# Curriculum Vitae: Jaroslav Bendl

## Personal information

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| ORCID | 0000-0001-9989-2720 |
| ResearcherID | J-8269-2014 |

## Education

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

## Employment summary & Participation on research projects

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| 01/2017 - present | **Postdoctoral Fellow** · Roussos Lab · Department of Genetics and Genomics Sciences · Icahn School of Medicine at Mount Sinai · Manhattan, New York. Participation on projects:<br>· R01AG057440 · Towards a comprehensive signaling pathway map of parahippocampal vulnerability in Alzheimer's Disease.<br>· R01AG050986-03 · National Institute of Health · Higher order chromatin and genetic risk for Alzhaimer's disease<br>· R01MH109677-02 · National Institute of Health · Risk genetic variants and cis regulation of gene expression in bipolar disorder |
| 03/2018 – present | **WOC Researcher** · James J. Peters, VA Medical Center · Bronx ·New York. Participation on projects:<br>· 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:<br>· GA16-06096S · Grant Agency of the Czech Republic: Clarifying the importance of dynamic tunnels for enzymatic catalysis: virtual simulation and fluorescence experiment<br>· 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:<br>· LQ1605 · Ministry of Education of the Czech republic<br>St. Anne´s University Hospital in Brno · Translational Medicine<br>· CZ.1.05/1.1.00/02.0123 · European Regional Development Fund<br>St. Anne´s University Hospital in Brno - International Clinical Research Center |
| 01/2012 - 07/2015 | **PhD student / technical stuff** · Faculty of Information Technology · Brno University of Technology. Participation on projects:<br>· FIT-S-11-2 · Brno University: Advanced recognition and presentation of multimedia data |

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| 01/2012 - 12/2016 | · <u>FIT-S-14-2299</u> · Brno University: Research and application of advanced methods in ICT<br>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

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| Programming skills | **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 |
| Operating systems | **GNU / Linux**: Intermediate knowledge of maintenance and configuration<br>(primary operating system for about six years) |
| Statistics | **R, WEKA** |
| 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<br>**PredictSNP2** · Development and maintenance · http://loschmidt.chemi.muni.cz/predictsnp2<br>**HotSpot Wizard 2** · Development and maintenance · http://loschmidt.chemi.muni.cz/hotspotwizard2<br>**FireProt** · Co-development · http://loschmidt.chemi.muni.cz/hotspotwizard2 |

## Internships & Academic stays

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

## International courses

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| 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

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| 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

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| 01/2019-01/2021 | **Young Investigator Award**, The Brain & Behavior Research Foundation (NARSAD)<br>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 |
| 11/2015 | **Best journal paper award · IMIA Yearbook · Category Bioinformatics and Translational Informatics**<br>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** |
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| | 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

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| 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

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| 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) |

## Research overview

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| 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 2,000 users worldwide. |
| Peer-reviewed papers | Wang M, Beckmann ND, Roussos P, Wang E, Zhou X, Wang Q, Ming C, Neff R, Ma W, Fullard J, Hauberg ME, Bendl J, Peters MA, Logsdon B, Wang P, Mahajan M, Mangravite LM, Dammer EB, Duong DM, Lah JJ, Seyfried NT, Levey AI, Buxbaum JD, Ehrlich M, Gandy S, Katsel P, 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, Bendl J, 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, Bendl J, Black J, 2017: NewProt - Protein Engineering Portal**. Protein Engineering, Design and Selection** 30: 441-7

Bendl J*, 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 Journal** 44: W479-W487

Bendl J*, 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, Bendl J, 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

Bendl J, 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*, Bendl J, 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*, Bendl J, 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, Bendl J, Brezovsky J, Prokop Z, Damborsky J, 2014. Maximizing the Efficiency of Multienzyme Process by Stoichiometry Optimization. **ChemBioChem** 15: 1891–1895

* These authors contributed equally

| Consortia authorship papers | Amiri A, et al., 2018. Transcriptome and epigenome landscape of human cortical development modeled in organoids. **Science** 362: 6420 (eaat6720)<br><br>Li M., et al., 2018. Integrative functional genomic analysis of human brain development and neuropsychiatric risks. **Science** 362: 6420 (eaat7615) |
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| Preprints | 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** 2019: 694281. |
| Book chapter | 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 |