

Jon Bråte

Senior Researcher at the Norwegian Institute of Public Health
Associate Professor at the University of Oslo

Date of birth: 12.03.1983

Nationality: Norwegian

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Current and previous positions

Senior Researcher, Norwegian Institute of Public Health, Norway (2024 – present)

Researcher, Norwegian Institute of Public Health, Norway (2020 – 2024)

Associate Professor, University of Oslo, Norway (2022 – present)

Senior Lecturer, Department of Biosciences, University of Oslo, Norway (2020 – 2021)

Researcher, Department of Biosciences, University of Oslo, Norway (2015 - 2019)

Post Doc, Department of Biosciences, University of Oslo, Norway (2012 – 2015)

Education

PhD, Department of Biology, University of Oslo, Norway (2008 – 2012)

Master of Science, Department of Molecular Biosciences, University of Oslo, Norway (2006 – 2008)

Bachelor of Science, Department Molecular Biosciences, University of Oslo, Norway (2003 – 2006)

Additional education

PRINCE2 7 Foundation Project Management course (2024).

Project Management for Post Docs by Institute for Co-creative Leadership, Ltd. (2013)

Development Program in Leadership by Institute for Co-creative Leadership, Ltd. (2012)

Courses in communication, teamwork and leadership by Scandinavian Training Design (2008 – 2009)

Visiting researcher & Collaborations

Visiting researcher at the lab of Iñaki Ruiz-Trillo, Institute de Biologia Evolutiva, Barcelona, Spain (2014)

Visiting researcher at the lab of Maja Adamska, Sars Centre, Bergen, Norway (2012)

Exchanging PhD at the lab of Mikhail Matz, University of Texas at Austin, USA (2010)

Grants and projects

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| 2025 | Frances and Augustus Newman Foundation: Analysis of viral agents in childhood leukemia (£14,000). My role in this project is to help design lab and bioinformatics protocols, as well as identification of viral agents in sequence data. |
| 2025 | European Commission: European Reference Laboratory (EURL) for food and waterborne viruses, 2026-2032. (€3.25 million). My role in this project is to implement tools for virus surveillance based on whole genome sequence data. |
| 2023 | Research Council of Norway (RCN): SICKSOIL: Linking Microbes, Organic Matter and Sick Soil Syndrome (€266.000). My role in this project is to investigate the diversity of viruses in various soil environments. |
| 2022 | ErC EU4Health: Development of NGS and bioinformatics tools for increased preparedness against infectious diseases (€1 million). |
| 2021 | ErC HERA Incubator: Method development and improved preparedness for future Covid-19 variants (€1.8 million). |

- 2019 RCN: Financial support for ERC Consolidator Grant application (€51,000).
- 2019 Invited to interview for ErC Starting Grant (June 2019).
- 2018 UNIFOR: Small grant for purchasing scientific equipment (€2,900).
- 2017 RCN: Mobility grant for PhD-students. Funding for my PhD student to stay at the lab of Iñaki Ruiz-Trillo at the Institut de Biologia Evolutiva, Barcelona, Spain (€5,800).
- 2017 Norwegian Academy of Science and Letters: Centre for Advanced Study (2019-2020). I am part of an international consortium of evolutionary biologists who recently was granted a two-year project on the concept of Evolvability.
- 2014 RCN: Young Research Talent grant (2015–2018). Three-year personal grant, including salary for a PhD-student (in total €786,000), for studying the role of non-coding RNAs in the evolution of animals (project nr. 240284).
- 2014 RCN: Mobility grant for post docs. Funding for a research stay in the lab of Iñaki Ruiz-Trillo at the Institut de Biologia Evolutiva, Barcelona, Spain (€9,500)
- 2011 RCN: Personal Post Doc grant (2012–2015). Three-year personal grant (in total €408,000) for studying the role of non-coding RNAs in the evolution of multicellularity (project nr. 213707).
- 2009 Molecular Life Science, UiO: Mobility grant for PhD-students. Visiting the lab of Mikhail Matz at the University of Texas at Austin (€2,800).

Commissions of trust

CAS Fellow: I was a Fellow at the Centre for Advanced Study (CAS) at the Norwegian Academy of Science and Letters (2019-2020). This is a part of the CAS project on Evolvability listed under Grants.

Marie Curie evaluator: The European Commission's Marie Skłodowska-Curie Individual Fellowships (2016-2018).

National Science Centre of Poland, grant reviewer: Reviewed a research proposal for the SONATA BIS-13 call (2023).

Peder Sather Center reviewer: Reviewer for the UC Berkeley Peder Sather Center grants (2019).

Board member, Department of Biology, University of Oslo, Norway (2012).

Peer reviewer for the journals Molecular Biology and Evolution, Scientific Reports, Proceedings of the Royal Society: Biological Sciences, BMC Plant Biology, Algal Research, European Journal of Protistology, Aquatic Microbial Ecology, Genes, IJMS and Applied and Environmental Microbiology. See my [reviewer profile on Web of Science](#).

PhD evaluation committee. I served as an external referee in a committee in 2017 for evaluating whether a PhD thesis was worthy of public defense. Institut de Ciències del Mar, ICM-CSIC, Spain.

Hiring committees. I served on several hiring committees for PhD and Post Doc fellowships at UiO and UiB.

Supervision of graduate students

Main supervisor: Eugenia Giovanna Grande (master, 2023 - 2025), Ina J. Andresen (PhD, 2015 – 2021), Arthur A. H. Blørstad (PhD, 2016 – 2019[†]), Hengyi Zhu (master, 2018 – 2019), Alexander H. Løvestad (master, 2015 – 2017), Shruti Mehrotra (master, 2015 – 2018). **Co-supervisor:** Tengjel Hvidsten Tjersland (2022 - present), Peter Arnesen (master, 2019 – present*), Renate M. Alling (master, 2017 – 2019), Øyvind S. Gulbrandsen (master, 2016 – 2018), Eirik Høy (master, 2015 – 2016), Line L. Røsæg (master, 2014 – 2016), Andreas Evenstad (master, 2014 – 2017), Ina J. Andresen (master, 2014 – 2015), Anders K. Krabberød (master, 2008 – 2010), Dan K. Ree (master, 2008 – 2010). [†]Deceased. *Not finished.

Teaching

Bioinformatics for Molecular Biology (MBV-INF4410/9410). I have organized and lead the course, in addition to giving lectures and teaching computer labs in analyzing genomics and transcriptomics data, basic Unix/command line, as well as basic Python and R programming.

Bioinformatics (BIOS3010). Teaching Unix, molecular phylogenetics and NGS analysis.

Genetics and Developmental Biology (BIOS3601). I teach Echinoderm development, animal organogenesis and Evo-Devo.

Special curriculum on the Evolution of Multicellularity. 2016. I organized a special curriculum on the subject of the evolution of multicellularity. Four students (one master and three PhD-students) participated. I formed the curriculum and participated in the oral examinations and grading.

Molecular Biology and Biological Methods (BIO2140). Organized the course in 2015, in addition to teaching wet labs and computer labs in environmental sequencing and transcriptomics. Was also involved in writing and grading the exams. 2009 – 2011: supervised colloquia and wet labs in molecular biology.

Elementary Biology (BIO1000). 2008 – 2010: Supervised lab work in genetics and phylogeny.

Classification and Phylogeny (BIO4210). 2008: Supervised lab work in molecular phylogenetic methods.

Experience with bioinformatics tools and methods

- **Genomic epidemiology** – Phylogenetic and phylogeographic analyses of virus genome data using tools such as Nextstrain, NextClade, TreeTime and BEAST.
- **Genomics** – various genome assemblers using both short- and long-read sequence data (e.g. Spades, Canu, Flye). Quality assessment, both of sequence data and assemblies (e.g. coverage, k-mer analysis, Kraken2, MetaBAT, BUSCO).
- **Transcriptomics** – Quality control of sequence data (e.g. MultiQC, Trimmomatic). *de novo* assembly using Trinity, reference assembly using HISAT2 or PASA. Small RNA mapping and analysis (e.g. using Bowtie1 and MirDeep2). Gene quantification using RSEM, HTSeq and Cufflinks.
- **Comparative transcriptomics** – Quality control of sequencing libraries using (sequencing depth, gene variation, PCA). Differential gene expression testing using DESeq2 and edgeR. Visualization of gene expression using heatmaps and gene plotting. GO-enrichment and orthology comparisons. Co-expression analysis and gene module identification with the WGCNA and Clust methods.
- **Molecular phylogeny and phylogenomics** – multiple sequence alignment with tools like Muscle and Mafft, alignment visualization and refinement using MacClade and Mesquite. Model selection (ModelTest). Phylogenetic analysis with tools like RAxML, Phylobayes and MrBayes.
- **Gene identification and annotation** – homology searches with Blast, gene prediction using Augustus and annotation with Transdecoder and phylogenetic analysis. Gene and isoform identification using Cufflinks. Ortholog/Paralog detection. Chimera detection using Blast and Chimera Slayer. Domain annotation using CD-search and InterProScan.
- **Protein structure analysis** – evolutionary comparisons of protein structure evolution using ConSurf and Pyre2 and visualization in PyMOL.
- **Programming.** I have extensive experience with the Unix operating system and command line environment. I run and adapt programs written in Python and Perl and I know basic Python programming. I am also experienced with the language R, and I prefer to work in R for instance for statistical analysis and visualization of genomic and gene expression data.
- **Automation/workflow managers.** I use Nextflow to write bioinformatics pipelines that can automate the steps involved in for instance genome assembly and analysis of viruses. These pipelines can be run locally or in HPC environments.
- **High-performance computing (HPC).** I have used HPC platforms for many years, in particular the Abel/Saga at UiO. I have experience from handling large datasets from Next Generation Sequencing projects, and know the challenges and pitfalls associated with data storage, backup, sharing, memory requirements and resource requirements in highly computer intensive projects.

Research and Publications

Peer reviewed research papers

Garcia, I., **Bråte, J.**, Fossum, E., Rohringer, A., Moen, L. V., Hungnes, O., Fjære, O., Zaragkoulias, K. and Bragstad, K. 2024. Recombinant SARS-CoV-2 Delta/Omicron BA.5 emerging in an immunocompromised long-term infected COVID-19 patient. *Scientific Reports*. <https://doi.org/10.1038/s41598-024-75241-3>.

Ondracka, A., Dudin, O. and **Bråte, J.** 2023. Time-resolved small RNA transcriptomics of the ichthyosporean *Sphaeroforma arctica*. *F1000Research*. doi: 10.12688/f1000research.133935.1.

Moen, L. V., Vollan, H. S., **Bråte, J.**, Hungnes, O. and Bragstad, K. 2022. Molecular Epidemiology of the Norwegian SARS-CoV-2 Delta Lineage AY.63. *Viruses*. doi: 10.3390/v14122734.

- Osnes, N. M., Alfsnes, K., **Bråte, J.**, Llorente, G. I., Riis, K. R., Instefjord, H. K., Elshaug, H., Vollan, S. H., Moen, L. V., Pedersen, N. B., Caugant, A. D., Stene-Johansen, K., Hungnes, O., Bragstad, K., Brynildsrud, O., Eldholm, V. 2021. The Impact of Global Lineage Dynamics, Border Restrictions and Emergence of the B.1.1.7 Lineage on the SARS-CoV-2 Epidemic in Norway. *Virus Evolution*. doi: 10.1093/ve/veab086
- Andresen, I. J., Orr, R. J. S., Shalchian-Tabrizi, K. and **Bråte, J.** 2021. Compartmentalization of mRNAs in the giant, unicellular green alga *Acetabularia acetabulum*. *Scientific Reports*. doi: 10.1016/j.algal.2021.102440.
- Andresen, I. J., Orr, R. J. S., Krabberød, A. K., Shalchian-Tabrizi, K. and **Bråte, J.** 2021. Genome sequencing and *de novo* assembly of the giant unicellular alga *Acetabularia acetabulum*. *Scientific Reports*. doi: 10.1038/s41598-021-92092-4.
- Gulbrandsen, Ø. S., Andresen, I. J., Krabberød, A. K., **Bråte, J.*** and Shalchian-Tabrizi, K. 2021. Phylogenomic analysis restructures the Ulvophyceae. *Journal of Phycology*. doi: 10.1111/jpy.13168. *Joint senior author.
- Dudin, O., Ondracka, A., Grau-Bové, X., Haraldsen, A. A. B., Toyoda, A., Suga, H., **Bråte, J.*** and Ruiz-Trillo, I. 2019. A unicellular relative of animals generates a layer of polarized cells by actomyosin-dependent cellularization. *eLife*. doi: 10.7554/eLife.49801. *Senior author, ncRNA work.
- Bråte, J.**, Fuss, J., Jakobsen, K. S. and Klaveness, D. 2019. A draft genome assembly and transcriptome sequencing of the golden algae *Hydrurus foetidus* (Chrysophyceae). *F1000Research*. doi: 10.12688/f1000research.16734.1
- Bråte, J.**, Neumann, R. S., Fromm, B., Haraldsen, A. A. B., Tarver, J. E., Suga, H., Donoghue, P. C. J., Peterson, K. J., Ruiz-Trillo, I., Grini, P. and Shalchian-Tabrizi, K. 2018. Unicellular origin of the animal microRNA pathway. *Current Biology*. 28:1-8. doi: 10.1016/j.cub.2018.08.018.
- Krabberød, A. K., Orr, R. J. S., **Bråte, J.**, Kristensen, T., Bjørklund, K. R. and Shalchian-Tabrizi, K. 2017. Single cell transcriptomics, mega-phylogeny and the genetic basis of morphological innovations in Rhizaria. *Molecular Biology and Evolution*. doi: https://doi.org/10.1093/molbev/msx075
- Bråte, J.**, Adamski, M., Neumann, S. R., Shalchian-Tabrizi, K. and Adamska, M. 2015. Regulatory RNA at the root of animals: dynamic expression of developmental lincRNAs in the calcisponge *Sycon ciliatum*. *Proc. Royal. Soc. B*. doi:10.1098/rspb.2015.1746
- Leininger, S., Adamski, M., Bergum, B., Guder, C., Liu, J., Laplante, M., **Bråte, J.**, Hoffmann, F., Fortunato, S., Jordal, S., Rapp, H. T. and Adamska, M. 2014. Developmental gene expression provides clues to relationships between sponge and eumetazoan body plans. *Nature Communications*. 5:3905. doi:10.1038/ncomms4905
- Bråte, J.**, Krabberød, A. K., Dolven, J. K., Ose, R. F., Kristensen, T., Bjørklund, K. R. and Shalchian-Tabrizi, K. 2012. Radiolaria associated with large diversity of marine alveolates. *Protist*. 163(5): 767-777.
- Zhao, S., Burki, F., **Bråte, J.**, Keeling, P., Klaveness, D. and Shalchian-Tabrizi, K. 2012. *Collodictyon* – an ancient lineage in the tree of eukaryotes. *Mol Biol Evol*. doi: 10.1093/molbev/mss001
- Krabberød, A. K., **Bråte, J.**, Dolven, J. K., Ose, R. F., Klaveness, D., Kristensen, T., Bjørklund, K. and Shalchian-Tabrizi, K. 2011. Radiolaria divided into Polycystina and Spasmaria in combined 18S and 28S rDNA phylogeny. *PLoS ONE*. 6(8): e23526. doi: 10.1371/journal.pone.0023526
- Klaveness, D., **Bråte, J.**, Patil, V., Shalchian-Tabrizi, K., Kluge, R., Gislerød, H. R. and Jakobsen, K. S. 2011. The 18S and 28S rDNA Identity and Phylogeny of the common lotic Chrysophyte, *Hydrurus foetidus*. *Eur J Phycol*. 46(3): 282-291
- Shalchian-Tabrizi, K., Røberg, K. R., Ree, D. K., Klaveness, D. and **Bråte, J.** 2011. Marine-freshwater colonizations of haptophytes inferred from phylogeny of environmental 18S rDNA sequences. *J Euk Microbiol*. 58: doi: 10.1111/j.1550-7408.2011.00547.x
- Bråte, J.**, Klaveness, D., Rygh, T., Jakobsen, K. S. and Shalchian-Tabrizi, K. 2010. Telonemia-specific environmental 18S rDNA PCR reveals unknown diversity and multiple marine-freshwater colonizations. *BMC Microbiology*. 10:168. doi: 10.1186/1471-2180-10-168
- Bråte, J.**, Logares, R., Berney, C., Ree, D. K., Klaveness, D., Jakobsen, K. S. and Shalchian-Tabrizi, K. 2010. Freshwater Perkinsea and marine-freshwater colonizations revealed by pyrosequencing and phylogeny of environmental rDNA. *ISME Journal*. doi:10.1038/ismej.2010.39.
- Logares, R., **Bråte, J.**, Heinrich, F., Shalchian-Tabrizi, K. and Bertilsson, S. 2010. Infrequent Transitions between Saline and Fresh Waters in One of the Most Abundant Microbial Lineages (SAR11). *Mol Biol Evol*. 27(2): 347-357.
- Burki, F., Inagaki, Y., **Bråte, J.**, Archibald, J. M., Keeling, P. J., Cavalier-Smith, T., Sakaguchi, M., Hashimoto, T., Horak, A., Kumar, S., Klaveness, D., Jakobsen, K. S., Pawlowski, J. and Shalchian-Tabrizi, K. 2009.

- Large-scale phylogenomic analyses reveal that two enigmatic protist lineages, Telonemia and Centroheliozoa, are related to photosynthetic chromalveolates. *Genome Biol Evol.* 1: 231-238.
- Logares, R., **Bråte, J.**, Bertilsson, S., Clasen, J. L., Shalchian-Tabrizi, K. and Rengefors, K. 2009. Infrequent marine-freshwater transitions in the microbial world. *Trends Microbiol.* doi: 17(9): 414-422.
- Shalchian-Tabrizi, K., **Bråte, J.**, Logares, R., Klaveness, D., Berney, C. and Jakobsen, K. S. 2008. Diversification of unicellular eukaryotes: cryptomonad colonizations of marine and fresh waters inferred from revised 18S rRNA phylogeny. *Env. Microbiol.* 10(10): 2635-2644.
- Patil, V., **Bråte, J.**, Shalchian-Tabrizi, K. and Jakobsen, K. S. 2008. Revisiting the phylogenetic position of *Synchroma grande*. *J Euk Microbiol.* 56(4): 394-396.

Conferences and meetings

- Bråte, J.** Genomic surveillance of HCV in Norway. Norwegian Consortium of Microbial Genomics. Invited talk. 2024.12.05.
- Bråte, J.** Genome sequencing and surveillance of viruses at FHI (NIPH). Norwegian Bioinformatics Days. 2024.05.28.
- Bråte, J.** SARS-CoV-2 sequencing at the Norwegian Institute of Public Health. Nordic Elixir meeting 2022 on Handling Pandemic Omics Data in the Nordics.
- Bråte, J.** Import og evolusjon av SARS-CoV-2 i Norge. SARS-CoV-2 NGS Workshop at NIPH, Oslo Norway. 2022.
- Bråte, J.** Dyrenes opprinnelse. Bio-konferansen 2019. Invited talk. Norsk Biologforening. Oslo, Norway.
- Bråte, J.** Evolution and development in single-celled eukaryotes. Seminar at the Evolvability Project at the Centre for Advanced Study. 2019. Norwegian Academy of Science and Letters, Oslo, Norway.
- Bråte, J.** Evolution and function of the ichthyosporean miRNA system. 7th Choanoflagellates & Friends Meeting. 2019. Institute of Evolutionary Biology, Barcelona, Spain.
- Bråte, J.** Studying protist evolution using single-cell transcriptomics. Annual CIME/NFM meeting. 2017.
- Haraldsen, A. A. B., **Bråte, J. et al.** Pre-metazoan origin of animal microRNAs. EuroEvoDevo 2016. European Society of Evolutionary Developmental Biology, Uppsala, Sweden.
- Bråte, J.** Long non-coding RNAs in the sponge *Sycon ciliatum*. Origin of multicellularity. Institut de Biologia Evolutiva (UPF-CSIC). Barcelona. 2013.
- Bråte, J.** Regulatorisk RNA – Evolusjon, utvikling og epigenetikk. Konferanse i bioteknologi og etikk for lærere. 2013. Skolelabben, UiO.
- Bråte, J.** 18S+28S phylogeny divides Radiolaria into Polycystina and Spasmaria and supports the Retaria hypothesis. VI European Congress of Protistology. 2011. Berlin, Germany.
- Bråte, J.** Radiolaria revealed as a reservoir of Marine alveolates. VI European Congress of Protistology. 2011. Berlin, Germany.
- Bråte, J.** Diversity of unculturable Radiolaria and their symbionts revealed by 18S rDNA phylogeny. The 18th meeting of the International Society for Evolutionary Protistology 2010. Kanazawa, Japan.
- Bråte, J.** Lake Finsevatn sediment diversity investigated by pyrosequencing. 2nd International Winter Limnology Symposium 2010. Liebenberg, Germany.
- Bråte, J.** 2008. Barriers to Dispersal: Few Marine - Freshwater Colonizations Revealed by Environmental Sequencing. NIVA Algesymposium 2008. Oslo, Norway.

Popular science and media

- «A teeny-weeny mystery: investigating the difference between you and me and a single-celled organism». Story on ScienceNordic on our paper in Current Biology 2018. <http://sciencenordic.com/teeny-weeny-mystery-investigating-difference-between-you-and-me-and-single-celled-organism>
- «Knøttlite mysterium: Hva er egentlig forskjellen på deg og en encellet skapning?». Interview in Forskning.no 04.02.19. <https://forskning.no/celler-evolusjon/knottlite-mysterium-hva-er-egentlig-forskjellen-pa-deg-og-en-encellet-skapning/1289155>
- «Leter etter skillet mellom encellede og flercellede dyr» 2017. Interview in Apollon 06.11.17. http://www.apollon.uio.no/artikler/2017/4_tema_flercellet.html
- «Tenk om». 2017. Radio show on NRK P2: <https://radio.nrk.no/serie/hva-hvis-ikke>
- «På spor av det første flercellede dyret». 2016. Interview Titan.uio.no: <https://titan.uio.no/node/1637>
- «Omvendt kreftjakt». 2016. News article Forskning.no: <http://forskning.no/celler-kreft-cellebiologi/2016/01/omvendt-kreftjakt>

- Bråte, J.** Genomets mørke materie. 2015. Popular science talk. “Frokost hos Kristine”. IBV, UiO.
- Bråte, J.** Genomets mørke materie. 2015. Talk at “Nettverkssamling for realfagslærere i Trondheim”.
- Bråte, J.** Genomets mørke materie: nye roller til ikke-kodende RNA. 2015. Talk in “Etterutdanningskurs i bioteknologi for lærere”. IBV, UiO.
- Bråte, J.** Genomets mørke materie - nye roller til ikke-kodende RNA. 2014. Talk at “Faglig-pedagogisk dag”. IBV School laboratory, UiO.
- Bråte, J.** Non-coding RNA and the Origin of Animals. 2014. Talk at the Institut de Biologia Evolutiva, Barcelona, Spain.
- Bråte, J.** Single Cell Protistology - Work in Progress. 2014. Talk at the Institut de Biologia Evolutiva, Barcelona, Spain.
- Bråte, J.** Betydningen av små RNA fragmenter for evolusjon, økologi og epigenetikk. 2013. Talk at “Konferanse om bioteknologi og etikk for lærere”. IBV School laboratory, UiO.
- Bråte, J.** Søppel-DNA: Hva er det og (hvorfor) trenger vi bry oss? 2013. Talk at “Fredagsforedrag”. Forsvarets Forskningsinstitutt (FFI).
- «Har gentestet urtidsdyr fra Ås: Menneskets aller fjerneste slektning». 2012. News article Apollon: <http://www.apollon.uio.no/artikler/2012/urdyret.html>
- Bråte, J.** and Shalchian-Tabrizi, K. «Søppel-gen» gjorde folk av oss? 2013. Chronicle in Aftenposten: <http://www.aftenposten.no/meninger/kronikker/Soppel-gen-gjorde-folk-av-oss-7128851.html>
- Bråte, J.** Encellede eukaryoter - hvordan studere dem genetisk? 2011. Popular science talk. “Frokost hos Kristine”. IBV, UiO.