

Jakub Mieczkowski

CONTACT INFORMATION	Nencki Institute of Experimental Biology Laboratory of Molecular Neurobiology	mobile: +48 502 098 544 e-mail: jmieczkowski@jmieczkowski.pl LinkedIn: www.linkedin.com/in/jmieczkowski
PROFESSIONAL EXPERIENCE	Nencki Institute of Experimental Biology Massachusetts General Hospital Harvard Medical School <i>Research Fellow in Genetics</i>	08.2016 – present 06.2013 – 06.2016
EDUCATION	Nencki Institute of Experimental Biology <i>Ph.D. in biology (with honors)</i> <ul style="list-style-type: none">• Specialty: Bioinformatics Faculty of Mathematics, Informatics and Mechanics University of Warsaw <i>M.Sc. in mathematics</i> <ul style="list-style-type: none">• Specialty: Applied Statistics	10.2008 – 03.2013 10.2003 – 09.2008
SCIENTIFIC VISITS	U753 INSERM, Institut Gustave Roussy, Mar., 2010, Paris, France. Linnaeus Centre for Bioinformatics, Uppsala University, Nov., 2009, Uppsala, Sweden.	
PUBLICATIONS	Gieryng, A., Pszczolkowska, D., Bocian, K., Dabrowski, M., Rajan, WD., Kloss, M., Mieczkowski, J. , Kaminska, B., Immune microenvironment of experimental rat C6 gliomas resembles human glioblastomas, Sci Rep. , 2017 Dec 14;7(1):17556 Cook, A. *, Mieczkowski, J. * , Tolstorukov, MY., Single-Assay Profiling of Nucleosome Occupancy and Chromatin Accessibility, Current Protocols in Molecular Biology , 120, 21.34.121.34.18 Mueller, B. *, Mieczkowski, J. * , Kundu, S., Wang, P., Sadreyev, R., Tolstorukov, MY., Kingston, RE., Widespread changes in nucleosome accessibility without changes in nucleosome occupancy during a rapid transcriptional induction, Genes & Dev. , 31(5):451, 2017. *co-first author Wang, X. *, Lee, RS. *, Alver, BH. *, Haswell, JR., Wang, S., Mieczkowski, J. , Drier, Y., Gillespie, SM., Archer, TC., Wu, JN., Tzvetkov, EP., Troisi, EC., Pomeroy, SL., Biegel, JA., Tolstorukov, MY., Bernstein, BE., Park, PJ., Roberts, CW., SMARCB1-mediated SWI/SNF complex function is essential for enhancer regulation, Nature Genetics , 49(2):289-295, 2017. *co-first author Deaton, AM., Gomez-Rodriguez, M., Mieczkowski, J. , Tolstorukov, MY., Kundu, S., Sadreyev, RI., Jansen, LET., RE. Kingston, <i>Enhancer regions show high histone H3. 3 turnover that changes during differentiation.</i> eLife , 5:e15316, 2016. Mieczkowski, J. * , Cook, A. *, Bowman, SK. *, Mueller, B., Alver, BH., Kundu, S., Deaton, AM., Urban, JA., Larschan, E., Park, PJ., Kingston RE., M. Tolstorukov, <i>MNase titration reveals differences between nucleosome occupancy and chromatin accessibility.</i> Nature Commun. , 7:11485, 2016. *co-first author Mieczkowski, J. * , Kocyk, M. *, Nauman, P., Gabrusiewicz, K., Sielska, M., Przanowski, P., Maleszewska, M., Rajan, W., Pszczolkowska, D., Tykocki, T., Grajkowska, W., Kotulska, K., Roszkowski, M., Kostkiewicz B., B. Kaminska, <i>Down-regulation of IKKβ expression in glioma-infiltrating microglia/macrophages is associated with defective inflammatory/immune gene responses in glioblastoma.</i> Oncotarget , 2015. *co-first author	

PUBLICATIONS	<p>Kruczyk M., Przanowski P., Dabrowski M., Swiatek-Machado K., Mieczkowski, J., Wallerman O., Ronowicz A., Piotrowski A., Wadelius C., Kaminska B., J. Komorowski Integration of genome-wide of Stat3 binding and epigenetic modification mapping with transcriptome reveals novel Stat3 target genes in glioma cells. Biochim Biophys Acta., 1839(11):1341-50, 2014.</p> <p>Przanowski, P., Dabrowski, M., Ellert-Miklaszewska, A., Kloss, M., Mieczkowski, J., Kaza, B., Ronowicz, A., Hu, F., Piotrowski, A., Kettenmann, H., Komorowski, J., B Kaminska The signal transducers Stat1 and Stat3 and their novel target Jmjd3 drive the expression of inflammatory genes in microglia. J Mol Med, 92(3):239-54, 2014.</p> <p>Kruczyk, M., Baltzer, N., Mieczkowski, J., Draminski, M., Koronacki, J., J Komorowski <i>Random reducts: A monte carlo rough set-based method for feature selection in large datasets.</i> Fundamenta Informaticae, 127,1-4,2013</p> <p>Mieczkowski, J., Swiatek-Machado, K., B. Kaminska, <i>Identification of Pathway Deregluation – Gene Expression Based Analysis of Consistent Signal Transduction.</i> PLoS One,7(7):e41541, 2012.</p> <p>Swiatek-Machado, K., Mieczkowski, J., Ellert-Miklaszewska, A., Swierk, P., Fokt, I., Szymanski, S., Skora, S., Szeja, W., Gryniewicz, G., Lesyng, B., Priebe, W., B. Kaminska, <i>Novel small molecular inhibitors disrupt the JAK/STAT3 and FAK signaling pathways and exhibit a potent antitumor activity in glioma cells.</i> Cancer Biol Ther, 13(8):657-70, 2012.</p> <p>Tyburczy, M. E., Kotulska, K., Pokarowski, P., Mieczkowski, J., Kucharska, J., Grajkowska, W., Roszkowski, M., Jozwiak S., B. Kaminska, <i>Novel proteins regulated by mTOR in subependymal giant cell astrocytomas of patients with tuberous sclerosis complex and new therapeutic implications.</i> Am J Path, 176, 1878-1890, 2010.</p> <p>Mieczkowski, J., Tyburczy, M. E., Dabrowski, M., P. Pokarowski, <i>Probe set filtering increases correlation between Affymetrix GeneChip and qRT-PCR expression measurements,</i> BMC Bioinformatics, 11:104, 2010.</p> <p>Dabrowski, M., Dojer, N., Zawadzka, M., Mieczkowski, J., B. Kaminska, <i>Comparative analysis of cis-regulation following stroke and seizures in subspaces of conserved eigensystems,</i> BMC Syst Biol, 4(1):86, 2010.</p>
SELECTED GRANTS	<p>2017 - 2019 Identification of epigenetic mechanisms contributing to glioma drug resistance, financed by National Science Centere, Principal Investigator, 220 000 EUR.</p> <p>2015 - 2020 An atlas of brain regulatory regions and regulatory networks - a novel systems biology approach to pathogenesis of selected neurological disorders, financed by National Science Centere, participant, 1 700 000 EUR.</p> <p>2011 - 2012 Identification of signalling pathways differentiating glioma and control cells using expression microarrays, financed by Ministry of Science and Higher Education, Principal Investigator, 25 000 EUR.</p>
TRAINING	<p>EMBO Practical Course: Analysis of High-Throughput Sequencing Data, 2012, Hinxton,England.</p> <p>Next Generation Sequencing Workshop, 2009, Bari, Italy.</p> <p>Computational Challenges of the Next Sequencing Technologies, 2009, Uppsala, Sweden.</p> <p>Tutorial on the Analysis of Next Sequencing, 2009, Uppsala, Sweden.</p>
COMPUTER SKILLS	R/Bioconductor, SAS, SPSS, STATA, Perl, Python, C/C++, PHP, SQL, L ^A T _E X 2 _ε , HTML, Adobe Illustrator, Linux user.
LANGUAGE SKILLS	Polish – Native, English – Advanced, Spanish – Elementary