

Marie Saitou

Curriculum Vitae · 2026

Evolutionary · Population · Functional Genomics

Faculty of Biosciences, Norwegian University of Life Sciences (NMBU), Ås, Norway

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Scholar	Google Scholar profile

Research profile

Evolutionary geneticist studying how genomic change generates biological diversity and how wild and domesticated populations respond to environmental and human-driven pressures. Research integrates structural variation, whole-genome duplication, population genomics, comparative transcriptomics, and gene-regulatory analysis across Atlantic salmon, aquatic and coastal systems, and vertebrate secretory biology.

Academic appointments

2020-present	Postdoctoral Fellow (Tenure-Track) and Principal Investigator Faculty of Biosciences / CIGENE, Norwegian University of Life Sciences, Norway
2020	Postdoctoral Scholar Section of Genetic Medicine, University of Chicago, USA
2017-2020	Postdoctoral Scholar Department of Biological Sciences, University at Buffalo, USA

Education

2017	PhD, Biological Anthropology Graduate School of Science, The University of Tokyo, Japan
2014	MSc, Biological Anthropology Graduate School of Science, The University of Tokyo, Japan
2012	BSc, Biological Anthropology Faculty of Science, The University of Tokyo, Japan

Research leadership and funded projects

2024-2027	HubSmolt · Work-package leader Research Council of Norway
2021-2025	SalmoSV · Project leader · FRIPRO Young Talent Research Council of Norway · NOK 8 million
2020-2023	SynchroSmolt · Work-package leader FHF - Norwegian Seafood Research Fund

Teaching

2024-present	Course coordinator, BIO322 Advanced Topics in Genomics MSc level, NMBU (teaching contributions also in 2021-2022)
2020-present	BIO326 Genome Sequencing: Tools and Analysis MSc level, NMBU

Completed PPUN400 Teaching and Learning in Higher Education, PPVE400 Master and PhD Supervision, and additional training in research leadership, supervision, mentoring, and course design.

Supervision and mentoring

Principal supervision has included one postdoctoral researcher, two PhD candidates, one master's student, and three international master's interns. Outcomes include completed PhD degrees, peer-reviewed publications and preprints, NMBU's 2024 best master's thesis award, and subsequent appointments at Lund University, the Roslin Institute / University of Edinburgh, the University of Oslo, and Kongju National University.

Selected awards and recognition

2026	SMBE Caregiver Award
2022	First Marie Skłodowska Curie Award - Recognition Prize, Japan Science and Technology Agency and Embassy of the Republic of Poland in Japan
2022	Young Scientist Initiative Award, Society of Evolutionary Studies, Japan
2021-2023	NMBU Talent Program 2.0 - Research Talents for Sustainability
2019	Young Investigator Award, Society for Molecular Biology and Evolution
2019	DeLill Nasser Award, Genetics Society of America
2019	Excellent Oral Presentation Award, Society of Evolutionary Studies, Japan

Academic and institutional service

2026	PhD internal examiner, NMBU
2025	Evaluator, Marie Skłodowska-Curie Actions Postdoctoral Fellowships
2024	PhD mid-term evaluation committee member, NMBU
2022-present	Early Career Reviewer, eLife
2017-present	Reviewer for journals including Molecular Biology and Evolution, Genome Biology and Evolution, G3, Genetics, PLOS Genetics, Molecular Ecology Resources, NAR Genomics and Bioinformatics, Reviews in Aquaculture, and Environmental Science & Technology
2020-2023	Organizer, CIGENE online invited seminar series, NMBU
2021	Organizer, Japan-Norway Symposium on Fish Endocrinology and Genomics

Selected publications and preprints

1. **Saitou, M.** (2026). Comparative transcriptomics suggests that breast secretory epithelium reuses gene repertoires conserved across vertebrates beyond mammals. *Genome Biology and Evolution*, evag130. doi
2. Røed, E. S., Ellis, C., Stevens, J. R., Chavarie, L., & **Saitou, M.** (2026). Resampling-based evaluation of a 79-SNP panel for hybrid classification across generations: a case study in European lobster (*Homarus gammarus*). *G3: Genes, Genomes, Genetics*. doi
3. Manousi, D., Naseer, S., Martin, S. A. M., Sandve, S. R., & **Saitou, M.** (2026). Gene gain and loss drive the diversification of giga immune genes in teleosts: structural and regulatory insights from Atlantic salmon. *Fish & Shellfish Immunology*, 110975. doi
4. Diblasi, C., Kwak, J. S., Manousi, D., et al., & **Saitou, M.** (2026). Ancient persistence and recurrent emergence of structural variants across divergent Atlantic salmon lineages. *bioRxiv*. doi
5. Chapis, M., Manousi, D., Diblasi, C., et al., & **Saitou, M.** (2026). Imputed graph-genotyped structural variants identify regulatory haplotypes associated with gene expression in Atlantic salmon. *bioRxiv*. doi
6. Diblasi, C., Manousi, D., Hazlerigg, D., et al., & **Saitou, M.** (2025). Large-scale eQTL analyses in Atlantic salmon reveal persistent dosage compensation 100 million years after genome duplication. *bioRxiv*. doi
7. Diblasi, C., & **Saitou, M.** (2025). Beyond inversions and deletions: evolutionary and functional insights from translocations, fissions, and fusions in animal genomes. *Heredity*. doi
8. Buso, P., Diblasi, C., Manousi, D., et al., & **Saitou, M.** (2025). Parallel selection in domesticated Atlantic salmon from divergent founders including on whole-genome duplication-derived homeologous regions. *Genome Biology and Evolution*, 17(4), evaf063. doi
9. Kwak, J. S., León-Tapia, M. Á., Diblasi, C., et al., & **Saitou, M.** (2024). Functional and regulatory diversification of *Period* genes responsible for circadian rhythm in vertebrates. *G3: Genes, Genomes, Genetics*, 14(10), jkae162. doi
10. **Saitou, M.**, Resendez, S., Pradhan, A. J., et al. (2021). Sex-specific phenotypic effects and evolutionary history of an ancient deletion polymorphism of the human growth hormone receptor. *Science Advances*, 7(39), eabi4476. doi
11. **Saitou, M.**, Gaylord, E. A., Xu, E., et al. (2020). Functional specialization of human salivary glands and origins of proteins intrinsic to human saliva. *Cell Reports*, 33(7), 108402. doi

A complete and automatically updated publication record is available through ORCID and Google Scholar.