

## SCIENTIFIC ARTICLES

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1. Fiorini MR, Amiri S, Dilllotti, AA, Yde Ohki CM, Smigielski L, Walitza S, Fon EA, Grunblatt E, Farhan SMK\*, **Thomas RA\*** Ensemblex: an accuracy-weighted ensemble genetic demultiplexing framework for population-scale scRNAseq sample pooling. *Genome Biology*. 2025 July 3; 26, 191. <https://doi.org/10.1186/s13059-025-03643-1> \*Equal contribution and co-corresponding.
2. Deyab G, **Thomas RA**, Ding XE, Li J, Sirois J, Al-Azzawi Z, Niu S, Durcan TM, Fon EA. Midbrain organoids with an SNCA gene triplication display dopamine-dependent alteration in network activity <https://doi.org/10.1101/2025.04.23.650231>
3. Fiorini MR, Li J, Fon EA, Farhan SMK\*, **Thomas RA\***. Neural networks reveal novel gene signatures in Parkinson disease from single-nuclei transcriptomes (under revision NPJ Parkinson's Disease, Aug 2025) *BioRxiv* <https://doi.org/10.1101/2024.11.19.24317547> \*Equal contribution and co-corresponding.
4. **Thomas RA\***, Fiorini MR, Amiri S, Fon EA, Farhan, SMK\*. ScRNAbox: Empowering Single-Cell RNA Sequencing on High Performance Computing Systems. *BMC-Bioinformatics*. 2024 Oct 1; 25, 319. <https://doi.org/10.1186/s12859-024-05935-y>. \* co-corresponding author.
5. **Thomas RA\***, Sirois JM, Li S, Gestin A, Deyab GE, Piscopo VE, Lépine P, Mathur M, Goldsmith TM, Chen XCQ, Soubannier V, Fawaz L, Durcan TM, Fon EA. CelltypeR: A framework to identify and characterize cell types in human midbrain organoids using flow cytometry. *iScience*. 2024 Sep 20;27(9) <https://doi.org/10.1016/j.isci.2024.110613> \*corresponding author.
6. Fiorini MR, Dilllotti AA, Farhan SMK\*, **Thomas RA\***. Transcriptomics of Human Brain Tissue in Parkinson's Disease: a Comparison of Bulk and Single-cell RNA Sequencing. *Molecular Neurobiology* 2024 April 05. <https://doi.org/10.1007/s12035-024-04124-5> \*\*Equal contribution and co-corresponding.
7. Dorion MF, Casas D, Schlaifer I., Yaqubi M, Fleming P, Karpilovsky, N, Chen CXQ, Nicouveau M, Piscopo VE, MacDougall, EJ, Alluli A, Goldsmith TM, Schneider A, Dorion S, Aprahamian N, MacDonald A, **Thomas RA**, Dudley RW, Hall JA, Fon EA, Antel JP, Stratton JA, Durcan TM, La Piana R, Healy LM. An adapted protocol to derive microglia from stem cells and its application in the study of CSF1R-related disorders. *Molecular Neurodegeneration*. 2024 April 05; 19, 31. <https://doi.org/10.1186/s13024-024-00723-x>
8. Eldeeb MA, Bayne AN, Fallahi A, Goiran T, MacDougall EJ, Soumbasis A, Zorca CE, Tabah J, **Thomas RA**, Karpilovsky N, Mathur M, Durcan TM, Trempe JF, Fon EA. TOM20 gates PINK1 Activity and Mediates Its Tethering of the TOM and TIM23 Translocases Upon Mitochondrial Stress. *PNAS* 2024 Feb 28; 121 (10) e2313540121. <https://doi.org/10.1073/pnas.2313540121>
9. **Thomas RA**, Cai E, Reintsch WE, Krahn AI, Han C, Shinde S, Laviviere R, Krahn A, Chen CXQ, Nguyen-Renou E, Deneault E, You Z, Durcan TM, Fon TM. A deep learning convolutional neural network distinguishes neuronal models of Parkinson's disease from matched controls. *bioRxiv* 2023:11:24. \*co-corresponding author. <https://doi.org/10.1101/2023.11.23.568499>
10. Vanderperre B, Muraleedharan A, Dorion MF, Larroquette F, Del Cid Pellitero E, Rajukulendran N, Chen CXQ, Lariviere R, Michaud-Tardif C, Chidiac R, Lipuma D, MacLeod G, **Thomas RA**, Wang Z, Reintsch WE, Luo W, Schlaifer I, Fuming Z, Xia K, Yan L, Steinhart Z, Linhardt RJ, Trempe JF, Liu J, Durcan TM, Angers S, Fon EA. A genome-wide CRISPR/Cas9 screen identifies genes that regulate the cellular uptake of  $\alpha$ -synuclein fibrils by modulating heparan sulfate proteoglycans. *bioRxiv* 2023:09:29 <https://doi.org/10.1101/2023.09.29.560170>

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11. Yu E, Lariviere R, **Thomas RA**, Liu L, Senkevich K, Rahayel S, Trempe JF, Fon EA, Gan-Or Z. Machine learning nominates the inositol pathway and novel genes in Parkinson's disease. *Brain*. 2023 Oct 10:1093/awad345. <https://doi.org/10.1093/brain/awad345>
12. Eldeeb MA, **Thomas RA**, Ragheb MA, Fallahi A, Fon EA. Mitochondrial quality control in health and in Parkinson's disease. *Physiological Reviews*. 2022 Apr 25. <https://doi.org/10.1152/physrev.00041.2021>
13. **Thomas RA\***, Maussion G\*, Demirova I, Gu G, Cai E, Chen CX, Abdian N, Strauss TJ, Kelai S, Nauleau-Javaudin A, Beitel LK, Ramoz N, Gorwood P, Durcan TM. Auto-qPCR: A Python based web app for automated and reproducible analysis of qPCR data. *Scientific Reports* 2021 Oct 11, 1–14. [doi: 10.1038/s41598-021-99727-6](https://doi.org/10.1038/s41598-021-99727-6) \*Equal contribution.
14. Mohamed NV, Sirois J, Ramamurthy J, Mathur M, Lepine P, Deneault E, Maussion G, Nicoulet M, Chen CX, Abdian N, Soubannier V, Cai E, Nami H., **Thomas RA**, Beitel LK, Dolt, K.S., Karamchandani, J, Kunath, K., Fon, EA, Durcan, TM. Midbrain organoids with an SNCA gene triplication model key features of synucleinopathy. *Brain Comm* 2021 Sept fcab223. <https://doi.org/10.1093/braincomms/fcab223>
15. Chen CX, Abdian N, Maussion G, **Thomas RA**, Demirova I, Cai E, Tabatabaei M, Beitel LK, Karamchandani J, Fon EA, Durcan TM. A Multistep Workflow to Evaluate Newly Generated iPSCs and Their Ability to Generate Different Cell Types. *Methods Protocols*. 2021 July 19;4(3),50. <https://doi.org/10.3390/mps4030050>
16. Mohamed NV, Mathur M, da Silva RV, **Thomas RA**, Lepine P, Beitel LK, Fon EA, Durcan TM. Generation of human midbrain organoids from induced pluripotent stem cells. *MNI Open Research*. 2021 Feb 11;3:1. <https://doi.org/10.12688/mniopenres.12816.2>
17. Tavassoly O, del Cid Pellitero E, Larroquette F, Cai E, **Thomas RA**, Soubannier V, Luo W, Durcan TM, Fon EA. Pharmacological Inhibition of Brain EGFR Activation by a BBB-penetrating Inhibitor, AZD3759, Attenuates  $\alpha$ -Synuclein Pathology in a Mouse Model of  $\alpha$ -Synuclein Propagation. *Neurotherapeutics*. 2021 Mar 12:1-9. <https://doi.org/10.1007/s13311-021-01017-6>
18. Vogel JW, La Joie R, Grothe MJ, Diaz-Papkovich A, Doyle A, Vachon-Preseu E, Lepage C, de Wael RV, **Thomas RA**, Iturria-Medina Y, Bernhardt B. A molecular gradient along the longitudinal axis of the human hippocampus informs large-scale behavioral systems. *Nature communications*. 2020 Feb 19;11(1):1-7. <https://doi.org/10.1038/s41467-020-14518-3>
19. **Thomas RA**, Metzen MG, Chacron MJ. Weakly electric fish distinguish between envelope stimuli arising from different behavioral contexts. *Journal of Experimental Biology*. 2018 Aug 1;221(15):jeb178244. <http://dx.doi.org/10.1242/jeb.178244>
20. **Thomas RA**, Gibon J, Chen CX, Chierzi S, Soubannier VG, Baulac S, Séguéla P, Murai K, Barker PA. The Nogo receptor ligand LGI1 regulates synapse number and synaptic activity in hippocampal and cortical neurons. *Eneuro*. 2018 Jul;5(4). <https://doi.org/10.1523/eneuro.0185-18.2018>
21. Gibon J, Unsain N, Gamache K, **Thomas RA**, De Leon A, Johnstone A, Nader K, Séguéla P, Barker PA. The X-linked inhibitor of apoptosis regulates long-term depression and learning rate. *The FASEB Journal*. 2016 Sep;30(9):3083-90. <https://doi.org/10.1096/fj.201600384r>
22. **Thomas RA**, Ambalavanan A, Rouleau GA, Barker PA. Identification of genetic variants of LGI 1 and RTN 4R (NgR1) linked to schizophrenia that are defective in NgR1–LGI 1 signaling. *Molecular genetics & genomic medicine*. 2016 Jul;4(4):447-56. <https://doi.org/10.1002/mgg3.215>

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23. Kommaddi R, **Thomas R**, Ceni C, Daigneault K, Barker PA. Trk-dependent ADAM17 activation facilitates neurotrophin survival signalling. FASEB 2011 March 16; fj.10-173740. <https://doi.org/10.1096/fj.10-173740>
24. Ceni C, Kommaddi R, **Thomas R**, Vereker E, McPherson PM, Ritter B, Liu X, Barker PA. The p75NTR intracellular domain is generated by neurotrophin-induced receptor cleavage to potentiate Trk signalling. Journal of Cell Science 2010 July 1;123(13):2299-307. <https://doi.org/10.1096/fj.10-173740>
25. **Thomas R**, Favell K, Morante-Redolat JM, Pool, M, Kent C, Wright M, Daignault K, Ferraro G, Montcalm S, Durocher Y, Fournier A, Perez-Tur J, Barker PA. LGI1 is a Novel Nogo Receptor 1 ligand that antagonizes myelin-based growth inhibition. Journal of Neuroscience 2010 May 12;30(19):6607-12. <https://doi.org/10.1523/JNEUROSCI.5147-09.2010>

## ANALYSIS SOFTWARE

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1. Deyab G, **Thomas RA**, Ding XE, Li J, Sirois J, Al-Azzawi Z, Niu S, Durcan TM, Fon EA. Midbrain organoids with an SNCA gene triplication display dopamine-dependent alteration in network activity <https://doi.org/10.1101/2025.04.23.650231>
2. Fiorini, MF, Amiri, S, **Thomas, RA**. **Ensemblex**: Ensemblex is an accuracy-weighted ensemble framework for genetic demultiplexing of pooled scRNAseq. **2024** <https://neurobioinfo.github.io/ensemblex/site/>
3. **Thomas, RA**, Fiorini, MF, Amiri, S. **scRNAbox**: a comprehensive pipeline for single-cell RNA sequencing analysis on HPC, supporting transcriptomics and feature sequencing. **2024** <https://neurobioinfo.github.io/scrnabox/site/>
4. Snide S, **Thomas, RA**, Aroomoogon, K. **Automated cilia analysis**: A Cell Profiler and Python pipeline to detect cilia, match each cilium to a nucleus and centriole and measure features of each component. **2023** <https://github.com/RhalenaThomas/AutomatedCiliaMeasurements>
5. Cai E, **Thomas, RA**, Snide, S. **CNN microscopy classifier**: Microscopy images processing and deep learning convolutional network to classify case vs control from high content imaging. **2023** [https://github.com/RhalenaThomas/DeepLearningCNN\\_DiseaseStatusClassifier](https://github.com/RhalenaThomas/DeepLearningCNN_DiseaseStatusClassifier)
6. **Thomas, RA**, Li S, Gestin, A. **CelltypeR**: An R library with functions for a workflow to use flow cytometry to quantify cell types within a complex tissue. **2023** <https://github.com/RhalenaThomas/CelltypeR>
7. **Thomas, RA**, Maussion, G, Gu, G, Demirova, I, Cai, E. **Auto-qPCR**: A program to automatically process qPCR data from csv files in any PCR machine and create a normalized table of RNA/DNA quantities, statistics, and bar charts. **2020** <https://github.com/neuroeddu/Auto-qPCR>
8. **Thomas, RA**, Cai E, Soubannier, V. **HistQ**: A Fiji macro written in jython to quantify staining in histology sections. **2019** <https://github.com/neuroeddu/HistQ>
9. **Thomas, RA**. and Cai, E. **CellQ**: A Fiji Macro written in jython macro to analyze 2D cell cultures counting cell density and positive cells for markers of interest. **2019** <https://github.com/neuroeddu/CellQ>
10. **Thomas, RA** and Cai, E. **OrgM**: A Fiji macro for automated measurement of object area, diameter and roundness from bright field images. **2019**. <https://github.com/neuroeddu/OrgM>

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11. **Thomas, RA** and Cai, E. **OrgQ**: A Fiji macro written in jython to analysis IF images of cryosections from organoid tissues. **2019**. <https://github.com/neuroeddu/OrgQ>

### INVITED TALKS AND ORAL PRESENTATIONS (last 6 years)

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1. Scalable Single-Cell Analysis and Deep Learning for Understanding Parkinson's Disease in iPSC-Derived Models. Université de Sherbrooke, Quebec, Canada. June 19<sup>th</sup>, 2024.
2. Single cell RNAseq analysis of different brain cells and midbrain organoids grown from iPSCs. Tissue engineering and Regenerative Medicine, Virtual Conference London UK. June 11-12, 2024.
3. Single Cell transcriptomic analysis workflow with scRNAbox. 10X Genomics Bioinformatics bootcamp: Getting started with analyzing single cell data. Webinar May 17<sup>th</sup>, 2024.
4. Toward single cell sequencing at a cohort level for identification of subgroup markers and pathways. International Single Cell Neurobiology Meeting. Holetown Barbados. May 21<sup>st</sup>-25<sup>th</sup>, 2023.
5. TechTalk: An overview of single cell RNA sequencing: from data collection to analysis. l'Association des Étudiant(e)s de l' Institute for Research in Immunology and Cancer and Dept of Biochemistry and Molecular Medicine (AÉIRIC), Université de Montréal, Marcell-Coutu Pavilion, Montréal, Québec, Canada. February 23<sup>rd</sup>, 2023.
6. Pseudotime trajectory analysis: getting your cells in order. Technical seminar on methods of single cell sequencing analysis organized by the Neuro Single Cell Group. McGill University, Montréal, Québec, Canada. December
7. Single cell sequencing analysis of midbrain organoid models of Parkinson's Disease. Joint Paris Brain Institute (ICM) – Montreal Neurological Institute-Hospital workshop: Studying brain development and disease at single-cell resolution. (Held Virtually in Paris and Montreal) October 20<sup>th</sup>, 2021.
8. Single cell RNA sequencing of human midbrain organoids modeling Parkinson's Disease. Healthy Lives Research Day (Virtual), June 7th-8, 2021.  
<https://www.youtube.com/watch?v=iKQZFw2e3oY&list=PLM9hDE9mNky4u-nRjusQ4tXpFFvDv4Vjn&index=17&t=6s>
9. Single cell transcriptomics: Taking advantage of heterogeneity. Novel Techniques in Neuroscience Panel: Healthy Lives Research Day (Virtual), June 7th-8, 2021.
10. A deep learning classifier to distinguish between human iPSC derived cells from Parkinson's Disease Patients and healthy controls. Joint McGill-ZNZ (Zurich Neuroscience Center) Workshop: Induced pluripotent stem cell-based modeling in brain disease research. (Held Virtual in Zurich and Montreal) December 8<sup>th</sup>, 2020.
11. Single cell analysis of midbrain organoids as a model for Parkinson's Disease. Healthy Brains for Healthy Lives Research Day (Virtual). August 17th-18, 2020.  
[https://www.youtube.com/watch?v=87liaPsib1Q&list=PLM9hDE9mNky7XwAydI9p3\\_JqWFgmkzSTx&index=21&t=3s](https://www.youtube.com/watch?v=87liaPsib1Q&list=PLM9hDE9mNky7XwAydI9p3_JqWFgmkzSTx&index=21&t=3s)
12. Midbrain organoids as a model of Parkinson's disease and single cell sequencing analysis. Presented at the Healthy Brains for Healthy Lives Research Series, February 11th, 2020. Thompson House, Montréal, Québec, Canada.

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13. Can we better understand the relationship between stem cells and neurons using computational models? Computational methods for Modeling and Precision Medicine in Neurodegeneration Workshop, November 4th, 2019. The Neuro, Montréal, Québec, Canada.
14. Development of quality control measures and analysis pipelines for Single cell sequencing analysis of midbrain organoids. Presented at the Stem Cell iPSC Seminar Series, May 30th, 2019. The Neuro, Montréal, Québec, Canada.
15. Single cell RNA sequencing of midbrain organoids as a model for Parkinson's Disease. Presented at the McGill Single Cell Club, September 2018. The McGill Genome Center, Montréal, Québec, Canada.

### CONFERENCE ABSTRACTS AND POSTER PRESENTATIONS (last 6 years)

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1. **Thomas RA**, Deyab G, Goldsmith TM, Lepine P, Sirois J, Chen CXQ, Mathur M, Omana V, Durcan TM, Fon EA. Defining vulnerable and preserved dopaminergic populations neurons in midbrain organoid models of Parkinson's disease using single cell transcriptomics. Gordon Research Conference: Parkinson's Disease. Waterville Valley, New Hampshire, USA. June 8-13, 2025. Presenter.
2. Lin S, **Thomas RA**, Larroquette F, Fon EA, Iturria-Medina Y. Transcriptomic-Neuroimaging Parkinson's Disease Stratification Reveals Distinctive Motor-Cognitive Subtrajectories. International Conference on Alzheimer's and Parkinson's Diseases and Related Neurological Disorders. Vienna, Austria. 2025. Contributor.
3. Fiorini MR, Li J, Fon EA, Farhan SMK\*, **Thomas RA\***. Leveraging Deep Neural Networks to Identify Single-Cell Gene Expression Profiles that Characterize Parkinson's Disease. American Society of Human Genetics Conference. Dever Colorado, USA. Nov 5-9, 2024. Supervisor.
4. **Thomas RA**, Goldsmith TM, Chen C.X-Q., Durcan TM, Fon EA. Analysis of scRNAseq of iPSC derived Brain Cells from Parkinson's Disease Patients with GBA Mutations. GBA1 Meeting. Montréal, Québec, Canada. June 27-29, 2024. Presenter.
5. **Thomas RA**, Fiorini MR, Goldsmith TM, Chen CXQ, Alluli A, Piscopo VE, Schlaifer I, Farhan SMK, Durcan TM, Fon EA. Analysis of scRNAseq from Parkinson's Disease Patients' Human iPSC Derived Neurons and Microglia Grown in Pooled Cultures. Healthy Brains for Healthy Lives Symposium. Montréal, Québec, Canada. May 8-9, 2024. Presenter.
6. Fiorini MR, Amiri S, Dilliot AA, Farhan SMK, **Thomas RA**. Ensemblx: an accuracy-weighted, probabilistic ensemble genetic demultiplexing framework for population-scale scRNAseq sample pooling. Healthy Brains for Healthy Lives Symposium. Montréal, Québec, Canada. May 8-9, 2024. Supervisor.
7. Fiorini MR, Amiri S, **Thomas RA**, Farhan, S. A consensus algorithm for genetic demultiplexing of scRNA-seq from pooled iPSC cultures of multiple subjects for cohort-scale analysis in neurodegenerative disease. American Society of Human Genetics 2023. Washington, DC, USA. November 1-5, 2023. Supervisor.
8. Yu Eric, Larivière R, **Thomas RA**, Fon EA, Gan-Or Z. Prioritization of causal genes at Parkinson's disease associated loci using machine learning. International Congress of Parkinson's Disease and Movement Disorder. Copenhagen, Denmark. Aug 27-31, 2023. Contributor.
9. Lin SJ, **Thomas RA**, Larroquette F, Degroot C, Fon EA, Iturria-Medina. Imaging-based subtyping differentiates clinical symptoms in Parkinson's Disease. Organization for Human Brain Mapping. Montréal, Québec, Canada. July 22-26, 2023. Contributor.

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10. **Thomas RA**, Cai E, Li JL, Reintsch W, Han C, Shinde S, Larivière R, Krahn A, Chen CXQ, Nguyen-Renou E, Durcan TM, Fon EA. Deep learning classification of Parkinson's Disease cells using single cell transcriptomics and high content microscopy. Parkinson's Disease Gordon Research Conference. Les Diablerets, VD, Switzerland. May 7-12, 2023. Presenter.
11. Fiorini MR, Amiri S, **Thomas RA**, Farhan, S. A pipeline for multiplexing Parkinson's disease iPSC-derived dopaminergic neurons and microglia for cohort-scale single cell RNA sequencing. Healthy Brains for Healthy Live Symposium. May 4-5, 2023. Supervisor.
12. Cai E, Reintsch W, Han C, Shinde S, Larivière R, Krahn A, Chen CXQ, Nguyen-Renou E, Durcan TM, Fon EA, **Thomas RA**. A convolutional neural network between Parkinson's disease and healthy cells using microscopy images. MAIN 2022. Montréal, Québec, Canada. December 9-10, 2022. Presenter.
13. Yu Eric, Larivière R, **Thomas RA**, Liu L, Senkevich K, Fon EA, Gan-Or Z. Machine learning reveals candidate genes from Parkinson's disease associated loci. American Society of Human Genetics. Los Angeles, USA. Oct 25-29, 2022. Contributor.
14. **Thomas RA**, Mathur M, Omana V, Sirois JM, Durcan TM, Fon EA. Differential gene expression analysis in midbrain organoid models of Parkinson's Disease using single cell RNA sequencing. Dopamine 2022. Montréal, Québec, Canada. May 21-25, 2022. Presenter.
15. **Thomas RA**, Sirois JM, Li S, Gestin A, Mathur, M, Durcan TM, Fon EA. Quantification of cell types in human midbrain organoids using a flow cytometry antibody panel. Dopamine 2022. Montréal, Québec, Canada. May 21-25, 2022. Presenter.
16. **Thomas RA**, Cai E, Gu G, Chen CXQ, Abdian N, Fon EA, Durcan TM. Quantitative characterization of variability in cortical neurons between healthy human induced pluripotent stem cell lines. Society for Neuroscience meeting, Chicago, USA. October 19-23, 2019. Presenter.
17. **Thomas RA**, Mohamed NV, Couturier C, Mathur M, Misic B, Ragoussis J, Durcan TM, Fon EA. Single cell RNA sequencing of midbrain organoids as a model for Parkinson's Disease. Keystone, Single Cell Biology. Breckenridge, USA. January 14-17, 2019. Presenter.