# JAROSLAV BENDL

**jaroslav.bendl@gmail.com; phone: 917-365-6690**

## PERSONAL

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|---|---|
| Address | 4 Martine Ave, Apt 511, 10606 White Plains |
| Immigration status | Lawful permanent resident / no visa sponsorship needed |
| ORC ID | https://orcid.org/0000-0001-9989-2720 |
| Google Scholar | https://scholar.google.com/citations?user=2x8JUYQAAAAJ&hl=en&oi=ao |
| NIH Biosketch | https://www.ncbi.nlm.nih.gov/myncbi/1Xsir7k6Qnjks/cv/186343/ |
| Personal bio | http://www.JaroslavBendl.site/ |

## EMPLOYMENT

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|---|---|
| 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 |

## SKILLS

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| **NGS analysis** | **Bulk & single cell epigenome (ATAC-, ChIP-seq), transcriptome (RNA-seq)**: Expert knowledge<br>**WGS, SNP-array**: Working knowledge |
| **Programming** | **General:** Procedural and object-oriented paradigm<br>**C, C++:** Intermediate knowledge, standard library STL, Qt<br>**Java:** Intermediate knowledge<br>**Python:** Intermediate knowledge<br>**Web technologies:** Intermediate knowledge of XHTML, XML, CSS, PHP, SQL, GWT<br>**Others:** basics in C#, ASP.NET, Bash, x86 assembler, LaTeX |
| **Statistics** | **R**: expert knowledge<br>**WEKA**: user knowledge |
| **Grid computing** | Portable batch system (average consumption about 250,000 CPU hours annually) |

## EDUCATION

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|---|---|
| 1/2017 - 12/2019 | **Postdoctoral training** (mentor: Panos Roussos)<br>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)<br>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)<br>Brno University of Technology (CZ) · Faculty of Information Technology |
| 1/2011 - 6/2011 | **Internship**<br>Gjøvik University College · Faculty of Computer Science, Media and Technology · Gjøvik, Norway |
| 7/2009 - 8/2011 | **Master Degree** (awarded: 8/22/2011) |

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|---|---|
| | Brno University of Technology (CZ) · Faculty of Information Technology<br>Study programme: Bioinformatics and Biocomputing |
| 9/2006 - 6/2009 | **Bachelor Degree** (awarded 6/16/2009)<br>Brno University of Technology (CZ) · Faculty of Information Technology<br>Study programme: Information Technology |

## HONORS/AWARDS

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| 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)**<br>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)

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|---|---|---|---|
| **Alzheimer's Association (PI)**<br>Epigenetic and transcriptomics mechanisms of Alzheimer's disease (AARF-21-722200) | 10/2021 - 10/2023 | $120,000 | AARF |

## TRAINEES

**This information is not available for the public version of my resume.**
**Summary: 10 MSc students, 1 PhD candidate, 2 junior bioinformaticians**

## TEACHING ACTIVITIES

| Activity | Level | Role | Number of students | Number of hours | Years Tought |
|---|---|---|---|---|---|
| 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 | 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 16;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 21;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 5;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 3;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 25;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 8;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 1;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 26;45.

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 11;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 24;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 18;47(20):10597–611.

13. Hoffman GE, Bendl J, Girdhar K, Roussos P. decorate: differential epigenetic correlation test. *Bioinformatics*. 2020 May 1;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 4;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 19;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;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. 2021 Mar 25;

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 18;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 5;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 14:1-6.

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 26;13(1):1-7.

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.

Non-peer reviewed publications

1. Roussos P, Rahman S, Dong P, Apontes P, Fernando M, Townsley K, Girdhar K, Bendl J, Shao Z, Misir R, Tsankova N, Kleopoulos SP, Brennand K, Fullard J, Roussos P. From compartments to gene loops: Functions of the 3D genome in the human brain. b*ioRxiv*. 2021.

2. Chandrashekar PB, Wang J, Hoffman GE, He C, Jin T, Alatkar S, et al. DeepGAMI: Deep biologically guided auxiliary learning for multimodal integration and imputation to improve phenotype prediction. *bioRxiv*. 2022.

3. 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.

4. Ruzicka WB, Mohammadi S, Fullard JF, Davila-Velderrain J, Subburaju S, Tso DR, et al. Single-cell multi-cohort dissection of the schizophrenia transcriptome. *medRxiv*. 2022.

5. Zhu K*, Bendl J*, Rahman S, Vicari JM, Coleman C, Clarence T, et al. Multi-omic profiling of the developing human cerebral cortex at the single cell level. *bioRxiv*. 2022.

6. Als TD, Kurki M, Grove J, Voloudakis G, Therrien K, Tasanko E, et al. Identification of 64 new risk loci for major depression, refinement of the genetic architecture and risk prediction of recurrence and comorbidities. *medRxiv*. 2022.

7. 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. *medRxiv*. 2022.

## VOLUNTARY PRESENTATIONS

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**, Hawai, 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 **VarI-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)