

Jon Bråte

Researcher at the University of Oslo (UiO)

Date of birth: 12.03.1983

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Current and previous positions

Researcher, Department of Biosciences, University of Oslo, Norway (since 2015)

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

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

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| 2018 | UNIFOR: Small grant for purchasing scientific equipment (€2,900). |
| 2017 | Research Council of Norway (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: In September and October 2019 I will be a Fellow of the Centre for Advanced Study (CAS) at the Norwegian Academy of Science and Letters. This is a part of the CAS project on Evolvability listed under Grants.

Proposal evaluator: The European Commission's Marie Skłodowska-Curie Individual Fellowships (2018-2016).
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, European Journal of Protistology, Aquatic Microbial Ecology and Genes. See my reviewer profile on Publons: <https://publons.com/author/1181302/jon-brate>

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.

Supervision of graduate students

Main supervisor: Arthur A. H. Blørstad (PhD, 2016 – 2019), Ina Jungersen Andresen (PhD, 2015 - present), Hengyi Zhu (master, 2018 – 2019), Alexander Hesselberg Løvestad (master, 2015 – 2017), Shruti Mehrotra (master, 2015 – 2018). **Co-supervisor:** Renate Marie Alling (master, 2017 – present), Øyvind Sætren Gulbrandsen (master, 2016 – 2018), Eirik Høye (master, 2015 – 2016), Line Lieblein Røsæg (master, 2014 – 2016), Andreas Evenstad (master, 2014 – 2017), Ina Jungersen Andresen (master, 2014 – 2015), Anders Kristian Krabberød (master, 2008 – 2010), Dan Kristofer Ree (master, 2008 – 2010).

Teaching

Bioinformatics for Molecular Biology (MBV-INF4410/9410). I am the main course organizer, 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.

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

- **Genomics** - genome assembly with Newbler, Spades and Canu. Various quality assessment (coverage, k-mer analysis).
- **Transcriptomics** – Quality control of sequence data using FastQC, Trimmomatic and Prinseq. *de novo* assembly using Trinity, reference assembly using TopHat/Cufflinks (Tuxedo pipeline). Small RNA mapping and analysis (e.g. using Bowtie1, MirMiner, MirDeep2*). Gene quantification using RSEM, HTSeq and Cufflinks.
- **Comparative transcriptomics** - Differential gene expression testing using DESeq2, edgeR (R packages) and the Tuxedo-pipeline. Quality control of sequencing libraries using PCA plots, distance clustering in R. Visualization of gene expression using heatmaps and gene plotting using R. Co-expression analysis and gene module identification with the WGCNA package in R.
- **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.
- **High-performance computing (HPC).** I have used the Abel HPC platforms for many years. 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

Research articles

- 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. In press.
- 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 an epithelium-like cell layer by actomyosin-dependent cellularization. *bioRxiv*. doi: <https://doi.org/10.1101/563726>.
- 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 calcsponge *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 Spasmalia 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 Pycol*. 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

- 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.