

## I. GENERAL INFORMATION

### Olga Vitek

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#### A Education

- Post-doc, 2006 Proteomics, Institute for Systems Biology, Seattle WA  
Supervisor: R. Aebersold
- PhD, 2005 Statistics, Purdue University, West Lafayette IN  
Co-advisors: B. A. Craig, Statistics, Purdue University and  
C. Bailey-Kellogg, Computer Science, Dartmouth College.  
Dissertation:  
*"An inferential approach to protein backbone nuclear magnetic resonance assignment"*
- M.S., 2001 Mathematical Statistics, Purdue University, West Lafayette IN
- M.S., 1997 Econometrics and Statistics, University of Geneva, Switzerland  
Advisor: E. Ronchetti, University of Geneva  
Dissertation: *"Tree-based classifiers with application to medical data"*
- B.S., 1995 Econometrics and Statistics, University of Geneva, Switzerland

#### B Previous Positions

- 2011 - 2014 Associate Professor, Statistics (90%) and Computer Science (10%), Purdue University
- 2012 - 2013 Visiting Associate Professor, Department of Radiology, Stanford University
- 2006 - 2011 Assistant Professor, Statistics (90%) and Computer Science (10%), Purdue University
- 2004 - 2004 Intern in Proteomics, Eli Lilly and Company, Indianapolis IN
- 2001 - 2005 Research assistant, Purdue University, West Lafayette IN
- 2000 - 2000 Member, Statistical Consulting Service, Purdue University, West Lafayette IN
- 1996 - 1999 Teaching assistant, University of Geneva, Switzerland
- 1997 - 1998 Statistician, University Hospitals, Geneva, Switzerland
- 1996 - 1997 Member, Laboratory of Applied Economics, University of Geneva, Switzerland

#### C Present Position

- 2014 - now Sy and Laurie Sternberg Interdisciplinary Chair and Associate Professor,  
College of Science, College of Computer and Information Science, Northeastern University
- 2014 - now Faculty Fellow, Barnett Institute for Chemical and Biological Analysis, Northeastern University
- 2014 - now Adjunct Associate Professor, Department of Statistics, Purdue University
- 2015 - now Faculty Affiliate, Tufts Clinical and Translational Sciences Institute

## **D Awards and Honors**

- 2014 Sy and Laurie Sternberg Interdisciplinary Chair, Northeastern University
- 2013 University Faculty Scholar, Purdue University
- 2011 National Science Foundation CAREER Award
- 2010 Outstanding Assistant Professor Teaching Award, Department of Statistics, Purdue University
- 2010 Graduate Student Mentoring Award, College of Science, Purdue University
- 2008 Teaching for Tomorrow Award, Office of the Provost, Purdue University
- 2008 Member, Sigma Xi
- 2005 Laha Travel Award, Institute of Mathematical Statistics
- 2004 Graduate School Dissertation Fellowship, Purdue University
- 2003 Charlie Sampson Best Poster Award, Midwest Biopharmaceutical Statistics Workshop, IN
- 1997 Prize of the Industrial Services of Geneva, Geneva, Switzerland

## **E Professional and Scholarly Associations**

- American Society for Mass Spectrometry (ASMS)
- American Statistical Association (ASA)
- The Association of Biomolecular Resource Facilities (ABRF)
- International Society for Computational Biology (ISCB)
- United States Human Proteome Organization (US HUPO)
- World Human Proteome Organization (HUPO)

## II. TEACHING

### A Teaching Assignments at Northeastern University

Semester	Title of the Course	Type	Median course evaluation*		Median instructor evaluation*		Respond / Enroll
			Vitek	CS faculty	Vitek	CS faculty	
Spring 2016	Topics in Statistics & Data	Grad					8 / 13
Fall 2015	Data Mining Techniques	MS	4.1	3.9	4.2	4.3	20 / 35
Spring 2015	Statistics for Big Data	Grad	4.4	3.3	4.9	4.1	8 / 13

### B Teaching Assignments at Purdue

Semester	Title of the Course	Type	Median course evaluation*		Median instructor evaluation*		Respond / Enroll
			Vitek	Dept.	Vitek	Dept.	
Spring 2014	Advanced Stat. Methodology	Grad	4.6	4.1	4.6	4.0	23 / 32
Fall 2013	Stat. Methods for Bioinformatics	Grad	4.3	-	4.3	-	8 / 12
Spring 2012	Advanced Stat. Methodology	Grad	4.3	4.1	4.7	4.0	14 / 27
Fall 2011	Stat. Methods for Bioinformatics	Grad	4.6	-	4.8	-	11 / 19
Spring 2011	Advanced Stat. Methodology	Grad	4.7	4.1	4.6	4.0	19 / 29
Fall 2010	Intermediate Stat. Methodology	Grad	4.9	4.4	4.9	4.4	21 / 34
Spring 2010	Advanced Stat. Methodology	Grad	4.5	4.1	4.5	4.0	12 / 16
Fall 2009	Stat. Methods for Bioinformatics	Grad	5.0	-	5.0	-	13 / 14
Spring 2009	Intermediate Stat. Methodology	Grad	4.6	4.4	4.6	4.4	9 / 14
Fall 2008	Intermediate Stat. Methodology	Grad	4.2	4.4	4.0	4.4	25 / 28
Spring 2008	Intermediate Stat. Methodology	Grad	4.7	4.4	4.7	4.4	9 / 11
Fall 2007	Stat. Methods for Bioinformatics	Grad	4.7	-	4.8	-	11 / 11
Spring 2007	Stat. Methods for Biology	So.-Gr.	4.2	3.7	4.6	3.8	27 / 36
Fall 2006	Stat. Methods for Biology	So.-Gr.	4.1	3.7	4.5	3.8	31 / 38

\* Student evaluation on a scale from 1="Very poor" to 5="Excellent".

## C Tutorials and Short Courses

- 2016 PRBB, Barcelona, Spain  
“EMBO targeted proteomics course”.  
1 week, lecturer.
- 2016 Varna, Italy.  
“EMBO advanced proteomics workshop.”.  
1 week, lecturer.
- 2016 University of Washington, Seattle WA.  
“Targeted proteomics course”.  
1 week, lecturer.
- 2016 Northeastern University, Boston, MA.  
“Computation & statistics for targeted proteomics.”.  
1 week, co-organizer.
- 2016 Annual Conference of the US Human Proteome Organization (US HUPO).  
“Design and analysis of quantitative proteomic experiments.”.  
1 day, co-instructor.
- 2016 Buck Institute, North San Francisco, CA.  
“Targeted proteomics course. ”.  
1 week, lecturer.
- 2016 ETH Zürich, Switzerland  
“Targeted proteomics course.”.  
1 week, lecturer.
- 2015 PRBB, Barcelona, Spain  
“EMBO targeted proteomics course: experimental design and data analysis”.  
1 week, lecturer.
- 2015 Cold Spring Harbor, NY.  
“Targeted quantitative proteomics”.  
1 week, lecturer.
- 2015 ETH Zürich, Switzerland.  
“Targeted proteomics”.  
1 week, co-instructor.
- 2015 Northeastern University, Boston MA.  
“Mass spectrometry-based proteomics: computation and statistics for discovery and targeted analysis”.  
1 week, co-organizer and co-instructor.
- 2015 University of Washington, Seattle WA.  
“Targeted quantitative proteomics”.  
1 week, co-instructor.
- 2015 Annual Conference of the US Human Proteome Organization (US HUPO).  
“Design and analysis of quantitative proteomic experiments.”.  
1 day, co-instructor.
- 2014 Barcelona, Spain.  
“EMBO practical course on targeted proteomics”.  
1 week, co-instructor.
- 2014 Brixen, Italy.  
The FEBS Advanced Lecture Course / 8th European Summer School on Advanced Proteomics.  
1 week, invited lecturer.

- 2014 Annual Conference of the US Human Proteome Organization (US HUPO).  
*"Quantitative proteomics"*.  
 1 day, organizer and co-instructor.
- 2014 University of Washington, Seattle WA.  
*"Targeted quantitative proteomics"*.  
 1 week, co-instructor.
- 2014 ETH Zürich, Switzerland.  
*"Targeted proteomics using selected reaction monitoring"*.  
 1 week, co-instructor.
- 2013 ETH Zürich, Switzerland.  
*"Selected reaction monitoring"*.  
 1 week, co-instructor.
- 2013 Annual Conference of the US Human Proteome Organization (US HUPO).  
*"Statistical methods for quantitative proteomics"*.  
 1 day, organizer and co-instructor.
- 2012 Annual World Congress of the World Human Proteome Organization (HUPO).  
*"Quantitative bottom-up proteomics"*.  
 1 day, co-instructor.
- 2012 Purdue Symposium on Statistics.  
*"Statistical design of experiments and linear mixed models, & applications in bioinformatics"*.  
 2 days, co-organizer and co-instructor.
- 2012 Annual Conference of the US Human Proteome Organization (US HUPO).  
*"Quantitative bottom-up proteomics"*.  
 1 day, co-instructor.
- 2011 International Conference on Intelligent Systems in Molecular Biology (ISMB).  
*"An insight into computational and statistical mass spectrometry-based proteomics"*.  
 1/2 day, co-instructor.
- 2011 Annual Conference of the US Human Proteome Organization (US HUPO).  
*"Quantitative bottom-up proteomics"*.  
 1 day, co-instructor.
- 2011 Australasian Proteomics Society Workshop.  
*"Statistical design & analysis of quantitative mass spectrometry-based proteomics"*.  
 1 day, co-instructor.
- 2011 Indian Institute of Sciences.  
*"Statistical Methods for High-Throughput Quantitative Experiments in Molecular Biology"*.  
 1 day, co-instructor.
- 2010 International Conference on Intelligent Systems in Molecular Biology (ISMB).  
*"An insight into computational and statistical mass spectrometry-based proteomics"*.  
 1/2 day, co-instructor.
- 2010 Research in Computational Molecular Biology (RECOMB) Satellite Conference on Computational Proteomics.  
*"Statistical design & analysis of quantitative mass spectrometry-based proteomic experiments"*.  
 1/4 day, instructor.
- 2010 Wrocław Institute of Technology, Poland.  
*"Computational and statistical analysis of biomolecular networks"*.  
 1 week, instructor.

## **D Other Contributions to Undergraduate Education**

1. Undergraduate student project: Mr. Yu Suo, Computer Science (Spring - Summer 2009) “*Computational analysis of post-translational modifications in mass spectrometry-based proteomics*”.
2. Undergraduate student project: Mr. Rob Gevers, Computer Science (Summer 2007 - Summer 2009) “*Computational analysis of search space in database-based identification of tandem mass spectra*”.
  - Best abstract award, Undergraduate Research and Poster Symposium, Purdue, 2008.
  - Honorable mention, Computing Research Association (CRA), 2008.
3. Vertical Integration of Research and Education in the Mathematical Sciences (VIGRE) Liftoff Seminar (Fall 2007, Fall 2008, Fall 2009, Fall 2010, Fall 2011). Department of Statistics, Purdue.

### III. DISCOVERY

#### A Publications

##### A.1 Refereed Research Publications

1. K. D. Bemis, A. Harry, L. S. Eberlin, C. R. Ferreira, S. M. van de Ven, P. Mallick, M. Stolowitz, O. Vitek. "Probabilistic segmentation of mass spectrometry images helps select important ions and characterize confidence in the resulting segments". *Molecular & Cellular Proteomics*, in press, 2016.
2. R. Ness, K. Sachs, O. Vitek. "From correlation to causality: statistical approaches to learning regulatory relationships in large-scale biomolecular investigations". *Journal of Proteome Research*, in press, 2016.
3. E. Borràs, E. Cantó, M. Choi, L. M. Villar, J. C. Ivarez-Cermeo, C. Chiva, X. Montalban, O. Vitek, M. Comabella, E. Sabid. "Protein-based classifier to predict conversion from clinically isolated syndrome to multiple sclerosis". *Molecular & Cellular Proteomics*, M115.053256, 2016.
4. S. Surinova, M. Choi, S. Tao, P. J. Schüffler, C.-Y. Chang, T. Clough, K. Vyslouil, M. Khoylou, J. Srovnal, Y. Liu, M. Matondo, R. Httenhain, H. Weisser, J. M. Buhmann, M. Hajdch, H. Brenner, O. Vitek, R. Aebersold. "Prediction of colorectal cancer diagnosis based on circulating plasma proteins". *EMBO Molecular Medicine*, in press, 2015.
5. S. Surinova, L. Radová, M. Choi, J. Srovnal, H. Brenner, O. Vitek, M. Hajdúch, R. Aebersold. "Non-invasive prognostic protein biomarker signatures associated with colorectal cancer". *EMBO Molecular Medicine*, 7:1153, 2015.
6. M. J. Rardin, B. Schilling, Lin.-Y. Cheng, B. X. MacLean, D. J. Sorenson, A. K. Sahu, M. J. MacCoss, O. Vitek and B. W. Gibson. "MS1 peptide ion intensity chromatograms in MS2 (SWATH) data independent acquisitions: Improving post acquisition analysis of proteomic experiments". *Molecular & Cellular Proteomics*, O115.048181, 2015.
7. A. Palmer, E. Ovchinnikova, M. Thune, R. Lavigne, B. Guevel, A. Dyatlov, O. Vitek, C. Pineau, M. Boren, T. Alexandrov. "Using collective expert judgements to evaluate quality measures of mass spectrometry images". *Bioinformatics* 31:i375, 2015.
8. K. D. Bemis, A. Harry, L. S. Eberlin, C. Ferreira, S. M. van de Ven, P. Mallick, M. Stolowitz, O. Vitek. "Cardinal: an R package for statistical analysis of mass spectrometry-based imaging experiments". *Bioinformatics*, 31:2418, 2015.
9. R. Bruderer, O. M. Bernhardt, T. Gandhi, S. M. Miladinovic, L.-Y. Cheng, S. Messner, T. Ehrenberger, V. Zantotelli, Y. Butscheid, C. Escher, O. Vitek, O. Rinner, L. Reiterd. "Extending the limits of quantitative proteome profiling with data-independent acquisition and application to acetaminophen treated 3D liver microtissues". *Molecular and Cellular Proteomics*, M114.044305, 2015.
10. Y. Liu, A. Buil, B. C. Collins, L. C. J. Gillet, L. C. Blum, L.-Y. Cheng, O. Vitek, J. Mouritsen, G. Lachance, T. D. Spector, E. T. Dermitzakis, R. Aebersold. "Quantitative variability of 342 plasma proteins in a human twin population". *Molecular Systems Biology*, 11:786, 2015.
11. N. Selevsek, C.-Y. Chang, L. C. Gillet, P. Navarro, O. M. Bernhardt, L. Reiter, L.-Y. Cheng, O. Vitek, R. Aebersold. "Reproducible and consistent quantification of the *Saccharomyces cerevisiae* proteome by SWATH-MS". *Molecular and Cellular Proteomics*, M113.035550, 2015.
12. M. Choi, C.-Y. Chang, T. Clough, D. Broudy, T. Killeen, B. MacLean, O. Vitek. "MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments". *Bioinformatics*, 30:2524-2526, 2014.
13. D. Broudy, T. Killeen, M. Choi, N. Shulman, D. R. Mani, S. E. Abbatiello, D. Mani, R. Ahmad, A. K. Sahu, B. Schilling, K. Tamura, Y. Boss, V. Sharma, B. W. Gibson, S. A. Carr, O. Vitek, M. J. MacCoss, B. MacLean. "A framework for installable external tools in Skyline". *Bioinformatics*, 30:2521-2523, 2014.
14. C.-Y. Chang, E. Sabidó, R. Aebersold, O. Vitek. "Targeted protein quantification using sparse reference label-

- ing". *Nature Methods*, 11:301-304, 2014.
15. S. Carr, S. E. Abbatiello, B. L. Ackermann, C. Borchers, B. Domon, E. W. Deutsch, R. P. Grant, A. N. Hoofnagle, R. Httenhain, J. M. Koomen, D. C. Liebler, T. Liu, B. MacLean, D. R. Mani, E. Mansfield, H. Neubert, A. G. Paulovich, L. Reiter, O. Vitek, R. Aebersold, L. Anderson, R. Bethem, J. Blonder, E. Boja, J. Botelho, M. Boyne, R. A. Bradshaw, A. L. Burlingame, D. Chan, H. Keshishian, E. Kuhn, C. Kinsinger, J. Lee, S.-W. Lee, R. Moritz, J. Oses-Prieto, N. Rifai, J. Ritchie, H. Rodriguez, P. R. Srinivas, R.R. Townsend, J. Van Eyk, G. Whiteley, A. Wiita, S. Weintraub. "Targeted peptide measurements in biology and medicine: best practices for mass spectrometry-based assay development using a fit-for-purpose approach". *Molecular and Cellular Proteomics*, Article M113.036095, 2014.
  16. F. Cerciello, M. Choi, A. Nicastrì, D. Bausch-Fluck, A. Ziegler, O. Vitek, E. Felley-Bosco, R. Stahel, R. Aebersold, B. Wollscheid. "Identification of a seven glycopeptide signature for malignant pleural mesothelioma in human serum by selected reaction monitoring". *Clinical Proteomics*, 10:16, 2013.
  17. S. Surinova, R. Hüttenhain, C.-Y. Chang, O. Vitek, R. Aebersold. "Automated SRM data analysis workflow for large scale targeted proteomic studies". *Nature Protocols*, 8:1602-1619, 2013.
  18. E. Sabidó, Y. Wu, L. Bautista, T. Porstmann, C.-Y. Chang, O. Vitek, M. Stoffel, R. Aebersold. "Targeted proteomics reveals strain-specific changes in the mouse insulin and central metabolic pathways after sustained high-fat diet", *Molecular Systems Biology*, 9, article 681, 2013.
  19. D. Yu, W. Huber, O. Vitek. "Shrinkage estimation of dispersion in Negative Binomial models for RNA-seq experiments with small sample size". *Bioinformatics*, 29:1275-1282, 2013.
  20. D. Yu, J. M. C Danku, I. Baxter, S. Kim, O. K. Vatamaniuk, O. Vitek, D. E. Salt. "High-resolution genome-wide scan of genes, gene-networks and cellular systems impacting the yeast ionome". *BMC Genomics*, 13:623, 2012.
  21. T. Clough, S. Thaminy, S. Ragg, R. Aebersold, O. Vitek. "Statistical protein quantification and significance analysis in label-free LC-MS experiments with complex designs". *BMC Bioinformatics*, 13:S16, 2012.
  22. K. Ma, O. Vitek, A. I. Nesvizhskii. "A statistical model-building perspective to identification of MS/MS spectra with PeptideProphet". *BMC Bioinformatics*, 13:S16, 2012.
  23. J. K. Muhlemann, H. Maeda, C.-Y. Chang, P. San Miguel, I. Baxter, B. Cooper, M. A. Perera, B. J. Nikolau, O. Vitek, J. A. Morgan, N. Dudareva. "Developmental changes in the metabolic network of snapdragon flowers". *PLoS One*, 7(7): e40381, 2012.
  24. E. Sabidó, O. Quehenberger, Q. Shen, C.-Y. Chang, I. Shah, A. M. Armando, A. Andreyev, O. Vitek, E. A. Dennis, R. Aebersold. "Targeted proteomics of the Eicosanoid biosynthetic pathway completes an integrated genomics-proteomics-metabolomics picture of cellular metabolism. *Molecular and Cellular Proteomics*, Article M111.014746, 2012.
  25. C.-Y. Chang, P. Picotti, R. Hüttenhain, V. Heinzlmann-Schwarz, M. Jovanovic, R. Aebersold, O. Vitek. "Protein significance analysis in selected reaction monitoring (SRM) measurements". *Molecular and Cellular Proteomics*, Article M111.014662, 2012.
  26. T. Ye, C. Zheng, S. Zhang, G. A. N. Gowda, O. Vitek, D. Raftery. "Add to Subtract: A simple method to remove complex background signals from the 1H nuclear magnetic resonance spectra of mixtures". *Analytical Chemistry*, 84, p. 994-1002, 2012.
  27. L. Käll, O. Vitek. "Computational mass spectrometry-based proteomics". *PLoS Computational Biology*, 7, e1002277, 2011.
  28. L. S. Riter, P. K. Jensen, J. M. Ballam, E. Urbanczyk-Wochniak, T. Clough, O. Vitek, J. Sutton, M. Athanas, M. F. Lopez, S. MacIsaac. "Evaluation of label-free quantitative proteomics in a plant matrix: A case study of the night-to-day transition in corn leaf". *Analytical Methods*, 3, p. 2733-2739, 2011.
  29. D. Yu, J. Danku, I. Baxter, S. Kim, O. K. Vatamaniuk, D. E. Salt, O. Vitek. "Noise reduction in genome-wide perturbation screens using linear mixed-effect models". *Bioinformatics*, 27, p. 2173-2180, 2011.



30. T. Clough, S. Braun, V. Fokin, I. Ott, S. Ragg, G. Schadow, O. Vitek. "Statistical design and analysis of label-free LC-MS proteomic experiments: A case study of coronary artery disease". *Methods in Molecular Biology*, 728, p.293-319, 2011.
31. C. Zheng, S. Zhang, S. Ragg, D. Raftery, O. Vitek. "Identification and quantification of metabolites in <sup>1</sup>H NMR spectra by Bayesian model selection". *Bioinformatics*, 27, p. 1637-1644, 2011.
32. A. L. Dill, L. S. Eberlin, A. B. Costa, C. Zheng, D. R. Ifa, L. Cheng, T. A. Masterson, M. O. Koch, O. Vitek, R. G. Cooks. "Multivariate statistical identification of human bladder carcinomas using ambient ionization imaging mass spectrometry". *Chemistry: A European Journal*, 17, p. 2897-2902, 2011.
33. B. Bodenmiller, S. Wanka, C. Kraft, J. Urban, D. Campbell, P. Pedrioli, B. Gerrits, P. Picotti, H. Lam, O. Vitek, M.-Y. Brusniak, B. Roschitzki, C. Zhang, R. Schlapbach, K. Shokat, A. Colman-Lerner, A. Nesvizhskii, M. Peter, R. Loewith, C. von Mering and R. Aebersold. "Phosphoproteomic analysis reveals interconnected system-wide responses to perturbations of kinases and phosphatases in yeast". *Science Signaling*, 3, rs4, 2010.
34. I. Baxter, J. N. Brazelton, D. Yu, Y. S. Huang, B. Lahner, E. Yakubova, Y. Li, J. Bergelson, J. O. Borevitz, M. Nordborg, O. Vitek, D. E. Salt. "A coastal cline in sodium accumulation in *Arabidopsis thaliana* is driven by natural variation of the sodium transporter *AtHKT1;1*". *PLoS Genetics*, in press, 2010.
35. A. L. Dill, L. S. Eberlin, A. B. Costa, C. Zheng, D. R. Ifa, L. Cheng, T. A. Masterson, M. O. Koch, O. Vitek, R. G. Cooks. "Multivariate statistical differentiation of renal cell carcinomas based on lipidomic analysis by ambient ionization imaging mass spectrometry". *Analytical and Bioanalytical Chemistry*, 398, p. 2969-2978, 2010.
36. T. Clough, M. Key, I. Ott, S. Ragg, G. Schadow, O. Vitek "Protein quantification in label-free LC-MS experiments". *Journal of Proteome Research*, 8, p. 5275-5284, 2009.
37. C. Sherwood, A. Eastham, L. W. Lee, J. Risler, O. Vitek, D. B. Martin. "Correlation between y-type ions observed in ion trap and triple quadrupole mass spectrometers". *Journal of Proteome Research*, 8, p. 4243-4251, 2009.
38. S. Zhang, C. Zheng, I. R. Lanza, K. S. Nair, D. Raftery, O. Vitek. "Interdependence of signal processing and analysis of urine <sup>1</sup>H NMR spectra for metabolic profiling. *Analytical Chemistry*, 81, p. 6080-6088, 2009.
39. O. Vitek. "Getting started in computational mass spectrometry-based proteomics". *PLoS Computational Biology*, 5, e1000366, 2009.
40. A. L. Oberg, O. Vitek. "Statistical design of quantitative mass spectrometry-based proteomic experiments". *Journal of Proteome Research*, 8, p. 2144-2156, 2009.
41. M.-Y. Brusniak, B. Bodenmiller, D. Campbell, K. Cooke, J. Eddes, S. Letarte, L. N. Mueller, V. Sharma, O. Vitek, R. Aebersold, J. D. Watts. "Corra: A LC-MS framework and computational tools for discovery and targeted mass spectrometry-based proteomics". *BMC Bioinformatics*, 9, p.542, 2008.
42. S. Letarte, M.-Y. Brusniak, D. Campbell, J. Eddes, C. J. Kemp, H. Lau, L. Mueller, A. Schmidt, P. Shannon, K. S. Kelly-Spratt, O. Vitek, H. Zhang, R. Aebersold and J. D. Watts. "Differential plasma glycoproteome of p19<sup>A</sup>RF skin cancer mouse model using the corra label-free LC-MS proteomics platform". *Proteomics: Clinical Applications*, 4, p.105-116, 2008.
43. I. R. Baxter, O. Vitek, B. Lahner, B. Muthukumar, M. Borghi, J. Morrissey, M. L. Guerinot, D. E. Salt. "The leaf ionome as a multivariable system to detect a plant's physiological status". *Proceedings of the National Academy of Sciences*, 105, p.12081-12086, 2008.
44. L. Hohmann, J. Eng, A. Gemmill, J. Klimek, O. Vitek, G. Reid, D. Martin. "Quantification of the compositional information provided by ammonium ions on a quadrupole-TOF mass spectrometer". *Analytical Chemistry*, 80, p.5596-5606, 2008.
45. A. Nesvizhskii, O. Vitek, R. Aebersold. "Analysis and validation of proteomic data generated by tandem mass spectrometry". *Nature Methods*, 4, p.787-797, 2007.
46. L. N. Mueller, O. Rinner, A. Schmidt, S. Letarte, B. Bodenmiller, O. Vitek, R. Aebersold, M. Muller. "Super-

- Hirn - a novel tool for high resolution LC-MS based peptide/protein profiling". *Proteomics*, 19, p.3470-3480, 2007.
47. O. Vitek, C. Bailey-Kellogg, B. A. Craig, J. Vitek. "Inferential backbone assignment for sparse data". *Journal of Biomolecular NMR*, 31, p.187-208, 2006.
  48. Z. Yi, O. Vitek, M. A. Qasim, S. M. Lu, W. Lu, M. Ranjbar, J. Li, M. C. Laskowski, C. Bailey-Kellogg, M. Laskowski. "Functional evolution within protein superfamilies". *Proteins: Structure, Function and Bioinformatics*, 63, p.697-708, 2006.
  49. O. Vitek, C. Bailey-Kellogg, B. A. Craig, P. Kuliniewicz, J. Vitek. "Reconsidering complete search algorithms for protein backbone NMR assignment". *Bioinformatics*, 21, p.ii230-ii236, 2005.
  50. L. S. Riter, O. Vitek, K. M. Gooding, B. D. Hodge, R. K. Julian, Jr. "Statistical design of experiments as a tool in mass spectrometry". *Journal of Mass Spectrometry*, 40, p.565-579, 2005.
  51. O. Vitek, J. Vitek, B. A. Craig, C. Bailey-Kellogg. "Model-based assignment and inference of protein backbone nuclear magnetic resonances", *Statistical Applications in Genetics and Molecular Biology*, 3, Article 6, 2004.
  52. J. C. Fleet, L. Wang, O. Vitek, B. A. Craig, H. J. Edenberg. "Gene expression profiling of Caco-2 BBe cells suggests a role for sSpecific signaling pathways during intestinal differentiation", *Physiological Genomics*, 13, p.57-68, 2003.
  53. T. V. Perneger, A.-C. Raë, J.-M. Gaspoz, F. Borst, O. Vitek, C. Héliot. "Screening for pressure ulcer risk in an acute care hospital: Development of a brief bedside scale". *Journal of Clinical Epidemiology*, 55, p.498-504, 2002.
  54. B. A. Craig, O. Vitek, M. A. Black, M. Tanurdzic, R. W. Doerge. "Designing microarrays." In *Proceedings of Applied Statistics in Agriculture, Kansas State University*, edited by George Milliken, p.159-182, 2001.
  55. S. Beer-Borst, A. Morabia, S. Hercberg, O. Vitek, M. S. Bernstein, P. Galan, R. Galasso, S. Giampaoli, S. Houterman, E. McCrum, S. Panico, F. Pannozzo, P. Preziosi, L. Ribas, L. Serra-Majem, W. M. M. Verschuren, J. Yarnell, M. E. Northridge. "Obesity and other health determinants across Europe: The Euralim Project". *Journal of Epidemiology and Community Health*, 54, p.424-430, 2000.
  56. S. Beer-Borst, S. Hercberg, A. Morabia, M. S. Bernstein, P. Galan, R. Galasso, S. Giampaoli, E. McCrum, S. Panico, P. Preziosi, L. Ribas, L. Serra-Majem, M. F. Vescio, O. Vitek, J. Yarnell, M. E. Northridge. "Dietary patterns in six European populations: results from Euralim, a collaborative European data harmonization and information campaign". *European Journal of Clinical Nutrition*, 54, p.253-262, 2000.

## A.2 Other Publications

1. R. Aebersbold, O. Kohlbacher, O. Vitek. "Computational Mass Spectrometry (Dagstuhl Seminar 15351)". In *Dagstuhl Reports*, 8:5, p.9-33, 2016.
2. R. Aebersbold, O. Kohlbacher, O. Vitek. "Computational Mass Spectrometry (Dagstuhl Seminar 13491)". In *Dagstuhl Reports*, 3:12, p.1-16, 2014.
3. O. Vitek. "Leading a statistical bioinformatics lab: it's all about finding balance". In *PLoS Computational Biology*, 9:e1003333, 2013.
4. M. Key, O. Vitek. "Designing experiments for sound statistical inference". In *Encyclopedia of Systems Biology*, W. Dubitzky, O. Wolkenhauer, H. Yokota, K.-H. Cho (Eds.), 2012.
5. O. Vitek. "An inferential approach to protein backbone nuclear magnetic resonance assignment". *Ph.D. dissertation*. Purdue University, USA, 2005.
6. O. Vitek, B. A. Craig, R. Becker. "Statistical sampling plan for monitoring egg quality in an egg breaking plant". *Technical Assistance Program*, Purdue University, 2000.
7. O. Vitek, B. A. Craig, R. Becker. "Statistical sampling plan for monitoring the quality of seed lots". *Technical Assistance Program*, Purdue University, 2000.

8. G. Antille Gaillard, N. Chavaz, E. El May, E. Ronchetti and O. Ryndina<sup>1</sup>, “Evaluation of postoperative improvement in functional autonomy in Treatment and Rehabilitation Centers of Canton Vaud, Switzerland” (in French). *Laboratory of Applied Economics*. University of Geneva, Switzerland, 1998.
9. S. Beer-Borst, A. Morabia, S. Hercberg, O. Vitek, M. S. Bernstein, P. Galan, R. Galasso, S. Giampaoli, S. Houterman, E. McCrum, S. Panico, F. Pannozzo, P. Preziosi, L. Ribas, L. Serra-Majem, W. M. M. Verschuren, J. Yarnell, M. E. Northridge. “Nutrition and Heart”. *Information brochures for general public and for health professionals*. University Hospital, Geneva, Switzerland, 1998.
10. O. Ryndina<sup>1</sup> “Tree-based classifiers with application to medical data”. *M.Sc. dissertation*. University of Geneva, Switzerland, 1997.
11. O. Ryndina<sup>1</sup>, D. Kustrimovic and M. Pfenninger, “Assessing fuel efficiency of cars on the Swiss market” (in French). *B.Sc. diploma project and CUEPE technical report 98.02*. University of Geneva, Switzerland, 1996.

### A.3 Software

All software is implemented in R, is open-source, and is publicly available at <http://olga-vitek-lab.org/software/>

1. **Cardinal**: Signal processing and statistical analysis of mass spectrometry-based imaging experiments.
  - John M. Chambers Statistical Software Award of the American Statistical Association, 2015
2. **MSstats**: Protein quantification in label-free and label-based LC-MS and SRM experiments.
3. **sparseQuant**: Protein quantification in Selected Reaction Monitoring (SRM) experiments with stable isotope labeled reference peptides, which utilize a reduced subset of the references.
4. **SRMstats**: Protein quantification in Selected Reaction Monitoring (SRM) experiments.
5. **sSeq**: Finding differentially expressed genes in RNA-seq experiments with a small sample size.
6. **HTSmix**: Interpretation of high-throughput perturbation screens measuring low-dimensional quantitative phenotypes.
7. **BQuant**: Fully automated, probabilistic database-based identification and quantification of metabolites in local regions of Nuclear Magnetic Resonance (NMR) spectra.
8. **MBA (Model-Based Assignment)**: A software for inferential assignment of protein backbone nuclear magnetic resonances. Implemented in Java.

## B Invited Lectures

1. Keystone Symposium on Molecular and Cellular Biology, Breckenridge, CO, 2017.  
*TBA.*
2. New York University (NYU), 2016.  
*TBA.*
3. Mass Spectrometry: Applications to the Clinical Lab (MSACL) 2016.  
*Statistical Inference for Mass Spectrometry Imaging.*
4. The Pennsylvania State University, University Park, PA 2016.  
*Statistical methods and tools for quantitative mass spectrometry-based proteomics.*
5. Proteomics Workshop, Brazilian Biosciences National Laboratory (LNBio) at the Brazilian Center for Research in Energy and Materials (CNPEM), Campinas, Brazil 2015.  
*Statistical methods for quantitative proteomics.*

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<sup>1</sup>Published as Olga Ryndina prior to 1999.

6. The Royal Society, Theo Murphy International Scientific Meeting, Chichley Hall, UK 2015.  
*Statistical Inference for Mass Spectrometry Imaging.*
7. OurCon: Imaging Mass Spectrometry Conference, Pisa, Italy 2015.  
*Statistical Inference for Mass Spectrometry Imaging.*
8. Meeting of the Association of Biomolecular Resource Facilities (ABRF), St. Louis 2015.  
*iPRG 2015 Study: Differential Abundance Analysis in Label-free Quantitative Proteomics.*
9. International Quantitative and Computational Biology (QCB) seminar series, Princeton University, 2014.  
*Statistical methods and tools for quantitative mass spectrometry-based proteomics.*
10. Research seminar, Research Center for Statistics, University of Geneva, Switzerland, 2014.  
*Statistical methods and tools for quantitative mass spectrometry-based proteomics.*
11. International Mass Spectrometry Conference (IMSC), Geneva, Switzerland 2014.  
*Statistical methods and tools for mass spectrometry-based proteomics.*
12. UCSF, San Francisco, 2014.  
*Statistical methods and tools for mass spectrometry-based proteomics.*
13. Bioconductor conference, Boston 2014.  
*Statistical methods and tools for mass spectrometry-based proteomics.*
14. Mass Spectrometry Special Interest Group (MS-SIG), International Conference on Intelligent Systems for Molecular Biology (ISMB), Boston 2014.  
*Nonlinear regression improves the accuracy of estimation and calibration in quantitative proteomics.*
15. Genentech, California, 2014.  
*MSstats: an R package for quantitative mass spectrometry-based proteomics.*
16. Annual Symposium of Canadian National Proteomics Network, 2014.  
*MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments.*
17. Annual Conference of the Association of the Biomedical Resource Facilities (ABRF), 2014.  
*Report of the Proteome Informatics Research Group.*
18. Annual Conference of the Association of the Biomedical Resource Facilities (ABRF), 2014.  
*Statistical methods for biomedical resource facilities.*
19. Annual Conference of the US Human Proteome Organization (US HUPO) 2014.  
*MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments.*
20. Department of Mathematics, Northeastern University, Boston 2014.  
*Statistical methods and tools for quantitative mass spectrometry-based proteomics.*
21. The Indo-USA workshop on Statistical Methods for Bioinformatics, Bangalore 2013.  
*Protein significance analysis in quantitative mass spectrometry-based proteomics.*
22. Mass Spectrometry Research Center, Vanderbilt University, 2013.  
*Statistical methods and software for mass spectrometry-based imaging.*
23. Mass Spectrometry Special Interest Group (MS-SIG), International Conference on Intelligent Systems for Molecular Biology (ISMB), Berlin, Germany 2013.  
*Statistical selection of informative features for protein quantification in DIA experiments.*
24. F. Hoffmann-La Roche Ltd, Basel Switzerland, 2013.  
*Statistical protein quantification from mass spectra.*
25. Statistics Seminar, Stanford University 2013.  
*Statistical methods and tools for quantitative mass spectrometry-based proteomics.*
26. Workshop on Targeted Peptide Measurements in Biology and Medicine, NIH 2013.  
*Statistical methods for analysis of targeted proteomic experiments.*

27. Statistics and Genomics Seminar, UC Berkeley 2013.  
*Statistical methods and tools for quantitative mass spectrometry-based proteomics.*
28. Proteomics Group Seminar, UCSF 2013.  
*Statistical methods and tools for quantitative mass spectrometry-based proteomics.*
29. Qatar Computing Research Institute, 2013.  
*Statistical proteomics and bioinformatics.*
30. Department of Statistics, UC Irvine, 2013.  
*Statistical methods and tools for quantitative mass spectrometry-based proteomics.*
31. Department of Electrical and Computer Engineering, UT at San Antonio, 2012.  
*Statistical methods and tools for quantitative mass spectrometry-based proteomics.*
32. Samuel Lunenfeld Research Institute, Toronto, Canada, 2012.  
*Statistical methods and tools for quantitative mass spectrometry-based proteomics.*
33. Department of Biostatistics, University of Washington, Seattle, 2012.  
*Statistical mass spectrometry-based proteomics.*
34. Department of Biostatistics, Stanford University, 2012.  
*Statistical mass spectrometry-based proteomics.*
35. Information Sciences in Imaging, Stanford University, 2012.  
*Statistical design and analysis of experiments for quantitative and imaging mass spectrometry-based proteomics.*
36. Mass Spectrometry Special Interest Group (MS-SIG), International Conference on Intelligent Systems for Molecular Biology (ISMB), Long Beach, 2012.  
*Statistical analysis can account for sparsity and redundancy in protein quantifications to save cost and gain deeper biological insight.*
37. ISMB, Swiss Federal Institute of Technology (ETH), Zürich Switzerland, 2012.  
*Protein quantification from mass spectra.*
38. F. Hoffmann-La Roche Ltd, Basel Switzerland, 2012.  
*Protein quantification from mass spectra.*
39. Department of Statistics, University of British Columbia, Vancouver Canada, 2012.  
*Protein quantification from mass spectra: statistical methods and tools for overcoming variation and sparsity.*
40. Annual meeting of the Center for Algorithmic and Systems Biology, UCSD, San Diego, 2012.  
*Statistical analysis can account for sparsity and redundancy in protein quantifications to save cost and gain deeper biological insight.*
41. Training Program in Biostatistics, Bioinformatics, Nutrition and Cancer, Texas A& M, 2012.  
*Protein quantification from mass spectra: statistical methods and tools for overcoming variation and sparsity.*
42. Joint meeting of the French Mass Spectrometry Society and the French Proteomics Society, Avignon, France 2011.  
*Statistical methods for quantitative proteomics.*
43. Qatar Computing Research Institute, Doha, Qatar, 2011.  
*An insight into computational and statistical mass spectrometry-based proteomics.*
44. The George Institute, University of Sydney, Australia, 2011.  
*Statistical framework for protein quantification with mass spectrometry-based proteomic experiments.*
45. Annual meeting of the Australasian Proteomics Society, Lorne, Australia, 2011.  
*Statistical Analysis of Quantitative Mass Spectrometry-Based Proteomic Experiments.*
46. Department of Bioinformatics and Biostatistics, University of Louisville, KY, 2010.  
*Mixed-effect models for high-throughput mass spectrometry-based proteomic profiling experiments.*

47. Commissariat à l’Energie Atomique et aux Energies Alternatives (CEA), Grenoble, France, 2010.  
*Statistical protein quantification in label-free LC-MS experiments: methods, software & case studies.*
48. Research and Training Center on Bioinformatics, Russian Academy of Sciences, Moscow, 2010.  
*An insight into computational and statistical mass spectrometry-based proteomics.*
49. The US Human Proteome Organization (US HUPO), Denver, CO, 2010.  
*Statistical experimental design and protein quantification in LC-MS experiments: methods, software and case study.*
50. Center for Bioinformatics Research, Indiana University at Bloomington, 2010.  
*Mixed-effect models for high-throughput mass spectrometry-based molecular profiling experiments.*
51. Training Program in Bioinformatics, Texas A& M, 2009.  
*Protein Quantification in Label-free LC-MS experiments.*
52. The US Human Proteome Organization (US HUPO), San Diego, CA, 2009.  
*Introduction to Statistical Principles in Designing Proteomics Experiments.*
53. Keystone Symposium “Omics Meets Cell Biology”, Breckenridge, CO, 2009.  
*Experimental Design from a Statistics Point of View.*
54. Swiss Federal Institute of Technology (ETH), Zürich, Switzerland, 2008.  
*Statistical design and analysis of LC-MS profiling experiments.*
55. Swiss Institute of Bioinformatics, Geneva, Switzerland, 2008.  
*Statistical design and analysis of LC-MS profiling experiments.*
56. Indiana University Purdue University, Indianapolis, IN, 2007.  
*Discovery of biomarkers of disease in a combined LC-MS and LC-MS/MS proteomics workflow.*
57. IBM T. J. Watson, Yorktown Heights, NY, 2007.  
*Discovery of biomarkers of disease in a combined LC-MS and LC-MS/MS proteomics workflow.*
58. New York University, New York, 2007.  
*Discovery of biomarkers of disease in a combined LC-MS and LC-MS/MS proteomics workflow.*
59. International Chinese Statistical Association Applied Statistics Symposium, Raleigh, NC, 2007.  
*Discovery of biomarkers of disease in a combined LC-MS and LC-MS/MS proteomics workflow.*
60. University of Illinois-Urbana Champaign, IL, 2007.  
*Discovery of biomarkers of disease in a combined LC-MS and LC-MS/MS proteomics workflow.*
61. Monsanto Company, St. Louis, MO, 2006.  
*A combined LC-MS and LC-MS/MS framework for quantitative peptide and protein profiling.*
62. Bioinformatics and statistical genetics seminar series, Purdue University, 2005.  
*A scalable inferential approach to protein backbone nuclear magnetic resonance assignment.*
63. Swiss Federal Institute of Technology (ETH), Zürich, Switzerland, 2005.  
*Inferential analysis of protein Nuclear Magnetic Resonance (NMR) spectra.*

## C Other Selected Presentations

1. Annual conference of the American Society for Mass Spectrometry, Minneapolis, MN, 2013.  
Oral presentation: *Statistical selection of informative features for protein quantification in data-independent spectral acquisition.*
2. Annual conference of the American Society for Mass Spectrometry, Vancouver, Canada, 2012.  
Oral presentation: *A statistical framework for protein significance analysis in SRM experiments with sparse labeled references.*

3. Keystone Symposium “Omics Meets Cell Biology”, Alpbach, Austria 2011.  
Oral presentation: *Statistical Methods and Tools for Protein Quantification in MS-based Proteomics*.
4. Joint Statistical Meetings, Vancouver, CA, 2010.  
Oral presentation: *Mixed-effect models for high-throughput mass spectrometry-based proteomic profiling experiments*.
5. Joint Statistical Meeting, Denver CO, 2008.  
Oral presentation: *Introducing bioinformatics as part of statistics curriculum at Purdue*.
6. Bioinformatics and statistical genetics seminar series, Purdue University, 2008.  
Oral presentation: *False discovery rates in database-based identification of tandem mass spectra*.
7. Bioinformatics and statistical genetics seminar series, Purdue University, 2006.  
Oral presentation: *Inferential approaches to peptide sequence identification and quantitative protein profiling in MS-based proteomics*.
8. Joint Statistical Meeting, Seattle, 2006.  
Oral presentation: *Determination of differentially abundant peptides and proteins in a combined LC-MS and LC-MS/MS proteomics workflow*.
9. New Researchers Conference, Seattle, 2006.  
Oral presentation: *Determination of differentially abundant peptides and proteins in a combined LC-MS and LC-MS/MS proteomics workflow*.
10. Joint Statistical Meeting, Minneapolis, 2005.  
Oral presentation: *Model search in highly dimensional constrained graphical models with application to protein backbone NMR assignment*.
11. Eastern North American Region (ENAR) meeting of the International Biometric Society, 2004.  
Oral presentation: *Inferential analysis of protein Nuclear Magnetic Resonance (NMR) spectra*.
12. Joint Statistical Meeting, San Francisco, 2003.  
Oral presentation: *Model-based analysis of protein backbone NMR*.
13. Bioinformatics and statistical genetics seminar series, Purdue University, 2002.  
Oral presentation: *Statistical issues in protein structure determination by nuclear magnetic resonance spectroscopy (NMR)*.
14. Bioinformatics and statistical genetics seminar series, Purdue University, 2002.  
Oral presentation: *Gene expression profiling of intestinal cell differentiation: biological and statistical issues*.
15. Bioinformatics and statistical genetics seminar series, Purdue University, 2000.  
Oral presentation: *Designing microarray experiments: chips, dips, flips, and skips*.

## **D Other Professional Activities**

### **D.1 Chaired Sessions and Discussants**

1. Session Chair. Conference of the International Society for Computational Biology, 2013.
2. Session Chair. Conference of the International Society for Computational Biology, 2012.
3. Session Chair. Annual conference of the American Society for Mass Spectrometry, 2012.
4. Session Co-chair. “Challenges and Opportunities in Statistical Bioinformatics” and “Scaling Data Analytics”, Purdue Symposium on Statistics, 2012.
5. Session Chair. “Proteomics: Function Prediction and Modeling”, Joint Statistical Meeting, Contributed Papers, 2010.
6. Discussant. Planning workshop on “Biomarkers for Precision Medicine Initiative”. Canadian Institutes of Health Research, 2010.

Health Research (CIHR), 2009.

## D.2 Editorial Positions

1. Guest co-editor, special issue on “Large-scale computational mass spectrometry and multi-omics” in *Journal of Proteome Research*, 2015-2016.
2. Editorial advisory board member, *Journal of Proteome Research*, 2015-2017.
3. Editorial board member, *Molecular and Cellular Proteomics*, since 2012.
4. Associate Editor. *Journal of Statistical Planning and Inference*, 2012-2014.
5. Co-editor. “*Statistical methods for MS-based proteomics*”, BMC Bioinformatics Supplement, 2012.

## E Funding

### E.1 Current

1. *CAREER: Sparse-sampling inference for functional proteomics, metabolomics and ionomics*  
NSF-BIO/DBI  
07/01/2011-07/01/2016  
PI: Olga Vitek. Total amount: \$546,822. Percent of the amount to Olga Vitek: 100%
2. *NSF S2I2 Scalable Data Analytics Institute*  
Northeastern University, Tier III grant  
06/12/2015 - open  
PI: Jan Vitek  
Total amount: \$75,000. Percent of the amount to Olga Vitek: 50%.

### E.2 Past

1. *Quantification of signal transduction pathways in Bayesian Network to facilitate tailored cancer therapy research*  
Eli Lilly and Co  
08/01/2014-12/01/2015  
PI: Olga Vitek. Total amount: \$39,000. Percent of the amount to Olga Vitek: 100%
2. *Desorption Electrospray Ionization Mass Spectrometry Imaging In Clinical Diagnostics*  
NIH  
04/01/2013 - 03/31/2015  
PI: Graham Cooks, Purdue.  
Total amount: \$393,780. Percent of the amount to Olga Vitek: 10%
3. *Pheromonal control of gamete determination and differentiation in Ceratopteris*  
NSF-BIO  
05/01/2013-04/30/2015  
PI: Jo Ann Banks, Purdue. Total amount: \$300,000. Percent of the amount to Olga Vitek: 20%
4. *New proteomic technologies for the analysis of tyrosine kinase signaling pathways*  
NIH-NIGMS-R01  
07/01/2010-07/01/2015  
PI: Weiguo Andy Tao, Purdue. Co-PI: Robert Geahlen, Scott McLuckey, Olga Vitek.  
Total amount: \$1,854,175. Percent of the amount to Olga Vitek: 10%.
5. *SI2: Conceptualization: Dynamic Languages for Scalable Data Analytics*  
NSF-SI2



- 10/01/2012 - 03/31/2014  
PI: Jan Vitek, Purdue. Co-PIs: William Cleveland, Ananth Grama, Suresh Jogannathan, Olga Vitek.  
Total amount: \$200,000. Percent of the amount to Olga Vitek: 5%.
6. *Computational imaging mass spectrometry*  
Canary Center at Stanford for Cancer Early detection  
01/01/2013-12/30/2013.  
PI: Olga Vitek.  
Total amount of award: \$19,000. Percent of the amount to Olga Vitek: 100%.
7. *A Tracing Virtual Machine for Statistical Computing*  
NSF-SI2-SSE  
12/01/2010-11/31/2013  
PI: Jan Vitek, Purdue. Co-PI: Olga Vitek.  
Total amount: \$489,082.90. Percent of the amount to Olga Vitek: 50%.
8. *Statistical methods and computing for functional interpretation of high-throughput experiments in molecular systems biology*  
Qatar Research Foundation  
08/15/2012-08/14/2013  
PI: Olga Vitek. Total amount: \$52,228. Percent of the amount to Olga Vitek: 100%
9. *Statistical validation of the G-Series RayBiotech arrays for biomarker screening*  
RayBiotech Biomarker Discovery Research Pilot Grant  
04/30/2010-04/30/2012  
PI: Olga Vitek.  
Total amount of award: \$10,000. Percent of the amount to Olga Vitek: 100%.
10. *Classification of multiple bacterial pathogens using light-scattering sensor imaging*  
Advanced BioImaging Systems  
05/30/2010-05/30/2011.  
PI: Olga Vitek.  
Total amount of award: \$45,317. Percent of the amount to Olga Vitek: 100%.
11. *Development of workflows for integration of high throughput data and clinical variables: Additional Indiana CTSI support.*  
IU School of Medicine/NIH  
05/01/2009-04/30/2010.  
PI: Connie Weaver. Co-PI: Olga Vitek.  
Total amount of award: \$53,036. Percent of the amount to Olga Vitek: 100%.
12. *Statistical design and analysis of selected reaction monitoring (SRM) experiments for quantitative proteomics*  
Purdue Research Foundation  
8/17/09 - 7/31/2010.  
PI: Olga Vitek.  
Total amount of award: \$16,750. Percent of the amount to Olga Vitek: 100%
13. *A proteomic roadmap to the endogenous protein complexes of the endoplasmic reticulum in key plant species*  
Purdue Discovery Park Seed Grant  
04/01/2009-03/31/2010.  
PI: Dan Szymanski, Agronomy, Purdue. Co-PI: Chris Staiger, Mark Hall, Olga Vitek.  
Total amount of award: \$50,000. Percent of the amount to Olga Vitek: 24%.
14. *Accurate quantification of protein abundance for clinical applications of mass spectrometry-based proteomics*  
IUPUI  
2/1/09-01/31/2010.  
PI: Olga Vitek.  
Total amount of award: \$20,000. Percent of the amount to Olga Vitek: 100% .

15. *Development of workflows for integration of high throughput data with clinical variables*  
IU School of Medicine/NIH  
1/1/09-05/31/2009.  
PI: Olga Vitek.  
Total amount of award: \$34,900. Percent of the amount to Olga Vitek: 100%.
16. *Proteomics and metabolomics analyses to identify biomarkers in osteosarcoma*  
Indiana University Cancer Center Translational Research Acceleration Collaboration (ITRAC),  
7/15/2007-7/14/2009  
PI: Susanne Ragg, IU School of Medicine. Co-PI: Gunther Schadow (IUPUI), Olga Vitek.  
Total amount of award: \$50,000. Percent of the amount to Olga Vitek: 10%.
17. *Proteomic and gene expression analysis to identify biomarkers in Wilms tumor*  
Indiana University Cancer Center Translational Research Acceleration Collaboration (ITRAC)  
5/15/08-5/14/09  
PI: Susanne Ragg, IU School of Medicine. Co-PI: Gunther Schadow (IUPUI), Olga Vitek.  
Total amount of award: \$50,000. Percent of the amount to Olga Vitek: 10%.
18. *Interfacing biological knowledge and statistical analysis for rapid interpretation of clinical proteomics experiments*  
Purdue University/IUPUI Intercampus Applied Research Program (IARP)  
5/1/2008-4/30/2009.  
PI: Gunther Schadow, IUPUI. Co-PI: Olga Vitek.  
Total amount of award: \$50,000. Percent of the amount to Olga Vitek: 50%.
19. *A hypothesis testing approach to identification and assessment of statistical significance of peptides and proteins in shotgun proteomics*  
Purdue University/Indiana University Collaboration in Life Sciences and Informatics Research (CLSIR)  
01/01/2007-12/31/2007  
PI: Olga Vitek. Co-PI: Predrag Radivojac, IU Bloomington.  
Total amount: \$50,000. Percent of the amount to Olga Vitek: 50%.
20. *Taking quantitative LC-MS profiling of blood samples in cardiovascular disease to a clinically relevant scale: a computational and statistical approach*  
Purdue University/Indiana University School of Medicine Collaboration in Biomedical Research (CBR)  
01/01/2007-12/31/2007  
PI: Olga Vitek. Co-PI: Susanne Ragg, IU School of Medicine.  
Total amount: \$50,000. Percent of the amount to Olga Vitek: 50%.

## **F Evidence of Involvement in the Graduate Research Program**

### **F.1 Graduated M.S. and Ph.D. Students**

#### **Ph.D. students:**

1. Ms. Meena Choi, Department of Statistics, Purdue, Spring 2016.
  - ThinkSwiss research scholarship, 2013
 Dissertation:  
*A flexible and versatile framework for statistical design and analysis of quantitative mass spectrometry-based proteomic experiments*  
First position: Post-doctoral Associate, College of Science, Northeastern University.
2. Mrs. Danni Yu, Department of Statistics, Fall 2013, Purdue.
  - I.W. Burr Dissertation Award, 2014
 Dissertation:  
*Estimation of variation in high-throughput molecular biology experiments with small sample size*

First position: Research Scientist, Eli Lilly and Company.

3. Mrs. Ching-Yun (Veavi) Chang, Department of Statistics, Summer 2013, Purdue.

Dissertation:

*Cost-effective and accurate protein quantification for large-scale targeted proteomics*

First position: Research Scientist, Eli Lilly and Company.

4. Mr. Tim Clough, Department of Statistics, Summer 2012, Purdue.

- StatCom leadership Award, 2011
- ThinkSwiss research scholarship, 2010

Dissertation:

*Statistical protein quantification and prioritization in label-free shotgun LC-MS/MS proteomics*

First position: Senior Biometrician, Novartis.

5. Mr. Cheng Zheng, PhD. Department of Statistics, Fall 2010, Purdue.

- I.W. Burr Dissertation Award, 2010
- Bilsland Fellowship 2009-2010.

Dissertation: *Model-based identification and quantification of metabolites in  $^1H$  NMR spectra*

First position: Senior Biostatistician, Novartis.

#### **M.S. students:**

1. Ms. Melissa Key, Department of Statistics, Purdue.  
First position: Research Scientist, Center for Computational Diagnostics, IUPUI.

## **F.2 Current Graduate Students**

#### **Current Post-docs:**

1. Mrs. Meena Choi, College of Science, Northeastern University.
2. Mr. Eralp Dogu Galitzine, College of Science, Northeastern University.
3. Mr. Cyril Galitzine, College of Science, Northeastern University.
4. Mr. Tsung-Heng Tsai, College of Science, Northeastern University.

#### **Current Ph.D. students:**

1. Mr. Kyle Bemis, Department of Statistics, Purdue.
  - John M. Chambers Statistical Software Award of the American Statistical Association, 2015
  - NSF Graduate Research Dissertation Fellowship, 2012
2. Mr. Lin-Yang Cheng, Department of Statistics, Purdue.
3. Mrs. April Harry, Department of Statistics, Purdue.
4. Mrs. Ting Huang, College of Computer and Information Sciences, Northeastern University
  - Lucille Zanghi '72 and Jim Dow '72 Graduate Fellowship in Bioinformatics 2015
5. Mr. Robert Ness, Department of Statistics, Purdue.
  - Institute of International Education Boren Fellowship, 2012

## **F.3 Other Activities:**

#### **Ph.D. Committee Member:**

1. Christopher Wilson, Engen Lab, Chemistry and Chemical Biology, Northeastern University
2. Catherine M. Rawlins, Agar Lab, Chemistry and Chemical Biology, Northeastern University

3. Michael Wleklinski, Department of Chemistry, Purdue.
4. Ms. Nadia Atallah, Department of Botany and Plant Pathology, Purdue.
5. Mrs. Kelly-Ann Dixon Hamil, Department of Statistics, Purdue.
6. Mr. Ariful Azad, Department of Computer Science, Purdue. Graduated Spring 2014.
7. Ms. Eunjung Lim, Department of Statistics, Purdue. Graduated Summer 2011.
8. Mr. Paul Livermore Auer, Department of Statistics, Purdue. Graduated Summer 2010.
9. Mr. Shahin Mohammadi, Department of Computer Science, Purdue.
10. Ms. Sudeshna Paul, Department of Statistics, Purdue. Graduated Fall 2009.
11. Ms. Sandra Lövenich, ETH Zürich. Graduated Summer 2009.

**M.S. Committee Member:**

1. Kyungmin Ahn, Veronica Crofts, Dan Dillon, Junyan Ge, Syed Haque, Qiming Huang, Xinyan Liu, Wen Wei Loh, Chris Morgan, Xuelu Ren, Xiaosu Tong, Pu-Tai Yang, Yi Yin, Shuai Edison Yu, Catherine Withey, Noah Whitman, Yang Zhao, Jing Zhu  
*Department of Statistics, Purdue University. Current and graduated M.S. students.*
2. Mr. Mourad Mellal  
*l'Université Joseph Fourier, Grenoble, France. Graduated Summer 2010.*

**Reading Courses:**

1. Mr. Qiming Huang (Summer 2012).  
*"Image-based classification of bacterial pathogens".*
2. Ms. Meena Choi (Fall 2010, Spring 2012).  
*"Statistical Bioinformatics".*
3. Mr. Tim Clough and Kelvin Ma, Statistics, Purdue (Spring 2008).  
*"Topics in computational biology".*
4. Ms. Johnna Anderson, Statistics, Purdue (Spring 2007).  
*"Topics in computational proteomics".*
5. Ms. Melissa Key, Statistics, Purdue (Spring 2007).  
*"Topics in computational proteomics".*

**Collaboration on Research Projects:**

1. Mr. Hao Chen, Biology, Purdue (Spring 2008).  
*"Ionic profiling of mutant strains of Arabidopsis thaliana".*
2. Mr. Shucha Zhang, DChemistry, Purdue (Spring 2008 - Spring 2009).  
*"Normalization in NMR-based metabolomic profiling experiments".*
3. Mr. Zuoyi Zhang, Statistics, Purdue (Spring 2007 - Fall 2007).  
*"Statistical interpretation of tandem mass spectra".* Financial support Spring 2007 - Fall 2007.
4. Ms. Joëlle Mühlemann, Horticulture and Landscape Architecture, Purdue (Summer 2009).  
*"Interpretation of metabolomic experiments in plants".*

**Other Mentoring:**

1. Graduate Women In Science Programs (WISP), Fall 2011.  
*Guest speaker.*

2. Reading group in computational biology, Spring 2007.  
*Organizer.*
3. Preparing Future Faculty I - GRAD 590B, Spring 2007.  
*Panel discussant.*
4. Purdue Graduate School workshop “Networking Skills: Optimizing your Conference Experience”, Spring 2007.  
*Panel discussant.*

## IV. ENGAGEMENT

### A Northeastern University

- F2015-S2016:** College of Science Dean Search Committee  
College of Science Computational Faculty Search Committee  
College of Computer and Information Science MS in Data Science Curriculum Design Committee
- F2014-S2015:** Hiring committee, College of Computer and Information Science

### B Purdue University

- F2013-S2014:** Hiring committee in computational statistics (Co-chair)  
Applied Methods PhD qualifying exam committee  
M. S. in Applied Statistics Exam committee  
Outstanding Assistant Professor Teaching Award committee  
Graduate Student Teaching Award committee  
Executive and Personnel committee  
Diversity committee  
College of Science Grade Appeals committee
- F2011-S2012:** I.W. Burr Award committee (Chair)  
L. J. Cote M.S. Excellence in Statistics Award committee  
Strategic Planning committee  
Applied Methods PhD qualifying exam committee  
M.S. in Applied Statistics exam committee
- F2010-S2011:** Applied Methods PhD qualifying exam committee (Chair)  
M.S. in Applied Statistics exam committee  
L.J. Cote award committee  
Strategic planning committee  
Hiring committee - advisory member
- F2009-S2010:** Applied Methods PhD qualifying exam committee (Chair)  
M.S. in Applied Statistics exam committee  
Hiring committee  
Student cases committee  
Faculty representative at the Commencement ceremony
- F2008-S2009:** Myra Samuels lecture committee (Chair)  
College of Science Faculty Council representative
- F2007-S2008:** Computational Statistics PhD qualifying exam committee  
Graduate admissions committee  
Hiring committee
- F2006-S2007:** Computational Statistics PhD qualifying exam committee  
Myra Samuels lecture committee

### C Professional

1. Co-organizer, Annual Conference of the US Human Proteome Organization (US HUPO), 2016.
2. Program Committee member, Annual International Conference on Research in Computational Molecular Biology (RECOMB), 2016.

3. Co-organizer. Schloss Dagstuhl Seminar on Computational Mass Spectrometry. August 2015.
4. Invited discussant, NSF workshop “Mass Spectrometry: Big Data to Knowledge”, 2015.
5. Member, Board of Directors, US Human Proteome Organization, 2015-2018.
6. Co-organizer, Annual Conference of the US Human Proteome Organization (US HUPO), 2015.
7. Program Committee member. MS & Proteomics, Intelligent Systems in Molecular Biology (ISMB), 2015.
8. Member, founding committee. Computational mass spectrometry special interested group. Since 2014.
9. Grant proposal reviewer. NIH, Spring 2014.
10. Grant proposal reviewer. NSF, Spring 2014.
11. Organizer. Workshop on “Software and Statistics in Mass Spectrometry”. International Mass Spectrometry Conference (IMSC), 2014.
12. Program committee member, Computational Systems Biology. European Conference on Computational Biology (ECCB), 2014.
13. Organizer. Workshop on Biostatistics. Annual Conference of the Association of the Biomedical Resource Facilities (ABRF), 2014.
14. Area program committee co-chair. Mass Spectrometry & Proteomics. Intelligent Systems in Molecular Biology (ISMB) 2014.
15. Education Committee member. US Human Proteome Organization (US HUPO), 2012-2014.
16. Co-organizer. Schloss Dagstuhl Seminar on Computational Mass Spectrometry. December 2013.
17. Grant proposal reviewer. NIH, Spring 2013.
18. Area program committee co-chair, Mass Spectrometry & Proteomics. Program committee member, Late Breaking Research. Intelligent Systems in Molecular Biology (ISMB) and European Conference on Computational Biology, 2013.
19. Member, Proteome Informatics Research Group (iPRG), Association of Biomedical Resource Facilities, since 2013.
20. Program Committee member. ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB) 2012.
21. Grant proposal reviewer. NIH, Spring 2012.
22. Grant proposal reviewer. NSF-BIO, Spring 2012.
23. Program Committee member. Mass Spectrometry & Proteomics, Intelligent Systems in Molecular Biology (ISMB), 2012.
24. Conference co-chair. Research in Computational Molecular Biology (RECOMB) Satellite Conference on Computational Proteomics, 2012.
25. Ad-hoc grant proposal reviewer. NIH, Fall 2011.
26. Grant proposal reviewer. NSF-BIO, Fall 2011.
27. Program Committee member. Mass Spectrometry & Proteomics, Intelligent Systems in Molecular Biology (ISMB) and European Conference on Computational Biology, 2011.
28. Program Committee member. Workshop on Emerging Computational Methods for the Life Sciences, 2011.
29. Program Committee member. Research in Computational Molecular Biology (RECOMB) Satellite Conference on Computational Proteomics, 2011.
30. Program Committee member. Late Breaking Research program, Intelligent Systems in Molecular Biology (ISMB), 2010.
31. Program Committee member. Workshop on Algorithms in Bioinformatics (WABI), 2010.
32. Program Committee member. Research in Computational Molecular Biology (RECOMB) Satellite Conference on Computational Proteomics, 2010.

33. Program Committee member. Invited Session on Nature-Inspired Collective Intelligence, International Conference on Computational Collective Intelligence (ICCCI), 2009.
34. Grant proposal reviewer. NSF-BIO, Fall 2009.
35. Grant proposal reviewer. Qatar National Research Foundation, Fall 2009.
36. Grant proposal reviewer. NSF-DMS, Fall 2008.
37. Referee for *Bioinformatics*, *Computational Statistics and Data Analysis*, *IEEE Transactions on Signal Processing*, *IEEE International Workshop on Genomic Signal Processing and Statistics GENSIPS'07*, *Journal of Proteome Research*, *Molecular and Cellular Proteomics*, *Mass Spectrometry Reviews*, *Pacific Symposium of Biocomputing*, *Physiological Genomics*, *The Plant Cell*, *PLoS Computational Biology*, *PLoS ONE*, *Statistical Applications in Genetics and Molecular Biology*, *Nature Biotechnology*, *Nature Methods*.