

## Nozomu Yachie, Ph.D.

### Professor

#### Director of Research

School of Biomedical Engineering  
Faculty of Applied Science & Faculty of Medicine  
**The University of British Columbia**  
2222 Health Sciences Mall, Vancouver, BC V6T 1Z3, Canada

### Specially Appointed Professor

Premium Research Institute for Human Metaverse Medicine  
**Osaka University**  
2-2 Yamadaoka, Suita, Osaka 565-0871, Japan

### Visiting Professor

Research Center for Advanced Science and Technology  
**The University of Tokyo**  
4-6-1 Komaba, Meguro-ku, Tokyo, Japan 153-8904

### Canada Research Chair in Synthetic Biology

### Allen Distinguished Investigator

### CIFAR Fellow

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## SELECTED RECOGNITIONS/FELLOWSHIPS

2024.09	<b>Nagase Grand Prize</b> The Frontier Salon Foundation
2024.03	<b>JSPS Prize</b> Japan Society for the Promotion of Science
2023.04-Today	<b>CIFAR Fellow</b> MacMillan Multiscale Human Program Canadian Institute for Advanced Research
2022.01	<b>Allen Distinguished Investigator Award</b> Allen Institute
2020.09-Today	<b>Canada Research Chair (Tier 2) in Synthetic Biology</b> Canadian Institute of Health Research (CIHR)
2020.04	<b>Minister's Young Scientists Award</b> Ministry of Education, Culture, Sports, Science and Technology, Japan
2014.10-2018.03	<b>PRESTO Researcher'ship</b> Japan Science and Technology Agency (JST)
2012.04-2014.03	<b>Banting Postdoctoral Fellowship</b> National Sciences and Engineering Research Council of Canada (NSERC)
2007.04-2012.03	<b>JSPS Fellowships (DC1, PD and 'to Research Abroad')</b> Japan Society for the Promotion of Science

## EDUCATION

2009.03 Ph.D., Systems Biology Program, SFC, **Keio University**  
2007.03 M.M.G., Bioinformatics Program, SFC, **Keio University**  
2005.03 B.A., Faculty of Environmental Information, SFC, **Keio University**

## POSITIONS HELD

2020.09-Today **Professor** (2023.07-Today)  
**Associate Professor** (2020.09-2023.06)  
**The University of British Columbia**  
School of Biomedical Engineering  
Faculty of Applied Science & Faculty of Medicine  
  
(July, 2022-Today)  
**Director of Research and Associate Director**  
School of Biomedical Engineering

2023.03-Today **Specially Appointed Professor**  
**Osaka University**  
Premium Research Institute for Human Metaverse Medicine (PRIME)

2020.09-Today **Visiting Professor** (2023.10-Today)  
**Visiting Associate Professor** (2020.09-2023.08)  
**The University of Tokyo**  
Research Center for Advanced Science and Technology (RCAST)

2023.04-Today **Guest Professor (Global)**  
**Keio University**  
Graduate School of Media and Governance

2014.06-2021.12 **Adjunct Associate Professor** (2015.04-2021.12)  
**Adjunct Assistant Professor** (2014.06-2015.03)  
**Keio University**  
Graduate School of Media and Governance, and  
Institute for Advanced Biosciences

2014.07-2020.08 **Associate Professor**  
**The University of Tokyo**  
Synthetic Biology Division,  
Research Center for Advanced Science and Technology (RCAST), and  
Department of Advanced Interdisciplinary Studies (AIS),  
Graduate School of Engineering  
  
(2015.04-2020.08)  
Department of Biological Sciences, Graduate School of Science  
  
(2018.04-2020.08)  
PEAK and GPES Programs, Graduate School of Arts and Sciences  
  
**Director** (2018.01-2019.10)  
Laboratories for Systems Biology and Medicine

- 2010.04-2014.06    **Postdoctoral Fellow** (with Dr. Frederick Roth)  
(April, 2010-November, 2010)  
**Harvard Medical School**  
Department of Biological Chemistry and Molecular Pharmacology  
(December, 2010-June, 2014)  
**University of Toronto**  
Donnelly Centre for Cellular and Biomolecular Research
- 2009.04-2010.03    **Postdoctoral Fellow** (with Dr. Masaru Tomita)  
**Keio University**  
Institute for Advanced Biosciences

## SIGNIFICANT CONTRIBUTIONS

(Yachie N is a +first and/or \*corresponding author)

**Genome editing:** In CRISPR-Cas9 genome editing, a guide RNA recruits Cas9 to a target genomic region adjacent to a protospacer adjacent motif (PAM) sequence, 5'-NGG-3', and Cas9 produces a DNA double-stranded break (DSB). This event promotes either gene deletion or transgene insertion through the induction of different DNA repair pathways, but DSBs are cytotoxic and the DSB-based editing outcomes are unpredictable. In collaboration with Dr. Keiji Nishida, we developed a new genome-editing tool, Target-AID, which fused cytidine deaminase (AID) to a nickase Cas9 and enabled highly precise targeted C→T substitutions without DSBs (**Science** 2016). In collaboration with Dr. Osamu Nureki, we also succeeded in increasing the targeting scope of Cas9 from a restrictive NGG to an NG PAM (Cas9-NG) and developed Target-AID-NG (**Science** 2018). Furthermore, my team developed a new base editor Target-ACEmax, which enables the simultaneous induction of C→T and A→G substitutions on a target DNA molecule and greatly expands the potential of base editing in therapeutics and biotechnology development (**Nature Biotechnology** 2020\*). We have also contributed to the development of an Cas12f-based compact genome-editing tool led by Drs. Atsushi Hoshino and Osamu Nureki (**Cell** 2023). Furthermore, to explore new genome editing tools apart from the CRISPR-Cas9 and other characterized genome editing tools, we have developed a tool to rapidly capture periodic and interspaced periodic repeats from genomic and metagenomic resources (**Nucleic Acids Research** 2019\*).

**Cell lineage tracing:** Several methods have been proposed to trace developmental cell lineages of multicellular organisms, whereby chromosome-embedded DNA barcodes are continuously mutated by Cas9 and inherited from mother to daughter cells, which lineage can be reconstructed according to the mutation patterns at the time of observation. However, none of these technologies has achieved high-resolution lineage tracing. To decipher the map of the whole-body mammalian (mouse) developmental process at the single-cell resolution, my team has outlined the key issues and perspectives in this field (**Science** 2022\*) and is developing new genetic circuits, mouse engineering, and high-performance computing technologies. Target-AID and Target-ACEmax, described above, were developed primarily for the purpose of high-resolution cell lineage tracing. We also developed a new deep distributed computing platform and succeeded in the precise lineage reconstruction of over 235 million mutated sequences generated by a simulator (**Nature Biotechnology** 2022\*).

**Retrospective clone isolation:** Questions such as "Did the chemotherapy-resistant clones exist in the initial cell population with a unique cellular status from the beginning?" or "Did any molecular factor underlie the observed stem cell differentiation fates?" highlight many unresolved biological questions. These could be addressed if clones that have once demonstrated a specific phenotype in a later phase of cell progression can be isolated from the initial cell population. The new concept of "retrospective clone isolation" has recently emerged to tackle the above-raised questions. A barcoded cell population is first propagated in such a system, and its subpopulation is subjected to a given assay. After identifying a barcoded clone of interest, the same clone (or its close relative) is isolated in a barcode-specific manner from the initial or any other subpopulation stored during the experiment. The isolated live clone can then be subjected to any following experiments, including omics measurements and reconstitution of a synthetic cell population with the isolates. We have recently established a high-performance retrospective isolation technology CloneSelect using CRISPR base editing (**bioRxiv** 2022\*). We have demonstrated that CloneSelect is applicable in human cancer cell lines, human pluripotent stem cells, mouse stem cells, yeast cells and E. coli cells.

**Cellular networks:** Cancers and human diseases are often mediated by complex cellular networks. We have demonstrated that genomic mutations involved in the disruption of protein interactions are highly enriched in cancers and other human diseases (**Cell** 2015). Furthermore, by harnessing DNA molecular tagging of protein-coding genes and massively parallel DNA sequencing, we have developed a new high-throughput protein interaction technology, BFG-Y2H (barcode fusion genetics-yeast two-hybrid). This technology enables a single researcher to screen the

protein interactions of at least 2.5 million protein pairs in 2–3 weeks (*Molecular Systems Biology* 2016+,\*). Using a similar DNA barcode-based approach, we have also developed another screening method to identify non-additive effects of multigenic mutations on given phenotypes (*Cell Systems* 2019\*).

**Automation and genomics:** My team has also been contributing to the development of laboratory automation and data analysis automation platforms. We have previously established humanoid robots to automate various molecular and cellular biology experiments and proposed the vision of robotic cloud biology (*Nature Biotechnology* 2017+). More recently, we have established a new semantic framework to efficiently share reproducible DNA materials and construction protocols within the broad life sciences community (*Nature Communications* 2022\*). Furthermore, we have developed a universal tool to interpret and translate high-throughput sequencing read structures, thereby accelerating the development of new sequencing-based assays (*Science Advances* 2023\*). In the genomics space, we have established a new theoretical framework to scalably measure the spatial genomics of large tissues without the need for a microscopy system (*Cell Systems* 2023\*).

## PUBLICATIONS

+Equal contribution. \*(Co-)corresponding authors. NY is **bolded and double-underlined**. Trainees from the laboratory are single-underlined.

### Preprints and manuscript in press or in revision

- 65- Okamura E, Mizuno S, Matsumoto S, Murata K, Tanimoto Y, Dinh THT, Suzuki H, Kang W, Ema T, Morimoto K, Kato K, Matsumoto T, Masuyama N, Kijima Y, Morimura T, Sugiyama F, Takahashi S, Mizutani E, Woltjen K, Yachie N & Ema M. Highly efficient transgenic mouse production using piggyBac and its application to rapid phenotyping at the founder generation. <https://www.biorxiv.org/content/10.1101/2023.12.10.570953v1>
- 64- Ishiguro S+, Ishida K+, Sakata RC+, Mori H, Takana M, King S, Bashth O, Ichiraku M, Masuyama N, Takimoto R, Kijima Y, Adel A, Toyoshima H, Seki M, Oh JH, Archambault A-S, Nishida K, Kondo A, Kuhara S, Aburatani H, Klein Geltink RI, Takashima Y, Shakiba N & Yachie N. A multi-kingdom genetic barcoding system for precise target clone isolation. <https://www.biorxiv.org/content/10.1101/2023.01.18.524633v1>
- 63- Baccouche A, Adel A, Yachie N, Fujii T & Genot AJ. License to cut: Smart RNA guides for conditional control of CRISPR-Cas9. <https://www.biorxiv.org/content/10.1101/2022.10.26.513620v1>
- 62- Baccouche A, Montagne K, Yachie N, Fujii T & Genot AJ. Quantitative assaying of SpCas9-NG with fluorescent reporters. <https://www.biorxiv.org/content/10.1101/2022.08.04.502727v1>

### Peer-reviewed articles

- 61- Nakane T, Nakagawa R, Ishiguro S, Okazaki S, Mori H, Shuto Y, Yamashita K, Yachie N, Nishimasu H & Nureki O. (2024) Structure and engineering of Brevibacillus laterosporus Cas9. *Communications Biology* 7, 803
- 60- Nakayama Y, Fujiu K, Oshima T, Matsuda J, Sugita J, Matsubara TJ, Liu Y, Goto K, Kani K, Uchida R, Takeda N, Morita H, Xiao Y, Hayashi M, Maru Y, Hasumi E, Kojima T, Ishiguro S, Kijima Y, Yachie N, Yamazaki S, Yamamoto R, Kudo F, Nakanishi M, Iwama A, Fujiki R, Kaneda A, Ohara O, Nagai R, Manabe I & Komuro I. (2024) Heart failure promotes multimorbidity through innate immune memory. *Science Immunology* 9, eade3814
- 59- Tsubouchi A, An Y, Kawamura Y, Yanagihashi Y, Murata Y, Teranishi K, Ishiguro S, Aburatani H, Yachie N & Ota S. (2024) Pooled CRISPR screening of high-content cellular phenotypes by ghost cytometry. *Cell Reports Methods*, 4, 100737
- 58- Kawasaki F, Mimori T, Mori Y, Aburatani H, Yachie N, Sato I & Ota S. (2023) Computational Design of Synthetic Optical Barcodes in Microdroplets. *Advanced Optical Materials*, 2302564
- 57- Hino T, Omura SN, Nakagawa R, Togashi T, Takeda SN, Hiramoto T, Tasaka S, Hirano H, Tokuyama T, Uosaki H, Ishiguro S, Kagieva M, Yamano H, Ozaki Y, Motooka D, Mori H, Kirita Y, Kise Y, Itoh Y, Matoba S, Aburatani H, Yachie N, Karvelis T, Siksnys V, Ohmori T, Hoshino A & Nureki O. (2023) An AsCas12f-based compact genome-editing tool derived by deep mutational scanning and structural analysis. *Cell* 186, 4920-4935.e23
- 56- Greenstreet L+, Afanassiev A+, Kijima Y+, Heitz M+, Ishiguro S, King S, Yachie N\* & Schiebinger G\*. (2023) DNA-GPS: A theoretical framework for optics-free spatial genomics and synthesis of current methods. *Cell Systems* 14, 844-859.e4

- 55- Yachie N\* & Nika Shakiba\*. (2023) Tenure time loopers.  
*Nature Biotechnology* 41, 1375–1377
- 54- Darwish M, Hattori S, Nishizono H, Miyakawa T, Yachie N & Takao K. (2023) Comprehensive behavioral analyses of mice with a glycine receptor alpha 4 deficiency.  
*Molecular Brain* 16, 44
- 53- Kijima Y, Evans-Yamamoto D, Toyoshima H & Yachie N\*. (2023) A universal sequencing read interpreter.  
*Science Advances* 9, add2793 (featured on the cover)
- 52- Masuyama N, Konno N & Yachie N\*. (2022) Molecular recorders to track cellular events (perspective).  
*Science* 377, 469-470
- 51- Mori H & Yachie N\*. (2022) A framework to efficiently describe and share reproducible DNA materials and construction protocols.  
*Nature Communications* 13, 2894
- 50- Nakagawa R, Ishiguro S, Okazaki S, Mori H, Tanaka M, Yachie N, Nishimasu H & Nureki O. (2022) Engineered *Campylobacter jejuni* Cas9 variant with enhanced activity and broader targeting range.  
*Communications Biology* 5, 211
- 49- Evans-Yamamoto D, Rouleau FD, Nanda P, Makanae K, Liu Y, Després PC, Matsuo H, Seki M, Dube AK, Ascencio D, Yachie N\* & Landry CR\*. (2022) BFG-PCA: tools and resources that expand the potential for binary protein interaction discovery.  
*Nucleic Acids Research* gkac045
- 48- Després PC, Dubé AK, Yachie N, Landry CR. (2022) High-Throughput Gene Mutagenesis Screening Using Base Editing.  
*Methods in Molecular Biology* 2477, 331-348
- 47- Konno N, Kijima Y+, Watano K+, Ishiguro S+, Ono K, Tanaka M, Mori H, Masuyama N, Pratt D, Ideker T, Iwasaki W & Yachie N\*. (2022) Deep distributed computing to reconstruct extremely large lineage trees.  
*Nature Biotechnology* 40, 566–575 (featured on the cover)
- 46- Suzuki G, Saito Y, Seki M, Evans-Yamamoto D, Negishi M, Kakoi K, Kawai H, Landry CR, Yachie N\* & Mitsuyama T\*. (2021) Machine learning approach for discrimination of genotypes based on bright-field cellular images.  
*npj Systems Biology and Applications* 7, 31
- 45- Fukushima T, Tanaka Y, Adachi K, Masuyama N, Asada S, Ishiguro S, Mori H, Seki M, Yachie N, Goyama S & Kitamura T. (2021) CRISPR/Cas9-mediated Base-editing Enables a Chain Reaction Through Sequential Repair of sgRNA Scaffold Mutations.  
*Scientific Reports* 11, 23889
- 44- Ishiguro S and Yachie N\* (2020) Highly-multiplexed analysis of genome editing outcomes in mammalian cells.  
*Methods in Molecular Biology* 2312, 193-223
- 43- Kim JH, Seo Y, Jo M, Jeon H, Kim YS, Kim EJ, Seo D, Lee WH, Kim SR, Yachie N, Zhong Q, Vidal M, Roth FP & Suk K. (2020) Interrogation of kinase genetic interactions provides a global view of PAK1-mediated signal transduction pathways.  
*Journal of Biological Chemistry* 295, 16906-16919
- 42- Sakata RC+, Ishiguro S+, Mori H+, Tanaka M, Tastuno K, Ueda H, Yamamoto S, Seki M, Masuyama N, Nishida K, Nishimasu H, Arakawa K, Kondo A, Nureki O, Tomita M, Aburatani H and Yachie N\* (2020) Base editors for simultaneous introduction of C-to-T and A-to-G mutations.  
*Nature Biotechnology* 38, 865-869 (featured on the cover)
- 41- Kim J-H, Seo Y, Jo M, Jeon H, Lee W-H, Yachie N, Zhong Q, Vidal M, Roth FP & Suk K. (2020) Yeast-Based Genetic Interaction Analysis of Human Kinome.  
*Cells (MPDI)* 9, 1156
- 40- Després PC, Dubé AK, Seki M, Yachie N\* and Landry CR\* (2020) Systematic perturbation of yeast essential genes using base editing.  
*Nature Communications* 11, 1871
- 39- Nishizono H, Darwish M, Uosaki H, Masuyama N, Seki M, Abe H, Yachie N and Yasuda R (2020) Use of Freeze-thawed Embryos for High-efficiency Production of Genetically Modified Mice.  
*Journal of Visualized Experiments* 158, e60808
- 38- Murai Y, Masuda T, Onuma Y, Evans-Yamamoto D, Takeuchi N, Mori H, Masuyama N, Ishiguro S, Yachie N and Arakawa K (2020) Complete Genome Sequence of *Bacillus* sp. Strain KH172YL63, Isolated from Deep-Sea

Sediment.

**Microbiology Resource Announcements** 9, e00291-20

- 37- Celaj A, Gebbia M, Musa L, Cote AG, Snider J, Wong V, Ko M, Fong T, Bansal P, Mellor JC, Seesankar G, Nguyen M, Zhou S, Wang L, Kishore N, Mani R, Stagljar I, Suzuki Y, **Yachie N\*** & Roth FP\* (2020) Dissecting Complex Multi-Drug Resistance Traits with High-Order Genetic Analysis.  
**Cell Systems** 9, 1–14
- 36- Marchant A, Cisneros AF, Dubé AK, Gagnon-Arsenault I, Ascencio D, Jain HA, Aubé S, Eberlein C, **Evans-Yamamoto D**, **Yachie N** & Landry CR. (2019) The role of structural pleiotropy and regulatory evolution in the retention of heteromers of paralogs.  
**eLife** 8, e46754
- 35- **Masuyama N**, **Mori H** & **Yachie N\*** (2019) DNA barcodes evolve for high-resolution cell lineage tracing.  
**Current Opinion in Chemical Biology** 52, 63-71
- 34- **Ishiguro S**, **Mori H** & **Yachie N\*** (2019) DNA event recorders send past information of cells to the time of observation.  
**Current Opinion in Chemical Biology** 52, 54-62
- 33- **Evans-Yamamoto D**, Takeuchi N, Masuda T, Murai Y, Onuma Y, **Mori H**, **Masuyama N**, **Ishiguro S**, **Yachie N** & Arakawa K (2019) Complete Genome Sequence of Psychrobacter sp. Strain KH172YL61, Isolated from Deep-Sea Sediments in the Nankai Trough, Japan.  
**Microbiology Resource Announcements** 8, e00326-19
- 32- Dandage R, Després PC, **Yachie N** & Landry CR (2019) beditor: A computational workflow for designing libraries of guide RNAs for CRISPR base editing.  
**Genetics** 212, 377-385
- 31- Mori H, Evans-Yamamoto D, Ishiguro S, Tomita M & **Yachie N\*** (2019) Fast and global detection of periodic sequence repeats in large genomic resources.  
**Nucleic Acids Research** 47, e8
- 30- Nishimasu H, Shi X, **Ishiguro S**, Gao L, Hirano S, Okazaki S, Noda T, Abudayyeh OO, Gootenberg JS, **Mori H**, Oura S, Holmes B, **Tanaka M**, **Seki M**, Hirano H, Aburatani H, Ishitani R, Ikawa M, **Yachie N**, Zhang F & Nureki O (2018) Engineered CRISPR-Cas9 nuclease with expanded targeting space.  
**Science** 361, 1259-1262
- 29- Després PC, Dubé AK, Nielly-Thibault L, **Yachie N** & Landry CR (2018) Double Selection Enhances the Efficiency of Target-AID and Cas9-Based Genome Editing in Yeast.  
**G3: Genes, Genomes, Genetics** 8, 3163-3171
- 28- Jo M+, Chung AY+, **Yachie N+**, Seo M, Jeon H, Nam Y, Seo Y, Kim E, Zhong Q, Vidal M, Park HC, Roth FP & Suk K (2017) Yeast genetic interaction screen of human genes associated with amyotrophic lateral sclerosis: identification of MAP2K5 kinase as a potential drug target.  
**Genome Research** 27, 1487-1500
- 27- Ghanegolmohammadia F, Yoshida M, Ohnuki S, Sukegawa Y, Okada H, Obara K, Kihara A, Suzuki K, Kojima T, **Yachie N**, Hirata D & Ohya Y (2017) Systematic analysis of Ca<sup>2+</sup> homeostasis in *Saccharomyces cerevisiae* based on chemical-genetic interaction profiles.  
**Molecular Biology of the Cell** 28, 3415-3427
- 26- **Yachie N**, Robotic Biology Consortium & Natsume T (2017) Robotic crowd biology with Maholo LabDroids (Correspondence).  
**Nature Biotechnology** 35, 310
- 25- Nishida K, Arazoe T, **Yachie N**, Banno S, Kakimoto M, Tabata M, Mochizuki M, Miyabe A, Araki M, Hara KY, Shimatani Z & Kondo A (2016) Targeted nucleotide editing using hybrid prokaryotic and vertebrate adaptive immune systems.  
**Science** 353, aaf8729
- 24- **Yachie N+\***, Petsalaki E+, Mellor JC, Weile J, Jacob Y, Verby M, Ozturk SB, Li S, Cote AG, Mosca R, Knapp JJ, Ko M, Yu A, Gebbia M, Sahni N, Yi S, Tyagi T, Sheykhkarimli D, Roth JF, Wong C, Musa L, Snider J, Liu Y-C, Yu H, Braun P, Stagljar I, Hao T, Calderwood MA, Pelletier L, Aloy P, Hill DE, Vidal M & Roth FP\* (2016) Pooled-matrix protein interaction screens using Barcode Fusion Genetics.  
**Molecular Systems Biology** 12, 863 (featured on the cover)
- 23- Rich MS, Payen C, Rubin AF, Ong GT, Sanchez MR, **Yachie N**, Dunham MJ & Fields S (2016) The Effects of Cis-Regulatory Mutations in the SUL1 Gene on Sulfate-Limited Fitness in Yeast.  
**Genetics** 203, 191-202

- 22- Sahni N, Yi S, Taipale M, Fuxman Bass JI, Coulombe-Huntington J, Yang F, Peng J, Weile J, Karras GI, Wang Y, Kovács IA, Kamburov A, Krykbaeva I, Lam MH, Tucker G, Khurana V, Sharma A, Liu Y-Y, **Yachie N**, Zhong Q, Shen Y, Palagi A, San-Miguel A, Fan C, Balcha D, Dricot A, Jordan DM, Walsh JM, Shah AA, Yang X, Stoyanova AK, Leighton A, Calderwood MA, Jacob Y, Cusick ME, Salehi-Ashtiani K, Whitesell LJ, Sunyaev S, Berger B, Barabási A-L, Charlotiaux B, Hill DE, Hao T, Roth FP, Xia Y, Walhout AJM, Lindquist S & Vidal M (2015) Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. **Cell** 3, 647-660
- 21- Soma A, Sugahara J, Onodera A, **Yachie N**, Kanai A, Watanabe S, Yoshikawa H, Ohnuma M, Kuroiwa H, Kuroiwa T & Sekine Y (2013) Identification of highly-disrupted tRNA genes in nuclear genome of the red alga, *Cyanidioschyzon merolae* 10D. **Scientific Reports** 3, 2321
- 20- Suzuki Y, Stam J, Novotny M, **Yachie N**, Lasken RS & Roth FP (2012) The Green Monster process for the generation of yeast strains carrying multiple gene deletions. **Journal of Visualized Experiments** 70, e4072
- 19- Nozaki T, **Yachie N**, Ogawa R, Kratz A, Saito R & Tomita M (2011) Tight associations between transcription promoter type and epigenetic variation in histone positioning and modification. **BMC Genomics** 12, 416
- 18- Nozaki T, **Yachie N**, Ogawa R, Saito R & Tomita M (2011) Computational analysis suggests a highly bendable, fragile structure for nucleosomal DNA. **Gene** 476, 10-14
- 17- **Yachie N**, Saito R, Sugiyama N, Tomita M & Ishihama Y (2011) Integrative features of the yeast phosphoproteome and protein-protein interaction map. **PLoS Computational Biology** 7, e1001064
- 16- Imamura H, **Yachie N**, Saito R, Ishihama Y & Tomita M (2010) Towards the systematic discovery of signal transduction networks using phosphorylation dynamics data. **BMC Bioinformatics** 11, 232
- 15- **Yachie N**, Saito R, Sugahara J, Tomita M & Ishihama Y (2009) In silico analysis of phosphoproteome data suggests a rich-get-richer process of phosphosite accumulation over evolution. **Molecular Cellular Proteomics** 8, 1061-1071
- 14- **Yachie N**, Ohashi Y & Tomita M (2008) Stabilizing synthetic data in the DNA of living organisms. **Systems and Synthetic Biology** 2, 19-25
- 13- Sugahara J, Kikuta K, Fujishima K, **Yachie N**, Tomita M & Kanai A (2008) Comprehensive analysis of archaeal tRNA genes reveals rapid increase of tRNA introns in the order Thermoproteales. **Molecular Biology and Evolution** 25, 2709-2716
- 12- Soma A, Onodera A, Sugahara J, Kanai A, **Yachie N**, Tomita M, Kawamura F & Sekine Y (2007) Permuted tRNA genes expressed via a circular RNA intermediate in *Cyanidioschyzon merolae*. **Science** 318, 450-453
- 11- Watanabe Y, Kishi A, **Yachie N**, Kanai A & Tomita M (2007) Computational analysis of microRNA-mediated antiviral defense in humans. **FEBS Letters** 581, 4603-4610
- 10- Matsui M, **Yachie N**, Okada Y, Saito R & Tomita M (2007) Bioinformatic analysis of post-transcriptional regulation by uORF in human and mouse. **FEBS Letters** 581, 4184-4188
- 9- **Yachie N**, Sekiyama K, Sugahara J, Ohashi Y & Tomita M (2007) Alignment-based approach for durable data storage into living organisms. **Biotechnology Progress** 23, 501-505
- 8- Negishi Y, Nakamura H, **Yachie N**, Saito R & Tomita M (2007) eXpanda: an integrated platform for network analysis and visualization. **In Silico Biology** 7, 141-144
- 7- Sugahara J, **Yachie N**, Arakawa K & Tomita M (2007) In silico screening of archaeal tRNA-encoding genes having multiple introns with bulge-helix-bulge splicing motifs. **RNA** 13, 671-681
- 6- **Yachie N**, Arakawa K & Tomita M (2006) On the interplay of gene positioning and the role of rho-independent terminators in *Escherichia coli*. **FEBS Letters** 580, 6909-6914

- 5- Shinoda K, Yachie N, Masuda T, Sugiyama N, Sugimoto M, Soga T & Tomita M (2006) HybGFS: a hybrid method for genome-fingerprint scanning.  
***BMC Bioinformatics*** 7, 479
- 4- Shinoda K, Sugimoto M, Yachie N, Sugiyama N, Masuda T, Robert M, Soga T & Tomita M (2006) Prediction of liquid chromatographic retention times of peptides generated by protease digestion of the Escherichia coli proteome using artificial neural networks.  
***Journal of Proteome Research*** 5, 3312-3317
- 3- Sugahara J, Yachie N, Sekine Y, Soma A, Matsui M, Tomita M & Kanai A (2006) SPLITS: a new program for predicting split and intron-containing tRNA genes at the genome level.  
***In Silico Biology*** 6, 411-418
- 2- Yachie N, Numata K, Saito R, Kanai A & Tomita M (2006) Prediction of non-coding and antisense RNA genes in Escherichia coli with Gapped Markov Model.  
***Gene*** 372, 171-181
- 1- Watanabe Y, Yachie N, Numata K, Saito R, Kanai A & Tomita M (2006) Computational analysis of microRNA target recognition in Caenorhabditis elegans.  
***Gene*** 365, 2-10

## TALKS

- 187- *Invited talk*, Sado Conference 2024, July 25, 2024 (Sado, Japan)
- 186- *Invited talk (plenary lecture)*, The 76th Annual Meeting of the Japan Society for Cell Biology, July 17, 2024 (Tsukuba, Japan)
- 185- *Invited talk*, Young Researchers' Meeting in Cell Biology, July 16, 2024 (Tsukuba, Japan)
- 184- *Invited talk*, The Frontier Salon, July 5, 2024 (Tokyo, Japan)
- 183- *Invited talk*, The Allen Frontier Symposium 2024, June 25, 2024 (Seattle, US)
- 182- *Invited talk*, The 54th Annual Meeting of the Japan Society of Developmental Biologists, June 20, 2024 (Kyoto, Japan)
- 181- *Invited talk*, Keio University, June 19, 2024 (Zoom)
- 180- *Invited talk*, Nagoya City University Life Science Seminar, June 18, 2024 (Nagoya, Japan)
- 179- *Invited talk*, The 27th Science in Japan Forum, June 13, 2024 (Washington DC, US)
- 178- *Invited talk*, Centre for Heart Lung Innovation, June 7, 2024 (Vancouver, Canada)
- 177- *Invited talk*, CIFAR McMillan Multiscale Human Meeting, May 3, 2024 (New York City, US)
- 176- *Invited talk*, Jichi Medical School, March 8, 2024 (Shimotsuke, Japan)
- 175- *Invited talk*, Osaka University WPI-PRIME International Symposium, Frontiers in Human Metaverse Medicine, February 29, 2024 (Osaka, Japan)
- 174- *Invited talk*, *The SANKEN International Symposium, Osaka University, Osaka University, January 12, 2024 (Osaka, Japan)*
- 173- *Invited talk*, The 46th Annual Meeting of the Molecular Biology Society of Japan, December 7, 2023 (Kobe, Japan)
- 172- *Session chair*, The 46th Annual Meeting of the Molecular Biology Society of Japan, December 6, 2023 (Kobe, Japan)
- 171- *Invited talk*, UBC LSI Seminar, September 22, 2023 (Vancouver, Canada)
- 170- *Invited talk*, UBC Advanced Genomics and Genome Engineering Workshop, September 8, 2023 (Vancouver, Canada)
- 169- *Session chair*, The 56th Annual Meeting of the Japanese Society of Developmental Biologists, June 23, 2023 (Sendai, Japan)
- 168- *Invited talk*, Central Institute for Experimental Animals, July 25, 2023 (Tokyo, Japan)
- 167- *Invited talk*, SynBYSS seminar series, July 20, 2023 (Zoom)
- 166- *Invited talk (keynote lecture)*, The 16th Annual Meeting of the Japanese Society for Epigenetics, June 19, 2023 (Tokyo, Japan)
- 165- *Invited talk (keynote lecture)*, The 8th Annual Meeting of the Japanese Society for Genome Editing, June 8, 2023 (Tokyo, Japan)
- 164- *Invited talk*, StemCellTalks, May 19, 2023 (Calgary, Canada)
- 163- *Invited talk*, University of Utah, May 5, 2023 (Utah, US)
- 162- *Invited talk*, Ochanomizu University, January 23, 2023 (Zoom)
- 161- *Invited talk*, Simon Fraser University, January 20, 2023 (Vancouver, Canada)
- 160- *Invited talk*, Kyoto University ASHBI Seminar, January 9, 2023 (Zoom)
- 159- *Invited talk*, Keio University School of Medicine, December 9, 2022 (Tokyo, Japan)
- 158- *Invited talk*, The 51st Annual Meeting of the Japanese Society for Immunology, December 8, 2022 (Kumamoto, Japan)
- 157- *Invited talk*, The University of Tokyo, School of Science, December 5, 2022 (Tokyo, Japan)
- 156- *Session chair*, The 45th Annual Meeting of the Molecular Biology Society of Japan, December 1, 2022 (Chiba, Japan)
- 155- *Invited talk*, SEEDS Conference 2022, October 9, 2022 (Tokyo, Japan)
- 154- *Invited talk*, The Virtual Human Development Consortium, October 5, 2022 (Vancouver, Canada)
- 153- *Invited talk*, University of Washington Genome Science Department Combi Seminar, September 28, 2022 (Seattle, US)
- 152- *Invited talk*, STEMCELL Technologies, September 23, 2022 (Zoom)
- 151- *Invited talk*, Japan Young Researchers Society of Biochemistry, August 28, 2022 (Sendai, Japan)
- 150- *Invited talk*, Juntendo University, July 27, 2022 (Tokyo, Japan)
- 149- *Invited talk*, Keio-Stanford Webinar: Pattern Formation and Stem Cell Development, July 22, 2022 (Zoom)



- 148- *Invited talk*, Boston Japanese Researcher's Society Izayoi Workshop, July 8, 2022 (Zoom)
- 147- *Invited talk*, JSPS Holistic Brain Project Workshop, June 23, 2022 (Zoom)
- 146- *Session chair*, ISSCR 2022 Modeling Stem Cells through Time and Space, June 17, 2022 (San Fransisco, US)
- 145- *Invited talk*, Genome BC board meeting, June 10, 2022 (Vancouver, Canada)
- 144- *Invited talk*, 55th Annual Meeting for the Japanese Society of Developmental Biology (JSDB2022), June 1, 2022 (Zoom)
- 143- *Invited talk*, CIHR Institutes of Genetics, IAB 44, May 28, 2022 (Vancouver, Canada)
- 142- *Invited talk*, Society of Biotechnology Japan Young Researchers Symposium, May 26, 2022 (Zoom)
- 141- *Invited talk*, CIFAR program meeting, May 22, 2022 (Toronto, Canada)
- 140- *Invited talk*, The University of Tokyo, Laboratory for Systems Biology and Medicine, April 17, 2021 (Zoom)
- 139- *Invited talk*, UBC BIG22, March 23, 2022 (Vancouver, Canada)
- 138- *Invited talk*, Future Trends and Emerging Technologies in Synthetic Biology (Japan-Australia Synthetic Biology Symposium), March 15, 2022 (Zoom)
- 137- *Invited talk*, BC Cancer Research Centre, January 17, 2022 (Zoom)
- 136- *Invited talk*, The 4th ExCELLS Symposium, National Institutes of Natural Sciences, December 20, 2021 (Zoom)
- 135- *Invited talk*, The Frontier of Animal and Plant Reseraches, Kobe Univeristy, December 15, 2021 (Zoom)
- 134- *Invited talk*, The 44th Annual Meeting of the Molecular Biology Society of Japan, December 3, 2021 (Zoom)
- 133- *Invited talk*, Japan Science for the Promotion of Science, Replication of Non-Genome Program, November 23, 2021 (Zoom)
- 132- *Invited talk*, Japanese San Francisco Bay Area Seminar, October 30, 2021 (Zoom)
- 131- *Invited talk*, BC Children's Hospital, October 27, 2021 (Zoom)
- 130- *Invited talk*, MIT Bioengineering, October 20, 2021 (Zoom)
- 129- *Invited talk*, BioDojo, April 30, 2021 (Zoom)
- 128- *Invited talk (keynote)*, UBC SBME Research Day, University of British Columbia, March 10, 2021 (Zoom)
- 127- *Invited talk*, 2021 BCRegMed Annual Symposium, May 18, 2021 (Zoom seminar)
- 126- *Invited talk*, BioDojo, April 30, 2021 (Zoom seminar)
- 125- *Invited talk (keynote)*, TRINITY Symposium (Keynote), Hiroshima University, March 17, 2021 (Zoom seminar)
- 124- *Invited talk*, NARA Institute of Science and Technology (NAIST), December 4, 2020 (Zoom seminar)
- 123- *Invited talk*, Notch Therapeutics, November 17, 2020 (Virtual seminar)
- 122- *Invited talk*, Cascadia 2020, November 5, 2020 (Virtual conference)
- 121- *Invited talk*, The University of British Columbia, BC Children PITCH seminar series, October 6, 2020 (Zoom seminar)
- 120- *Invited talk*, Japan Science and Technology Agency, National Bioscience Database Center, October 4, 2020 (Virtual conference)
- 119- *Invited talk*, LADEC2020, October 3, 2020 (Virtual conference)
- 118- *Invited talk*, The University of British Columbia, MSL seminar series, September 23, 2020 (Zoom seminar)
- 117- *Invited talk*, CRISPR and Beyond: Perturbations at Scale to Understand Genomes, September 23, 2020 (Wellcome Genome Campus, UK, Virtual conference)
- 116- *Invited talk*, The 64th Annual Meeting of the Japan College Rheumatology, August 23, 2020 (Virtual conference)
- 115- *Invited talk*, The University of Tokyo, School of Medicine, April 14, 2020 (Zoom seminar)
- 114- *Invited talk*, The University of Tokyo, The Institute of Medical Science, April 5, 2020 (Zoom seminar)
- 113- *Invited talk*, NEDO Festa, December 18, 2019 (Osaka, Japan)
- 112- *Invited talk*, AMED Symposium, December 13, 2019 (Tokyo, Japan)
- 111- *Session chair*, The 42nd Annual Meeting of the Molecular Biology Society of Japan, December 6, 2019 (Fukuoka, Japan)
- 110- *Invited talk*, Augmented Cell Engineering Symposium, December 4, 2019 (Tokyo, Japan)
- 109- *Invited talk*, Hiroshima University, November 26, 2019 (Hiroshima, Japan)
- 108- *Invited talk*, Frontiers in Genome Engineering 2019, November 26, 2019 (Kobe, Japan)
- 107- *Invited talk*, Kumamoto University, November 21, 2019 (Kumamoto, Japan)
- 106- *Invited talk*, Asian Synthetic Biology Association 2019, October 28, 2019 (Chengdu, China)
- 105- *Invited talk*, Takeda New Insight Cross Talk Meeting, October 19, 2019 (Tokyo, Japan)
- 104- *Invited talk*, The University of Tokyo Friday Lecture for High School and University Students, October 18, 2019 (Tokyo, Japan)
- 103- *Invited talk*, University of Toronto, Donnelly Centre, October 10, 2019 (Toronto, Canada)
- 102- *Invited talk*, NARA Institute of Science and Technology (NAIST), September 24, 2019 (Nara, Japan)
- 101- *Invited talk*, The 91st Annual Meeting of Genetic Society of Japan, September 13, 2019 (Fukui, Japan)
- 100- *Invited talk*, The 68th Annual Meeting of Japan Society of Analytical Chemistry 2019, September 11, 2019 (Chiba, Japan)
- 99- *Invited talk*, Society of Young Scientists in Biophysics, Summer School, August 28, 2019 (Kobe, Japan)
- 98- *Invited talk*, Takato Symposium, August 22, 2019 (Takato, Japan)
- 97- *Invited talk*, The 40th Annual Meeting of Japanese Society of Inflammation and Regeneration, July 16, 2019 (Kobe, Japan)
- 96- *Invited talk*, Nagoya University, July 8, 2019 (Nagoya, Japan)
- 95- *Invited talk*, The 13th Intn'l Workshop on Advanced Genomics, June 26, 2019 (Tokyo, Japan)
- 94- *Invited talk*, The University of Tokyo, Graduate School of Agricultural and Life Sciences, June 19, 2019 (Tokyo, Japan)
- 93- *Invited talk*, Advanced Biomeasurement Meeting, May 24, 2019 (Tokyo, Japan)
- 92- *Invited talk*, Q-Bio Meeting: Interface between Immunology & Quantitative Biology, May 20, 2019 (Tokyo, Japan)
- 91- *Invited talk*, TECAN, April 24, 2019 (Tokyo, Japan)
- 90- *Invited talk*, The 63rd Annual Meeting of the Japan College Rheumatology, April 15, 2019 (Kyoto, Japan)
- 89- *Invited talk*, Tohoku University, March 19, 2019 (Sendai, Japan)
- 88- *Invited talk*, Single Cell Biology Meets Diagnostics, March 5, 2019 (Uppsala, Sweden)
- 87- *Invited talk*, JSPS "Cell Diversity" Workshop, February 28, 2019 (Sendai, Japan)
- 86- *Invited talk*, Keystone Symposium: Genome Engineering, February 22, 2019 (Victoria, Canada)

- 85- *Invited talk (keynote lecture)*, Life Science Frontier Meeting 2018, October 6, 2018 (Mishima, Japan)
- 84- *Invited talk*, Max Planck Institute Florida for Brain Sciences, December 10, 2018 (Palm Beach, US)
- 83- *Invited talk*, University of Texas, December 7, 2018 (Texas, US)
- 82- *Invited talk*, The 41st Annual Meeting of the Molecular Biology Society of Japan, November 28, 2018 (Yokohama, Japan)
- 81- *Invited talk*, Asian Synthetic Biology Association, November 23, 2018 (Jeju, South Korea)
- 80- *Invited talk*, Cell Mapping Symposium, October 29, 2018 (San Diego, US)
- 79- *Invited talk*, JST IMPACT Noji Artificial Cell Program, September 28, 2018 (Tokyo, Japan)
- 78- *Invited talk*, NARA Institute of Science and Technology (NAIST), September 27, 2018 (Nara, Japan)
- 77- *Invited talk*, Japanese Biochemical Society, September 26, 2018 (Kyoto, Japan)
- 76- *Invited talk*, Joint Yeast Biology Symposium, September 13, 2018 (Fukuoka, Japan)
- 75- *Invited talk*, Japanese Society for Biotechnology, DBTL Symposium, September 7, 2018 (Osaka, Japan)
- 74- *Invited talk*, Japanese Society for Biotechnology, Mammalian cell culture, September 7, 2018 (Osaka, Japan)
- 73- *Invited talk*, BIO tech 2018, June 28, 2018 (Tokyo, Japan)
- 72- *Invited talk*, The 3rd Annual Meeting of The Japanese Society for Genome Editing, June 19, 2018 (Hiroshima, Japan)
- 71- *Invited talk*, CIFAR Genetic Networks Workshop, June 2, 2018 (Toronto, Canada)
- 70- *Invited talk*, The University of British Columbia, May 28, 2018 (Vancouver, Canada)
- 69- *Invited talk*, University of Toronto, Donnelly Centre, May 23, 2018 (Toronto, Canada)
- 68- *Invited talk (plenary lecture)*, PROTEO 18th Annual Symposium (Plenary Talk), May 18, 2018 (Quebec City, Canada)
- 67- *Invited talk*, Club d'édition génomique de l'Université Laval, May 16, 2018 (Quebec City, Canada)
- 66- *Invited talk*, Nippon Medical School, May 11, 2018 (Tokyo, Japan)
- 65- *Invited talk*, Forum-Management for Tomorrow, April 26, 2018 (Tokyo, Japan)
- 64- *Invited talk*, Osaka University IPR Seminar: BioNetworks in Health and Diseases, April 18, 2018 (Osaka, Japan)
- 63- *Invited talk*, 17th Congress on the Japanese Society for the Regenerative Medicine, March 23, 2018 (Yokohama, Japan)
- 62- *Invited talk*, Japan Association of Technology Executives, March 12, 2018 (Tokyo, Japan)
- 61- *Invited talk*, Annual Meeting for Systems and Synthetic E. coli Biology, March 20, 2018 (Awaji, Japan)
- 60- *Invited talk*, National Institute for Basic Biology, March 5, 2018 (Okazaki, Japan)
- 59- *Invited talk*, ConBio2017: Single Cell Biology Symposium, December 6, 2017 (Kobe, Japan)
- 58- *Invited talk*, ConBio2017: ShinBio Symposium, December 6, 2017 (Kobe, Japan)
- 57- *Invited talk*, Japanese Society for Cell Synthesis Research, October 20, 2017 (Kyoto, Japan)
- 56- *Invited talk*, Kyoto University, Institute for Frontier Medical Sciences, September 20, 2017 (Kyoto, Japan)
- 55- *Invited talk*, Japan Human Proteome Organization (JHUPO), July 27, 2017 (Osaka, Japan)
- 54- *Invited talk*, Kyoto University, Graduate School of Agriculture, July 18, 2017 (Kyoto, Japan)
- 53- *Invited talk*, Kyushu University, Medical Institute of Bioregulation, July 6, 2017 (Fukuoka, Japan)
- 52- *Invited talk*, Japan Research Industries and Industrial Technology Association (JRIA), June 29, 2017 (Tokyo, Japan)
- 51- *Invited talk*, Japan Bioindustry Association, May 15, 2017 (Tokyo, Japan)
- 50- *Invited talk*, Japanese Society of Developmental Biologists, May 10, 2017 (Tokyo, Japan)
- 49- *Invited talk*, CIFAR Genetic Networks Workshop, April 27, 2017 (Tokyo, Japan)
- 48- *Invited talk*, Tottori University, Chromosome Engineering Research Center, April 17, 2017 (Tottori, Japan)
- 47- *Invited talk*, RIKEN Sakura Symposium, March 30, 2017 (Yokohama, Japan)
- 46- *Invited talk*, Annual Meeting for Systems and Synthetic E. coli Biology, March 15, 2017 (Awaji, Japan)
- 45- *Invited talk*, The University of Tokyo, School of Pharmaceutical Sciences, February 27, 2017 (Tokyo, Japan)
- 44- *Invited talk*, Physical Approaches for Growing and Evolving Populations, February 11, 2017 (Tokyo, Japan)
- 43- *Invited talk*, Okinawa Institute of Science and Technology Graduate University (OIST), February 8, 2017 (Okinawa, Japan)
- 42- *Invited talk*, Japanese Society for Quantitative Biology, January 8, 2017 (Okazaki, Japan)
- 41- *Invited talk*, The molecular Biology Society of Japan, December 2, 2016 (Yokohama, Japan)
- 40- *Invited talk*, International Conference on Single Cell Research 2016, November 16, 2016 (Tokyo, Japan)
- 39- *Invited talk*, The 8th IMS Seminar on Human Disease Biology, RIKEN IMS, October 28, 2016 (Tokyo, Japan)
- 38- *Invited talk*, Informatics in Biology, Medicine and Pharmacology, September 30, 2016 (Tokyo, Japan)
- 37- *Invited talk*, Bayer Innovation Day, September 8, 2016 (Yokohama, Japan)
- 36- *Invited talk*, Keio University, School of Medicine, August 9, 2016 (Tokyo, Japan)
- 35- *Invited talk*, Kyoto University, School of Medicine, June 16, 2016 (Kyoto, Japan)
- 34- *Invited talk*, The University of Tokyo, BIO UT 2016 (Plenary Talk), April 23, 2016 (Tokyo, Japan)
- 33- *Invited talk*, CIFAR Genetic Networks Workshop, April 16, 2016 (Toronto, Canada)
- 32- *Invited talk*, The University of Tokyo, Institute of Medical Science, IIS Retreat, March 31, 2016 (Tokyo, Japan)
- 31- *Invited talk*, Chemical Society of Japan, March 27, 2016 (Kyoto, Japan)
- 30- *Invited talk*, The University of Tokyo, Institute of Industrial Science, March 19, 2016 (Tokyo, Japan)
- 29- *Invited talk*, International Symposium on Genome Microbiology, March 6, 2016 (Tokyo, Japan)
- 28- *Invited talk*, Spiber, Inc., March 1, 2016 (Tsuruoka, Japan)
- 27- *Invited talk*, BMB2015: Illumina Seminar, December 1, 2015 (Kobe, Japan)
- 26- *Invited talk*, BMB2015: Single Cell Workshop, December 1, 2015 (Kobe, Japan)
- 25- *Invited talk*, Kobe University, Innovative BioProduction Kobe, August 5, 2015 (Kobe, Japan)
- 24- *Invited talk*, RIKEN Center for Sustainable Resource Center, July 29, 2015 (Wako, Japan)
- 23- *Invited talk*, Toyota Physical and Chemical Research Institute, July 27, 2015 (Tokyo, Japan)
- 22- *Invited talk*, NARA Institute of Science and Technology (NAIST), July 22, 2015 (Nara, Japan)
- 21- *Invited talk*, Cancer and Metabolism, July 16, 2015 (Kanazawa, Japan)
- 20- *Invited talk*, NGS Field, July 2, 2015 (Tsukuba, Japan)
- 19- *Invited talk*, RIKEN Quantitative Biology Center, QBic Retreat, June 21, 2015 (Osaka, Japan)

- 18- *Invited talk*, Illumina Genome Summit 2015, June 4, 2015 (Tokyo, Japan)
- 17- *Invited talk*, RIKEN Quantitative Biology Center, May 26, 2015 (Osaka, Japan)
- 16- *Invited talk*, Kyoto University, Center for iPS Research and Application, May 25, 2015 (Kyoto, Japan)
- 15- *Invited talk*, Keio IAB-Osaka BIKEN Joint Workshop, March 5, 2015 (Osaka, Japan)
- 14- *Invited talk*, The University of Tokyo, Graduate School of Science, February 9, 2015 (Tokyo, Japan)
- 13- *Invited talk*, National Institute of Advanced Industrial Science and Technology (AIST), December 26, 2014 (Tokyo, Japan)
- 12- *Invited talk*, Okazaki Institute for Integrative Bioscience, November 21, 2014 (Okazaki, Japan)
- 11- *Invited talk*, The University of Tokyo, Graduate School of Science, November 18, 2014 (Nara, Japan)
- 10- *Invited talk*, Mie University, School of Medicine, October 29, 2014 (Mie, Japan)
- 9- *Invited talk*, Advanced Telecommunications Research Institute International, October 14, 2014 (Mie, Japan)
- 8- *Invited talk*, RIKEN Tanabata Meeting, Yokohama, Japan, July 11, 2014
- 7- *Invited talk*, Harvard Medical School, Center of Cancer Systems Biology Retreat 2013, MA, USA, September 12, 2013
- 6- *Invited talk*, Yokohama City University, School of Medicine, Yokohama, Japan, October 1, 2012
- 5- *Invited talk*, RIKEN Plant Science Center, Yokohama, Japan, October 4, 2012
- 4- *Invited talk*, Harvard Medical School, Center of Cancer Systems Biology Retreat 2012, MA, USA, September 14, 2012
- 3- *Invited talk*, Harvard Medical School, Center of Cancer Systems Biology, MA, USA, April 10, 2012
- 2- *Invited talk*, Brandeis University, MA, USA, April 9, 2012
- 1- *Invited talk*, National Institute of Genetics, Mishima, Japan, February 19, 2009

### Peer-reviewer participation

- **For journals:** *Science*, *Nature* (4), *Nature Biotechnology* (5), *Nature Methods*, *Nature Genetics*, *Nature Chemical Biology*, *Nature Nanotechnology*, *Nature Communications* (6), *Nature Protocols*, *Cell Genomics*, *Cell Reports*, *Cell Reports Methods*, *iScience*, *Molecular Systems Biology*, *Genome Biology*, *GEN Biotechnology*, *Nucleic Acids Research* (2), *PNAS* (2), *Bioinformatics*, *BMC Bioinformatics* (2), *BMC Biology*, *Journal of Theoretical Biology* (3), *Journal of Proteomics*, *Journal of Molecular Biology*, *Scientific Reports* (3), *PLOS One*, *npj Systems Biology and Applications* (6), *Journal of Visualized Experiments*
- **Grants:** NSERC (a total of 2 applications), Japan Science and Technology Agency (227), Japan Society for the Promotion of Science (45), Medicine by Design (6 applications), CIFAR (35), Stem Cell Network