Curriculum Vitae

Personal information

Martin Machyna

Work experience

April 2022 – Present

Bioinformatics Data Scientist, Paul-Ehrlich-Institut (Germany)

- Applying deep learning models for novel virus prediction
- Applying machine learning to biomarker discovery
- Analysis of genome integration sites of transposable elements
- RNA-seq, miRNA-seq data analysis

January 2014 – March 2022

Postoctoral Associate, Yale University (USA)

- Development of hybridization-capture NGS method for RNA-chromatin interaction sites identification
- Analysis of NGS data: ChIP-seq, HiC-seq, ChIRP-seq, RAP-seq, TimeLapse-seq, nucleotide, SLAM-seq
- Bayesian statistical modeling

September 2009 – January 2014

PhD Student, Max Planck Institute of Molecular Cell Biology and Genetics (Germany)

- Analysis of iCLIP-seq and ChiP-seq data
- Analysis of microscopy data: FRET, protein colocalization,

September 2006 – June 2009

Undergraduate and Master Student, Institute of Molecular Genetics of Czech Academy of Sciences (Czech Republic)

- Investigating role of CD9 tetraspanin in regulation of mast cells activation

September 2005 – June 2006

Internship Student, Institute of Physiology of Czech Academy of Sciences (Czech Republic)

- Investigated physiology of cholinergic neurons in response to covalent agonists

Education and training

September 2009 – January 2014

PhD., International Max Planck Research School for Molecular and Cellular Biology (IMPRS – MCBB) and Technische Universität Dresden (Germany)

- Functional genomics and transcription regulation
- Nuclear organization

September 2007 – June 2009

Mgr. (MSc.), Charles University (Czech Republic)

- Molecular immunology

September 2004 – June 2007
Bc. (BSc.), Charles University (Czech Republic)

- Molecular biology and cell physiology

Additional information

Publications

Hufsky F., …, **Machyna M.**, …, Marz M. (2023). “The International Virus Bioinformatics Meeting 2023”, **Viruses**, 15(10):2031.

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Lu-Culligan W.J., Connor LJ., Xie Y., Ekundayo B.E., Rose B.T., **Machyna M.**, Pintado-Urbanc A.P., Zimmer J.T., Vock I.W., Bhanu N.V., King M.C., Garcia B.A., Bleichert F., Simon M.D. (2023). “Acetyl-methyllysine marks chromatin at active transcription start sites”, **Nature**, 622(7981):173-179.

Machyna M., Courchaine E., Gelles-Watnick S., Straube K., Sarah Sauyet, Jade Enright and Neugebauer K.N. (2022). “The coilin N-terminus mediates multivalent interactions between coilin and Nopp140 to form and maintain Cajal bodies”, **Nature Communications**, 13, 6005.

Biancon G., Joshi P., Zimmer J.T., Hunck T., Gao Y., Lessard M.D., Courchaine E., Barentine A.E.S., **Machyna M.**, Botti V., Qin A., Gbyli R., Patel A., Song Y., Viero G., Neuenkirchen N., Lin H., Bewersdorf J., Simon MD., Neugebauer K.M., Tebaldi T. and Halene S. (2022). “Precision analysis of mutant U2AF1 activity reveals deployment of stress granules in myeloid malignancies”, **Molecular Cell**, 82(6):1107-1122.e7.

Machyna, M., Kiefer, L. & Simon, M. D. (2020). “Enhanced nucleotide chemistry and toehold nanotechnology reveals lncRNA spreading on chromatin”, ***Nature Structural and Molecular Biology***, 27(3):297-304.
Featured front cover article

Machyna, M., & Simon, M. D., “Principles and Practices of Hybridization Capture Experiments to Study Long Noncoding RNAs That Act on Chromatin” RNA Worlds: New Tools for Deep Exploration, Cech, T. R., Steitz, J. A., Atkins, J. F., ***New York : Cold Spring Harbor Perspectives in Biology,*** 2019, 221–237.

Machyna, M., & Simon, M. D. (2017). “Catching RNAs on chromatin using hybridization
capture methods.“, ***Briefings in Functional Genomics***, 17(2):96-103.

Sexton, A. N., **Machyna, M.,** & Simon, M. D. (2016).“Capture Hybridization Analysis of DNA Targets.“ ***Methods in Molecular Biology*** (Clifton, NJ), 1480(Chapter 8), 87–97.

Machyna M., Neugebauer K.M., Staněk D. (2015). “Coilin: The First 25 years”, ***RNA Biology*** 12(6), 590–596.

Machyna M., Kehr S., Straube K., Kappei D., Buchholz F., Butter F., Ule J., Hertel J., Stadler P.F., Neugebauer K.M. (2014). “*The Coilin Interactome Identifies Hundreds of Small Noncoding RNAs that Traffic through Cajal Bodies*”, ***Molecular Cell***, *56*(3), 389–399.

Hálová I., Dráberová L., Bambousková M., **Machyna M.**, Stegurová L., Smrz D., Dráber P. (2013). “*Crosstalk between tetraspanin CD9 and transmembrane* *adaptor protein non-T cell activation linker (NTAL) in mast cell activation and chemotaxis*”, ***Journal of Biological Chemistry***, 288(14):9801-14.

Machyna M., Heyn P., & Neugebauer K. M. (2013). “*Cajal bodies: where form meets function*”, ***Wiley interdisciplinary reviews. RNA***, 4(1).

Tripsianes K., Madl T., **Machyna M.**, Fessas D., Englbrecht C., Fischer, U., Neugebauer, K. M., Sattler M. (2011). “*Structural basis for dimethylarginine recognition by the Tudor domains of human SMN and SPF30 proteins*”, ***Nature Structural & Molecular Biology***, 18, 1414–1420.

Projects

BLOODVIR
- Development of surveillance system for detection of known and novel virus infection in human blood
- Identification of virus infection biomarkers from blood miRNA

thCHART
- Development of LNA and toehold-based hybridization capture method for RNA enrichment
- Charles H Revson senior fellowship in biomedical science
- *U.S. Patent application 16/412,527*: “Compositions and Methods for Improved RNA Capture”

Cajal body assembly
- Combining information from ChiP-seq, iCLIP-seq and mass spectrometry to understand assembly of phase-separated and non-membrane bound organelles

Memberships

Selected conference presentations
- Harnessing enhanced nucleotide chemistry and toehold nanotechnology to reveal lncRNA spreading on chromatin. *RNA Biology Symposium, Bethesda NIH*, 2019 (Poster)
- An enhanced hybridization capture approach reveals different modes of lncRNA spreading on chromatin. *RNA Society Symposium, Berkeley, CA*, 2018 (Talk)
- Coilin-RNA interactome identifies hundreds of mammalian snoRNAs that localize to Cajal bodies. *Eukarytic mRNA processing, Cold Spring Harbor*, 2013 (Talk)

Other Relevant Information