim, Viktória Doma, Uğur Çakır, Magdalena Kuras, Lazaro Hiram Betancourt, Indira Pla, Aniel Sanchez, Yutaka Sugihara, Roger Appelqvist, Henriett Oskolas, Boram Lee, Jéssica Guedes, Gustavo Monnerat, Gabriel Reis Alves Carneiro, Fábio C. S. Nogueira, Gilberto B. Domont, Johan Malm, Bo Baldetorp, Elisabet Wieslander, István Balázs Németh, A. Marcell Szász, **Runyu Hong**, Krzysztof Pawlowski, Melinda Rezeli, Ho Jeong Kwon, Jozsef Timar, David Fenyő, Sarolta Kárpáti, György Marko-Varga, Jeovanis Gil. (2025) Mitochondrial proteome landscape unveils key insights into melanoma severity and treatment strategies. **Cancer**.

Yize Li, Eduard Porta-Pardo, Collin Tokheim, Matthew H. Bailey, Tomer M. Yaron, et. al., Clinical Proteomic Tumor Analysis Consortium (Contributors include **Runyu Hong**). (2023) Pan-cancer proteogenomics connects oncogenic drivers to functional states. **Cell**.

Yifat Geffen, Shankara Anand, Yo Akiyama, Tomer M. Yaron, Yizhe Song, et. al., Clinical Proteomic Tumor Analysis Consortium (Contributors include **Runyu Hong**). (2023) Pan-cancer analysis of post-translational modifications reveals shared patterns of protein regulation. **Cell**.

Francesca Petralia, Weiping Ma, Tomer M. Yaron, Francesca Pia Caruso, Nicole Tignor, Joshua M. Wang, Daniel Charytonowicz et al., Clinical Proteomic Tumor Analysis Consortium (Contributors include **Runyu Hong**). (2024) Pan-cancer proteogenomics characterization of tumor immunity. **Cell**.

Joshua Wang, **Runyu Hong**, Jimin Tan, Wenke Liu, David Fenyő. (2024) Uncovering clinically relevant omics signatures from pan-cancer imaging and multi-omics data integration. **Cancer Research**.

Wen-Wei Liang, Rita Jui-Hsien Lu, Reyka G. Jayasinghe, Steven M. Foltz, et. al., Clinical Proteomic Tumor Analysis Consortium (Contributors include **Runyu Hong**). (2023) Integrative multi-omic cancer profiling reveals DNA methylation patterns associated with therapeutic vulnerability and cell-of-origin. **Cancer Cell**.

Runyu Hong, David Fenyő. (2022) When blockchain meets artificial intelligence: An application to cancer histopathology. **Cell Reports Medicine**.

Runyu Hong, David Fenyő. (2022) Deep Learning and Its Applications in Computational Pathology. **BioMedInformatics**.

Runyu Hong, Wenke Liu, David Fenyő. (2022) Predicting and Visualizing STK11 Mutation in Lung Adenocarcinoma Histopathology Slides Using Deep Learning. **BioMedInformatics**.

Herbert H. Loong, Tao Liu, Thirupathi Pattipaka, **Runyu Hong**, Timothy W. Smith, Stefanie Knoll, Vincent Pretre, Rafael Caparica, Fen Ye, Anna F. Farago. (2022) Heterogeneity and Prognostic Diagnosis of KRAS-Mutated Population and KRAS G12C Subtype among Patients with Advanced NSCLC: A Real-world Study Aided by Machine Learning Approaches. **Annals of Oncology**

Runyu Hong, Wenke Liu, Deborah DeLair, Narges Razavian, David Fenyő. (2021) Predicting endometrial cancer subtypes

and molecular features from histopathology images using multi-resolution deep learning models. **Cell Reports Medicine**

Randie H. Kim, Sofia Nomikou, Nicolas Coudray, George Jour, Zarmeena Dawood, **Runyu Hong**, Eduardo Esteva, Theodore Sakellaropoulos, Douglas Donnelly, Una Moran, Aristides Hatzimemos, Jeffrey S. Weber, Narges Razavian, Ioannis Aifantis, David Fenyő, Matija Snuderl, Richard Shapiro, Russell S. Berman, Iman Osman, Aristotelis Tsirigos. (2021) Deep learning and pathomics analyses reveal cell nuclei as important features for mutation prediction of BRAF-mutated melanomas. **The Journal of Investigative Dermatology**

Lazaro Hiram Betancourt, Jeovanis Gil, Aniel Sanchez, Viktória Doma, Magdalena Kuras, Jimmy Rodriguez Murillo, Erika Velasquez, Uğur Çakır, Yonghyo Kim, Yutaka Sugihara, Indira Pla Parada, Beáta Szeitz, Roger Appelqvist, Elisabet Wieslander, Charlotte Welinder, Natália Pinto de Almeida, Nicole Woldmar, Matilda Marko-Varga, Jonatan Eriksson, Krzysztof Pawłowski, Bo Baldetorp, Christian Ingvar, Håkan Olsson, Lotta Lundgren, Henrik Lindberg, Henriett Oskolas, Boram Lee, Ethan Berge, Marie Sjögren, Carina Eriksson, Dasol Kim, Ho Jeong Kwon, Beatrice Knudsen, Melinda Rezeli, Johan Malm, **Runyu Hong**, Peter Horvath, A. Marcell Szász, József Tímár, Sarolta Kárpáti, Peter Horvatovich, Tasso Miliotis, Toshihide Nishimura, Harubumi Kato, Erik Steinfelder, Madalina Oppermann, Ken Miller, Francesco Florindi, Quimin Zhou, Gilberto B. Domont, Luciana Pizzatti, Fábio C. S. Nogueira, Leticia Szadai, István Balázs Németh, Henrik Ekedahl, David Fenyő, György Marko-Varga. (2021) The human melanoma proteome atlas— Complementing the Melanoma Transcriptome. **Clinical and Translational Medicine**.

Lazaro Hiram Betancourt, Jeovanis Gil, Yonghyo Kim, Viktória Doma, Uğur Çakır, Aniel Sanchez, Jimmy Rodriguez Murillo, Magdalena Kuras, Indira Pla Parada, Yutaka Sugihara, Roger Appelqvist, Elisabet Wieslander, Charlotte Welinder, Erika Velasquez, Natália Pinto de Almeida, Nicole Woldmar, Matilda Marko-Varga, Krzysztof Pawłowski, Jonatan Eriksson, Beáta Szeitz, Bo Baldetorp, Christian Ingvar, Håkan Olsson, Lotta Lundgren, Henrik Lindberg, Henriett Oskolas, Boram Lee, Ethan Berge, Marie Sjögren, Carina Eriksson, Dasol Kim, Ho Jeong Kwon, Beatrice Knudsen, Melinda Rezeli, **Runyu Hong**, Peter Horvatovich, Tasso Miliotis, Toshihide Nishimura, Harubumi Kato, Erik Steinfelder, Madalina Oppermann, Ken Miller, Francesco Florindi, Qimin Zhou, Gilberto B Domont, Luiciana Pizzatti, Fábio CS Nogueira, Peter Horvath, Leticia Szadai, József Tímár, Sarolta Kárpáti, A Marcell Szász, Johan Malm, David Fenyő, Henrik Ekedahl, István Balázs Németh, György Marko-Varga. (2021) The human melanoma proteome atlas—Defining the molecular pathology. **Clinical and Translational Medicine**.

Liang-Bo Wang*, Alla Karpova*, Marina A Gritsenko*, Jennifer E Kyle*, Song Cao*, Yize Li*, Dmitry Rykunov†, Antonio Colaprico†, Joseph H Rothstein†, **Runyu Hong**†, Vasileios Stathias†, MacIntosh Cornwell†, Francesca Petralia†, Yige Wu, Boris Reva, Karsten Krug, Pietro Pugliese, Emily Kawaler, Lindsey K Olsen, Wen-Wei Liang, Xiaoyu Song, Yongchao Dou, Michael C Wendl, Wagma Caravan, Wenke Liu, Daniel Cui Zhou, Jiayi Ji, Chia-Feng Tsai, Vladislav A Petyuk, Jamie Moon, Weiping Ma, Rosalie K Chu, Karl K Weitz, Ronald J Moore, Matthew E Monroe, Rui Zhao, Xiaolu Yang, Seungyeul Yoo, Azra Krek, Alexis Demopoulos, Houxiang Zhu, Matthew A Wyczalkowski, Joshua F McMichael, Brittany L Henderson, Caleb M Lindgren, Hannah Boekweg, Shuangjia Lu, Jessica Baral, Lijun Yao, Kelly G Stratton, Lisa M Bramer, Erika Zink, Sneha P Couvillion, Kent J Bloodsworth, Shankha Satpathy, Weiva Sieh, Simina M Boca, Stephan Schürer, Feng Chen, Maciej Wiznerowicz, Karen A Ketchum, Emily S Boja, Christopher R Kinsinger, Ana I Robles, Tara Hiltke, Mathangi Thiagarajan, Alexey I Nesvizhskii, Bing Zhang, DR Mani, Michele Ceccarelli, Xi S Chen, Sandra L Cottingham, Qing Kay Li, Albert H Kim, David Fenyő, Kelly V Ruggles, Henry Rodriguez, Mehdi Mesri, Samuel H Payne, Adam C Resnick, Pei Wang, Richard D Smith, Antonio Iavarone, Milan G Chheda, Jill S Barnholtz-Sloan, Karin D Rodland, Tao Liu, Li Ding, Clinical Proteomic Tumor Analysis Consortium. (2021) Proteogenomic and metabolomic characterization of human glioblastoma. **Cancer Cell**.

Michael A Gillette, Shankha Satpathy, Song Cao, Saravana M Dhanasekaran, Suhas V Vasaikar, Karsten Krug, Francesca Petralia, Yize Li, Wen-Wei Liang, Boris Reva, Azra Krek, Jiayi Ji, Xiaoyu Song, Wenke Liu, **Runyu Hong**, Lijun Yao, Lili Blumenberg, Sara R Savage, Michael C Wendl, Bo Wen, Kai Li, Lauren C Tang, Melanie A MacMullan, Shayan C Avanessian, M Harry Kane, Chelsea J Newton, MacIntosh Cornwell, Ramani B Kothadia, Weiping Ma, Seungyeul Yoo, Rahul Mannan, Pankaj Vats, Chandan Kumar-Sinha, Emily A Kawaler, Tatiana Omelchenko, Antonio Colaprico, Yifat Geffen, Yosef E Maruvka, Felipe da Veiga Leprevost, Maciej Wiznerowicz, Zeynep H Gümüş, Rajwanth R Veluswamy, Galen Hostetter, David I Heiman, Matthew A Wyczalkowski, Tara Hiltke, Mehdi Mesri, Christopher R Kinsinger, Emily S Boja, Gilbert S Omenn, Arul M Chinnaiyan, Henry Rodriguez, Qing Kay Li, Scott D Jewell, Mathangi Thiagarajan, Gad Getz, Bing Zhang, David Fenyő, Kelly V Ruggles, Marcin P Cieslik, Ana I Robles, Karl R Clauser, Ramaswamy Govindan, Pei Wang, Alexey I Nesvizhskii, Li Ding, DR Mani, Steven A Carr, Clinical Proteomic Tumor Analysis Consortium. (2020) Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. **Cell**.

Yongchao Dou, Emily A Kawaler, Daniel Cui Zhou, Marina A Gritsenko et. al., Clinical Proteomic Tumor Analysis Consortium (Contributors include **Runyu Hong**). (2020) Proteogenomic characterization of endometrial carcinoma. **Cell**.

David J Clark, Saravana M Dhanasekaran, Francesca Petralia, Jianbo Pan, Xiaoyu Song, Yingwei Hu, Felipe da Veiga Leprevost, Boris Reva, Tung-Shing M Lih et. al., Clinical Proteomic Tumor Analysis Consortium (Contributors include **Runyu Hong**). (2019) Integrated proteogenomic characterization of clear cell renal cell carcinoma. **Cell**.

Runyu Hong, Lixue Cheng, Yao Yao, Ben Knowles, Yurun Zhang, Michael Kerins, Irina Shkel, M. Thomas Record. (2017) Predicting and Interpreting the Hofmeister Effects of Different Salts with Nucleic Bases and Aromatic Compounds Using

HONORS AND AWARDS

Key Contributor Award, Regeneron	2025
Special MacCracken Award	2021
1st Place Winner, NYU Langone Health Datathon	2019
Graduated with Highest Distinction	2017
Undergraduate Academic Achievement Award	2017
University Book Store Academic Excellence Award	2017
Albert J. & Adelaide E. Riker Academic Merit Award	2017
University of Wisconsin Department of Chemistry Scholarship	2016
Daughters of Demeter Outstanding Junior Scholarship	2015
Henry Steenbock Academic Merit Award	2014
Dean's List (6 times)	2013-2016

SELECTED PRESENTATIONS

<i>Oral Presentation</i>	
CPTAC Annual Scientific Symposium	National Cancer Institute, USA, 2020
Panoptes: A Multi-resolution Deep Learning Tool to Predict and Visualize Histopathologic Features	
CPTAC Imaging SIG Webinars (invited)	The Cancer Imaging Archive by NCI, USA, 2020
Proteogenomic analysis of Glioblastoma	
CPTAC Imaging SIG Webinars (invited)	The Cancer Imaging Archive by NCI, USA, 2019
Imaging-Omic correlation studies utilizing CPTAC data	
<i>Poster Presentation</i>	
AACR Annual Meeting 2024	San Diego, USA, 2024
Uncovering clinically relevant omics signatures from pan-cancer imaging and multi-omics data integration	
CPTAC Annual Scientific Symposium	National Cancer Institute, USA, 2019
Predicting and Visualizing Mutations in Cancer Histopathology Images Using Deep Learning	
EMBL Conference: From Images to Knowledge with ImageJ and Friends.	Heidelberg, Germany, 2018
Using Deep Learning Methods to Identify Neutrophil Infiltrations in Histology Images	
Deep Learning to Accelerate Drug Development: A NYC Symposium	New York, USA, 2018
Using Deep Learning Methods to Identify Neutrophil Infiltrations in Histology Images	
Experimental Biology (EB) Meeting	Chicago, USA, 2017
Predicting and Interpreting the Hofmeister Effects of Different Salts with Nucleic Bases and Aromatic Compounds	
Using Solubility Assay	
UW-Madison Undergraduate Symposium	Madison, USA, 2017
Predicting and Interpreting the Hofmeister Effects of Different Salts with Nucleic Bases and Aromatic Compounds	
Using Solubility Assay	

REVIEW AND EDIT RECORD

BioMedInformatics	Guest Editor (1 time)
BioMedInformatics	Reviewer (10 times)
Journal of Imaging	Reviewer (9 times)
Mathematical Biosciences and Engineering	Reviewer (7 times)
Journal of Translational Medicine	Reviewer (6 times)
Cell Reports Medicine	Reviewer (4 times)
Cancers	Reviewer (3 times)
Physics in Medicine and Biology	Reviewer (2 times)
Informatics	Reviewer (2 times)
Molecular & Cellular Proteomics	Reviewer (2 times)
PLOS Computational Biology	Reviewer (2 times)
BioMed	Reviewer (2 times)
Data	Reviewer (2 times)

Mathematics
Information
Electronics
Applied Sciences

Reviewer (2 times)
Reviewer (1 time)
Reviewer (1 time)
Reviewer (1 time)

FUNDING

Vilcek Travel Grant	2021
Sackler Travel Grant	2018-2020
Dean's Student Travel Grant	2018
Hilldale Undergraduate Research Fellowship	2016-2017
Allen Memorial Daughters of Demeter Scholarship	2016
Biochemistry Score/Super-G Scholarship	2016

TEACHING

Course Instructor and Teaching Assistant, New York University. 2020.09-2021.12

Course: Machine Learning (BMSC-GA 4439/BMIN-GA 1004)

Responsibilities: Prepared and taught 2 lectures for a class of 50 graduate students. Held weekly office hours. Prepared and graded quizzes, assignments, and course projects.

Teaching Assistant, New York University 2021.01-2021.05

Course: Deep Learning in Medicine (BMSC-GA 4493/BMIN-GA 3007)

Responsibilities: Prepared and taught 3 practical lectures for a class of 30 graduate students. Held weekly office hours. Prepared and graded assignments.

Teaching Assistant, NYU Langone Health 2020.04-2020.06

Course: Imaging Analysis

Responsibilities: Helped setting up a series of online bioinformatics courses at NYU Langone Health during the pandemic. Assisted the instruction of the course with about 200 students.

Tutor, University of Wisconsin Madison 2014.09-2017.05

Subject: Chemistry

Responsibilities: Helped on average 30 undergraduate students per month with their course work.

STUDENTS MENTORED

• Zi Zhu, Graduate Intern, Regeneron Pharmaceuticals	2026
• Junyang Deng, Graduate Intern, Regeneron Pharmaceuticals	2025
• Kristin Fullerton, PhD Intern, Regeneron Pharmaceuticals	2024
• Henry Webb, Co-op student, Regeneron Pharmaceuticals	2023
• Joshua Shofaro, Mentored student, Regeneron Pharmaceuticals	2023
• Michael Chen, Fenyő Lab master thesis student, New York University	2020
• Tinatin Nikvashvili, Lionnet Lab master student intern, New York University	2020
• Bea Szeitz, Fenyő Lab PhD student intern, New York University	2020
• Joshua Wang, Fenyő Lab MD/PhD student, New York University	2019
• Yang Liu, Fenyő Lab volunteer researcher, New York University	2018

PROFESSIONAL ASSOCIATIONS

-
- The New York Academy of Sciences
 - Association for the Advancement of Artificial Intelligence

LEADERSHIP EXPERIENCE

Lab Safety Officer, Fenyő lab 2020-2022

Responsibilities: In charge of the safety of Fenyő lab during the COVID-19 pandemic.

Student Host and Interviewer, Vilcek Institute 2020-2021

Responsibilities: Hosted and interviewed graduate program applicants

Diversity & Inclusion Chair, Vilcek Student Council <i>Responsibilities:</i> Organized social activities for graduate students.	2019-2020
President, CSSA of NYU Grossman School of Medicine <i>Responsibilities:</i> Held the celebrations and events during Chinese festivals.	2018-2019
Shared Governance Committee Member, Associated Students of Madison <i>Responsibilities:</i> Represented non-Wisconsin-resident students to advocate for tuition freeze	2015-2016

Selected Media Coverage

National Cancer Institute (NCI) News and Announcements Machine Learning Predicts Molecular Features of Endometrial Cancer with Exceptionally High Accuracy https://proteomics.cancer.gov/news_and_announcements/machine-learning-predicts-molecular-features-endometrial-cancer-exceptionally?cid=eb_govdel	Sep 24, 2021
BioArtMED Cell Reports Medicine Multi-resolution deep learning model predicts molecular subtypes and molecular characteristics of endometrial cancer https://mp.weixin.qq.com/s/Wvq1NX_49Gii8N-13Gip2q	Sep 29, 2021
Netease News Multi-resolution deep learning model predicts molecular subtypes and molecular characteristics of endometrial cancer https://www.163.com/dy/article/GL5GQOJ60532HZIO.html	Sep 30, 2021
Cell Reports Medicine Q&A: Runyu Hong and David Fenyö https://doi.org/10.1016/j.xcrm.2021.100507	Jan 18, 2022