

JAROSLAV BENDL

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PERSONAL

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NIH Biosketch <https://www.ncbi.nlm.nih.gov/myncbi/1Xsir7k6Qnjks/cv/186343/>
Github <https://github.com/xbendl>
Personal bio <http://www.JaroslavBendl.site/>

EMPLOYMENT

10/2021 - present **Assistant Professor** / Team leader of the Multi-omics Data Integration Group at Center for Disease Neurogenomics · Roussos Lab · Department of Genetics and Genomics Sciences · Icahn School of Medicine at Mount Sinai · New York
1/2020 – 9/2021 **Senior Scientist** · Roussos Lab · Department of Genetics and Genomics Sciences · Icahn School of Medicine at Mount Sinai · New York
1/2017 – 12/2019 **Postdoctoral Fellow** · Roussos Lab · Department of Genetics and Genomics Sciences · Icahn School of Medicine at Mount Sinai · New York
1/2012 - 12/2016 **PhD candidate** · International Clinical Research Centre / Loschmidt Laboratories · St. Anne's University Hospital Brno · Brno, Czech Republic

EDUCATION

1/2017 - 12/2019 **Postdoctoral training** (mentor: Panos Roussos)
Roussos Lab · Department of Genetics and Genomics Sciences · Icahn School of Medicine at Mount Sinai · New York
4/2015 - 7/2015 **Internship** (mentor: Yaochi Zhou)
Griffith University · Institute for Glycomics · Laboratory of Molecular Biology and Bioinformatics · Gold Coast, Australia
9/2011 - 10/2016 **Ph.D. Degree** (mentor: Jaroslav Zendulka; awarded: 10/10/2021)
Brno University of Technology (CZ) · Faculty of Information Technology
1/2011 - 6/2011 **Internship**
Gjøvik University College · Faculty of Computer Science, Media and Technology · Gjøvik, Norway
7/2009 - 8/2011 **Master Degree** (awarded: 8/22/2011)
Brno University of Technology (CZ) · Faculty of Information Technology
Study programme: Bioinformatics and Biocomputing
9/2006 - 6/2009 **Bachelor Degree** (awarded 6/16/2009)
Brno University of Technology (CZ) · Faculty of Information Technology
Study programme: Information Technology

HONORS/AWARDS

10/2016 **Dean's Award** for outstanding dissertation thesis
4/2016 **Finalist of Joseph fourier prize for computer sciences, French Embassy at Prague**
11/2015 **Best Journal Paper Award** · IMIA Yearbook · Category Bioinformatics and Translational Informatics
4/2012 **Best Conference Paper Award** · Student conference EEICT · Category Bioinformatics and Biomedical engineering

8/2011	Dean's award for very good study results during master studies and very good knowledge during state final examination
6/2009	Dean's award for very good study results during bachelor studies and very good knowledge during state final examination

PAST GRANTS (PI role only)

Funding source	Dates	Direct Costs	Suppl.
Brain & Behavior Research Foundation (PI) Unraveling the Mechanism Underlying Bipolar Disorder by Integrated Analysis of Gene Expression, Chromatin Accessibility and Genetic Association Studies (27209)	1/2019 - 1/2021	\$70,000.00	Young Investigator Award

ACTIVE GRANTS (PI role only)

Alzheimer's Association (PI) Epigenetic and transcriptomics mechanisms of Alzheimer's disease (AARF-21-722200)	10/2021 - 10/2023	\$120,000	AARF
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TRAINEES

Name	Level of Trainee	Role in Training (Inclusive dates)	Training venue	Current status
Milos Musil	MSc student	Master thesis supervision 9/2014 - 6/2015	Computational work	Assistant Professor
Ondrej Salanda	MSc student BSc student	Master thesis supervision 9/2014 - 6/2015 Bachelor thesis supervision 9/2012 - 6/2014	Computational work	Industry
Miroslav Kadlec	MSc student BSc student	Master thesis supervision 9/2014 - 6/2015 Bachelor thesis supervision 9/2012 - 6/2014	Computational work	Graduate student
Frantisek Malinka	MSc student	Master thesis supervision 9/2013 - 6/2014	Computational work	Graduate student
David Pavlik	MSc student	Master thesis supervision 9/2013 - 6/2014	Computational work	Instustry
Pelikan Ondrej	MSc student	Master thesis supervision 9/2012 - 6/2014	Computational work	Industry
Jiri Trlica	BSc student	Bachelor thesis supervision 9/2012 - 6/2014	Computational work	Industry
Martin Hyrs	MSc student	Bachelor thesis supervision /2011 - 6/2012	Computational work	Graduate student
Vladimir Brigant	BSc student	Bachelor thesis supervision 9/2011 - 6/2012	Computational work	Industry
Vojtech Salanda	BSc student	Bachelor thesis supervision 9/2011 - 6/2012	Computational work	Industry
Yixuan Ma	PhD student	PhD thesis co-supervision 9/2021 - present	Computational work	Graduate student
Rebecca Mahoney	Visiting student	Research project supervision 1/2022 - present	Computational work	Graduate student

Claire Coleman	Junior bioinformatician	Research project supervision 5/2022 - present	Computational work	Junior bioinformatician
Prashant Fnu	Junior bioinformatician	Research project supervision 7/2021 - present	Computational work	Senior Bioinformatician
Mikaela Koutrouli	Visiting student	Research project supervision 7/2023 - present	Computational work	Graduate student

TEACHING ACTIVITIES

Activity	Level	Role	Number of students	Number of hours	Years Taught
Bioinformatics I (practises)	MSc students	Lecturer	20	4 hrs / month	2012-2015 (summer semester)
Web programming (practises)	BSc students	Lecturer	60	4 hrs / month	2013 (summer semester)
Introduction to Programming (practises)	BSc students	Lecturer	40	8 hrs / month	2011 (winter semester)

PUBLICATIONS

Peer reviewed original contributions * first author / shared first author
senior / corresponding author

1. Bendl J*, Stourac J, Salanda O, Pavelka A, Wieben ED, Zendulka J, Brezovsky J, Damborsky J. PredictSNP: robust and accurate consensus classifier for prediction of disease-related mutations. *PLoS Comput Biol.* 2014 Jan; 10(1):e1003440.
2. Kurumbang NP, Dvorak P, Bendl J, Brezovsky J, Prokop Z, Damborsky J. Computer-assisted engineering of the synthetic pathway for biodegradation of a toxic persistent pollutant. *ACS Synth Biol.* 2014 Mar ;3(3): 172–81.
3. Dvorak P, Kurumbang NP, Bendl J, Brezovsky J, Prokop Z, Damborsky J. Maximizing the efficiency of multienzyme process by stoichiometry optimization. *Chembiochem.* 2014 Sep; 15(13):1891–5.
4. Bednar D, Beerens K, Sebestova E, Bendl J, Khare S, Chaloupkova R, Prokop Z, Brezovsky J, Baker D, Damborsky J. FireProt: Energy- and Evolution-Based Computational Design of Thermostable Multiple-Point Mutants. *PLoS Comput Biol.* 2015 Nov; 11(11):e1004556.
5. Bendl J*, Musil M*, Stourac J*, Zendulka J, Damborsky J, Brezovsky J. Predictsnp2: A unified platform for accurately evaluating SNP effects by exploiting the different characteristics of variants in distinct genomic regions. *PLoS Comput Biol.* 2016 May; 12(5):e1004962.
6. Bendl J*, Stourac J*, Sebestova E, Vavra O, Musil M, Brezovsky J, Damborsky J. HotSpot Wizard 2.0: automated design of site-specific mutations and smart libraries in protein engineering. *Nucleic Acids Res.* 2016 Jul;44(W1): W479-87.
7. Schwarte A, Genz M, Skalden L, Nobili A, Vickers C, Melse O, Kuipers R, Joosten H-J, Stourac J, Bendl J, Black Jon, Haase Peter, Baakman Coos, Damborsky J, Bornscheuer U, Vriend G, Venselaar H. NewProt - a protein engineering portal. *Protein Eng Des Sel.* 2017 Jun; 30(6):441–7.
8. Musil M, Stourac J, Bendl J, Brezovsky J, Prokop Z, Zendulka J, Martinek T, Bednar D, Damborsky J. FireProt: web server for automated design of thermostable proteins. *Nucleic Acids Res.* 2017 Apr; 45: W393–W399.
9. Fullard JF, Hauberg ME, Bendl J, Egervari G, Cirnaru M-D, Reach SM, Motl J, Ehrlich ME, Hurd YL, Roussos P. An atlas of chromatin accessibility in the adult human brain. *Genome Research.* 2018 Aug; 28(8):1243–52.

10. Wang M, Beckmann ND, Roussos P, Wang E, Zhou X, Wang Q, et al. The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. *Scientific Data*. 2018 Sep; 5:180185.
11. Hoffman GE, [Bendl J](#), Voloudakis G, Montgomery KS, Sloofman L, Wang Y-C, et al. CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. *Scientific Data*. 2019 Sep; 6(1):180.
12. Hoffman GE, [Bendl J](#), Girdhar K, Schadt EE, Roussos P. Functional interpretation of genetic variants using deep learning predicts impact on chromatin accessibility and histone modification. *Nucleic Acids Res*. 2019 Nov; 47(20):10597–611.
13. Hoffman GE, [Bendl J](#), Girdhar K, Roussos P. decorate: differential epigenetic correlation test. *Bioinformatics*. 2020 May; 36(9):2856–61.
14. Hauberg ME*, Creus-Muncunill J*, [Bendl J](#)*, Kozlenkov A, Zeng B, Corwin C, et al. Common schizophrenia risk variants are enriched in open chromatin regions of human glutamatergic neurons. *Nature Communications*. 2020 Nov; 11(1):5581.
15. Espeso-Gil S, Halene T, [Bendl J](#), Kassim B, Ben Hutta G, Iskhakova M, et al. A chromosomal connectome for psychiatric and metabolic risk variants in adult dopaminergic neurons. *Genome Medicine*. 2020 Feb; 12(1):19.
16. Novikova G, Kapoor M, Tcw J, Abud EM, Efthymiou AG, Chen SX, et al. Integration of Alzheimer's disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. *Nature Communications*. 2021 Mar; 12(1):1610.
17. Hoffman GE, Ma Y, Montgomery KS, [Bendl J](#), Jaiswal MK, Kozlenkov A, et al. Sex differences in the human brain transcriptome of cases with schizophrenia. *Biol Psychiatry*. 2022 Jan; 91(1):92-101.
18. Zhao B, Li T, Yang Y, Wang X, Luo T, Shan Y, et al. Common genetic variation influencing human white matter microstructure. *Science*. 2021 Jun; 372(6548).
19. Cirnaru M-D, Song S, Tshilenge K-T, Corwin C, Mleczko J, Aguirre CG, et al. Transcriptional and epigenetic characterization of early striosomes identifies Foxf2 and Olig2 as factors required for development of striatal compartmentation and neuronal phenotypic differentiation. *Elife*. 2021 Oct; 10:e659790.
19. Zeng B, [Bendl J](#), Kosoy R, Fullard JF, Hoffman GE, Roussos. Multi-ancestry eQTL meta-analysis of human brain identifies candidate causal variants for brain-related traits. *Nature Genetics*. 2022 Feb; 54(2):161-169.
20. Girdhar K, Hoffman GE, [Bendl J](#), Rahman S, Dong P, Liao W, et al. Acetylated Chromatin Domains Link Chromosomal Organization to Cell- and Circuit-level Dysfunction in Schizophrenia and Bipolar Disorder. *Nature Neuroscience*. 2022 Apr; 25(4):474-83.
21. Zhao B, Li T, Smith SM, Xiong D, Wang X, Yang Y, Luo T, Zhu Z, et al. Common variants contribute to intrinsic human brain functional networks. *Nature Genetics*. 2022 Apr; 54(4):508-17.
22. Liu D, Zinski A, Mishra A, Noh H, Park GH, Qin Y, et al. Impact of schizophrenia GWAS loci converge onto distinct pathways in cortical interneurons vs glutamatergic neurons during development. *Molecular Psychiatry*. 2022 Jun; 27(10):4218-4233
23. Kosoy R*, Fullard JF*, Zeng B*, [Bendl J](#)*, Dong P, Rahman S, et al. Genetics of the human microglia regulome refines Alzheimer's disease risk loci. *Nature Genetics*. 2022 Aug; 54(8):1145-54.
24. Mattheisen M, Grove J, Als TD, Martin J, Voloudakis G, Meier S, Demontis D, [Bendl J](#), et al. Identification of shared and differentiating genetic architecture for autism spectrum disorder, attention-deficit hyperactivity disorder and case subgroups. *Nature Genetics*. 2022 Oct; 54(10):1470-8.
25. Dong P, Hoffman GE, Apontes P, [Bendl J](#), Rahman S, Fernando MB, et al. Population-level variation in enhancer expression identifies disease mechanisms in the human brain. *Nature*

Genetics. 2022 Oct; 54(10):1493-503.

26. [Bendl J](#), Hauberg ME, Girdhar K, Im E, Vicari JM, Rahman S, et al. The three-dimensional landscape of cortical chromatin accessibility in Alzheimer's disease. *Nature Neuroscience*. 2022 Oct; 25(10):1366-78.

27. Fulton SL, Wenderski W, Lepack AE, Eagle AL, Fanutza T, Bastle RM, et al. Rescue of deficits by Brwd1 copy number restoration in the Ts65Dn mouse model of Down syndrome. *Nature Communications*. 2022 Oct;13(1):1-7.

28. Demontis D, Walters GB, Athanasiadis G, Walters R, Therrien K, Farajzadeh L, Voloudakis G, [Bendl J](#), ..., Børglum AD. Genome-wide analyses of ADHD identify 27 risk loci, refine the genetic architecture and implicate several cognitive domains. *Nature Genetics*. 2023 Feb; 55(2):198-208.

29. Wang E, Wang M, Guo L, Fullard JF, Micallef C, [Bendl J](#), Song W-M, Ming C, Huang Y, Li Y, Yu K, Peng J, Bennett DA, De Jager PL, Roussos P, Haroutunian V, Zhang B. Genome-wide methylomic regulation of multiscale gene networks in Alzheimer's disease. *Alzheimer's & Dementia*. 2023 Aug; 19(8):3472-3495.

30. Als TD, Kurki M, Grove J, Voloudakis G, Therrien K, Tasanko E, et al. Depression pathophysiology, risk prediction of recurrence and comorbid psychiatric disorders using genome-wide analyses. *Nature Medicine*. 2023 Jul; 29(7):1832-1844.

31. Burstein D, Griffen TC, Therrien K, [Bendl J](#), Venkatesh S, Dong P, et al. Genome-wide analysis of binge-eating disorder identifies the first three risk loci and implicates iron metabolism. *Nature Genetics*. 2023 Sep; 55(9):1462-1470.

32. Ma Y*, [Bendl J](#)*, Hartley BJ, Fullard JF, et al. Activity-Dependent Transcriptional Program in NGN2+ Neurons Enriched for Genetic Risk for Brain-Related Disorders. *Biological Psychiatry*. 2023 Jul; S0006-3223(23)01426-9.

33. Mathilde Pruvost, Julia Patzig, Camila Yattah, et al. The stability of the myelinating oligodendrocyte transcriptome is regulated by the nuclear lamina. *Cell Reports*. 2023 Aug; 42(8):112848.

34. Coleman C, Wang M, Wang E, Micallef C, Shao Z, Vicari JM, Li Y, Yu K, Cai D, Peng J, Haroutunian V, Fullard JF#, [Bendl J](#)#, Zhang B#, Roussos P#. Multi-omic atlas of the parahippocampal gyrus in Alzheimer's disease. *Scientific Data*. 2023 Jul; 10(1):602.

35. Rahman S, Dong P, Apontes P, Fernando MB, Kosoy R, Townsley KG, Girdhar K, [Bendl J](#), Shao Z, Misir R, Tsankova N, Kleopoulus SP, Brennand KJ, Fullard JF, Roussos P. Lineage specific 3D genome structure in the adult human brain and neurodevelopmental changes in the chromatin interactome. *Nucleic Acids Res*. 2023 Oct; gkad798.

36. Zhu K*, [Bendl J](#)*, Rahman S, Vicari JM, Coleman C, Clarence T, Latouche O, Tsankova NM, Li A, Brennand KJ, Lee D. Multi-omic profiling of the developing human cerebral cortex at the single-cell level. *Science Advances*. 2023 Oct 12;9(41); eadg3754.

37. Chandrashekar PB, Alatkari S, Wang J, Hoffman GE, He C, Jin T, Khullar S, [Bendl J](#), Fullard JF, Roussos P, Wang D. DeepGAMI: deep biologically guided auxiliary learning for multimodal integration and imputation to improve genotype-phenotype prediction. *Genome Medicine*. 2023 Dec;15(1):1-9.

39. Ruzicka WB, Mohammadi S, Fullard JF, Davila-Velderrain J, Subburaju S, Tso DR, et al. Single-cell multi-cohort dissection of the schizophrenia transcriptome. *Science*. 2024 May 24; eadg5136.

40. Zeng B, [Bendl J](#)*, Deng C, Lee D, Masir R, Reach SM, Kleopoulos SP, Auluck P, Marengo S, Lewis DA, Haroutunian V, Ahituv N, Fullard JF, Hoffman GE, Roussos P. Genetic regulation of cell-type specific chromatin accessibility shapes the etiology of brain diseases. *Science*. 2024 May 24; eadh4265.

41. Emani PS, Liu JJ, Clarke D, Jensen M, Warrell J, ... Bendl J, ... Wang D, Geschwind D, Gerstein M. Single-cell genomics and regulatory networks for 388 human brains. *Science*. 2024 May 24; eadi5199.

Books and book chapters

1. Sebestova E, [Bendl J](#), Brezovsky J, Damborsky J. Computational tools for designing smart libraries. *Methods Mol Biol*. 2014;1179:291–314.
2. Fullard JF, [Bendl J](#)*, Roussos P. ATAC-seq and psychiatric disorders. *Epigenetics in Psychiatry*. Elsevier; 2021. p. 143–62.

Preprints (In review)

1. Dong P, [Bendl J](#), Misir R, Shao Z, Edelstien J, Davis DA, et al. Transcriptome and chromatin accessibility landscapes across 25 distinct human brain regions expand the susceptibility gene set for neuropsychiatric disorders. *bioRxiv*. 2022.
2. Hoffman GE, Lee D, [Bendl J](#), Fnu P, Hong A, Casey C, Alvia M, Shao Y, Argyriou S, Therrien K, Venkatesh S, Voloudakis G, Haroutunian V, Fullard JF, Roussos P. Efficient differential expression analysis of large-scale single cell transcriptomics data using dreamlet. *BioRxiv*. 2023.
3. Fulton SL, [Bendl J](#), Gameiro-Ros I, Fullard JF, Al-Kachak A, Lepack AE, Stewart AF, Singh S, Poller WC, Bastle RM, Hauberg ME, Fakira AK, Chen M, Durand-de Cuttoli R, Cathomas F, Ramakrishnan A, Gleason K, Shen L, Tamminga CA, Milosevic A, Russo SJ, Swirski F, Blitzer RD, Slesinger PA, Roussos P, Maze I. ZBTB7A regulates MDD-specific chromatin signatures and astrocyte-mediated stress vulnerability in orbitofrontal cortex. *BioRxiv*, 2023/5/4.
4. Girdhar K, [Bendl J](#)*, Baumgartner A, Therrien K, Venkatesh S, Mathur D, Dong P, Rahman S, Kleopoulos SP, Misir R, Reach SM. The neuronal chromatin landscape in adult schizophrenia brains is linked to early fetal development. *medRxiv*. 2023 Oct 3.
* co-first author
5. Lee D, Porras C, Spencer C, Pjanic M, Weiler P, Kosoy R, [Bendl J](#), NM P, Wang X, Zheng S, Therrien K. Plasticity of Human Microglia and Brain Perivascular Macrophages in Aging and Alzheimer's Disease. *medRxiv*, 2023:2023-10.
6. Wang Q, Antone J, Alsop E, Reiman R, Funk C, [Bendl J](#), Dudley JT, Liang WS, Karr TL, Roussos P, Bennett DA, De Jager PL, Serrano GE, Beach TG, Van Keuren-Jensen K, Mastroeni D, Reiman EM, Readhead BP. A public resource of single cell transcriptomes and multiscale networks from persons with and without Alzheimer's disease. *bioRxiv*, 2023.10. 20.563319.
7. Kosoy R, Fullard JF, [Bendl J](#), Kleopoulos S, Shao Z, Argyriou S, Mathur D, Vicari J, Ma Y, Humphrey J, Brophy E, Raj T, Katsel P, Voloudakis G, Lee L, Bennett DA, Haroutunian V, Hoffman G, Roussos P. Alzheimer's disease transcriptional landscape in ex-vivo human microglia. *Research Square*, 2024/1/26 (doi.org/10.21203/rs.3.rs-3851590/v1).
8. Yixuan M, Girdhar K, Hoffman GE, Fullard J, [Bendl J](#)#, Roussos P#. Sex differences in brain cell-type specific chromatin accessibility in schizophrenia. *Research Square*, 2024/4/10 (https://doi.org/10.21203/rs.3.rs-4158509/v1).
co-senior author
9. Francis M, Gorman BR, Bigdeli TB, Genovese G, Voloudakis G, [Bendl B](#), Zeng B, ..., Saiju Pyarajan. Multi-ancestry genome-wide association meta-analysis of mosaic loss of chromosome Y in the Million Veteran Program identifies 167 novel loci. *medRxiv*. 2024/4/5 (doi.org/10.1101/2024.04.24.24306301).

VOLUNTARY PRESENTATIONS

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| 7/2023 | AAIC , Amsterdam, Netherlands: Transcriptomic profiling of prefrontal cortex reveals shared mechanisms underlying Alzheimer's and Parkinson's Diseases (poster) |
| 8/2022 | AAIC , San Diego, USA: Neuronal, glial and microglial maps of epigenetic and transcriptomics |

- dysregulations in Alzheimer's disease ([poster & short talk](#))
- 4/2022 **Charleston Conference on Alzheimer's Disease, Huwai, USA**, Hawaii, USA: Cell-type and brain region landscape in Alzheimer's disease ([oral presentation](#))
- 9/2021 **ASHG**: Lineage-specific analysis of epigenome and transcriptome changes in postmortem brains from Schizophrenia and Bipolar Disorder ([oral presentation](#))
- 3/2020 **Charleston Conference on Alzheimer's Disease**, Charleston, USA: Unraveling the mechanism underlying Alzheimer's disease by integrated analysis of gene expression, chromatin accessibility and genetic association studies ([oral presentation](#))
- 10/2019 **ASHG**, Houston, USA: Cell type and brain region-specific differential chromatin accessibility analysis in Alzheimer's disease ([poster](#))
- 4/2018 **Neuroscience Annual Retreat**, New York, USA: Profiling of chromatin accessibility and gene expression in stimulated neuronal cells of childhood-onset schizophrenia patients ([poster](#))
- 4/2017 **Neuroscience Annual Retreat**, New York, USA: Chromatin accessibility maps of human postmortem brain reveal epigenome brain-region-specific and cell-type-specific signatures ([poster](#))
- 7/2016 **ENBIK**, Loucen, Czech republic: PredictSNP2: Consensual predictor of the effect of nucleotide substitution on the development of monogenic diseases ([oral presentation](#))
- 7/2015 **Varl-SIG**, Dublin, Ireland: PredictSNP 2.0: A unified platform for prediction of disease-related mutations in entire human genome ([oral presentation](#))
- 9/2014 **Biochemical congress SSBMB and CSBMB**, Bratislava, Slovakia: HotSpot Wizard 2.0: Automated prediction of mutagenesis targets ([oral presentation](#))
- 6/2014 **ENBIK**, Kouty, Czech republic: PredictSNP 1.0: Predictor of the effect of amino acid substitutions on the protein function ([oral presentation](#))
- 7/2013 **SNP-SIG**, Berlin, Germany: PredictSNP: Robust and accurate consensus classifier for prediction of disease-related mutations ([poster presentation](#))
- 4/2012 **Student conference EEICT**, Brno, Czech republic: Integration system for functional annotation of single nucleotide polymorphism ([oral presentation](#))

TEACHING ACTIVITIES

Journals	17x review of article for peer-reviewed journals (https://orcid.org/my-orcid?)
Conferences	5x review of article for student conferences EEICT and Excel@FIT
Theses	3x review of Bachelor Thesis, 7x review of Diploma Thesis
Grants	1x review for Stichting Alzheimer Onderzoek (stopalzheimer.be) 2022-2024 Reviews for fellowships at Alzheimer's Association (>10)