

## Jon Bråte

Researcher at the University of Oslo (UiO)

Date of birth: 12.03.1983

Nationality: Norwegian

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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, Institut 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

- Norwegian Research Council: Mobility grant for PhD-students (2017). Funding for a PhD student to stay at the lab of Iñaki Ruiz-Trillo at the Institut de Biologia Evolutiva, Barcelona, Spain (57.000 NOK).
- Norwegian Academy of Science and Letters: Centre for Advanced Study (2019-2020). I am part of an international consortium of evolutionary biologists who recently got funded a project on the concept of Evolvability.
- Norwegian Research Council: Young Talented Researcher grant (2015 – 2018). Three-year personal grant, including salary for a PhD-student (in total 7,67 mill NOK), for studying the role of non-coding RNAs in the evolution of animals.
- Norwegian Research Council: Mobility grant for post docs (2014). Funding for a research stay in the lab of Iñaki Ruiz-Trillo at the Institut de Biologia Evolutiva, Barcelona, Spain (93.000 NOK).
- Norwegian Research Council: Personal Post Doc grant (2012 – 2015). Three-year personal grant (in total 3,98 mill NOK) for studying the role of non-coding RNAs in the evolution of multicellularity.
- Molecular Life Science, UiO: Mobility grant for PhD-students (2009). Visiting the lab of Mikhail V. Matz at the University of Texas at Austin (28.000 NOK).

### Commissions of trust

**Proposal evaluator**: The European Commission's Marie Skłodowska-Curie Individual Fellowships (2017 and 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 – present), Alexander Hesselberg Løvestad (master, 2015 – 2017), Shruti Mehrotra (master, 2015 – present). **Co-supervisor:** Renate Marie Alling (master, 2017 – present), Ina Jungersen Andresen (PhD, 2015 - present), 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 and Spades. Quality assessment using PreQC.
- **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 Blast2GO and phylogent. Gene and isoform identification using Cufflinks. Ortholog/Paralog detection. Chimera detection using Blast and Chimera Slayer.
- **Protein structure analysis** - evolutionary comparisons of protein structure evolution using ConSurf and Phyre2 and visualization in PyMOL.

## **Research and Publications**

### **Research articles**

- 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.**, Neumann, R. S., Fromm, B., Haraldsen, A. A. B., Grini, P. and Shalchian-Tabrizi, K. 2016. Pre-metazoan origin of animal miRNAs. *bioRxiv*. doi: <http://dx.doi.org/10.1101/076190>.
- 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 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

- “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](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 urtdyr 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.