

荒川和晴 業績目録

Research Contributions

Research Publications

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Research Paper

- Bino T, Arakawa K, Aoki K, "Possible roles of CAHS proteins form Tardigrade in osmotic stress tolerance in mammalian cells", Cell Structure and Function, 2024, in press.
- Ikeda H, Oshibuchi K, Yang J, Fukuda S, Arakawa K*, " Complete genome sequence of Bulleidia sp. 10714-15 isolated from human colon cancer patients " , Microbiol Resour Announc, 2024, 0:e00937-24. (Publisher)
- Yamamoto PK, Fujimoto Y, Warashina T, Arakawa K*, " Complete genome sequences of two Paenibacillus isolated from pegmatite in Fukushima, Japan " , Microbiol Resour Announc, 2024, 0:e00938-24. (Publisher)
- Ito L, Masui M, Galipon J, Arakawa K*, " Complete genome sequence of polylactic acid degrading Rhodopseudomonas palustris strain R1 isolated from rice field soil " , Microbiology Resource Announcements, 2024,0:e00814-24. (Publisher)
- Takahashi H, Warashina T, Takahashi Y, Tanaka M, Suzuki K, Morita T, Arakawa K*, " Complete genome sequence of Serratia plymuthica SWSY-3.47 " , Microbiology Resource Announcements, 2024,0:e00815-24.
- Ichimura R, Tanaka K, Nakato G, Fukuda S, Arakawa K*, " Complete genome sequence of Mediterraneibacter gnavus strain RI1, isolated from human feces " , Microbiology Resource Announcements, 2024,0:e00863-24. (Publisher)
- Craig H, Malay A, Hayashi F, Mori M, Arakawa K, Numata K, "Post-Translational Modifications in Spider Silk Influence Conformation and Dimerization Dynamics", MRS Bulletin, 2024, in press.
- Sugiura K, Yoshida Y, Hayashi K, Arakawa K, Kunieda T, Matsumoto M, "Sexual dimorphism in the tardigrade Paramacrobiotus metropolitanus transcriptome", Zoological Lett., 2024, in press.
- Yoshida Y, Hirayama A, Arakawa K*, "Transcriptome analysis of the tardigrade Hypsibius exemplaris exposed to the DNA-damaging agent bleomycin", Proc Jpn Acad Ser B Phys Biol Sci., 2024, in press.
- Miyake A, Harada S, Sugiyama D, Matsumoto M, Hirata A, Miyagawa N, Toki, R, Edagawa S, Kuwabara K, Okamura T, Sato A, Amano K, Hirayama A, Sugimoto M, Soga T, Tomita M, Arakawa K, Takebayashi T, Iida M, " Reliability of Time-Series Plasma Metabolome Data over 6 Years in a Large-Scale Cohort Study " , Metabolites, 2024, 14(1):77.
- Kato S, Yuzawa S, Takeda T, Arakawa K, " Complete genome sequence of Kitasatospora aureofaciens Tü117 " , Microbiology Resource Announcements, 2024, 13:e01014-23. (Publisher)

- Michalczyk & Gross V, Arakawa K, " Progress in research on water bears presented at the 15th International Symposium on Tardigrada (Krakow, 22nd-26th of August 2022) ", Zoological Journal of the Linnean Society, 2024, 200(1):1-11.
- Fleming J, Pisani D, Arakawa K, " The evolution of temperature and desiccation-related protein families in Tardigrada reveals the complex acquisition of extremotolerance ", Genome Biology and Evolution, 2024:evad217. ([PubMed](#))
- Naruki M, Watanabe A, Warashina T, Morita T, Arakawa K*, " Complete genome sequence of Limnobacter thiooxidans CS-K2T, isolated from freshwater lake sediments in Bavaria, Germany ", Microbiology Resource Announcements, 2023,13:e00992-23. ([Publisher](#))
- Oshibuchi K, Yang J, Obana N, Fukuda Shinji, Arakawa K*, " Complete genome sequence of Solobacterium moorei JCM 10645T isolated from a human stool sample ", Microbiology Resource Announcements, 2023,13:e00965-23. ([Publisher](#))
- Kawashima T, Watanabe Y, Arakawa K, " Complete genome sequence of Actinoplanes sichuanensis strain 03-723T ", Microbiology Resource Announcements, 2023, 14:e00662-23. ([Publisher](#))
- Tanaka S, Arakawa K*, " Reply to Tanaka and Kunieda: Control protein GFP also shows a mesh-like structure in desiccating tardigrade cells ", PNAS, 2023, 120(48):e2316451120. ([PubMed](#))
- Suzuki Y, Fukazawa A, Sugawara K, Galipon J, Arakawa K*, "Complete genome sequence of PETase type IIa-harboring Marinobacter nanhaiticus D15-8W, isolated from a South China Sea sediment", Microbiol Resour Announc, 2023, 12:e00868-23. ([Publisher](#))
- Sato A, Arakawa K, Kakui K, " Two new species in Leptocheliidae (Crustacea: Peracarida: Tanaidacea) from Japan, with notes on their phylogenetic position and aspects of morphology ", Zoologischer Anzeiger, 2023, 306:51-68. ([Publisher](#))
- Arakawa K, Hirose T, Inada T, Ito T, Kai T, Oyama M, Tomari Y, Yoda T, Nakagawa S, "Non-domain Biopolymers: flexible molecular strategies to acquire biological functions", Genes to Cells, 2023, 28(8):539-552.
- Nakamura H, Kono N, Mori M, Masunaga H, Numata K, Arakawa K*, " Composition of Minor Ampullate Silk Makes Its Properties Different from Those of Major Ampullate Silk ", Biomacromolecules, 2023, 24(5):2042-2051. ([PubMed](#))
- Watanabe Y, Arakawa K*, " Molecular mechanisms of the high performance of spider silks revealed through multi-omics analysis ", Biophysics and Physicobiology, 2023, e200014. ([Publisher](#))
- Arakawa K*, " A Nanopore Sequencing Course for Graduate School Curriculum ", Methods Mol. Biol, 2023, 2632:113-127. ([PubMed](#))
- Takasuka K, Arakawa K, " The Method of Eliminating the Wolbachia Endosymbiont Genomes from Insect Samples Prior to a Long-Read Sequencing ", Methods Mol. Biol, 2023, 2632:101-112. ([PubMed](#))
- Arakawa K*, " Ultralow-Input Genome Library Preparation for Nanopore Sequencing with Droplet MDA ", Methods Mol. Biol, 2023, 2632:91-100. ([PubMed](#))
- Tanaka S, Aoki K, Arakawa K*, " In vivo expression vector derived from anhydrobiotic tardigrade

genome enables live imaging in Eutardigrada ” , PNAS, 2023, 120 (5): e2216739120. ([PubMed](#))

- Arakawa K*, Kono N, Malay A.D, Tateishi A, Ifuku N, Masunaga H, Sato R, Tsuchiya K, Ohtoshi R, Pedrazzoli D, Shinohara A, Ito Y, Nakamura H, Tanikawa A, Suzuki Y, Ichikawa T, Fujita S, Fujiwara M, Tomita M, Blamires S.J, Chuah J-A, Craig H, Foong C.P, Greco G, Guan J, Holland C, Kaplan D.L, Sudesh K, Mandal B.B, Norma-Rashid.Y, Oktaviani N.A, Preda R.C, Pugno N.M, Rajkhowa R, Wang X, Yazawa K, Zheng Z, Numata K, “ 1000 spider silkomes: Linking sequences to silk physical properties ” , Science Advances, 2022, 8(41):eabo6043. ([Publisher](#))
- Iwai H, Mori M, Tomita M, Kono N, Arakawa K, “ Molecular Evidence of Chemical Disguise by the Socially Parasitic Spiny Ant *Polyrhachis lamellidens* (Hymenoptera: Formicidae) When Invading a Host Colony ” , Frontiers in Ecology and Evolution, 2022, 10:915517. ([Publisher](#))
- Ishikawa S, Huang M, Tomita A, Kurihara Y, Watanabe R, Iwai H, Arakawa K*, "Complete Genome Sequences of Four Bacteria Isolated from the Gut of a Spiny Ant (*Polyrhachis lamellidens*)", Microbiol Resour Announc, 2022, 11:e00333-22. ([Publisher](#))
- Takeda T, Fukumitsu N, Yuzawa S, Arakawa K*, "Complete Genome Sequence of *Streptomyces albus* Strain G153", Microbiol Resour Announc, 2022, 11:e00332-22. ([Publisher](#))
- Huang M, Miura MC, Inose R, Sato A, Kamezaki K, Tomita T, Mori M, Arakawa K, Kanai A, "Dataset for proteomic analysis of *Escherichia coli* before and after severe heat shock stress", Journal of Proteome Data and Methods, 2022, 4:1.
- Yoshida Y, Satoh T, Ota C, Tanaka S, Horikawa DD, Tomita M, Kato K, Arakawa K*, "Time-series transcriptomic screening of factors contributing to the cross-tolerance to UV radiation and anhydrobiosis in tardigrades", BMC Genomics, 2022, 23:405. ([Publisher](#))
- Miyazawa K, Itoh S, Yoshida Y, Arakawa K, Okumura H, "Tardigrade Secretory-Abundant Heat-Soluble Protein Varies Entrance Propensity Depending on the Amino-Acid Sequence", Journal of Physical Chemistry B, 2022, 126(12):2361-2368. ([Publisher](#))
- Kurihara Y, Iwai H, Kono N, Tomita M, Arakawa K, "Initial parasitic behaviour of the temporary social parasitic ant *Polyrhachis lamellidens* can be induced by host-like cuticles in laboratory environment", Biology Open, 2022, 11(3):bio058956. ([Publisher](#))
- Arakawa K*, "Examples of Extreme Survival: Tardigrade Genomics and Molecular Anhydrobiology", Annu Rev Anim Biosci., 2022, 10:17-37. ([PubMed](#))
- Kono N, Ohtoshi R, Malay A.D, Mori M, Masunaga H, Yoshida Y, Nakamura H, Numata K, Arakawa K “ Darwin ’ s bark spider shares a spidroin repertoire with *Caerostris extrusa* but achieves extraordinary silk toughness through gene expression ” , Open Biol, 2021, 11(12): 210242. ([PubMed](#))
- Kakui K, Fleming J.F, Mori M, Fujiwara Y, Arakawa K*, “ Comprehensive transcriptome sequencing of Tanaidacea with proteomic evidences for their silk ” , Genome Biology and Evolution, 2021, 13(12):evab281. ([PubMed](#))
- Murai Y, Yagi-Utsumi M, Fujiwara M, Tanaka S, Tomita M, Kato K, Arakawa K*, “ Multiomics study of a heterotardigrade, *Echiniscus testudo*, suggests the possibility of convergent evolution of abundant heat-soluble proteins in Tardigrada ” , BMC Genomics, 2021, 22:813. ([PubMed](#))
- Yagi-Utsumi M, Aoki K, Watanabe H, Song C, Nishimura S, Satoh T, Yanaka S, Ganser C, Tanaka S, Schnapka V, Goh EW, Furutani Y, Murata K, Uchihashi T, Arakawa K, Kato K, “ Desiccation induced fibrous condensation of CAHS protein in an anhydrobiotic tardigrade ” , Sci Rep, 2021, 11 :21328. ([PubMed](#))

- Kono N, Nakamura H, Ohtoshi R, Arakawa K*, "Transcriptomic data during development of a two-spotted cricket *Gryllus bimaculatus*", Data in Brief, 2021, 38:107388. ([PubMed](#))
- Kono N, Nakamura H, Arakawa K, "The complete mitochondrial genome of *Trichonephila clavipes* (Araneae: Araneidae)", Mitochondrial DNA B Resour, 2021, 6(10):2986-2988. ([PubMed](#))
- Iwai H, Kurihara Y, Kono N, Tomita M, Arakawa K, "The evidence of temporary social parasitism by *Polyrhachis lamellidens* (Hymenoptera, Formicidae) in a *Camponotus obscuripes* colony (Hymenoptera, Formicidae)", Insectes Sociaux, 2021, 68:375–382. ([Publisher](#))
- Miyazawa K, Itoh S, Watanabe H, Uchihashi T, Yanaka S, Yagi-Utsumi M, Kato K, Arakawa K, Okumura H, "Tardigrade secretory-abundant heat-soluble protein has a flexible β -barrel structure in solution and keeps this structure in dehydration", Journal of Physical Chemistry B, 2021, 125, 9145 - 9154. ([PubMed](#))
- Kono N, Nakamura H, Mori M, Yoshida Y, Ohtoshi R, Malay A.D, Pedrazzoli Moran DA, Tomita M, Numata K, Arakawa K*, " Multicomponent nature underlies the extraordinary mechanical properties of spider dragline silk ", PNAS, 2021, 118(31): e2107065118. ([PubMed](#))
- Fleming J, Pisani D, Arakawa K, "New Tardigrade Opsins and Differential Expression Analyses shows ontogenic variation in light perception", Genome Biology and Evolution, 2021, 13(8):evab164. ([PubMed](#))
- Watanabe Y, Arakawa K*, "Complete Genome Sequences of Two *Lysobacter* Strains Isolated from Sea Water (*Lysobacter caseinilyticus*) and Soil (*Lysobacter helvus*) in South Korea", Microbiol Resour Announc, 2021,10(28):e00337-21. ([PubMed](#))
- Kono N, Nakamura H, Tateishi A, Numata K, Arakawa K, "The balance of crystalline and amorphous regions in the fibroin structure underpins the tensile strength of bagworm silk", Zoological Letters, 2021,7(1):11. ([PubMed](#))
- Watanabe Y, Takeuchi N, Yang J, Obana N, Morinaga K, Kusada H, Tamaki H, Fukuda S, Arakawa K*, "Complete Genome Sequence of *Atopobiaceae* bacterium strain P1, Isolated from Mouse Feces", Microbiol Resour Announc, 2021, 10(28):e00627-21. ([PubMed](#))
- Takahashi H, Yang J, Yamamoto H, Fukuda S, Arakawa K*, "Complete Genome Sequence of *Adlercreutzia equolifaciens* subsp. *celatus* DSM18785", Microbiol Resour Announc, 2021, 10 :e00354-21. ([PubMed](#))
- Yoshida Y, Horikawa DD, Sakashita T, Yokota Y, Kobayashi Y, Tomita M, Arakawa K*, "RNA sequencing data for gamma radiation response in the extremotolerant tardigrade *Ramazzottius varieornatus*", Data in Brief, 2021, 36:107111. ([PubMed](#))
- Fujiwara M, Kono N, Hirayama A, Malay A, Nakamura H, Ohtoshi R, Numata K, Tomita M, Arakawa K*, "Xanthurenic acid is the main pigment of *Trichonephila clavata* gold dragline silk", Biomolecules, 2021, 11(4):563. ([PubMed](#))
- Warashina, T, Yamamura S, Suzuki H, Amachi S, Arakawa K, "Complete Genome Sequence of *Geobacter* sp. Strain SVR, an Antimonate-reducing Bacterium Isolated from Antimony-rich Mine Soil", Microbiol Resour Announc, 2021, 10:e00142-21. ([PubMed](#))
- Berger CA, Brewer MS, Kono N, Nakamura H, Arakawa K, Kennedy SR, Wood HM, Adams SA, Gillespie RG, "Shifts in morphology, gene expression, and selection underlie web loss in Hawaiian *Tetragnatha* spiders", BMC Ecol Evol, 2021, 21(1):48. ([PubMed](#))
- Arakawa K, Mori M, Kono N, Suzuki T, Gotoh T, Shimano S, "Proteomic evidence for the silk fibroin genes of spider mites (order Trombidiformes: family Tetranychidae)", J Proteomics, 2021,

239:104195. ([PubMed](#))

- Nishimura K, Ikarashi M, Yasuda Y, Sato M, Cano Guerrero M, Galipon J, Arakawa K, "Complete Genome Sequence of *Sphingomonas paucimobilis* Strain Kira, Isolated from Human Neuroblastoma SH-SY5Y Cell Cultures Supplemented with Retinoic Acid.", *Microbiol Resour Announc*, 2021, 10 (6):e01156-20. ([PubMed](#))
- Arakawa K*, Numata K, "Reconsidering the "glass transition" hypothesis of intrinsically unstructured CAHS proteins in desiccation tolerance of tardigrades", *Mol Cell*, 2021, 81(3):409-410. ([PubMed](#))
- Fleming J, Arakawa K, "Systematics of Tardigrada: A reanalysis of tardigrade taxonomy with specific reference to Guil et al (2019)", *Zoologica Scripta*, 2021, 50(3):376-382. ([Publisher](#))
- Malay AD, Suzuki T, Katashima T, Kono N, Arakawa K, Numata K, "Spider silk self-assembly via modular liquid-liquid phase separation and nanofibrillation", *Science Advances*, 2020, 6(45):eabb6030. ([Publisher](#))
- Kono N, Nakamura H, Mori M, Tomita M, Arakawa K, "Spidroin profiling of cribellate spiders provides insight into the evolution of spider prey capture strategies", *Sci Rep*. 2020, 24;10(1):15721. ([PubMed](#))
- Kondo K, Mori M, Tomita M, Arakawa K, "Pre - treatment with D942, a furancarboxylic acid derivative, increases desiccation tolerance in an anhydrobiotic tardigrade *Hypsibius exemplaris*", *FEBS Open Bio*, 2020, 10(9):1774-1781. ([Publisher](#))
- Sakata R. C, Ishiguro S, Mori H, Tanaka M, Tatsuno K, Ueda H, Yamamoto S, Seki M, Masuyama N, Nishida K, Nishimasu H, Arakawa K, Kondo A, Nureki O, Tomita M, Aburatani H, Yachie N, " Base editors for simultaneous introduction of C-to-T and A-to-G mutations " , *Nature Biotechnology*, 2020. ([PubMed](#))
- Inoue H, Shibata S, Ii K, Inoue J, Fukuda S, Arakawa K, "Complete Genome Sequence of *Bifidobacterium longum* Strain Jih1, Isolated from Human Feces", *Microbiol Resour Announc*, 2020, 9:e00319-20. ([Publisher](#))
- Kurihara Y, Kawai S, Sakai A, Galipon J, Arakawa K*, "Complete Genome Sequence of *Halomonas meridiana* Strain Eplume2, Isolated from a Hydrothermal Plume in the Northeast Pacific Ocean", *Microbiol Resour Announc*, 2020, 9:e00330-20. ([Publisher](#))
- Seo K, Tanaka K, Fukuda S, Arakawa K*, "Complete Genome Sequences of Two *Cutibacterium acnes* Strains Isolated from an Orthopedic Surgical Site", *Microbiol Resour Announc*, 2020, 9 :e00290-20. ([Publisher](#))
- Takahashi Y, Takahashi H, Galipon J, Arakawa K*, "Complete Genome Sequence of *Halomonas meridiana* Strain Slthf1, Isolated from a Deep-Sea Thermal Vent", *Microbiol Resour Announc*, 2020 , 9:e00292-20. ([Publisher](#))
- Murai Y, Masuda T, Onuma Y, Evans-Yamamoto D, Takeuchi N, Mori H, Masuyama N, Ishiguro S, Yachie N, Arakawa K*, "Complete Genome Sequence of *Bacillus* sp. Strain KH172YL63, Isolated from Deep-Sea Sediment", *Microbiol Resour Announc*, 2020, 9:e00291-20. ([Publisher](#))
- Takeyama N, Huang M, Sato K, Galipon J, Arakawa K*, "Complete Genome Sequence of *Halomonas hydrothermalis* Strain Slthf2, a Halophilic Bacterium Isolated from a Deep-Sea Hydrothermal-Vent Environment", *Microbiol Resour Announc*, 2020, 9:e00294-20. ([Publisher](#))
- Arakawa K*, "Simultaneous metabarcoding of eukaryotes and prokaryotes to elucidate the community structures within tardigrade microhabitats", *Diversity*, 2020, 12(3):110. ([Publisher](#))

- Sugiura K, Arakawa K, Matsumoto M, "Distribution of *Macrobiotus shonaicus* Stec, Arakawa & Michalczyk, 2018 (Tardigrada: Eutardigrada: Macrobiotidae) in Japan", *Zootaxa*, 2020, 4767(1):56-70. ([Publisher](#))
- BioHackathon 2015, "BioHackathon 2015: Semantics of data for life sciences and reproducible research", *F1000 Research*, 2020, 9:136. ([Publisher](#))
- Mapalo MA, Arakawa K, Baker CM, Persson DK, Mirano-Bascos D, Giribet G, "The Unique Antimicrobial Recognition and Signaling Pathways in Tardigrades with a Comparison Across Ecdysozoa", *G3 (Bethesda)*, 2020, 10(3):1137-1148. ([PubMed](#))
- Stec D, Krzywański, Arakawa K*, Michalczyk, "A new redescription of *Richtersius coronifer*, supported by transcriptome, provides resources for describing concealed species diversity within the monotypic genus *Richtersius* (Eutardigrada).", *Zool. Lett.*, 2020, 6:2. ([PubMed](#))
- Tamaki S, Nishino K, Ogawa T, Maruta T, Sawa Y, Arakawa K, Ishikawa T, "Comparative proteomic analysis of mitochondria isolated from *Euglena gracilis* under aerobic and hypoxic conditions", *PLoS One*, 2019, 14(12):e0227226. ([PubMed](#))
- Yoshida Y, Sugiura K, Tomita M, Matsumoto M, Arakawa K*, "Comparison of the transcriptomes of two tardigrades with different hatching coordination", *BMC Developmental Biology*, 2019, 19(1):24. ([PubMed](#))
- Kondo K, Mori M, Tomita M, Arakawa K*, "AMPK activity is required for the induction of anhydrobiosis in a tardigrade *Hypsibius exemplaris*, and its potential upregulator is PP2A", *Genes to Cells*, 2019, 24(12):768-780. ([PubMed](#))
- BioHackathon 2013/2014, "BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services", *F1000 Research*, 2019, 8:1677. ([Publisher](#))
- Craig RJ, B&ndel KB, Arakawa K, Nakada T, Ito T, Bell G, Colegrave N, Keightley PD, Ness RB, "Patterns of population structure and complex haplotype sharing among field isolates of the green alga *Chlamydomonas reinhardtii*", *Molecular Ecology*, 2019, 28(17):3977-3993. ([Publisher](#))
- Yoshida Y, Novel RW, Arakawa K, Baxter M, "Horizontal Gene Transfer in Metazoa: Examples and Methods", *Horizontal Gene Transfer*, 2019, 203-226. ([Publisher](#))
- Masuda T, Kono N, Tomita M, Arakawa K, "Strand-specific Single-stranded DNA Sequencing (4 S-seq) of *E. coli* genomes", *Bio-protocol*, 2019, 9(15): e3329. ([Publisher](#))
- Tsurumaki M, Deno S, Galipon J, Arakawa K*, "Complete Genome Sequence of Halophilic Deep-Sea Bacterium *Halomonas axialensis* Strain Althf1", *Microbiol Resour Announc*, 2019, 8:e00839-19. ([Publisher](#))
- Saito M, Nishigata A, Galipon J, Arakawa K*, "Complete Genome Sequence of *Halomonas sulfidaeris* Strain Esulfide1 Isolated from a Metal Sulfide Rock at a Depth of 2,200 Meters, Obtained Using Nanopore Sequencing", *Microbiol Resour Announc*, 2019, 8(23):e00327-19. ([Publisher](#))
- Nagata S, Ii KM, Tsukimi T, Miura MC, Galipon J, Arakawa K*, "Complete genome sequence of *Halomonas olivaria*, a moderately halophilic bacterium isolated from olive processing effluents, obtained by nanopore sequencing", *Microbiol Resour Announc*, 2019, 8:e00144-19.
- Evans-Yamamoto D, Takeuchi N, Masuda T, Murai Y, Onuma Y, Mori H, Masuyama N, Ishiguro

- S, Yachie N, Arakawa K*, "Complete genome sequence of *Psychrobacter* sp. strain KH172YL61, isolated from deep-sea sediments in the Nankai Trough, Japan", *Microbiol Resour Announc*, 2019, 8:e00326-19. ([PubMed](#))
- Kono N, Nakamura H, Ohtoshi R, Pedrazzoli Moran DA, Shinohara A, Yoshida Y, Fujiwara M, Mori M, Tomita M, Arakawa K*, " Orb-weaving spider *Araneus ventricosus* genome elucidates the spidroin gene catalogue ", *Sci. Rep.* 9(1):8380, 2019. ([PubMed](#))
 - Kono N, Arakawa K*, " Nanopore sequencing: review of potential applications in functional genomics ", *Development, Growth & Differentiation*, 61(5):316-326, 2019. ([PubMed](#))
 - Kono N, Nakamura H, Ohtoshi R, Tomita M, Numata K, Arakawa K*, " The bagworm genome reveals a unique fibroin gene that provides high tensile strength ", *Communications Biology*, 2019, 2:148. ([Publisher](#))
 - Sugiura K, Minato H, Suzuki AC, Arakawa K, Kunieda T, Matsumoto M, "Comparison of sexual reproductive behavior in two species of Macrobiotidae (Tardigrada: Eutardigrada)", *Zool. Sci.*, 2019, 36(2):120-127. ([PubMed](#))
 - Ohshima Y, Kono N, Yokota Y, Watanabe S, Sasaki I, Ishioka NS, Sakashita T, Arakawa K*, "Anti-tumor effects and potential therapeutic response biomarkers in α -emitting meta-211 At-astato-benzylguanidine therapy for malignant pheochromocytoma explored by RNA-sequencing", *Theranostics* 2019, 9(6):1538-1549. ([Publisher](#))
 - Ii KM, Kono N, Paulino-Lima IG, TomitaM, Rothschild LJ, Arakawa K*, "Complete Genome Sequence of *Arthrobacter* sp. Strain MN05-02, a UV-Resistant Bacterium from a Manganese Deposit in the Sonoran Desert", *J Genomics*, 2019, 7:18-25. ([PubMed](#))
 - Fleming J, Kristensen R, Sørensen Martin, Park T, Arakawa K, Blaxter M, Rebecchi L, Guidetti R, Williams T, Roberts N, Vinther J, Pisani D, "Molecular palaeontology illuminates evolution of ecdysozoan vision", *Proceedings of the Royal Society B*, 2018, 285(1892):20182180. ([PubMed](#))
 - Kono N, Tomita M, Arakawa K*, "Accelerated laboratory evolution reveals the influence of replication on the GC skew in *Escherichia coli*", *Genome Biol. Evol.*, 2018, 10(11):3110-3117. ([PubMed](#))
 - Arakawa K*, Kono N, Ohtoshi R, Hiroyuki N, Tomita M, The complete mitochondrial genome of *Eumeta variegata* (Lepidoptera: Psychidae), *Mitochondrial DNA B Resour*, 2018, 3(2):812-813. ([Publisher](#))
 - Arakawa K* "The complete mitochondrial genome of *Echiniscus testudo* (Heterotardigrada: Echiniscidae)", *Mitochondrial DNA B Resour*, 2018, 3(2):810-811. ([Publisher](#))
 - Yoshida Y, Konno S, Nishino R, Murai Y, Tomita M, Arakawa K, "Ultralow Input Genome Sequencing Library Preparation from a Single Tardigrade Specimen", *J. Vis. Exp.*, 2018, 137 :e57615. ([PubMed](#))
 - Stec D, Arakawa K*, Michalczyk J, "An integrative description of *Macrobiotus shonaicus* sp. nov. (Tardigrada: Macrobiotidae) from Japan with notes on its phylogenetic position within the hufelandi group", *PLoS One*, 2018, 13(2):e0192210. ([PubMed](#))
 - Ohta T, Kawashima T, Shinozaki NO, Dobashi A, Hiraoka S, Hoshino T, Kanno K, Kataoka T, Kawashima S, Matsui M, Nemoto W, Nishijima S, Suganuma N, Suzuki H, Taguchi Y, Takenaka Y, Tanigawa Y, Tsuneyoshi M, Yoshitake K, Sato Y, Yamashita R, Arakawa K, Iwasaki W, "Collaborative environmental DNA sampling from petal surfaces of flowering cherry *Cerasus yedoensis* 'Somei-yoshino' across the Japanese archipelago", *J.*

Plant Res., 2018, 131(4):709-717. ([PubMed](#))

- Kono N, Tomita M, Arakawa K, "eRP arrangement: a strategy for assembled genomic contig rearrangement based on replication profiling in bacteria", BMC Genomics, 2017, 18(1):784. ([PubMed](#))
- Malay A, Arakawa K, Numata K, "Analysis of repetitive amino acid motifs reveals the essential features of spider dragline silk proteins", PLoS One, 2017, 12(8):e0183397. ([PubMed](#))
- Yoshida Y, Koutsovoulos G, Laetsch DR, Stevens L, Kumar S, Horikawa DD, Ishino K, Komine S, Kunieda T, Tomita M, Blaxter M, Arakawa K*, "Comparative genomics of the tardigrades *Hypsibius dujardini* and *Ramazzottius varieornatus*", PLoS Biol, 2017, 15(7):e2002266. ([PubMed](#))
- Tanaka Y, Ogawa T, Maruta T, Yoshida Y, Arakawa K, Ishikawa T., "Glucan synthase-like 2 is indispensable for paramylon synthesis in *Euglena gracilis*", FEBS Lett, 2017, 591(10): 1360-1370. ([PubMed](#))
- Iwai H, Horikawa DD, Arakawa K, Tomita M, Komatsu T, Maruyama M, "Rearing and observation of immature stages of the hoverfly *Microdon katsurai* (Diptera, Syrphidae)", Biodiversity Data Journal, 2016, 4:e10185. ([PubMed](#))
- Hashimoto T, Horikawa DD, Saito Y, Kuwahara H, Kozuka-Hata H, Shin-I T, Minakuchi Y, Ohishi K, Motoyama A, Aizu T, Enomoto A, Kondo K, Tanaka S, Hara Y, Koshikawa S, Sagara H, Miura T, Yokobori S, Miyagawa K, Suzuki Y, Kubo T, Oyama M, Kohara Y, Fujiyama A, Arakawa K, Katayama T, Toyoda A, Kunieda T, "Extremotolerant tardigrade genome and improved radiotolerance of human cultured cells by tardigrade-unique protein", Nat. Commun., 2016, 7:12808. ([PubMed](#))
- Arakawa K*, Yoshida Y, Tomita M, "Genome sequencing of a single tardigrade *Hypsibius dujardini* individual", Sci. Data, 2016, 3:160063. ([PubMed](#))
- Arakawa K*, "No evidence for extensive horizontal gene transfer from the draft genome of a tardigrade", PNAS, 2016, 113(22):E3057. ([PubMed](#))
- Yoshida Y, Tomiyama T, Maruta T, Tomita M, Ishikawa T, Arakawa K*, "De novo assembly and comparative transcriptome analysis of *Euglena gracilis* in response to anaerobic conditions", BMC Genomics, 2016, 17(1):182. ([PubMed](#))
- Kono N, Nakamura H, Ito Y, Tomita M, Arakawa K*, "Evaluation of the impact of RNA preservation methods of spiders for de novo transcriptome assembly", Molecular Ecology Resources, 2016, 16(3): 662-672 ([PubMed](#))
- Horikawa DD, Arakawa K, "Tardigrades - Ultimate animals surviving extreme environments", SFC Journal, 2015, 15(1), 246-260. ([Publisher](#))
- Oshita K, Tomita M, Arakawa K, "G-Links: a gene-centric link acquisition service", F1000 Research, 2015, 3:285. ([PubMed](#))
- Tanaka S, Tanaka J, Miwa Y, Horikawa DD, Katayama T, Arakawa K, Toyoda A, Kubo T, Kunieda T, "Novel Mitochondria-Targeted Heat-Soluble Proteins Identified in the Anhydrobiotic Tardigrade Improve Osmotic Tolerance of Human Cells", PLoS One, 2015, 10:e0118272. ([PubMed](#))
- Miyamoto M, Motooka D, Gotoh K, Imai T, Yoshitake K, Goto N, Iida T, Yasunaga T, Horii T, Arakawa K, Kasahara M, Nakamura S, "Performance comparison of second- and third-generation sequencers using a bacterial genome with two chromosomes", BMC Genomics, 2014, 15:699. ([PubMed](#))

- Kono N, Arakawa K, Sato M, Yoshikawa H, Tomita M, Itaya M, "Undesigned selection for replication termination of bacterial chromosomes", J. Mol. Biol. 2014, 426(16):2918-2927. ([PubMed](#))
- Arakawa K*, Tomita M, "Genome Analysis Workshop: a Personal Genomics class at Keio SFC", Keio SFC Journal, 2014, 14(1):158-177. ([Publisher](#))
- Nakada T, Tsuchida Y, Arakawa K, Ito T and Tomita M, "Hybridization between Japanese and North American *Chlamydomonas reinhardtii* (Volvocales, Chlorophyceae)", Phycological Research, 2014, 62(3):232-236. ([Publisher](#))
- BioHackathon 2011/2012, "BioHackathon series in 2011 and 2012: penetration of ontology and Linked Data in life science domains", Journal of Biomedical Semantics, 2014, 5:5. ([Publisher](#))
- Arakawa K, Tomita M, "Merging Multiple Omics Datasets In Silico: Statistical Analyses and Data Interpretation", Methods Mol. Biol. 2013, 985:459-470. ([PubMed](#))
- Itaya H, Oshita K, Arakawa K, Tomita M, "GEMBASSY: an EMBOSS Associated Software Package for Comprehensive Genome Analyses", Source Code for Biology and Medicine, 2013, 8(1):17. ([PubMed](#))
- Horikawa DD, Cumbers J, Sakakibara I, Rogoff D, Leuko S, Harnoto R, Arakawa K, Katayama T, Kunieda T, Toyoda A, Fujiyama A, Rothschild LJ, "Analysis of DNA Repair and Protection in the Tardigrade *Ramazzottius varieornatus* and *Hypsibius dujardini* after Exposure to UVC Radiation", PLoS One, 2013, 8(6):e6479. ([PubMed](#))
- Hisano Y, Ota S, Arakawa K, Muraki M, Kono N, Oshita K, Sakuma T, Tomita M, Yamamoto T, Okada Y, Kawahara A, "Quantitative assay for TALEN activity at endogenous genomic loci", Biology Open, 2013, 2(4):363-367. ([Publisher](#))
- BioHackathon 2010, "The 3rd DBCLS BioHackathon: improving life science data integration with semantic Web technologies", Journal of Biomedical Semantics, 2013, 4:6. ([Publisher](#))
- Arakawa K, "Comparative metabolomics of anhydrobiosis in tardigrade *Ramazzottius varieornatus*", Journal of Japanese Society for Extremophiles, 2013, 11(2), 75-82. ([Publisher](#))
- Yamaguchi A, Tanaka S, Yamaguchi S, Kuwahara H, Takamura C, Ohmi S, Horikawa DD, Toyoda A, Katayama T, Arakawa K, Fujiyama A, Kubo T, Kunieda T, "Two families of novel abundant heat-soluble proteins in an anhydrobiotic tardigrade", PLoS One, 2012, 7(8):e44209. ([PubMed](#))
- Kono N, Arakawa K*, Tomita M, "Validation of bacterial replication termination models using simulation of genomic mutations", PLoS One, 2012, 7(4): e34526. ([PubMed](#))
- Arakawa K*, Tomita M, "Measures of Compositional Strand Bias Related to Replication Machinery and its Applications", Current Genomics, 2012, 13(1):4-15. ([PubMed](#))
- BioHackathon 2009, "The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications", Journal of Biomedical Semantics, 2011, 2:4. ([PubMed](#))
- Toya Y, Kono N, Arakawa K*, Tomita M, "Metabolic flux analysis and visualization", Journal of Proteome Research, 2011, 10(8):3313-3323. ([PubMed](#))
- Oshita K, Arakawa K*. Tomita M, "KBWS: an EMBOSS associated package for accessing bioinformatics web services", Source Code for Biology and Medicine, 2011, 6(1):8. ([PubMed](#))

- Kono N, Arakawa K*, Tomita M, "Comprehensive prediction of chromosome dimer resolution sites in bacterial genomes", BMC Genomics, 2011, 12(1):19. ([PubMed](#))
- BioHackathon2008, "The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows", Journal of Biomedical Semantics, 2010, 1:8. ([PubMed](#))
- Arakawa K*, Kido N, Oshita K, Tomita M, "G-language Genome Analysis Environment with REST and SOAP Web Service Interfaces", Nucleic Acids Research, 2010, 48:W700-W705. ([PubMed](#))
- Arakawa K*, Suzuki H, Tomita M, "Quantitative analysis of replication-related mutation and selection pressures in bacterial chromosomes and plasmids using generalised GC skew index", BMC Genomics, 2009, 10:640. ([PubMed](#))
- Kono N, Arakawa K*, Ogawa R, Kido N, Oshita K, Ikegami K, Tamaki S, Tomita M, "Pathway Projector: Web-based Zoomable Pathway Browser using KEGG Atlas and Google Maps API", PLoS One, 2009, 4(11):e7710. ([PubMed](#))
- Arakawa K*, Oshita K, Tomita M, "A web server for interactive and zoomable Chaos Game Representation images", Source Code for Biology and Medicine, 2009, 4:6. ([PubMed](#))
- Arakawa K*, Tamaki S, Kono N, Kido N, Ikegami K, Ogawa R, Tomita M, "Genome Projector: zoomable genome map with multiple views", BMC Bioinformatics, 2009, 10:31. ([PubMed](#))
- Arakawa K*, Suzuki H, Tomita M, "Computational Genome Analysis Using The G-language System", Genes, Genomes and Genomics, 2008, 2(1): 1-13. ([PDF](#))
- Ogawa Y, Arakawa K*, Kaizu K, Miyoshi F, Nakayama Y, Tomita M, "Comparative study of circadian oscillatory network models of Drosophila", Artificial Life, 2008, 14(1):29-48. ([PubMed](#))
- Arakawa K, Tomita M, "Selection effects on the positioning of genes and gene structures from the interplay of replication and transcription in bacterial genomes", Evolutionary Bioinformatics, 2007, 3:279-286. ([PubMed](#))
- Arakawa K, Tomita M, "The GC skew index: a measure of genomic compositional asymmetry and the degree of replicational selection", Evolutionary Bioinformatics, 2007, 3:145-154. ([PubMed](#))
- Tamaki S, Arakawa K*, Kono N, Tomita M, "Restauro-G: A Rapid Genome Re-Annotation System for Comparative Genomics", Genomics Proteomics Bioinformatics, 2007, 5(1): 53-58. ([PubMed](#))
- Ishii N, Nakahigashi K, Baba T, Robert M, Soga T, Kanai A, Hirasawa T, Naba M, Hirai K, Hoque A, Ho PY, Kakazu Y, Sugawara K, Igarashi A, Harada A, Masuda T, Sugiyama N, Togashi T, Hasegawa M, Takai Y, Yugi K, Arakawa K, Iwata N, Toya Y, Nakayama Y, Nishioka T, Shimizu K, Mori H, Tomita M, "Multiple High-Throughput Analyses Monitor the Response of E. coli to Perturbations", Science, 2007, 316(5824): 593-597. ([PubMed](#))
- Sugahara J, Yachie N, Arakawa K*, Tomita M, "In Silico Screening of Archaeal tRNA-encoding Genes Having Multiple Introns with Bulge-Helix-Bulge Splicing Motifs", RNA, 2007, 13(5): 671-681. ([PubMed](#))
- Arakawa K, Uno R, Nakayama Y, Tomita M, "Validating the significance of genomic properties of Chi sites from the distribution of all octamers in Escherichia coli", Gene, 2007, 392(1-2):239-246. ([PubMed](#))

- Arakawa K, Saito R, Tomita M, "Noise-reduction filtering for accurate detection of replication termini in bacterial genomes", FEBS Letters, 2007, 581(2):253-258. ([PubMed](#)).
- Arakawa K, Tomita M, "G-language System as a platform for large-scale analysis of high-throughput omics data", Journal of Pesticide Science, 2006, 31(3):282-288([PDF](#))
- Kono N, Arakawa K*, Tomita M, "MEGU: Pathway mapping web-service based on KEGG and SVG", In Silico Biology, 2006, 6(6):621-655. ([PubMed](#)).
- Yachie N, Arakawa K*, Tomita M, "On the Interplay of Gene Positioning and the Role of Rho-Independent Terminators in Escherichia coli", FEBS Letters, 2006, 580(30):6909-6914. ([PubMed](#)).
- Arakawa K, Yamada Y, Shinoda K, Nakayama Y, Tomita M, "GEM System: Automatic prototyping of cell-wide metabolic pathway models from genomes", BMC Bioinformatics, 2006, 7:168 ([PubMed](#))
- Arakawa K, Nakayama Y, Tomita M, "GPAC: Benchmarking the sensitivity of genome informatics analysis to genome annotation completeness", In Silico Biology, 2006, 6:0006 ([PubMed](#))
- Arakawa K, Suzuki H, Fujishima K, Fujimoto K, Ueda S, Matsui M, Tomita M, "Comprehensive software suite for bioinformatics analysis of cDNAs", Genomics Proteomics Bioinformatics, 2005, 3(3):179-188 ([PubMed](#))
- Arakawa K, Kono N, Yamada Y, Mori H, and Tomita M, "KEGG-based pathway visualization tool for complex omics data", In Silico Biology, 2005, 5:0039 ([PubMed](#))
- Arakawa K, Mori K, Ikeda K, Matsuzaki T, Kobayashi Y, Tomita M, "G-language Genome Analysis Environment: a workbench for nucleotide sequence data mining", Bioinformatics, 2003, 19(2):305-306 ([PubMed](#))
- Uno R, Nakayama Y, Arakawa K, Tomita M, "The orientation bias of Chi sequences is a general tendency of G-rich oligomers", Gene, 2000, 259(1-2):207-215 ([PubMed](#))

Reviews and Others

- 田中冴, 荒川和晴, "クマムシ用ベクターの開発と乾眠過程のライブイメージング", バイオサイエンスとインダストリー, 2024, 82(4), 388-389.
- 田中冴, 荒川和晴, "「死なない」クマムシのライブイメージング", バイオサイエンスとインダストリー, 2024, 82(4), 368-369.
- 荒川和晴, " 覧古考新：ナノポアシーケンシング ", 実験医学, 2023, 41(9), 1450-1455.
- 荒川和晴, " クモ糸の構造と力学物性のデータベース化 - 人工クモ糸材料の創出に貢献 - ", バイオサイエンスとインダストリー, 2023, 81(3), 220-221.
- 田中冴, 荒川和晴, " 最強生物クマムシの乾眠メカニズムの解析 ", Keio SFC Journal, 2023, 22(2), 178-190. ([Publisher](#))
- 荒川和晴, " クモ 1,000 種の解析からクモ糸高機能発現メカニズムを解明する ", 実験医学, 2023, 41(4), 580-584. ([Publisher](#))
- 荒川和晴, " 生物材料・生体機能発現と液相分離：クマムシ乾眠とクモ糸 ", 生化学, 2022, 94(4), 537-547. ([Publisher](#))
- 荒川和晴, " クモ糸高機能発現メカニズムの解明：人工クモ糸の強度を倍化する SpiCE の発見 ", 生物物理, 2022, 62(3), 181-183. ([Publisher](#))
- 荒川和晴, "1,000 種のクモの解析から明らかになってきたクモ糸の可能性と多様性ービッグデータからクモ糸タンパクの配列と物性の関係を明らかにー", 生物の科学 遺伝, 2022, 74(6):677-683. ([Publisher](#))

- Blaxter M, Arakawa K, "Tardigrade in space", The Biologist, 2018, 65(1):14-17. ([Publisher](#))
- 荒川和晴, " 超高機能構造タンパク質探索に向けたクモ類網羅的シーケンシング ", 高分子, 2018, 67, 135-136.
- 河野暢明, 荒川和晴, " 解析困難な長鎖リピート配列の解析に挑むクモ系遺伝子を例に ", 実験医学, 2018, 36(1), 49-53. ([Publisher](#))
- 荒川和晴, " 概論—ナノポアシーケンサーがもたらす未来 ", 実験医学, 2018, 36(1), 2-8. ([Publisher](#))
- Arakawa K, Blaxter M, "Life without water", Biochemist, 2017, 39(6), 14-17. ([Publisher](#))
- 谷内江望, 荒川和晴, " 基礎研究の入口かつ出口としての好奇心 ", 実験医学, 2017, 35(13), 2190-2196. ([Publisher](#))
- 荒川和晴, " 最強生物クマムシの御家騒動とオープンサイエンス ", バイオサイエンスとインダストリー, 2017, 75(2), 150. ([Publisher](#))
- 荒川和晴, "G-language System による生物情報データベース活用法 ", 計測と制御, 2014, 53(5), 419-425. ([Publisher](#))
- 荒川和晴, " 変わりゆく研究者コミュニティと学会の群雄割拠 ", 実験医学, 2013, 31(6), 952. ([Publisher](#))
- 堀川大樹, 阿部 渉, 荒川和晴, 会津智幸, 片山俊明, 國枝武和, 鈴木 忠, 豊田 敦, " 研コミュ白書 第4回クマムシ研究者コミュニティ：市民との対話ツールとしてのクマムシ ", 細胞工学, 2012, 31(11). ([Web](#)).
- 荒川和晴, " 生命活動とは何か - 生命情報科学が向うべき道 ", 日本バイオインフォマティクス学会ニュースレター, 2012, 25:2-3. ([PDF](#)).
- 荒川和晴, 入江直樹, 谷上賢瑞, 中村昇太, " 研コミュ白書 第3回 NGS 現場の会：次世代シーケンサーの現場にいる人たちの交流の場 ", 細胞工学, 2012, 31(9). ([Web](#)).
- 荒川和晴, "G-language Project: バイオインフォマティクス研究のためのワークベンチ ", 日本バイオインフォマティクス学会ニュースレター, 2012, 24:4-5 ([PDF](#)).
- 八谷剛史, 入江直樹, 荒川和晴, "Close Up 実験法：次世代シーケンサー活用術 ", 実験医学, 2011, 7月号
- Arakawa K, Yachie N, Tomita M, "Visualizing Complex Omics Information - Scientific Visualization for Genomics and Systems Biology", BIOforum Europe 2008, 6:27-29 ([PDF](#)).
- Arakawa K, Tomita M, "Large-scale Modeling for Systems Biology", BIOforum Europe, 2006, 10:54-55 ([PDF](#)).
- 荒川和晴, " 次世代バイオインフォマティクスツールを目指して -G-language Project-", 日本バイオインフォマティクス学会ニュースレター, 2006, 12:3-4 ([PDF](#)).

Books

- "SFC バイオの軌跡 ", 荒川和晴 (編), KEIO SFC JOURNAL, 2023, 22(2). ([Publisher](#))
- "Nanopore Sequencing - Methods and Protocols", Arakawa K (Ed.), 2023, ISBN:978-1-0716-2995-6. ([Publisher](#))
- " 新種発見！ 見つけて、調べて、名付ける方法 ", 共著, 山と溪谷社, 2022, ISBN-13: 978-4635063203 ([Amazon](#))
- " 実験医学別冊 最強のステップ UP シリーズ ロングリード WET&DRY 解析ガイド シーケンスをもっと自由に！ ", 編集, 羊土社, 2021, ISBN-13: 978-4-7581-2253-5 ([Publisher](#))
- " 次世代シーケンサー DRY 解析教本 改訂第2版 ", 共著, 学研メディカル秀潤社, 2019, ISBN-13: 978-4780909838 ([Amazon](#))
- " どこでも 誰でも より長く ナノポアシーケンサーが研究の常識を変える！ ", 企画: 荒川和晴, 実験医学 2018 年 1 月号 Vol.36 No.1 ([Publisher](#))
- " 人工知能学大辞典 ", 人工知能学会 編, 共立出版, 2017 ([Amazon](#))
- " 水の生き物 (学研の図鑑 LIVE) ", 武田正倫 監修, 学研, 2016 ([Amazon](#))
- " オープンソースで学ぶバイオインフォマティクス ", オープンバイオ研究会編, 東京電機大学出版, 2008 ([Amazon](#))
- "Metabolomics - The Frontier of Systems Biology", 共著, Springer-Verlag, 2005:211-220

([Amazon](#))

- ・ "メタボローム研究の最前線", 共著, シュプリンガー・フェアラク, 2003:191-197 ([Amazon](#))

Books (Translations)

- ・ "R と Bioconductor を用いたバイオインフォマティクス", 共著, シュプリンガー・フェアラク, 2007, ISBN 978-4-431-73464-2 ([Amazon](#))

Educational Tools

- ・ "ミクロモンスター LED 内臓ズーム顕微鏡 & 調査キット", 学研教育出版, 2015 ([Amazon](#))

Invited Talks/Lectures

- ・ Arakawa K, "Design and mass production of high performance biomaterials to realize the next industrial revolution", International Conference on Climate Change and Net Zero Carbon Emissions, 2024, (11/10), Taichung, Taiwan
- ・ Arakawa K, "Design and Mass Production of High Performance Biomaterials to Realize the Next Industrial Revolution", International Symposium on Carbon-negative Futures, 2024, (11/6), Taichung, Taiwan
- ・ 荒川和晴, "最強生物クマムシはどのようにして生と死のはざまを生きるのか", Science-ome, 2024, (1/24), Online
- ・ 荒川和晴, "MIMB: Nanopore Sequencing", ナノポア現場の会 2023, (11/24), Tokyo, Japan
- ・ 荒川和晴, "P2 Solo によるコガネグモ科クモゲノムの網羅的シーケンシング", Nanopore Day Tokyo 2023, (6/6), Tokyo, Japan
- ・ 荒川和晴, "極限環境生物クマムシの乾眠を実現する多様な非ドメイン型タンパク", タンパク質研究シンポジウム ~ タンパク質研究はいま新たなステージに入ろうとしている!~, 2022 (12/12), Tokyo, Japan
- ・ 荒川和晴, "非モデル生物のナノポアシーケンシング: クマムシ・クモ・ミドリムシ", 第 45 回日本分子生物学会年会, 2022 (11/30), Makuhari, Japan
- ・ 荒川和晴, "最強素材クモ糸と最強生物クマムシのゲノミクス", イベリアトゲイモリゲノム解説記念シンポジウム, 2022 (9/25), Okazaki, Japan
- ・ Tomita M and Arakawa K, "Tsuruoka Science Park & #8211; Innovations in the twenty years of scientific adventure", Australia-Japan Forum on the Innovation-hub Ecosystem, 2021 (11/29), Online
- ・ 荒川和晴, "いまこそ本当に面白い生物の研究を - 最強素材クモ糸と最強生物クマムシの観点から", 第 44 回日本分子生物学会年会, 2021(12/1), Yokohama, Japan
- ・ 荒川和晴, "極限環境生物クマムシはどのようにして生と死のはざまを生きるか", 2021 年度 生理学研究所研究会「極限環境適応」, 2021 (11/11), Online
- ・ 荒川和晴, "オモロイ生物のゲノム解析: クマムシとミドリムシを例に", Virtual Nanopore Day Japan, 2021 (10/28), Online
- ・ 荒川和晴, "節足動物が紡ぐ「糸」の進化", 日本昆虫学会第 81 回大会, 2021 (9/5), Online
- ・ Arakawa K, "Learning from extraordinary abilities of nature: tardigrades and spider silk", SaSSOH, 2019 (9/19), Sapporo, Japan
- ・ 荒川和晴, "反モデル生物学: 生物は例外こそが面白い", 第 59 回 生命科学夏の学校, 2019 (8/31), Sapporo, Japan
- ・ Arakawa K, "Sequencing 1,000 spiders to elucidate the design mechanisms of spider silk proteins", International Silk Conference, 2019 (6/13), Trento, Italy

- ・ 荒川和晴, " 比較ゲノム解析による極限環境微生物の紫外線耐性関連遺伝子の網羅的探索 ", 第 92 回日本細菌学会総会, 2019 (4/24), Sapporo, Japan
- ・ 荒川和晴, " 超高機能構造タンパク質探索に向けたクモ類網羅的シーケンシング ", 第 41 回日本分子生物学会年会, 2018 (11/28), Yokohama, Japan
- ・ 荒川和晴, " クモ類網羅的シーケンシングによるクモ系超高機能発現メカニズムの解明 ", 第 91 回日本生化学会大会, 2018 (9/25), Kyoto, Japan
- ・ 荒川和晴, " 生物に学ぶタンパク素材によるものづくり ~ 人工クモ系の挑戦 ", 日本蜘蛛学会 第 50 回大会, 2018 (8/26), Hiroshima, Japan
- ・ 荒川和晴, " ナノポアシーケンスによる de novo ゲノムアセンブリー ~ メガスケールからギガスケールまで ", オックスフォード・ナノポア現場の会, 2018 (8/20), Tokyo, Japan
- ・ Arakawa K, Michalczyk & #321;, Fujimoto S, Murai Y, Tomita M, "Phylum-wide genome sequencing of Tardigrada", 14th International Symposium on Tardigrada, 2018 (8/2), Copenhagen, Denmark
- ・ 荒川和晴, " 網羅的シーケンシングによるクモ系超高機能発現メカニズムの解明 ", 第 9 回日本昆虫科学連合・日本学術会議共催シンポジウム「昆虫の恵み」, 2018 (7/28), Tokyo, Japan
- ・ 荒川和晴, " 非脊椎動物における遺伝子水平伝搬の偽陽性を正しく理解する - クマムシでの事例 ", 2017 年度生命科学系合同年次大会, 2017 (12/6), Kobe, Japan
- ・ 荒川和晴, " 「非モデル生物のマルチオミクス解析 - クモ系とクマムシの解析」, 龍谷大学ワークショップ「NGS データの多彩な活用」, 2017 (11/12), Shiga, Japan
- ・ 荒川和晴, " 「超微量 DNA/RNA からのシーケンスライブラリ作成が実現するクマムシ一匹からのゲノム・トランスクリプトーム解析」, タカラバイオ 次世代シーケンスで開く新たな世界 NGS プレミアムセミナー, 2017 (10/26), Tokyo, Japan
- ・ 荒川和晴, " 「バイオテクノロジーと未来の都市 / 遺伝子デザイン」 ~ 微生物の可視化と生命のデザイン、都市の目には見えない生命体 ~ ", Innovative City Forum 2017, 2017 (10/13), Tokyo, Japan
- ・ 荒川和晴, " クマムシはどのようにして生と死のはざまを生きるか ", 第 24 回自然科学研究機構シンポジウム 極限環境における生命 ~ 生命創成の探究に向けて ~, 2017 (9/18), Tokyo, Japan
- ・ 荒川和晴, " クモ類網羅的シーケンシングによる超高機能構造タンパク探索 ", 第 69 回日本生物工学会大会, 2017 (9/12), Tokyo, Japan
- ・ Arakawa K, "Untangling the spider silk genes using nanopore long reads", 第一回オックスフォードナノポア現場の会, 2017 (8/22), Tokyo, Japan
- ・ 荒川和晴, " 非脊椎動物における遺伝子水平伝搬の偽陽性を正しく理解する - クマムシでの事例 ", 遺伝研 研究会「生物種間における遺伝情報の水平移動」, 2017 (8/2), Mishima, Japan
- ・ 荒川和晴, " 非モデル生物研究者の恋しさとせつなさと (NGS の) 心強さと ", 第五回 NGS 現場の会研究会, 2017 (5/23), Sendai, Japan
- ・ Arakawa K, "Untangling the spider silk genes using nanopore long reads", London Calling 2017, 2017 (5/5), London, UK
- ・ 荒川和晴, " 超高機能構造タンパク質による素材産業革命に向けたクモ類網羅的シーケンシング ", IIBMP 一般公開講演, 2016 (10/1), Tokyo, Japan
- ・ 荒川和晴, " 超高機能構造タンパク質探索に向けたクモ類網羅的トランスクリプトーム解析 ", BioFinanceGuild 2016, 2016 (8/26), Tsuruoka, Japan
- ・ 荒川和晴, " クモ系高機能発現メカニズムの解明に向けた網羅的トランスクリプトームシーケンシング ", 日本蜘蛛学会 48 回大会 公開シンポジウム「クモ系研究の最前線: 進化・生態・機能」, 2016 (8/20), Kashiwa, Japan
- ・ 荒川和晴, " 非モデル生物のマルチオミクス解析 - クモ系とクマムシの解析 ", 東京農業大学生物資源ゲノム解析センター 2016 年度セミナー, 2016 (7/29), Tokyo, Japan
- ・ 荒川和晴, " 網羅的シーケンシングによるクモ系高機能発現メカニズムの解明 ", イルミナゲノムサミット 2016, 2016 (6/1), Tokyo, Japan
- ・ 荒川和晴, "de novo トランスクリプトームアセンブリーによるクモ系高機能発現メカニズムの解明 ", 海洋地球インフォマティクス 2016 - 情報・データの科学技術が社会の新しい扉を拓く -, 2016 (5/11), Tokyo, Japan
- ・ 荒川和晴, "PacBio ロングリードが可能にするクモ及びクマムシのゲノム解析 ", 第 2 回 PacBio 現場の会, 2016 (2/23), Tokyo, Japan
- ・ Arakawa K, "Design and mass production of high performance biomaterials to realize the next Industrial revolution", Illumina ELEVATE, 2016, (1/31), Siem Reap, Cambodia
- ・ 荒川和晴, " 超高機能構造タンパク質探索に向けたクモ類網羅的トランスクリプトーム解析 ", Illumina iSchool プロフェッショナル Webinar, 2015 (11/27), Tokyo, Japan
- ・ 荒川和晴, " 生命情報科学ってなんだ? ", 生命情報科学若手の会第 7 回研究会, 2015 (10/2

-), Tsuruoka, Japan
- ・荒川和晴, "生物は、かくも「デザイン」されている：細胞、クマムシから宇宙まで、生命のデザインを語るトークセッション", WXD (ワイアード・バイ・デザイン) トークセッション, 2015 (5/31), Tokyo, Japan
 - ・荒川和晴, "クマムシから見える生の境界線", WIRED デスフェス, 2014 (11/30), Tokyo, Japan
 - ・荒川和晴, "生命活動のサスペンド & レジュームを可能にするクマムシ乾眠の分子機構 加えて個人ゲノム時代のゲノムリテラシー教育について", 東海大学 医学部 基礎医学系 分子生命科学 情報生物医学研究室セミナー, 2014 (3/7), Isehara, Japan
 - ・荒川和晴, "パーソナルゲノム時代のリテラシーと教育", MEDALS 創薬研究におけるバイオデータベース講習会, 2013 (12/12), Tokyo, Japan
 - ・荒川和晴, "生命活動のサスペンド & レジュームを可能にするクマムシ乾眠の分子機構", JAMSTEC BIOGEOS 領域セミナー, 2013 (11/27), Yokosuka, Japan
 - ・荒川和晴, "De Novo の達人", NGS 現場の会 第三回研究会, 2013, (9/5), Kobe, Japan
 - ・荒川和晴, "ヨコヅナクマムシはどのようにして生と死のはざまを生きるか", 山口大学理学部附属生命パスウェイ解析センター講演会, 2013 (2/26), Yamaguchi, Japan
 - ・荒川和晴, "生命活動はどのように始まり、そしてどのように止まるか - ヨコヅナクマムシ乾眠機構からのアプローチ", 定量オミックスワークショップ, 2013 (1/22), Osaka, Japan
 - ・荒川和晴, "ヨコヅナクマムシ極限環境耐性のマルチオミクス解析", インシリコ・メガバンク研究会, 2012 (7/11), Sendai, Japan
 - ・荒川和晴, "マルチオミクス解析とバイオインフォマティクスによる微生物代謝のシステムバイオロジー - 全細胞シミュレーションに向けて", 東北大学 加齢研セミナー, 2011 (10/27), Sendai, Japan
 - ・荒川和晴, "全細胞シミュレーションに向けたマルチオミクス解析とモデリング環境の開発", 東北大学第 25 回生体生命工学研究会, 2011 (10/26), Sendai, Japan
 - ・荒川和晴, "バイオインフォマティクス環境の整備：AmazonEC2 クラウドの活用", 生命情報科学若手の会 沖縄セミナー, 2011, Okinawa, Japan
 - ・荒川和晴, "バイオインフォマティクスの最新動向 - 全細胞シミュレーションに向けて", CAMM フォーラム, 社団法人 企業研究会, 2010, Tokyo, Japan
 - ・荒川和晴, "バクテリアゲノム解析", オープンバイオ講習会, 東京大学医科学研究所, 2008, Tokyo, Japan
 - ・荒川和晴, "インハウスバイオインフォマティクス環境構築コース：G-language と Perl によるゲノム解析実習", KAST 財団法人神奈川科学技術アカデミー, 2005, Tokyo, Japan
 - ・内藤泰宏, 荒川和晴, "システム生物学研究における Xserve を利用したソフトウェア開発と実行", バイオ研究に活用するアップルソリューションセミナー, 2004, Kobe, Japan

Talks

- ・荒川和晴, Flemming J, 杉浦健太, 吉田祐貴, Auvinen S, 田中冴, 鳥飼直生, 石川創良, 鈴木忠, "雲仙における環境 DNA 調査", 第 9 回クマムシ学研究会, 2024 (12/7, Nagano, Japan
- ・Arakawa K, "Sequence design for high-performance artificial spider silk", 1st Asia&Pacific Bioinformatics Joint Conference, 2024 (10/24), Naha, Japan
- ・中村浩之, 伊藤雄介, 佐藤知香子, 渡部康羽, 荒川和晴, "クモ系の配列と物性の連関", 2023 (8/26) Kumamoto, Japan
- ・Arakawa K and Ishikawa T, "Construction of accurate gene model and draft genome sequencing and assembly of *Euglena gracilis* Z", 2nd Annual International Congress on Euglenoids 2022 (11/7), Online
- ・Arakawa K, Tanaka S, "Tardigrades are shining models of anhydrobiosis research", 15th International Symposium on Tardigrada, 2022 (8/24), Krakow, Poland
- ・荒川和晴, "クマムシ乾眠関連遺伝子についての現時点での知見の整理", 第 6 回クマムシ学研究会, 2022 (1/16), Online
- ・Arakawa K and Ishikawa T, "Draft genome sequencing and assembly of *Euglena gracilis* Z and basecalling of Base J", 1st Annual International Congress on Euglenoids 2021 (11/8), Online
- ・荒川和晴, "1,000 種のクモの解析から明らかになってきたクモ系の可能性 と多様性", 日本蜘蛛学会第 52 回大会, 2020 (11/21), Online
- ・荒川和晴, "見えてきたクマムシ乾眠の分子機構", 第 70 回 人工知能学会 分子生物情報研究会 (SIG-MBI), 2020, (3/13), Kanazawa, Japan

- ・荒川和晴, " 極限環境動物クマムシの乾眠機構の解明 ", ExCELLS シンポジウム, 2019 (11/18), Okazaki, Japan
- ・荒川和晴, " 広がりつつあるクマムシゲノムリソースからの展望 ", 第 4 回クマムシ学研究会, 2019 (9/8), Osaka, Japan
- ・荒川和晴, "1000 Spiders: ImPACT プロジェクト基礎研究の成果 ", 日本蜘蛛学会第 51 回大会, 2019 (8/25), Tsuruoka, Japan
- ・荒川和晴, " クモ類網羅的シーケンシングによるクモ糸超高機能発現メカニズムの解明 ", 第 68 回人工知能学会分子生物情報研究会 (SIG-MBI), 2019 (3/9), Kanazawa, Japan
- ・Arakawa K, "Sequencing 1,000 spiders to elucidate the design mechanisms of spider silk proteins", 21st International Congress of Arachnology, 2019 (2/14), Christchurch, New Zealand
- ・荒川和晴, " クマムシ乾眠機構の適応と進化 ", 第 41 回日本分子生物学会年会, 2018 (11/28), Yokohama, Japan
- ・荒川和晴, " 山形県鶴岡市で発見した新種のクマムシ、ショウナイチョウメイムシ ", 第 22 回オープンバイオ研究会, 2018 (3/9), Kanazawa, Japan
- ・荒川和晴, " 比較ゲノム解析による極限環境微生物の紫外線耐性関連遺伝子の網羅的探索 ", 第 65 回人工知能学会分子生物情報研究会 (SIG-MBI), 2018 (3/9), Kanazawa, Japan
- ・荒川和晴, 河野暢明, 藤原正幸, 中村浩之, 大川麟太郎, 篠原麻夏, Daniel Pedrazzoli, 高井幸, 斧澤佑紀, 吉田祐貴, 阿部望美, 石井菜穂子, 富田勝, " クモ類網羅的シーケンシングによる超高機能発現メカニズムの解明 ", 日本蜘蛛学会 第 49 回大会, 2017 (11/5), Okinawa, Japan
- ・荒川和晴, " クマムシ乾眠機構の適応と進化 ", 第一回慶應ライフサイエンスシンポジウム, 2017 (8/28), Tokyo, Japan
- ・荒川和晴, " クマムシは本当に「天然変性タンパクのガラス化によって乾眠する」のか? ", 第二回クマムシ学研究会, 2017 (8/5), Tokyo, Japan
- ・Arakawa K, Kono K, Fujiwara M, Nakamura N, Ohtoshi R, Tomita M, "Sequencing 1,000 spiders to elucidate the design mechanisms of spider silk proteins", ISMB/ECCB 2017 (7/25), Prague, Czech Republic
- ・Arakawa K, "Multi-Omics Strategy to Unveil the Molecular Mechanisms of Non-Classical Model Organisms", 13th MicRO Alliance Meeting, 2016 (11/8), Kyoto, Japan
- ・Arakawa K, "No evidence for extensive horizontal gene transfer from the draft genome of a tardigrade", IIBMP 2016 (9/30), Tokyo, Japan
- ・荒川和晴, " クマムシ一匹からのマルチオミクス解析 ", 第一回クマムシ学研究会, 2016 (4/10), Hiyoshi, Japan
- ・荒川和晴, "Adaptation strategies of tardigrades to rapidly desiccating environments", 第 89 回日本細菌学会総会, 2016 (3/23), Osaka, Japan
- ・荒川和晴, " クマムシゲノムに大規模な水平伝播は存在しない ", 第 60 回人工知能学会分子生物情報研究会 (SIG-MBI) / 第 20 回オープンバイオ研究会, 2016 (3/17), Kanazawa, Japan
- ・荒川和晴, " 生命活動を停止してまで「乾燥」という環境変化に適応したクマムシ ", BMB2015, 2015 (12/3), Kobe, Japan
- ・荒川和晴, " 生命活動のサスペンド&レジューム機構から見る「生」と「死」の境界 ", 山田研究会「生物と非生物をつなぐ」, 2015, (11/18) Shuzenji, Japan
- ・荒川和晴, 河野暢明, 藤原正幸, 中村浩之, 伊藤雄介, 富田勝, " クモ類の網羅的シーケンシング ", 日本蜘蛛学会第 47 回大会, 2015 (8/23), Kyoto, Japan
- ・荒川和晴, " 非古典的モデル生物遺伝子資源の活用に向けた NGS 解析 ", NGS 現場の会 第 4 回研究会, 2015 (7/2), Tsukuba, Japan
- ・Arakawa K, Fujimoto S, Tomita M, "De novo genome sequencing of various tardigrades with ultra low input", 13th International Symposium on Tardigrada, 2015 (6/23), Modena, Italy
- ・荒川和晴, " ゲノムの配列から機能を予測する ~ 非モデル生物遺伝子資源の活用に向けて ", 第 57 回人工知能学会分子生物情報研究会 (SIG-MBI) / 第 19 回オープンバイオ研究会, 2015 (3/21), Kanazawa, Japan
- ・荒川和晴, " ゲノムの配列から機能を予測する ~ 非モデル生物遺伝子資源の活用に向けて ", 第二回 阪大微研 x 慶應先端生命 合同研究会, 2015 (3/5), Osaka, Japan
- ・荒川和晴, " クマムシの乾燥耐性に関するマルチオミクス ", 第 7 回 Evo-Devo 青年の会, 2014 (10/11), Mishima, Japan
- ・荒川和晴, " パーソナルゲノム時代のリテラシー教育 - 慶應 SFC での事例 ", 生命医薬情報学連合大会 2014, 2014 (10/3), Sendai, Japan
- ・荒川和晴, " 生命活動のサスペンド&レジューム機構 ", 阪大微研 x 慶應先端生命 合同研究会, 2014 (4/18), Tsuruoka, Japan
- ・荒川和晴, " クマムシにおける乾眠の早さの違いはどこからうまれるのか ", 生命情報科学若手の会 第五回研究会, 2014 (2/17), Chiba, Japan

- ・ 荒川和晴, "生命活動はどのように始まり、そしてどのように止まるか - クマムシ乾眠機構からのアプローチ", 定量生物学の会 第六回年会, 2013 (11/24), Osaka, Japan
- ・ 荒川和晴, "パーソナルゲノム時代のリテラシー教育", 生命医薬情報学連合大会, 2013 (10/31), Tokyo, Japan
- ・ Arakawa K, "Molecular mechanisms of cryptobiosis in tardigrade *Ramazzottius varieornatus* - the third state between life and death", 7th AYRCOB, 2013 (9/10), Tokyo, Japan
- ・ Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Multi-Omics Study of Tardigrade *Ramazzottius Varieornatus* Reveals Dynamic Metabolic Response During Anhydrobiosis", Plant & Animal Genome Asia 2013, 2013 (3/18), Singapore, Singapore
- ・ 荒川和晴, "ヨコヅナクマムシはどのようにして生と死のはざまを生きるか", 生命情報科学若手の会 第四回研究会, 2013, (3/1), Okazaki, Japan
- ・ 荒川和晴, "生命活動はどのように始まり、そしてどのように止まるか - ヨコヅナクマムシ乾眠機構からのアプローチ", 定量オミックスワークショップ, 2013 (1/22), Osaka, Japan
- ・ Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Metabolomics of tardigrade *Ramazzottius varieornatus* reveals dynamic metabolic response during anhydrobiosis", 第 35 回日本分子生物学会年会, 2012 (12/13), Fukuoka, Japan
- ・ Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Metabolomics of tardigrade *Ramazzottius varieornatus* reveals dynamic metabolic response during anhydrobiosis", JST-BBSRC Workshop on Systems Redox Regulation, 2012 (10/25), Tsuruoka, Japan
- ・ 荒川和晴, "生命活動とは何か - 生命と非生命の境界線を探る", 4 会合同シンポジウム「これからの生命科学を考える」, 2012 (10/16), Tokyo, Japan
- ・ Arakawa K, "Multi-omics study of the molecular mechanisms of extremotolerance in tardigrade *Ramazzottius varieornatus*", 日本微生物生態学会, 2012 (9/20), Toyohashi, Japan
- ・ Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Metabolomics of tardigrade *Ramazzottius varieornatus* reveals dynamic metabolic response during anhydrobiosis", 12th International Symposium on Tardigrada, 2012 (6/25), Porto, Portugal
- ・ 荒川和晴, "ヨコヅナクマムシ乾眠機構のメタボローム解析", 極限環境生物学会, 2012 (6/23), Tokyo, Japan
- ・ 荒川和晴, "《クリックちゃん》を創るためには何が必要か - G-language Project のアプローチ", 第 4 8 回人工知能学会 分子生物情報研究会 (SIG-MBI) / 第 1 5 回オープンバイオ研究会, 2012 (3/24), Ishikawa, Japan
- ・ Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Metabolomics of tardigrade *Ramazzottius varieornatus* reveals dynamic metabolic response during anhydrobiosis", 第 34 回日本分子生物学会年会, 2011 (12/14), Yokohama, Japan
- ・ 荒川和晴, "ヨコヅナクマムシのマルチオミクス解析", 生命情報科学若手の会 第 3 回研究会, 2011 (10/16), Okazaki, Japan
- ・ 荒川和晴, "ヨコヅナクマムシのマルチオミクス解析", 生命情報科学若手の会 沖縄セミナー, 2011 (9/3), Okinawa, Japan
- ・ Arakawa K, "G-language Project: the last 10 years and beyond", BOSC, 2011 (7/16), Vienna, Austria
- ・ 荒川和晴, "Dashcode 3 による次世代ウェブアプリケーション開発", BH10.10 統合データベース技術情報交換ワークショップ, 2010 (10/19), Shuzenji, Japan
- ・ 荒川和晴, "ウェブサービス統合のためのユーザインタフェース", BH10.10 統合データベース技術情報交換ワークショップ, 2010 (10/19), Shuzenji, Japan
- ・ 荒川和晴, "複製するメディアとしてのバクテリアゲノムの秩序", 生命情報科学若手の会 第二回研究会, 2010 (10/9), Mishima, Japan
- ・ 荒川和晴, "ポストク in silico 実現のために。", ライフサイエンスパー vol.2 オープンバイオ研究会 × 生命情報科学若手の会, 2010 (9/3), Tokyo, Japan
- ・ 荒川和晴, "複製によって形成されたバクテリアゲノム構造の解析", 日本進化学会大会, 2010 (8/3), Tokyo, Japan
- ・ Arakawa K, Kido N, Oshita K, Tomita M, "G-language Bookmarklet: a gateway for Semantic Web, Linked Data, and Web Services", BOSC, 2010 (7/9), Boston, USA
- ・ Arakawa K, Kono N, Tomita M, "バクテリアゲノム構造のバイオインフォマティクス", 第 83 回日本細菌学会総会, 2010, Yokohama, Japan
- ・ Kunieda T, Kuwahara H, Horikawa DD, Toyoda A, Katayama T, Arakawa K, Yamaguchi A, Shin-I T, Ohishi K, Motoyama A, Aizu T, Hasebe Y, Kido N, Kanehisa M, Kubo T, Kohara Y, Fujiyama A, "Genome analysis and functional proteomics of anhydrobiotic extremotolerant tardigrade, *Ramazzottius cf. varieornatus*", MBSJ2009, 2009, Yokohama, Japan
- ・ Kunieda T, Kuwahara H, Horikawa DD, Toyoda A, Katayama T, Arakawa K, Shin-I T, Ohishi K, Motoyama A, Aizu T, Kohara Y, Fujiyama A, "The tardigrade genome of an anhydrobiotic extremotolerant species, *Ramazzottius varieornatus*", ISEPEP3, Tsukuba, Japan

- Kunieda T, Kuwahara H, Horikawa DD, Toyoda A, Katayama T, Arakawa K, Shin-I T, Ohishi K, Motoyama A, Aizu T, Kohara Y, Fujiyama A, "The tardigrade genome of an anhydrobiotic extremotolerant species, *Ramazzottius varieornatus*", 11th International Symposium on Tardigrada, 2009, Tuebingen, Germany
- Katayama T, Arakawa K, Hasebe Y, Kido N, Kunieda T, Toyoda A, Shin-I T, Horikawa DD, Kuwahara H, Ohishi K, Motoyama A, Aizu T, Kanehisa M, Kohara Y, Fujiyama A, "Draft genome sequence assembly and preliminary annotations of *Ramazzottius varieornatus* genome", 11th International Symposium on Tardigrada, 2009, Tuebingen, Germany
- Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Comparative metabolome profiling of active and anhydrobiotic states of Tardigrade *Ramazzottius varieornatus*", 11th International Symposium on Tardigrada, 2009, Tuebingen, Germany
- Arakawa K, Kido N, Oshita K, Tomita M, "Web Service Interface for G-language Genome Analysis Environment", BOSC, 2009, Stockholm, Sweden
- 荒川和晴, 富田勝, "仮説推論・検証型 生命情報科学のためのソフトウェアとインタフェース - G-language・GEM System・Genome Projector・E-Cell 3D -", 第一回生命情報科学若手の会, 2009, Mishima, Japan
- Arakawa K, "E-Cell 3D: 3-Dimensional Visualization of Dynamic Cell Simulation", BOSC, 2008, Toronto, Canada
- 荒川和晴, "G-language Genome Analysis Environment 2 に向けて", 第36回人工知能学会分子生物情報研究会 (SIG-MBI) / 第9回オープンバイオ研究会, 2008, Ishikawa, Japan
- Arakawa K, Saito R, Tomita M, "Noise-reduction filtering for accurate detection of replication termini in bacterial genomes", JSBi2007, 2007, Tokyo, Japan
- 荒川和晴, "E-Cell 3D: 細胞シミュレーションの三次元可視化", 第7回オープンバイオ研究会, 2007, Apple Store Ginza-Tokyo, Japan
- Arakawa K, "E-Cell Simulation Environment and E-Cell 3D visualization front-end", ISMB, Vienna, Austria
- Arakawa K, "Latest developments of the G-language Genome Analysis Environment in 2007", BOSC, Vienna, Austria
- Arakawa K, "E-Cell 3D: 3-Dimensional Visualization Front-End for E-Cell Simulation Environment", BOSC 2007, Vienna, Austria
- 荒川和晴, "微生物ゲノムの解析: 複製開始点と tRNA 予測の事例紹介 (おまけつき)", かずさバイオインフォマティクスセミナー, 2007, Kazusa, Japan
- 荒川和晴, "IAB におけるソフトウェアリソースの紹介: G-language と E-Cell", 生物情報の相互運用性 2007, 2007, Tokyo, Japan
- 荒川和晴, "E-Cell 3D プロジェクトの紹介", 第35回人工知能学会分子生物情報研究会 (SIG-MBI) / 第六回オープンバイオ研究会, 2007, Ishikawa, Japan
- 荒川和晴, "細胞シミュレーションのためのソフトウェア環境", 第一回機能ゲノミクス研究会 / ゲノム情報利用ワークショップ 2007, 2007, Kazusa, Japan
- 荒川和晴, "システム生物学のためのシステム", 第三回複雑ネットワーク研究会, 2006, Fujisawa, Japan
- 荒川和晴, "E-Cell 3D: 細胞シミュレーションの新しい見方", 第三回オントロジー研究会 / 第四回オープンバイオ研究会, 2006, Tokyo, Japan
- Arakawa K, "From Genome to Pathways and Simulation", The 21st Century COE Young Scientist Workshop 2006 in Shonan, 2006, Fujisawa, Japan
- Arakawa K, "G-language Project Updates", BOSC, 2006, Fortaleza, Brazil
- 荒川和晴, "From Genome to Pathways and Simulation", 第二回複雑ネットワーク研究会, 2006, Tokyo, Japan
- 荒川和晴, "GPAC: アノテーション精度に対する解析手法の感受性解析", 第三回オープンバイオ研究会, 2006, Ishikawa, Japan
- 荒川和晴, "G-language Project", 第二回オープンバイオ研究会, 2005, Yokohama, Japan

- Arakawa K, "G-language Project in 2005", BOSC, 2005, Detroit, USA
- 荒川和晴, "G-language Genome Analysis Environment", 第一回オープンバイオ研究会, 2005, Ishikawa, Japan
- 荒川和晴, "G-language Genome Analysis Environment", オープンバイオ BoF, 2004, Yokohama, Japan
- Arakawa K, "GEM System: Automatic generation of dynamic cell-wide metabolic pathway model from the genome", 21COE Young Scientist Symposium, 2004, Tsuruoka, Japan
- Arakawa K, "G-language Genome Analysis Environment", BOSC, 2004, Glasgow, UK
- 荒川和晴, "G-language Genome Analysis Environment", 生物情報資源の構築・提供側にとっても, 利用者側にとっても嬉しい環境を求めて: GRID, Web services, 言語など, 2003, Mishima, Japan
- Arakawa K, "Metabolomics for whole E.coli modeling", E.coli Symposium, 2003, Awaji, Japan
- Arakawa K, "G-language genome analysis environment", E.coli Symposium, 2003, Awaji, Japan

Posters (Selected)

- Arakawa K, "Learning from extraordinary abilities of nature: tardigrades and spider silk", 2nd JAG-FoS, 2019 (9/28), Kyoto, Japan
- Arakawa K, "Phylum-wide genome sequencing of Tardigrada with ultra-low input", ISMB/ECCB 2019, 2019 (7/22), Basel, Switzerland
- 荒川和晴, 河野暢明, 中村浩之, 大川麟太郎, 富田勝, 沼田圭司, "超高機能構造タンパク質データベースの開発", トーゴの日シンポジウム 2017, 2017 (10/4), Tokyo, Japan
- Arakawa K, Fujimoto S, Tomita M, "De novo genome sequencing of various tardigrades with ultra low input", ISMB/ECCB 2015, 2015 (7/12), Dublin, Ireland
- 荒川和晴, 富田勝 "ドゥジャルダンヤマクマムシのドラフトゲノム解析", 第 37 回日本分子生物学会年会, 2014, (11/25), Yokohama, Japan
- 荒川和晴, "クマムシにおける乾眠の早さの違いはどこからうまれるのか", 生命情報科学若手の会 第五回研究会, 2014 (2/17), Chiba, Japan
- 荒川和晴, 富田勝 "クマムシにおける乾眠の早さの違いはどこからうまれるのか", 第 36 回日本分子生物学会年会, 2013, (12/4), Kobe, Japan
- 荒川和晴, "微量サンプルシーケンスで切り拓く微小な非モデル生物の分子生物学", NGS 現場の会 第三回研究会, 2013, (9/4), Kobe, Japan
- Arakawa K, Tomita M, "De novo transcriptome sequencing and assembly of tardigrade species from ultra low input mRNA-Seq", ISMB/ECCB, 2013 (7/22), Berlin, Germany
- 荒川和晴, "ヨコヅナクマムシはどのようにして生と死のはざまを生きるか", 生命情報科学若手の会 第四回研究会, 2013, (3/1), Okazaki, Japan
- Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Metabolomics of tardigrade Ramazzottius varieornatus reveals dynamic metabolic response during anhydrobiosis", 第 35 回日本分子生物学会年会, 2012 (12/13), Fukuoka, Japan
- Arakawa K, Tomita M, "Measures of compositional strand bias related to replication machinery and its applications", The 8th 3R Symposium, 2012 (11/27), Awaji, Japan
- Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Metabolomics of tardigrade Ramazzottius varieornatus reveals dynamic metabolic response during anhydrobiosis", FOSBE2012, 2012 (10/22), Tsuruoka, Japan
- Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Metabolomics of tardigrade Ramazzottius varieornatus reveals dynamic metabolic response during anhydrobiosis", 生命医薬情報学連合大会, 2012 (10/15), Tokyo, Japan

- Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Quantitative metabolomics of extremotolerant tardigrade *Ramazzottius varieornatus* reveals dynamic response during anhydrobiosis", ECCB, 2012 (9/10), Basel, Switzerland
- Arakawa K, Kono N, Tomita M, "Genome Projector and Pathway Projector", The First 10 Years of UniProt Symposium, 2012 (9/8), Basel, Switzerland
- 荒川和晴, " パーソナルゲノム時代に向けたゲノム解析の実践教育 ", NGS 現場の会, 2012 (5/25), Osaka, Japan
- Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Metabolomics of tardigrade *Ramazzottius varieornatus* reveals dynamic metabolic response during anhydrobiosis", 第 34 回日本分子生物学会年会, 2011 (12/14), Yokohama, Japan
- 荒川和晴, " ヨコヅナクマシゲノムの構造・機能アノテーションにおける mRNA-Seq データの活用 ", NGS 現場の会, 2011 (5/29), 熱海, Japan
- Arakawa K, Oshita K, Kono N, Kido N, Tomita M, "G-language System: an ecosystem of bioinformatics suites", 第 33 回日本分子生物学会年会, 2010 (12/10), Kobe, Japan
- Arakawa K, Tomita M, "Quantitative analysis of replication-related mutation and selection pressures in bacterial chromosomes and plasmids using generalised GC skew index", 3R Symposium, 2010 (10/29), Toyama, Japan
- Arakawa K, Kido N, Oshita K, Tomita M, "G-language Bookmarklet: a gateway for Semantic Web, Linked Data, and Web Services", ECCB, 2010 (9/27), Ghent, Belgium
- Arakawa K, Kido N, Oshita K, Tomita M, "G-language Bookmarklet: a gateway for Semantic Web, Linked Data, and Web Services", ISMB, 2010 (7/12), Boston, USA
- Arakawa K, Kido N, Oshita K, Tomita M, "G-language Bookmarklet: オンライン生命情報リソースへのお手軽ゲートウェイ", 第 13 回オープンバイオ研究会, 2010, Ishikawa, Japan
- Arakawa K, Kido N, Oshita K, Tomita M, "REST/SOAP Web Service API for G-language System", GIW, 2009, Yokohama, Japan
- Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Comparative metabolome profiling of active and anhydrobiotic states of Tardigrade *Ramazzottius varieornatus*", 第 32 回日本分子生物学会年会, 2009, Yokohama, Japan
- 荒川和晴, 鈴木治夫, 富田 勝, " バクテリア染色体及びプラスミドにかかる複製選択圧の定量解析 ", 第 11 回日本進化学会大会, Sapporo, Japan
- Arakawa K, Ito T, Kunieda T, Horikawa D, Soga T, Tomita M, "Comparative metabolome profiling of active and anhydrobiotic states of Tardigrade *Ramazzottius varieornatus*", ISEPEP3, 2009, Tsukuba, Japan
- Arakawa K, Tomita M, "G-language Genome Analysis Environment Version 2: Integrated workbench for computational genome sequence analysis", ISMB, 2009, Stockholm, Sweden
- 荒川和晴, 木戸信博, 大下和希, 富田勝, "G-language Project:BioHackathon 2009 のサマリー", 第 11 回オープンバイオ研究会, 2009, Ishikawa, Japan
- 荒川和晴, 富田勝, " ゲノム解析ワークベンチ G-language GAE v.2", BMB2008 (第 31 回日本分子生物学会年会・第 81 回日本生化学会大会 合同大会), 2008, Kobe, Japan
- Arakawa K, Tomita M, "G-language Genome Analysis Environment Version 2: Integrated workbench for computational genome sequence analysis", GIW2008, 2008, Gold Coast, Australia
- Arakawa K, Tomita M, "The GC skew index: a quantitative measure of genomic compositional asymmetry", 3R Symposium 2008, 2008, Tsumagoi, Japan
- Arakawa K, Saito R, Tomita M, "Noise-reduction filtering for accurate detection of replication-related selection in bacterial genomes", ISMB, 2008, Toronto, Canada
- Arakawa K, Hattori R, Kouchi H, Yamada Y, Kishi A, Kobayashi Y, Tomita M, "G-language Genome Analysis Environment Version 2: Integrated workbench for computational genome sequence analysis", APBC2008, 2008, Kyoto, Japan
- Arakawa K, Saito R, Tomita M, "Noise-reduction filtering for accurate detection of replication termini in bacterial genomes", JSBi2007, 2007, Tokyo, Japan
- 荒川和晴, 谷内江望, 富田勝, "E-Cell 3D: 細胞シミュレーションデータの三次元可視化", BMB2007 (第 30 回日本分子生物学会年会・第 80 回日本生化学会大会合同大会), 2007, Yokohama, Japan
- Arakawa K, Yachie N, Tomita M, "E-Cell Simulation Environment 3D: 3-dimensional visualization of cellular simulation results.", ISMB, 2007, Vienna, Austria
- Arakawa K, Ogawa Y, Tomita M, "Database driven approach for automatic construction of dynamic cell-wide metabolic pathway models", ICSB, 2006, Yokohama, Japan
- Arakawa K, Kono N, Tamaki S, Yoshida H, Tomita M, "GEM System version 2 for the analysis of metabolic pathways", ISMB, 2006, Fortaleza, Brazil

- Arakawa K, Tomita M, "Rapid prototyping of cell-wide metabolic pathway models from the genome sequence", SwissProt 20 Years, 2006, Fortaleza, Brazil
- Arakawa K, Ogawa Y, Nakayama Y, Tomita M, "Database driven approach for automatic construction of dynamic models of cell-wide metabolic pathways", IUBMB, 2006, Kyoto, Japan
- 荒川和晴, 小川雪乃, 中山洋一, 富田勝, "各種データベースを利用した大規模代謝シミュレーションモデルの自動生成", 第28回日本分子生物学会年会, 2005, Fukuoka, Japan
- Arakawa K, Uno R, Nakayama Y, Tomita M, "Computational analysis of Chi orientation in Escherichia coli based on genomic nucleotide composition", 3R Symposium, 2005, Awaji, Japan
- Arakawa K, Ogawa Y, Nakayama Y, Tomita M, "Database driven approach for automatic construction of dynamic models of cell-wide metabolic pathways", ISMB, 2005, Detroit, USA
- 荒川和晴, 中山洋一, 富田勝, "ゲノム情報に基づいた大規模動的代謝パスウェイモデルの自動生成", 第27回日本分子生物学会年会, 2004, Kobe, Japan
- Arakawa K, Yamada Y, Shinoda K, Nakayama Y, Tomita M, "GEM System: Automatic generation of dynamic cell-wide metabolic pathway model from the genome", ICSB, 2004, Heidelberg, Germany
- Arakawa K, Yamada Y, Shinoda K, Nakayama Y, Tomita M, "GEM System: Automatic generation of dynamic cell-wide metabolic pathway model from the genome", 21COE Young Scientist Symposium, 2004, Tsuruoka, Japan
- Arakawa K, Yamada Y, Shinoda K, Nakayama Y, Tomita M, "GEM System: Automatic generation of dynamic cell-wide metabolic pathway model from the genome", ISMB, 2004, Glasgow, UK
- 荒川和晴, 山田洋平, 駒井宏美, 篠田幸作, 中山洋一, 富田勝, "大規模パスウェイモデルの自動生成", 第26回日本分子生物学会年会, 2003, Kobe, Japan
- Arakawa K, Yamada Y, Komai H, Shinoda K, Nakayama Y, Tomita M, "Automatic generation of cell-wide pathway model from complete genome", GIW, 2003, Yokohama, Japan
- Arakawa K, Nakayama Y, Tomita M, "Frequency of short palindromes decreases around Chi-sites in Escherichia coli", 3R Symposium, 2003, Awaji, Japan
- Arakawa K, Hattori R, Yamada Y, Kobayashi Y, Kouchi H, Atsuko Kishi, Tomita M, "G-language genome analysis environment version 2", E.coli Symposium, 2003, Awaji, Japan
- Arakawa K, Hattori R, Yamada Y, Kobayashi Y, Kouchi H, Atsuko Kishi, Tomita M, "G-language genome analysis environment version 2", CBI, 2003, Tokyo, Japan
- Arakawa K, Yamada Y, Komai H, Shinoda K, Nakayama Y, Tomita M, "Automatic generation of cell-wide pathway model from complete genome", CBI, 2003, Tokyo, Japan
- Arakawa K, Yamada Y, Komai H, Shinoda K, Nakayama Y, Tomita M, "Automatic generation of cell-wide pathway model from complete genome", ISMB, 2003, Brisbane, Australia
- Arakawa K, Yamada Y, Komai H, Shinoda K, Nakayama Y, Tomita M, "Automatic generation of cell-wide pathway model from complete genome", First IECA Conference on Systems Biology of E.coli, 2003, Tsuruoka, Japan

- Arakawa K, Mori K, Matsuzaki T, Hattori R, Yamada Y, Tomita M, "Development and Implementation of the G-language Genome Analysis Environment Version 2", RECOMB, 2003, Berlin, Germany
- Arakawa K, Mori K, Matsuzaki T, Hattori R, Yamada Y, Tomita M, "Development and Implementation of the G-language Genome Analysis Environment Version 2", Frontier of Microbial Genome Research, 2003, Kazusa, Japan
- Arakawa K, Mori K, Matsuzaki T, Hattori R, Yamada Y, Tomita M, "Development and Implementation of the G-language Genome Analysis Environment Version 2", Genome Informatics 13: 529-530 (2002), Universal Academy Press Inc, Tokyo (ISBN 4-946443-79-7), Tokyo, Japan
- 荒川和晴, 森航哉, 松崎建君, 服部亮, 山田洋平, 富田勝, "G-language Genome Analysis Environment Version 2 の設計と開発", 第 25 回日本分子生物学会年会, 2002, Yokohama, Japan
- Arakawa K, Mori K, Tomita M, "G-language Genome Analysis Environment", US-JAPAN Joint Workshop on Systems Biology of Useful Microorganisms, 2002, Tsuruoka, Japan
- Arakawa K, Mori K, Tomita M, "G-language Genome Analysis Environment", ISMB, 2002, Edmonton, Canada
- Arakawa K, Mori K, Tomita M, "G-language Genome Analysis Environment", RECOMB, 2002, Washington D.C., U.S.A.
- Arakawa K, Mori K, Tomita M, "G-language Genome Analysis Environment", Frontier of Microbial Genome Research, 2002, Kazusa, Japan
- Arakawa K, Mori K, Tomita M, "G-language Genome Analysis Environment", 2nd ASM and TIGR Conference on Microbial Genomes, 2002, Las Vegas, U.S.A.
- Arakawa K, Mori K, Tomita M, "G-language Genome Analysis Environment", Genome Informatics 12: 326-327 (2001), Universal Academy Press Inc, Tokyo (ISBN 4-946443-72-X), Tokyo, Japan
- Arakawa K, Mori K, Tomita M, "G-language Genome Analysis Environment", 第 24 回日本分子生物学会年会, 2001, Yokohama, Japan
- Arakawa K, Mori K, Uno R, Nakayama Y, Tomita M, "G-language Genome Analysis Environment", 3R Symposium, 2001, Kobe, Japan
- Arakawa K, Mori K, Tomita M, "G-language Genome Analysis Environment", Fall Symposium at Institute for Advanced Biosciences, 2001, Tsuruoka, Japan
- Arakawa K, Uno R, Nakayama Y, Tomita M, "Computational Analysis of the Strand Bias of the Chi Sequences and Other Oligonucleotides in Bacterial Genomes", Genome Informatics 11: 311-312 (2000), Universal Academy Press Inc, Tokyo (ISBN 4-946443-65-11), Tokyo, Japan
- 荒川和晴, 鶴野レイナ, 中山洋一, 富田勝, "バクテリアゲノムにおける χ 配列および G-rich オリゴ配列の方向性に関する解析", 第 23 回日本分子生物学会年会, 2000, Kobe, Japan

Funding

- ・ Academic Year 2024-2026 経済産業省中小企業政策推進事業費補助金（成長型中小企業等研究開発支援事業）Go-Tech 「シングルセルレパトア解析とAI駆動科学に基づいた抗体医薬品開発プラットフォームの確立」 20241018 財東北第11号.
- ・ Academic Year 2022-2032 文部科学省 データ創出・活用型マテリアル研究開発プロジェクト事業 MEXT Program: Data Creation and Utilization-Type Material Research and Development Project JPMXP1122714694
- ・ Academic Year 2021-2025 KAKENHI Grant-in-Aid for Transformative Research (A), No. 21H05279, from the Japan Society for the Promotion of Science (JSPS).
- ・ Academic Year 2019-2024 生命創生探求センター ExCELLS 課題研究 (一般) Cooperative Study Program of Exploratory Research Center on Life and Living Systems(ExCELLS) No. 19-501
- ・ Academic Year 2018-2019 生命創生探求センター ExCELLS 課題研究 (シーズ発掘)
- ・ Academic Year 2017-2020 KAKENHI Grant-in-Aid for Scientific Research (B), No. 17H03620, from the Japan Society for the Promotion of Science (JSPS).
- ・ Academic Year 2016-2019 New Energy and Industrial Technology Development Organization (NEDO)
- ・ Academic Year 2016-2017 Astrobiology Center of National Institutes of Natural Sciences (NINS).
- ・ Academic Year 2014-2019 ImPACT from the Cabinet Office, Government of Japan
- ・ Academic Year 2014-2015 Grant for Basic Science Research Projects from The Sumitomo Foundation.
- ・ Academic Year 2010 新領域融合研究センター 融合研究シーズ探索提案 (共同提案者)
- ・ Academic Year 2010-2013 KAKENHI Grant-in-Aid for Young Scientists (A), No.22681029, 2010, from the Japan Society for the Promotion of Science (JSPS).
- ・ Academic Year 2008-2009 KAKENHI Grant-in-Aid for Young Scientists (B), No.20710158, 2008, from the Japan Society for the Promotion of Science (JSPS).
- ・ Academic Year 2007 KAKENHI Grant-in-Aid for Young Scientists (Start-up), No.19810021, 2007, from the Japan Society for the Promotion of Science (JSPS).
- ・ Academic Year 2004-2006 KAKENHI Grant-in-Aid for JSPS Fellows, from the Japan Society for the Promotion of Science (JSPS).
- ・ Academic Year 2004 The Ryoichi Sasakawa Young Leaders Fellowship Fund.
- ・ Academic Year 2003 Taikichiro Mori memorial research grants.

Patent

- ・ "ポリペプチド、核酸、成形体、組成物及びその製造方法、並びに物性向上剤", 中村浩之・荒川和晴・沼田圭司・河野暢明, 特許第 7177453 号
- ・ "ユーグレナのパラミロン含有量を増加させる方法", 田中 優史・小川 貴央・丸田 隆典・石川 孝博・荒川 和晴・鈴木 健吾, 特許第 6242525 号

Media Appearance

- ・ NHK Yamagata News 2017.07.28 6:55 ~ 7:00, 7:45-8:00
- ・ NHK 「あさイチ」 2017.03.02 8:15-9:54
- ・ Radio Nikkei RN2 2013.08.26-30
- ・ Futurescape, FM Yokohama 2013.08.10

Media Recognitions

- ・ "日本蜘蛛学会の人に聞いてみた 本物のクモのAmazingな力", DVD & 動画配信

- でーた (2019年7月号), 06/20 2019 ([URL](#))
- "生命というレンズを通じて見る、環境とモビリティの「これから」: クラリティ PHEV × 生命科学", WIRED, 11/21 2018 ([URL](#))
 - "New Species of Tardigrade Discovered in Japanese Parking Lot", GIZMODO, 2/28 2018 ([URL](#))
 - "A new species of tardigrade lays eggs covered with doodads and streamers", Science News, 2/28 2018([URL](#))
 - "New tardigrade species Macrobiotus shonaicus sp. nov. identified in Japan", Science Daily, 2/28 2018 ([URL](#))
 - "A Totally New Species of Tardigrade Was Just Discovered in a Japanese Carpark", Science Alert, 2/28 2018 ([URL](#))
 - "An Even-Weirder-Than-Usual Tardigrade Just Turned Up in a Parking Lot", Live Science, 2/28 2018 ([URL](#))
 - "A New Tardigrade Species is Found Hiding in a Parking Lot", Outer Places, 2/28 2018 ([URL](#))
 - "Newly Discovered Tardigrade Species Is Not Cute", Inverse Science, 2/28 2018 ([URL](#))
 - "Mysterious Moss Piglet: Researchers discover new tardigrade species", PLOS Research News, 2/28 2018 ([URL](#))
 - "New tardigrade species Macrobiotus shonaicus sp. nov. identified in Japan", Eurek Alert, 2/28 2018 ([URL](#))
 - "New tardigrade species Macrobiotus shonaicus sp. nov. identified in Japan", PHYS ORG, 2/28 2018 ([URL](#))
 - "New Tardigrade Species Found in Parking Lot", Popular Mechanics, 3/1 2018 ([URL](#))
 - "New tardigrade found in Japanese car park", COSMOS, 3/1 2018 ([URL](#))
 - "New species of 'indestructible' tardigrade discovered in a parking lot in Japan", Daily Mail, 3/1 2018 ([URL](#))
 - "New species of tardigrade discovered in Japan", Brinkwire, 3/1 2018 ([URL](#))
 - "New Tardigrade Discovered: Mystery Eight-Legged Micro-Animal Found Lurking In Parking Lot", Newsweek, 3/1 2018 ([URL](#))
 - "New Tardigrade Species Found In Moss From Parking Lot In Japan", International Business Times US, 3/1 2018 ([URL](#))
 - "A new species of tardigrade was found in a Japanese car park and it's even more peculiar than others", International Business Times UK, 3/1 2018 ([URL](#))
 - "New species of tardigrade found in a Japanese car park", Alphr, 3/1 2018 ([URL](#))
 - "New Species of Tardigrade Found In Japan: Earth 's Smallest Animal Discovered At A Parking Lot In Tsuruoka", Latestly, 3/1 2018 ([URL](#))
 - "Macrobiotus shonaicus sp. nov, une nouvelle espèce de tardigrade", Actualité Houssenia Writing, 3/1 2018 ([URL](#))
 - "Spesies Baru Hewan Abadi Tardigrada Ditemukan di Jepang", TEMPO, 3/1 2018 ([URL](#))
 - "New species of tardigrade, world's most indestructible creature, discovered in parking lot in Japan", USA Today, 3/1 2018 ([URL](#))
 - "New Species of 'Indestructible' Animal Found in Surprising Place", National Geographic, 3/1 2018 ([URL](#))
 - "Scientists discover strange new water bear species", UPI, 3/1 2018 ([URL](#))
 - "New Tardigrade Species Found in Parking Lot in Japan", Smithsonian, 3/1 2018 ([URL](#))
 - "Nieuw Beerdiertje ontdekt opeen parkeerplaats In Japan", Scientias, 3/1 2018 ([URL](#))
 - "New Tardigrade Species That Lays Unique Eggs Dicovered In A Parking Lot In Japan", Tech Times, 3/1 2018 ([URL](#))
 - "New species of tardigrade, world's most indestructible creature, discovered in parking lot in Japan", Tennessean, 3/1 2018 ([URL](#))
 - "New 'indestructible' species of tardigrade found lurking in Japanese parking lot", Aol, 3/2 2018 ([URL](#))
 - "New Tardigrade Species Discovered In Parking Lot", Valuewalk, 3/1 2018 ([URL](#))
 - "New Tardigrade Species Found In Japan", 14U News, 3/1 2018 ([URL](#))
 - "New Species Of Tardigrade, World ' s Most Indestructible creature, discovered In Parking Lot In Japan", King5 News, 3/1 2018 ([URL](#))
 - "New Species Of Tardigrade, World ' s Most Indestructible creature, discovered In Parking Lot In Japan", abc10, 3/1 2018 ([URL](#))
 - "New Species Of Tardigrade, World ' s Most Indestructible creature, discovered In Parking Lot In Japan", 12newsnow, 3/1 2018 ([URL](#))
 - "Scientists discover strange new water bear species", Breitbart, 3/1 2018 ([URL](#))

- "New Tardigrade Species Found In Japan", The Africom, 3/1 2018 ([URL](#))
- "New species of near-indestructible tardigrades found in parking lot", Mother Nature Network, 3/1 2018 ([URL](#))
- "New Tardigrade Species That Unique Eggs Discovered in a Parking Lot Japan", Infosurhoy, 3/1 2018 ([URL](#))
- "Scientists Have Found A New Kind Of Amazing Supersweet", The Bobr Times, 3/1 2018 ([URL](#))
- "A New Species of Tardigrade Has Been Found in a Japanese Parking Lot", Atlas Obscura, 3/1 2018 ([URL](#))
- "New species of tardigrade, world", Todays News, 3/1 2018 ([URL](#))
- "New Even Stranger Species Of Tardigrade Found In Japanese Parking Lot", IFL Science!, 3/1 2018 ([URL](#))
- "New Species Of Tardigrade Discovered In Japanese Parking Lot", GIZMODO AU, 3/2 2018 ([URL](#))
- "New tardigrade species with unusual eggs found in Japanese parking lot", ZME Science, 3/2 2018 ([URL](#))
- 山形で「最強生物」クマムシの新種 慶応大先端研, 日本経済新, 3/2 2018 ([URL](#))
- "A New Type of Tardigrade Just Turned Up in a Parking Lot", Scientific American, 3/2 2018 ([URL](#))
- "New species of tardigrade, world's most indestructible creature, discovered in Japanese car park", The Herald Scotland, 3/2 2018 ([URL](#))
- "New tardigrade found in Japanese auto park", Newburgh Gazette, 3/2 2018 ([URL](#))
- "Tiny 'moss piglet' micro-animal that could survive in space found living in car park", METRO, 3/2 2018([URL](#))
- "Tardigrade : Une nouvelle espèce découverte dans un parking japonais", Science Post, 3/2 2018 ([URL](#))
- "New Even Stranger Species Of Tardigrade Found In Japanese Parking Lot", True Viral News, 3/2 2018([URL](#))
- "Descoberta nova espécie de urso-d'água ainda mais estranha do que o habitual", ZAP, 3/2 2018 ([URL](#))
- "New Tardigrade Species Found in Parking Lot in Japan 10ThousandCouple", 10000 Couple, 3/2 2018 ([URL](#))
- 「見つけた！新種クマムシ 鶴岡・国内 27 番目、名に「庄内」, 山形新聞, 3/2 2018 26 面 ([URL](#))
- 「新種のクマムシを山形県で発見、慶応大」, ナショナルジオグラフィック, 3/2 2018 ([URL](#))
- 「最強生物 "クマムシ" 新種、山形で発見」, PC Watch, 3/2 2018 ([URL](#))
- 「最強生物クマムシの新種 山形県のアパート駐車場で発見！慶應大」, ハザードラボ, 3/2 2018 ([URL](#))
- "Image of the Day: Tardigrade Eggs", The Scientist, 3/2 2018 ([URL](#))
- "Japanilaiselta parkkipaikalta löytyi maailman sitkein eläin; selviää avaruudessa ja voi muuttua ihmiseksi", Helsingin Sanomat, 3/2 2018 ([URL](#))
- "A New Species Of Tardigrade Discovered in a Japanese Car Park", The Talking Democrat, 3/2 2018 ([URL](#))
- "New species of tardigrade found in a Japanese car park", PC&Tech Authority, 3/2 2018 ([URL](#))
- "New species of microscopic tardigrade discovered in a Japanese parking lot", BGR, 3/2 2018 ([URL](#))
- "A New Tardigrade Species is Found Hiding in a Parking Lot", Helsingin Sanomat, 3/3 2018 ([URL](#))
- 「最強生物クマムシの新種発見」, 庄内日報, 3/3 2018 7 面
- 「最強生物クマムシの新種、山形の駐車場で発見」, Discovery Channel, 3/4 2018 ([URL](#))
- 「慶大、新種のクマムシを発見 「ショウナイチョウメイムシ」と命名」, 財経新聞, 3/5 2018 ([URL](#))
- "An even-weirder-than-usual tardigrade just turned up in a parking lot", Fox News, 3/5 2018 ([URL](#))
- "New Species of Tardigrade Found in Japan", Sci-News, 3/5 2018 ([URL](#))
- "Stata scoperta una nuova specie di tardigrado", GALILEO, 3/5 2018 ([URL](#))
- "Strange new "water bear" species discovered in a parking lot in Japan", Big Think, 3/6 2018 ([URL](#))
- "Investigador japonés descubre una nueva especie de tardigrado en un estacionamiento", El Ciudadano, 3/6 2018 ([URL](#))
- 「鶴岡で新種のクマムシ...名前の一部に「ショウナイ」, 読売新聞, 3/9 2018 29 面 ([URL](#))
- "New Tardigrade Species Found In Japanese Carpark", Asian Scientist, 3/9 2018 ([URL](#))

- ・「最強生物クマムシの新種を山形県鶴岡市内で発見 慶應義塾大学」, 大学ジャーナルオンライン, 3/9 2018 ([URL](#))
- ・「<クマムシ>鶴岡市で新種発見、アパート駐車場で採取したコケから「庄内」の地名加え命名」, 河北新聞, 3/13 2018 23 面 ([URL](#))
- ・「山形」「最強生物」クマムシ新種、鶴岡で見つかる」, 朝日新聞, 3/22 2018 25 面 ([URL](#))
- ・"Tiny tardigrades might hold the key to the origin of life", The Japan Times, 3/23 2018 ([URL](#))
- ・"5 new species discovered in 2018 2.TARDIGRADES", INDIA TODAY, 4/24 2018 ([URL](#))
- ・"Scientists just found the 168th species of Japanese tardigrade in a mossy parking lot", QUARTZ, 3/2 2018 ([URL](#))
- ・「遺伝子が明かす、最強生物クマムシの強さと進化の道筋」, JST Science Portal, ([URL](#))
- ・「sci tech file クマムシに問う、生命とは何か？クモ糸が紡ぐ、素材革命の夢」, AXIS, vol. 189, 74-79. ([URL](#))
- ・「王蟲そっくり！超低温や宇宙でも生きる 地上最強クマムシをゲノム解析」, excite ニュース 2017 (8/11) ([URL](#))
- ・「ドゥジャルダンヤマクマムシとヨコヅナクマムシのゲノムを比較解析 - 慶大」, マイナビニュース 2017 (8/7) ([URL](#))
- ・「地上最強生物」クマムシ 2 種の比較ゲノム解析 慶應義塾大学」, 大学ジャーナル ONLINE 2017 (8/13) ([URL](#))
- ・「慶大先端研（鶴岡）クマムシの乾眠遺伝子解明 "最強" の謎に迫る 関連研究の基盤に」, 山形新聞 8 月 5 日 26 面
- ・"Peu & peu, le tardigrade nous r  v  le ses secrets de r  sistance extr  me", Science Post, 7/31, 2017 ([URL](#))
- ・"The Hardy ' Water Bear ' Did Not Get All Its Superpowers From Other Species", The WIRE, 7/31, 2017 ([URL](#))
- ・「慶大先端研の吉田さんら 特定の遺伝子の存在発見 クマムシゲノム解説 医療やバイオへの応用期待」, 庄内日報 7 月 30 日 1 面
- ・「“最強”クマムシ遺伝情報解説」, NHK, 7/28 2017 ([URL](#))
- ・"Secrets of the world's toughest creatures revealed " , BBC, 7/28 2017 ([URL](#))
- ・"The microscopic critter that can survive almost anything " , CNN, 7/28 2017 ([URL](#))
- ・"Secrets of Earth's 'indestructible' creatures revealed: Study of tardigrade DNA pinpoints proteins that let them survive for up to 30 YEARS without food or water " , Daily Mail, 7/28 2017 ([URL](#))
- ・"Tardigrade's DNA reveals water bears ' secrets " , UPI, 7/28 2017 ([URL](#))
- ・"Tardigrade: Les scientifiques auraient perc   une partie des secrets de l'animal qui pourrait survivre l ' apocalypse " , Le Huffington Post, 7/28 2017 ([URL](#))
- ・"Les tardigrades, ces animaux qui r  sistent & tout " , Le Monde, 7/28 2017 ([URL](#))
- ・"This microscopic critter can survive almost anything " , PIX11, 7/28 2017 ([URL](#))
- ・"Secrets of world ' s toughest creatures revealed " , The Nation, 7/28 2017 ([URL](#))
- ・"Tardigrade genomes help explain how they survive without water " , New Scientist, 7/28 2017 ([URL](#))
- ・"Genomic Analysis Leaves Tardigrade Phylogeny Unclear " , The Scientist, 7/28 2017 ([URL](#))
- ・"Tardigrades aren ' t champion gene swappers after all " , Science News, 7/28 2017 ([URL](#))
- ・"How tardigrades come back from the dead " , WIRED, 7/28 2017 ([URL](#))
- ・"Tardigrades Are Still a Complete Evolutionary Mystery " , GIZMODO, 7/28 2017 ([URL](#))
- ・"Why Are Tardigrades the World ' s Hardest Creature? DNA Offers Clues " , Smithsonian, 7/28 2017 ([URL](#))
- ・"Tardigrades: A Microscopic Creature That Seems Invincible " , Rush Hour Daily, 7/28 2017 ([URL](#))
- ・"Tardigrade genetic secrets unveiled " , COSMOS, 7/28 2017 ([URL](#))
- ・"When all other life ends, the one likeliest to endure " , The Indian EXPRESS, 7/28 2017 ([URL](#))
- ・"The Secrets of Unkillable Tardigrades Found in Their DNA " , Popular Mechanics, 7/28 2017 ([URL](#))
- ・"Le g  nome des Tardigrades r  v  le quelques myst  res " , Actualit  , Houssenia Writing, 7/28 2017 ([URL](#))
- ・"Los Secretos Del Genoma Del Tard  grado, Una Especie Indestructible " , euronews, 7/28 2017 ([URL](#))
- ・"Tardigrade Study Reveals More Secrets About these Fascinating Life Forms " , labroots, 7/28 2017 ([URL](#))
- ・"Some Biologists Aren't Impressed By Apocalypse-Proof Tardigrades " , Inverse Science, 7/28 2017 ([URL](#))

- "Tardigrade genome reveals secrets of their toughness and evolution ", Earth Archives, 7/28 2017 ([URL](#))
- "DNA shows tiny tardigrades are just as cool as we thought ", Sciblogs, 7/28 2017 ([URL](#))
- "Tardigrade 's DNA reveals water bears ' secrets ", Breitbart, 7/28 2017 ([URL](#))
- "DNA Analysis Reveals Why ' Water Bears ' Are the World ' s Toughest Animal ", Seeker, 7/28 2017 ([URL](#))
- "New Tardigrade Study Reveals Where These Mystery Microbeasts Came From ", Science alert, 7/28 2017 ([URL](#))
- "The Tardigrade ' s Extraordinary Weirdness Continues ", Mental Floss, 7/28 2017 ([URL](#))
- "Secrets of the amazing tardigrades revealed by their DNA ", Phys.org, 7/28 2017 ([URL](#))
- "Research Round-Up: Tardigrades ' genes help them survive extreme conditions ", PLOS Research News, 7/28 2017 ([URL](#))
- "Secrets of the amazing tardigrades revealed by their DNA ", Science Daily, 7/28 2017 ([URL](#))
- "Tardigrade genome sequences reveal mystery of amazing resilience ", Slash Gear, 7/28 2017 ([URL](#))
- "Secrets and techniques of the world ' s hardest creatures revealed ", The Real News, 7/28 2017 ([URL](#))
- "Les secrets de l'invincible tardigrade décryptés par des chercheurs ", RTS, 7/28 2017 ([URL](#))
- "DNA Analysis Reveals Why 'Water Bears' Are the World's Toughest Animals ", LIVE SCIENCE, 7/28 2017 ([URL](#))
- "Tardigrades aren ' t champion gene swappers after all ", Irrann Daily, 7/28 2017 ([URL](#))
- "Tardigrades Are Still A Complete Evolutionary Mystery ", Gizmodo Australia, 7/28 2017 ([URL](#))
- 「「最強生物」クマムシの乾燥に強い遺伝子発見 慶大など仕組み解明」日本経済新聞 2017 年 7 月 28 日朝刊 28 面 ([URL](#))
- "Don't Get Too Caught Up With Secondary Findings" - [Kazuharu Arakawa](#), Front Line Genomics 2017 June 17th ([URL](#))
- 「タウンキャンパスの未来 《座談会》地域に生きる、地域を生かす」三田評論 No.1206 (2016 年 12 月号) ([URL](#))
- 「緩歩動物クマムシの単一個体のゲノムシーケンシング」Nature Japan 著者インタビュー ([URL](#))
- 「Wm の憂鬱、定点観測 = スパイバー (2)、とうとうクモなど新資源獲得に着手した」日経バイオテク ONLINE Vol.2481 ([URL](#))
- 「クマムシの乾眠や高機能繊維クモ系の解析から、生物の本質へ迫る」Life Technologies NEXT no.35 May 2016 ([URL](#))
- 「クマムシから学ぶ生命」読売新聞 山形版 2015 年 5 月 27 日朝刊 30 面 ([URL](#))
- 「クマムシは生きながら死ぬ」WIRED vol.14 2014.11.25 ([URL](#))
- 「ゲノム新時代 変わる医療」AERA 1 月 20 日号 2014 ([URL](#))
- 「【リアル逆襲】(03) お母さんは水槽——倫理と救命のはざままで」日本経済新聞 朝刊 1 月 4 日 2014 ([URL](#))
- "Gene Browser with a Google Feel" Bio-IT World 2008 (March 1st) ([URL](#))
- 「国際オープンバイオ第 8 回年会ウィーンで日本の先進性を発表」日経バイオテク BTJ ジャーナル 2007 年 8 月号 20(2) 5-6 ([PDF](#))
- "Keio University Researchers Wow ISMB Crowd With New 3D Front End for E-Cell Platform" BioInform 2007 11(30) (July 27th) ([URL](#))
- 「ゲノム解析で慶大生ら受賞」日経産業新聞 8 月 22 日 8 面 2002
- 「ゲノム解析で新ソフト」庄内日報 1 月 10 日 1 面 2002
- 「ゲノム解析簡単に」日経産業新聞 12 月 12 日 2001

Awards

- 2025.09 日本生物物理学会 Biophysics and Physicobiology Editors' Choice Award 2024
- 2023.03 SFC Faculty Award to recognize particularly outstanding achievements
- 2022.06 日本発生生物学会 DGD Awards Editor-in-Chief Prize (Most cited)
- 2020.06 日本発生生物学会 DGD Awards Wiley Prize (Most downloaded)

- 2019.02 山形県科学技術奨励賞
- 2016.10 日本バイオインフォマティクス学会 Oxford Journals JSBi Prize.
- 2016.03 Open Science Award 2015 by DBCLS: 2nd place in software division (for Crick-chan).
- 2010.12 Mashup Award 6th: Team Lab Shanghai Award (for G-language Bookmarklet).
- 2008.10 Mashup Award 4th: Google Award (for GenomeProjector).
- 2003.09 Chem-Bio Informatics Society Best Poster Award.
- 2003.03 Keio University President Award (慶應義塾塾長賞).
- 2002.08 ISMB Best Poster Award by SGI.
- 2002.04 SFC Student Award "G-language Genome Analysis Environment".
- 2002.03 SFC Student Award "Bioinformatics Project".