





Nanopore Direct Sequencing of RNA To map RNA modifications in human transcriptomes

We seek candidates with a fresh Bio-engineering PhD degree to apply bioinformatic skills to decode RNA modifications using nanopore direct RNA sequencing. RNA is at the forefronts of the central dogma, bridging the genetic information between DNA and protein. The human transcriptomes are post-transcriptionally modified with various chemical moieties, which regulate biology. Dysregulation of RNA modifications is directly linked to human diseases, such as cancer and neurodegeneration.

Nanopore direct RNA sequencing is currently the state-of-the-art technology to map RNA modifications. Our position is NIH-funded at Thomas Jefferson University, Philadelphia, USA, which offers intellectual growth and the potential for long-term stability.

For more information, please see the following publications and our website:

- Tavakoli, S, Nabizadeh, M, Makhamreh, A, Gamper, H, Rezapour, NK, Hou, YM, Wanunu, M, Rouhanifard, SH. (2023) Semi-quantitative detection of pseudouridine modifications and type I/II hypermodifications in human mRNAs using direct, long-read sequencing. *Nat Commun* 14(1):334. PMID:36658122; PMCID:PMC9852470
- Gamper, H, McCormick, C, Makhamreh, A, Wanunu, M, Rouhanifard, SH, Hou, YM. (2023) Enzymatic synthesis of RNA standards for mapping and quantifying RNA modifications in sequencing analysis. *Methods in Enzymology*, Academic Press, https://doi.org/10.1016/bs.mie.2023.04.024, PMID: 37925177
- Hou, YM, Nakano, Y. (2024) Breaking the deadlock in genetic code expansion. Invited for an article in **News & Views**, commenting on the paper in *Nature* "Adding α , α -disubstituted and β-linked monomers to the genetic code of an organism. **Nature Chem Biology**, PMID: 38467845. https://www.nature.com/articles/s41589-024-01579-4
- Avila, YI, Rebolledo, LP, Skelly, E, de Freitas Saito, R, Wei, H, Lilley, D, Stanley RE, Hou, YM, Yang, H, Sztuba-Solinska, J, Chen, SJ, Dokholyan, NV, Tan, C, Li, K, He, X, Zhang, X, Miles, W, Franco, E, Binzel, DW, Guo, P, Afonin, KA (2024) Cracking the code: Enhancing molecular tools for progress in nanotechnology. *ACS Applied Bio Materials*, PMID: 38833534; PMCID: PMC11190997.
- Masuda, I, Hou, YM. (2024) A tRNA modification pattern that facilitates interpretation of the genetic code. Submitted to *Frontier in Microbiology*, PMID: 38933027; PMCID: PMC11199890.
- Namani, S, Kavetsky, K, Lin, CY, Maharjan, S, Gamper, H, Li, NS, Piccirilli, J, Hou*, YM, Drndic*, M. (2024) Unraveling RNA conformation dynamics in mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episode syndrome with solid-state nanopores. *ACS Nano*, PMID: 38906834, DOI:10.1021/acsnano.4c04625

- Maharjan, S, Gamper, H, Yamaki, Y, Christian, T, Henley, RY, Li, NS, Suzuki, T, Suzuki, T, Piccirilli, JA, Wanunu, M, Seifert, E, Wallace, DC, Hou, YM. (2024) Post-transcriptional methylation of mitochondrial-tRNA differentially contributes to mitochondrial pathology. *Nature Commun* 15(1):9008, doi: 10.1038/s41467-024-53318-x; PMID: 39424798; PMCID:PMC11489592
- Makhamreh, A, Tavakoli, S, Fallahi, A, Kang, X, Gamper, H, Nabizadehmashhadtoroghi, M, Jain, M, Hou, YM, Rouhanifard, SH, Wanunu, M. (2024) Nanopore signal deviations from pseudouridine modifications in RNA are sequence-specific; quantification requires dedicated synthetic controls. *Sci Rep.* 14(1): 22457. DOI: 10.1038/s41598-024-72994-9; PMID: 39341872; PMCID:PMC11438862.
- Nakano, Y, Gamper, H, McGuigan, H, Maharjan, S, Sun, Z, Yigit, E, Grunberg, S, Krishnan, K, Li, NS, Piccirilli, JA, Kleiner, R, Nichols, N, Hou, YM. (2025) Genome-wide profiling of tRNA modifications by Induro-tRNAseq reveals coordinated changes. *Nat Commun*, PMID: 39865096; PMCID: PMC 11770116; DOI: 10.1038/s41467-025-56348-1.
- Fanari, O, Tavakoli, S, Qiu, Y, Makhamreh, A, Nilan, K, Akeson, S, Meseonznik, M, McCormick, CA, Block, D, Gamper, H, Jain, M, Hou, YM, Wanunu, M, Rouhanifard, SH. (2025) Probing enzyme-dependent pseudouridylation using direct RNA sequencing to assess neuronal epitranscriptome plasticity. *Cell Systems*, 2025 Mar 18:101238, doi: 10.1016/j.cels.2025.101238; PMID: 40118059

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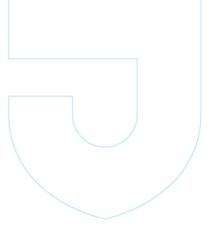
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