

Curriculum Vitae: Jaroslav Bendl

Personal information

Name	Jaroslav Bendl
Telephone	+1-917-365-6690
Address	52 East 97th St, Apt 3M, 10029 New York
E-mail	jaroslav.bendl@mssm.edu
ORCID	0000-0001-9989-2720
ResearcherID	J-8269-2014
NIH Biosketch	https://www.ncbi.nlm.nih.gov/myncbi/1Xsir7k6Qnjks/cv/186343/
Professional Bio	http://www.JaroslavBendl.me

Education

09/2011 - 10/2016	Ph.D. Degree Brno University of Technology (CZ) · Faculty of Information Technology Dissertation topic: Prediction of the effect of amino acid substitutions on protein function
07/2009 - 08/2011	Master Degree Brno University of Technology (CZ) · Faculty of Information Technology Study programme: Bioinformatics and Biocomputing
09/2006 - 06/2009	Bachelor Degree Brno University of Technology (CZ) · Faculty of Information Technology Study programme: Information Technology

Employment summary & Participation on research projects

01/2020 - present	Senior Scientist · Roussos Lab · Department of Genetics and Genomics Sciences · Icahn School of Medicine at Mount Sinai · Manhattan, New York.
01/2017 – 12/2019	Postdoctoral Fellow · Roussos Lab · Department of Genetics and Genomics Sciences · Icahn School of Medicine at Mount Sinai · Manhattan, New York. Participation on projects: <ul style="list-style-type: none"> · R01AG057440 · Towards a comprehensive signaling pathway map of parahippocampal vulnerability in Alzheimer's Disease. · R01AG050986-03 · National Institute of Health · Higher order chromatin and genetic risk for Alzheimer's disease · R01MH109677-02 · National Institute of Health · Risk genetic variants and cis regulation of gene expression in bipolar disorder
03/2018 – 12/2019	Computational Biologist · James J. Peters, VA Medical Center · Bronx · New York. Participation on projects: <ul style="list-style-type: none"> · BX004189 Million Veteran Project: Large-scale transcriptome and epigenome association analysis across multiple traits.
01/2016 - 12/2016	Research Assistant · Loschmidt Laboratories · Department of Experimental Biology, Faculty of Science · Masaryk University · Brno, Czech Republic. Participation on projects: <ul style="list-style-type: none"> · GA16-06096S · Grant Agency of the Czech Republic: Clarifying the importance of dynamic tunnels for enzymatic catalysis: virtual simulation and fluorescence experiment · LM2015055 · Ministry of Education of the Czech republic: The national infrastructure C4SYS - Centre for Systems Biology
01/2012 - 12/2016	Research Assistant · International Clinical Research Centre · St. Anne's University Hospital Brno · Brno, Czech Republic. Participation on projects: <ul style="list-style-type: none"> · LQ1605 · Ministry of Education of the Czech republic St. Anne's University Hospital in Brno · Translational Medicine

01/2012 - 07/2015	<ul style="list-style-type: none"> · CZ.1.05/1.1.00/02.0123 · European Regional Development Fund St. Anne's University Hospital in Brno - International Clinical Research Center PhD student / technical stuff · Faculty of Information Technology · Brno University of Technology. Participation on projects: <ul style="list-style-type: none"> · FIT-S-11-2 · Brno University: Advanced recognition and presentation of multimedia data · FIT-S-14-2299 · Brno University: Research and application of advanced methods in ICT
01/2012 - 12/2016	Consultancy on bioinformatics and protein stabilization for biotech company ENANTIS Ltd. Participation on EU Project NewProt (KBBE.2011.3.6-01).

Bioinformatics and IT experience

Programming skills	General: Procedural and object-oriented paradigm C, C++: Intermediate knowledge, standard library STL, Qt Java: Intermediate knowledge Python: Intermediate knowledge Web technologies: Intermediate knowledge of XHTML, XML, CSS, PHP, SQL, GWT Others: basics in C#, ASP.NET, Bash, x86 assembler, LaTeX
Operating systems	GNU / Linux: Intermediate knowledge of maintenance and configuration (primary operating system for about six years)
Statistics	R: expert knowledge WEKA: user knowledge (used within both R/Python pipelines)
Grid computing	Portable batch system (average consumption about 5,000-10,000 CPU days per year)
Responsibilities	PredictSNP1 · Development and maintenance · http://loschmidt.chemi.muni.cz/predictsnp1 PredictSNP2 · Development and maintenance · http://loschmidt.chemi.muni.cz/predictsnp2 HotSpot Wizard 2 · Development and maintenance · http://loschmidt.chemi.muni.cz/hotspotwizard2 FireProt · Co-development · http://loschmidt.chemi.muni.cz/hotspotwizard2

Internships & Academic stays

4/2015 - 7/2015	Griffith University (Australia) · Institute for Glycomics · Laboratory of Molecular Biology and Bioinformatics Topic: Development of computational predictor of mRNA half-life
1/2011 - 6/2011	Gjøvik University College (Norway) · Faculty of Computer Science, Media and Technology Topic: Study courses in the area of machine learning and pattern recognition

International courses

6/2018	Epigenomics bootcamp , Columbia University, New York, USA
3/2012	Winter school in methods in bioinformatics , Universitat Rovira i Virgili, Tarragona, Spain
7/2011	Summer school on bioinformatics , Comenius University, Bratislava, Slovakia

Pedagogical activities

2011 - 2015	Bioinformatics practices: lecturing practical exercises (6 lectures per semester)
2011 - 2015	Supervision of bachelor theses: 4x (2 theses awarded by Dean's prize)
2012 - 2015	Supervision of diploma theses: 8x (3 theses awarded by Dean's prize)

Honors and awards

03/2020	Finalist and selected attendee of Charleston Conference on Alzheimer's Disease
10/2019	Poster Award by NanoCollect and ActiveMotif (ASHG conference)

01/2019-01/2021	Young Investigator Award , The Brain & Behavior Research Foundation (NARSAD) Name of the project: Unraveling the Mechanism Underlying Bipolar Disorder by Integrated Analysis of Gene Expression, Chromatin Accessibility and Genetic Association Studies
10/2016	Dean's award for outstanding dissertation thesis
04/2016	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 Award for PredictSNP article (doi 10.1371/journal.pcbi.1003440): ranked among the top 4 articles out of 1,594 articles published and cited in 2014
04/2012	Best conference paper award · Student conference EEICT · Category Bioinformatics and Biomedical engineering Award for conference article "Integration System for Functional Annotation of Single Nucleotide Polymorphism"
08/2011	Dean's award for very good study results during master studies and very good knowledge during state final examination
06/2009	Dean's award for very good study results during bachelor studies and very good knowledge during state final examination

Peer review activities

Journals	>10x review of article for peer-reviewed journals (https://publons.com/author/200326)
Conferences	5x review of article for student conferences EEICT and Excel@FIT
Theses	3x review of Bachelor Thesis, 7x review of Diploma Thesis

Talks and presentations at conferences

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)

Research overview

Summary	Co-author of 13 publications with >350 citations, 1 book-chapter and 4 software tools (FireProt, PredictSNP1, PredictSNP2 and HotSpot Wizard 2) with more than 10,000 users worldwide.
Peer-reviewed papers	<ul style="list-style-type: none"> • Espeso-Gil S*, Halene T*, <u>Bendl J</u>, Kassim B, ..., Schahram A, 2020: A chromosomal connectome for psychiatric and metabolic risk variants in adult dopaminergic neurons. Genome Medicine 12. • Hoffman GE, Bendl J, Girdhar K, Roussos P, 2020: decorate: differential epigenetic correlation test. Bioinformatics. • Hoffman GE, <u>Bendl J</u>, ..., Roussos P, 2019: CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data 6. • Hoffman GE, <u>Bendl J</u>, Girdhar K, Schadt EE, Roussos P., 2019: Functional interpretation of genetic variants using deep learning predicts impact on chromatin accessibility and histone modification. Nucleic Acids Research: gkz808. • Wang M, Beckmann ND, ..., <u>Bendl J</u>, ..., Haroutunian V, Schadt E, Zhang B, 2018: The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. Scientific Data 5: 180185. • Fullard JF, Hauberg ME, <u>Bendl J</u>, Egervari G, Cirnaru M-D, Reach SM, Motl J, Ehrlich ME, Hurd YL, Roussos P, 2018: An atlas of chromatin accessibility in the adult human brain. Genome Research 8: 1243-1252. • Schwarte A, Genz M, Skalden L, Nobili A, Vickers C, Melse O, Kuipers R, Joosten HJ, Stourac J, <u>Bendl J</u>, ..., Venselaar H, 2017: NewProt - Protein Engineering Portal. Protein Engineering, Design and Selection 30: 441-7 • <u>Bendl J</u>*, Stourac J*, Sebestova E, Vavra O, Musil M., Brezovsky J, Damborsky J, 2016: HotSpot Wizard 2.0: Automated Design of Site-Specific Mutations and Smart Libraries in Protein Engineering. Nucleic Acids Research 44: W479-W487 • <u>Bendl J</u>*, Musil M*, Stourac J*, Zendulka J, Damborský J, Brezovsky J, 2016: PredictSNP2: A Unified Platform for Accurately Evaluating SNP Effects by Exploiting the Different Characteristics of Variants in Distinct Genomic Regions. PLOS Computational Biology 12: e1004962 • Bednar D*, Beerens K*, Sebestova E, <u>Bendl J</u>, Khare S, Chaloupkova R, Prokop Z, Brezovsky J, Baker D, Damborsky J, 2015. FireProt: Energy- and Evolution-Based Computational Design of Thermostable Multiple-Point Mutants. PLoS Computational Biology 11: e1004556 • <u>Bendl J</u>, Stourac J, Salanda O, Pavelka A, Wieben ED, Zendulka J, Brezovsky J, Damborsky J, 2014. PredictSNP: Robust and Accurate Consensus Classifier for Prediction of Disease-Related Mutations. PLoS Computational Biology 10: e1003440 • Musil M*, Stourac J*, <u>Bendl J</u>, Brezovsky J, Prokop Z, Zendulka J, Martinek T, Bednar D, Damborsky J, 2017: FireProt: web server for automated design of thermostable proteins. Nucleic Acids Research 45: W393-399 • Kurumbang NP*, Dvorak P*, <u>Bendl J</u>, Brezovsky J, Prokop Z, Damborsky J, 2014. Computer-Assisted Engineering of the Synthetic Pathway for Biodegradation of a Toxic Persistent Pollutant. ACS Synthetic Biology 3: 172–181 • Dvorak P, Kurumbang NP, <u>Bendl J</u>, Brezovsky J, Prokop Z, Damborsky J, 2014. Maximizing the Efficiency of Multienzyme Process by Stoichiometry Optimization. ChemBioChem 15: 1891–1895

Preprints	<ul style="list-style-type: none"> Novikova G, Kapoor M, Julia TC, Abud EM, Efthymiou AG, Cheng H, Fullard JF, Bendl J, Roussos P, Poon WW, Hao K. Integration of Alzheimer's disease genetics and myeloid cell genomics identifies novel causal variants, regulatory elements, genes and pathways. BioRxiv: 694281. Bowles K, Pugh DA, Farrell K, ..., Goate AM, 2019. 17q21. 31 sub-haplotypes underlying H1-associated risk for Parkinson's disease and progressive supranuclear palsy converge on altered glial regulation BioRxiv: 860668.
Book chapter	<ul style="list-style-type: none"> Sebestova E, Bendl J, Brezovsky J, Damborsky J, 2014. Computational Tools for Designing Smart Libraries. In Directed Evolution Library Creation: Methods and Protocols, Methods in Molecular Biology, 2nd edition, Humana Press, New York, pp. 291-314
Consortia authorship papers	<ul style="list-style-type: none"> Breen M, et al., 2019: Global landscape and genetic regulation of RNA editing in cortical samples from individuals with schizophrenia. Nature Neuroscience 22: 1402–1412 PsychENCODE Consortium, 2019: Revealing the brain's molecular architecture. Science 362: 6420 Gandal MJ, 2018: Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder Science 362: 6420 Amiri A, et al., 2018. Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science 362: 6420 Li M., et al., 2018. Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science 362: 6420