PROFILE FOR INSTITUTE WEBSITE

Current photo in graphic file e.g. 2024, 2023.	
Name and surname, Title	**Hiroaki Taniguchi, PhD, DSc**
Position	Associate Professor/Team Leader of Genome Editing and Transcriptional Regulation
Hirsch Index and Number of citations (according to Scopus) on the day of completing the form	H-index 21 2368
Research areas (in points, min. 200 characters, max. 500 characters)	– Utilizing Crispr-Cas9 for genome editing to functionally validate hot spot mutations in cancer driver genes. – Investigating the potential link between NFE2L1 and Parkinson's disease onset.
Total number of completed research projects; currently implemented research projects (title and number) and selected max. 3 completed projects (title and number) from the newest ones, i.e. 2024, 2023, 2022…	– **Currently** – NCN2020/39/O/NZ5/02467 Analysis of the molecular mechanism of phosphorylated α-synuclein and ubiquitinated protein accumulation caused by dopaminergic neuron-specific NFE2L1 gene knockout (Till 2026 Sep 30). – **Completed** – Grant agreement No 815668. BovReg - Identification of functionally active genomic regions relevant to phenotypic diversity and plasticity in cattle (Work package 6 leader) – NCN 2017/25/B/NZ5/02762 - Study of transcriptional networks disruption on the development of liver cancer: functional analysis of the HNF4A gene mutation using CRISPR/Cas9 system – NCN 2017/01/X/NZ9/01263 Potencjalna rola systemu ubikwityno-proteasomowego w ciałku żółtym bydła
Total number of publications; ORCID (number and hyperlink to the profile); SCOPUS (number and hyperlink to the profile); indicate selected publications (max. 5)	– **58 Publications (Scopus)** – ORCID: 0000-0001-7270-390X, **https://orcid.org/0000-0001-7270-390X** – SCOPUS 35785003500, **https://www.scopus.com/authid/detail.uri?authorId=35785003500** – **Selected Publications (5)** – 1. Łuczyńska K, Zhang Z, Pietras T, Zhang Y, **Taniguchi H**. NFE2L1/Nrf1 serves as a potential therapeutical target for neurodegenerative diseases. Redox Biol. 2023 69:103003.

	– 2. Śmiech M, Leszczyński P, Wardell C, Poznański P, Pierzchała M, **Taniguchi H**. Oncogenic Mutation BRAF V600E Changes Phenotypic Behavior of THLE-2 Liver Cells through Alteration of Gene Expression. Int J Mol Sci. 2022 23(3) 1548: – 3. **Taniguchi H**, Fujimoto A, Kono H, Furuta M, Fujita M, Nakagawa H. Loss-of-function mutations in Zn-finger DNA-binding domain of HNF4A cause aberrant transcriptional regulation in liver cancer. Oncotarget. 2018 9(40):26144-26156. – 4. Fujimoto A*, Furuta M*, Totoki Y*, Tsunoda T*, Kato M*, Shiraishi Y, Tanaka H, **Taniguchi H** et al. Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. Nat.Genet. 2016; 48: 500-509.* contributed equally – 5. Endo K, **Taniguchi H***, Karim MR*, Krejci A, Kinameri E, Siebert M, Ito K, Bray SJ, Moore AW. Chromatin modification of Notch targets in olfactory receptor neuron diversification. Nat.Neurosci. 2012; 15: 224-233. *contributed equally
Total number of patents; selected patents (max. 2) and a hyperlink to personal patent achievements (UP RP), on the day of completing the form	1. METHOD AND DEVICE FOR ARRANGING CELLS USING LASER – **https://patentscope.wipo.int/search/en/detail.jsf?docId=WO2016039397&_cid=P21-LT5ZS1-21385-1** 2.A method to prevent epithelial to mesenchymal transition and cancer metastasis – **https://jglobal.jst.go.jp/detail?JGLOBAL_ID=201603006129951965**
Selected scientific achievements from the newest, i.e. 2023, 2022, 2021... (in points, min. 800 characters, max. 1000 characters)	– We demonstrated that mutations in HNF4A (Oncotarget 2018), HNF1A (Genes 2022, Cancers 2021) and NRF2 (IJMS 2021) genes contribute to hepatocellular carcinoma (HCC) progression, highlighting potential diagnostic and therapeutic targets. Furthermore, BRAF mutations, particularly V600E, activate oncogenic pathways in liver cells, underscoring the complexity of liver cancer development (2022 IJMS). – In neurodegenerative disorders, NFE2L1 regulates protein turnover through the ubiquitin-proteasome system. NFE2L1 activation, explored as a potential therapeutic approach for Alzheimer's and Parkinson's diseases, is less studied compared to its homolog NFE2L2. We proposed that understanding these transcription factors offers insights into neurodevelopment, neurodegenerative diseases, and potential therapeutic strategies (BBRC 2017, Redox Biology 2023). – We demonstrated that PRDM3, a transcription factor, plays a significant role in neurogenesis. Its expression increases during neurogenesis, and its knockout accelerates neuronal differentiation while promoting non-neuronal cell growth. GATA6, another transcription factor, synergistically regulates PRDM3 expression, with retinoic acid receptors further enhancing this effect (2020 IJMS).
Number and list of defended PhD students from the latest, i.e. 2024, 2023, 2022...	– Effi Haque (Supervisor) 2022 – Pawel Leszczyński (Supporting Supervisor) 2021 – Magdalena Śmiech (Supporting Supervisor) 2021

Organizational activities, dissemination of knowledge and others (in points, min. 300 characters, max. 1000 characters)	– Lab website: https://hiroataniguchi.wixsite.com/polska-epigenetics