

CURRICULUM VITAE

Kristen M. Naegle
<http://naegle.wustl.edu>

Education: B.S. (EE) University of Washington, 2001
M.S. (EE) University of Washington, 2004
S.M. (BE) Massachusetts Institute of Technology, 2006
Ph.D. (BE) Massachusetts Institute of Technology, 2010

Professional Experience

University of Virginia:

Department of Biomedical Engineering; Associate Professor 2018-Present
Department of Computer Science and Engineering; Courtesy Appointment 2018-Present
Center for Public Health Genomics; Resident Faculty, 2018-Present
Data Sciences Institute: Member, 2018-Present

Washington University in St. Louis:

Department of Biomedical Engineering; Assistant Professor 2012-2018
Department of Computer Science and Engineering; Courtesy Appointment 2016-2018
Siteman Cancer Center, Member; 2015-2018

Massachusetts Institute of Technology:

Department of Biological Engineering and the Koch Institute for Integrative Cancer Research; Postdoctoral Associate 2010-2011

Industry Experience:

Philips Ultrasound, Engineering Intern (2001-2002)
Intel, Engineering Intern (2000)
Hewlett Packard, Engineering Intern (1996-1999)

Training Mentors:

Postdoctoral advisor: Michael B. Yaffe (MIT)

Ph.D. advisor: Douglas A. Lauffenburger (MIT), close collaboration with Forest M. White (MIT)

Academic Honors and Awards

NCI/SAGE Integrative Approaches to Cancer Metastasis workshop, June 2017
Siebel Scholar, class of 2010
International Society for Computational Biology Travel Award, RECOMB August 2010
Keystone Symposium Travel Award, March 2010
Medtronic Fellowship, 2004
Intel SRC Master's Scholarship 2003-2004
Intel Undergraduate scholarship, tuition and books, 1999-2001
B.S. *Magna Cum Laude*, Phi Beta Kappa, University of Washington, 2001

Funding

R21 CA 212726-01A1 (Naegle)	07/01/2017 - 06/30/2020	1.20 CM Effort
NIH/NCI (IMAT)	\$133,333 Annual Direct Costs	
A molecular toolkit for the production of tyrosine phosphorylated proteins		
SIP pre-R01 (Naegle)	01/01/2018-12/31/2019	1.0 CM Effort
Siteman Cancer Center	\$100,000 Annual Direct Costs	
Discovering the role of pleckstrin homology domain phosphorylation		
R21 NCI 231853-01 (Naegle)	08/03/2018-08/02/2020	1.0 CM Effort
NIH/NCI	\$130,500 Annual Direct Costs	
Inferring kinase activity profiles from phosphoproteomic data		

Research Interests

Molecular/Cell Bioengineering; Quantitative Cell Biology; Systems Biology – proteomics, post-translational modifications, cell signaling, cell networks, machine learning, domain-motif interactions, protein-protein interactions

Professional Activities

Washington University Affiliations

Center for Biological Systems Engineering, Member 2012-2018

Siteman Cancer Center, Member 2014-2018

Division of Biological and Biomedical Sciences, Division faculty in the following programs: Computational and Systems Biology, Computational and Molecular Biophysics, and Molecular Cell Biology 2012-2018

Memberships:

Biomedical Engineering Society (BMES) 2008-present

International Society for Computational Biology (ISCB) 2009-present

Biophysical Society (BPS) 2016

American Association for Cancer Research (AACR), Associate Member 2010-present

Institute of Electrical and Electronics Engineers (IEEE), 2002-2004

Editorial Duties:

1. PLoS Computational Biology: Guest Editor (1 article 2014)

Reviewer Duties:

1. Journal of Proteomics, 2011-present
2. Molecular and Cellular Proteomics, 2012-present
3. PLoS One, 2012-present
4. CPT: Pharmacometrics and Systems Pharmacology, 2012-present
5. NPG: Scientific Reports, 2014-present
6. BMC Bioinformatics, 2014-present
7. Briefings in Bioinformatics, 2015-present
8. Nature Chemical Biology, 2015-present
9. Journal of Molecular Biology, 2016-present
10. PLoS Computational Biology, 2016-present
11. Nature Biotechnology, 2018-present
12. DATABASE (Oxford), 2018-present

External Review Work: Grants

1. UK Medical Research Council grant Peer Review, 2018
2. NIH/NCI Study Section R21/R33 Imaging and Molecular Analysis Technologies (IMAT), October 2016, ad hoc
3. NIH Study Section Biodata Management and Analysis (BDMA) June 2016, ad hoc

Conference Duties:

1. Platform Session Co-Chair, Biomedical Engineering Society Annual Meeting, Phoenix AZ, October 2017.
2. Track Co-Chair, Biomedical Engineering Society Annual, Bioinformatics, Computational and Systems Biology, San Antonio TX, October 2014.
3. Platform Session Co-Chair, Biomedical Engineering Society Annual Meeting, Bioinformatics, Computational and Systems Biology, Seattle WA, September 2013.
4. Workshop Co-Chair, PNNL Signatures Workshop, Biological and Social Networks Session, Richland WA, May 2013.

Publications

Journal Articles:

1. Sloutsky, Roman, and **Kristen M. Naegle**. "Accuracy through Subsampling of Protein Evolution: An Ensemble Approach to Testing Accuracy and Reconstructing the History of Protein Family Divergence." *In Review*. (BioRxiv Preprint: doi: <https://doi.org/10.1101/170787>, 2017)
2. Tom Ronan, Shawn Anastasio, Zhijie Qi, Pedro Henrique S. Vieira Tavares, Roman Sloutsky, and **Kristen M. Naegle**. "OpenEnsembles: A Python Resource for Ensemble Clustering", *Journal of Machine Learning Research* (2018, in press)

3. Sloutsky, Roman and **Kristen. M. Naegle**. Proteome-Level Analysis Indicates Global Mechanisms for Post-Translational Regulation of RRM Domains. *J. Mol. Biol.* 1–4 (2017). doi:10.1016/j.jmb.2017.11.001
4. Mooradian, Arshag D., Jason M. Held, and **Naegle, K. M.** Using ProteomeScout: A Resource of Post-Translational Modifications, Their Experiments, and the Proteins they Annotate. *Curr. Protoc. Bioinforma.* **13**, 13.32.1-13.32.27 (2017).
5. Schaberg, Katherine E., Venkatesh S Shirure, Elizabeth A Worley, Steven C George, and **Kristen M Naegle**. “Ensemble Clustering of Phosphoproteomic Data Identifies Differences in Protein Interactions and Cell-Cell Junction Integrity of HER2-Overexpressing Cells.” *Integr. Biol.* 9 (2017): 539–47. doi:10.1039/C7IB00054E.
6. Sloutsky, Roman, and **Kristen M. Naegle**. “High-Resolution Identification of Specificity Determining Positions in the LacI Protein Family Using Ensembles of Sub-Sampled Alignments.” *Plos One* 11, no. 9 (2016): e0162579.
7. Noren, David P., Byron L. Long, Raquel Norel, Kahn Rhissorakrai, Kenneth Hess, Chenyue Wendy Hu, Alex J. Bisberg, et al. “A Crowdsourcing Approach to Developing and Assessing Prediction Algorithms for AML Prognosis.” *PLOS Computational Biology* 12, no. 6 (2016): e1004890. *Naegle lab (Tom Ronan, Jennifer Flynn, Kristen M. Naegle) participated as a team in the AML consortium.
8. Ronan, Thomas, Zhijie Qi, and **Kristen M Naegle**, “Avoiding pitfalls when clustering biological data”, *Science Signaling*, 9, no. 432 (2016): re6. Invited Review.
 - a. Made the banner of the home page of *Science* the week of publication.
 - b. Most tweeted *Science Signaling* article.
9. Ronan, Thomas, Jennifer L. McDonnell-Obermann, Laurel Huelsmann, ***Kristen M. Naegle**, and *Linda J. Pike. “The seven EGF receptor agonists each elicit a unique signature of recruitment of downstream signaling proteins”, *Journal of Biological Chemistry* 291, no. 12 (2016): 5528-5540 *co-corresponding
 - a. Article of the week in March 2016.
 - b. 2016 Highlights issue
 - c. Rated “Exceptional” by Faculty of 1000
10. Holehouse, Alex S, and **Kristen M. Naegle**. “Reproducible Analysis of Post-Translational Modifications in Proteomes—Application to Human Mutations.” *PLoS ONE* 10, no. 12 (2015): 1–19.
11. ***Naegle, Kristen M.**, Nancy R Gough, and *Michael B Yaffe. “Criteria for Biological Reproducibility : What Does ‘n’ Mean ?” *Science Signaling* 8, no. 371 (2015): 2–5. *co-corresponding
12. Matlock, Matthew K, Alex S Holehouse, and **Kristen M Naegle**. “ProteomeScout: A Repository and Analysis Resource for Post-Translational Modifications and Proteins.” *Nucleic Acids Research* 43, no. D1 (November 20, 2015): D521–30.
13. Cho, Yongcheol, Roman Sloutsky, **Kristen M Naegle**, and Valeria Cavalli. “Injury-Induced HDAC5 Nuclear Export Is Essential for Axon Regeneration.” *Cell* 155, no. 4 (November 2013): 894–908.
14. Iwai, Leo K, Leo S Payne, Maciej T Luczynski, Francis Chang, Huifang Xu, Ryan W Clinton, Angela Paul, Edward A. Esposito, Scott Gridley, Birgit Leitinger, **Kristen M Naegle**, and Paul H. Huang. “Phosphoproteomics of Collagen Receptor Networks Reveals SHP-2 Phosphorylation Downstream of Wild-Type DDR2 and Its Lung Cancer Mutants.” *The Biochemical Journal* 454, no. 3 (September 15, 2013): 501–13.
15. Sloutsky, Roman, Nicolas Jimenez, S Joshua Swamidass, and **Kristen M Naegle**. “Accounting for Noise When Clustering Biological Data.” *Briefings in Bioinformatics* 14, no. 4 (July 2013): 423–36. doi:10.1093/bib/bbs057.
16. **Naegle, Kristen M**, Forest M White, Douglas A Lauffenburger, and Michael B Yaffe. “Robust Co-Regulation of Tyrosine Phosphorylation Sites on Proteins Reveals Novel Protein Interactions.” *Molecular BioSystems* 8, no. 10 (August 1, 2012): 2771–82.
17. **Naegle, Kristen M**, Roy E Welsch, Michael B Yaffe, Forest M White, and Douglas A Lauffenburger. “MCAM: Multiple Clustering Analysis Methodology for Deriving Hypotheses and Insights from High-Throughput Proteomic Datasets.” *PLoS Computational Biology* 7, no. 7 (July 2011): e1002119.
18. ***Naegle, Kristen M**, *Melissa Gymrek, Brian A Joughin, Joel P Wagner, Roy E Welsch, Michael B Yaffe, Douglas A Lauffenburger, and Forest M White. “PTMScout, a Web Resource for Analysis of High Throughput Post-Translational Proteomics Studies.” *Molecular & Cellular Proteomics : MCP* 9, no. 11 (November 2010): 2558–70. *authors contributed equally
19. *Joughin, Brian A, ***Kristen M Naegle**, *Paul H Huang, Michael B Yaffe, Douglas A Lauffenburger, and Forest M White. “An Integrated Comparative Phosphoproteomic and Bioinformatic Approach Reveals a Novel Class of MPM-2 Motifs Upregulated in EGFRvIII-Expressing Glioblastoma Cells.” *Molecular BioSystems* 5, no. 1 (January 2009): 59–67. *authors contributed equally

Conference Proceedings:

1. **Naegle K**, Gupta S, Allstot D, "Design Considerations for a 10GHz CMOS Transmit-Receive Switch", IEEE International Symposium on Circuits and Systems, May 2005, Kobe Japan.

Conference Abstracts:

1. "Statistically robust detection of group-specific signal from specificity determining positions in protein families" Roman Sloutsky and Kristen M. Naegle. Biomedical Engineering Society Annual Meeting, Minneapolis, October 2016.
2. "Predicting Kinase Activities from Phosphoproteomic Measurements. Shweta Ravi and Kristen Naegle. Biomedical Engineering Society Annual Meeting, Minneapolis, October 2016.
3. "Analysis of SH2 specificity determinants" Roman Sloutsky and Kristen M. Naegle. Biophysical Society Meeting, Los Angeles, CA, February 2016.
4. "High-throughput quantitative phosphoproteomic dataset analysis using combinatorial parametric unsupervised learning". August 2010, Lisbon. RECOMB 2010.
5. "PTMScout: A web resource for analysis of high-throughput proteomic studies of post-translational modifications". March 2010, Quebec, QC. Keystone Symposia - Biomolecular Interaction Networks: Function and Disease.
6. "High Throughput Enrichment Analysis of Unsupervised Learning Algorithms in Application to Phosphoproteomic Networks". January 2009, Cambridge, MA. Cells, Circuits and Computation.

Presentations

Invited Talks

1. University of Illinois Chicago, Bioengineering Department Seminar, March 15th, 2019
2. Northwestern University, Biomedical Engineering Department Seminar, October 25th, 2018
3. Invited Speaker, FASEB meeting on Protein Kinase Signaling Network Regulation, Colorado, July 2018
4. University of Virginia, Data Science Institute and Biomedical Engineering, May 16th, 2018
5. Cornell University, Biomedical Engineering Department Seminar, March 8th, 2018
6. University of Minnesota, Biomedical Engineering Department Seminar, February 7th, 2018
7. Purdue, Department of Biomedical Engineering, January 10, 2018
8. Moffitt Cancer Center, Tampa Florida, December 1, 2016.
9. Invited Speaker, 4th Midwest Quantitative Biology Symposium, Purdue, October 22nd, 2016.
10. "Unsupervised learning to unravel differential cell fate outcomes", FASEB meeting on Protein Kinase Signaling Network Regulation, Colorado, July 2016.
11. NIH Computational Biology Department Seminar, May 2nd, 2016
12. University of Virginia, Biomedical Engineering Department Seminar, April 29th, 2016
13. **Keynote address** at the Biomedical Computation at Stanford (BCATS) symposium. April 6, 2015
14. Seminar at The Institute of Cancer Research, Royal Cancer Hospital, London, September 19, 2014.
15. Seminar at Pacific Northwest National Labs COIN seminar, Richland WA, November 2012.
16. "How to use PTMScout to understand the role of post-translational modifications in cell signaling and cancer", AACR-NCI Conference on Systems Biology: Confronting the Complexity of Cancer, San Diego CA, February 2011.
17. "PTMScout for analysis and storage of high-throughput post-translational modification data, a tutorial". Pfizer Corporation, Cambridge MA, June 2010.
18. "A Combinatorial Unsupervised Learning Framework for Prediction of Post-Translational Modification Functions in Signaling Networks". Merck-CSBi Symposium, Boston MA, June 2010.
19. "An integrated Phosphoproteomic and Bioinformatic Approach Reveals a Novel Class of MPM-2 Antigen", Merrimack seminar series, Cambridge MA, July 2008.

Conferences (Platform Talks)

1. "ASPEN: Analyzing and Reconstructing Paralog Divergence Using Ortholog Subsampling". BMES Annual Meeting, October 19, 2018 Atlanta, GA.
2. "Ensemble Clustering Infers Signaling Differences Resulting From HER2 Overexpression". BMES Annual Meeting, October 17, 2017 Phoenix, AZ.
3. "Using the principals of domain modularity to enhance phosphoprotein production". EMBO Workshop The Modularity of signaling proteins and networks, September 20-25, 2016 Seefeld in Tirol, Austria.
4. "ProteomeScout: A community resource for proteins and post-translational modifications", PTMs in Cell Signaling, Copenhagen Bioscience Conferences, September 2014
5. "Improved Clustering of Molecular Measurements Using Ensemble Approaches". Biomedical Engineering Society (BMES) Annual Meeting, San Antonio TX, October 2014.

6. "PTMScout: Understanding protein post-translational modifications". Biomedical Engineering Society (BMES) Annual Meeting, Seattle WA. September 2013.
7. "Robust Clustering of ERBB Phosphorylation Dynamics Predicts Protein Macromolecular Complex Formation and Reveals a Role for Novel Components of the ERBB Network". Biomedical Engineering Society (BMES) Annual Meeting, Hartford CT, October 2011.
8. "An integrated Phosphoproteomic and Bioinformatic Approach Reveals a Novel Class of MPM-2 Antigen". Biomedical Engineering Society (BMES) Annual Meeting, St. Louis MO, October 2008.

Teaching, Training, and Administration

Courses Taught

Washington University in St. Louis:

1. BME 5913 – Molecular Systems Biology: Computation and measurements for understanding cell physiology and disease (Spring 2013, 2014, 2015; Fall 2015; Spring 2017; Fall 2017)
2. BME 538 – Cell Signal Transduction (Fall 2014, Spring 2016, Spring 2018)
3. MATLAB Bootcamp for incoming BME Students (2014-2017): Established curriculum, organize, and recruit graduate lecturer

Special Lectures:

1. BME 301B Quantitative Physiology: Special Lectures (2) (An introduction to systems biology: 2018)
2. BME 140 Special Lecture (Networks in Biology and Society: 2012, 2013, 2014, 2015, 2016, 2017)
3. BME 5068 Fundamentals of Molecular Cell Biology. (Cell Signaling: Spring 2017, Spring 2018)
4. CHEM 482 (Post-translational Modifications: Spring 2017)
5. Faculty Spotlight Parent and Family Weekend (The Kevin Bacon Number, October 2015)

Massachusetts Institute of Technology: (Past)

1. BE 309 – Instrumentation and Measurement for Biological Systems (Course module development and TA) (Fall 2005)

Postdoctoral Associates

1. Amjad Nasir (2018-present)
2. Zeenat Shyr, joint with Maria Remedi (2017-present) through NIH training grant

Graduate Students Trained

1. Roman Sloutsky (PhD, August 2017): Robust algorithms for detecting hidden structure in biological data. Current Position: Postdoctoral Associate at University of Massachusetts Amherst with Dr. Margaret Stratton
2. Tom Ronan (PhD, November 2017): Binding Affinity and Specificity of SH2 Domain Interactions in Receptor Tyrosine Kinase Signaling Networks

Master Students Trained

1. Summer Elias, (WUSTL, BME), 2018: Reevaluating kinase evolution.

Rotation Students

1. Jessica Miller (MSTP/BME), 2012
2. Nathan Wong (BME), 2012
3. Alex Holehouse (Comp. Biophysics), 2012
4. Richard Hauser (BME), 2012
5. Matthew Matlock (MSTP/Comp Sys Bio), 2013
6. Shouyi Wei (BME), 2013
7. Will Pittman (BME), 2013
8. Jennifer Soll (Statistical Genetics), 2014
9. Jennifer Flynn (Comp Sys Bio), 2014
10. Aura Ferreira (BME), 2014
11. Zach Beller (MSTP), 2015
12. Matthew Curtis (BME), 2015
13. Paul Jang (BME), 2016
14. Avinash Ramu (Statistical Genetics), 2016
15. Yuanzi Sun (ChemE), 2017
16. Kaiser Loell (Comp Sys Bio), Spring 2018
17. Ryan Friedman (Comp Sys Bio), Spring 2018
18. Paige Hall (Biochemistry), Spring 2018

19. Ethan Stancliffe (Comp Sys Biol), Summer 2018
20. Jaquelin Garcia (Biochemistry), Summer 2018

Undergraduate Researchers

1. Elizabeth Worley (WUSTL BME), 2012-2014
2. Tedan Hu (UMSL Biochemistry), Summer 2012
3. Nikolay Shenkov (University of Richmond), Summer 2012
4. Kellie Stoka (WUSTL BME), Spring Semester 2013
5. Cong Zhang (WUSTL BME), Spring 2013
6. Jennifer Flynn (Truman Biology, Siteman Cancer Center), Summer 2013
7. Junwoo Suh (WUSTL BME), Summer/Fall 2013
8. Emily Gale (Swarthmore), Summer 2014 Amgen
9. Zhijie Qi (WUSTL BME), 2014-2015
10. Jordan Banks (University of Illinois), BiomedRAP
11. Pedro de Silva Vierira Taveres (Brazil Scientific Mobility Program), Summer 2015
12. Shweta Ravi (WUSTL BME), Spring/Summer 2016
13. Ramya Palaniappan (Case Western), Summer 2016
14. Varun Krishnamurthy (WUSTL CSE), Fall 2016
15. Erin Tevonian (UIUC BME), Siteman Cancer Center, Summer 2017
16. Liezel Tipples (Univ. of Guam), Genome Institute, Summer 2017
17. Yuanyuan He (WUSTL BME), Spring and Summer 2018
18. Yunli Chu (WUSTL BME), Spring 2018

High School Students

1. Cassidy Manns, Summer 2012
2. Elizabeth Love, Summer 2013
3. Ramya Palaniappan, Summer 2015 (Young Scientist's Program), Fall 2015
4. Shawn Anastasio, Summer 2015
5. David White (Young Scientist's Program), Summer 2017
6. Jynette Hall (SEPA), Summer 2018

Theses Advised (student, defense year, PI)

1. Yun Zhao, 2013, Anthony French
2. Ben Borgo, 2014, Jim Havranek
3. Laura Marquardt, 2014, Shelly Sakiyama-Elbert
4. Chaoyi Kang, 2016, Igor Effimov
5. Shivam Shah, 2016, Steve Thomopoulos
6. Rebecca Gilson, 2017, Sam Achilefu
7. Adam Joyce, 2017, Jim Havranek
8. Dov Lerman-Sinkoff, 2018, Deanna Barch
9. Allison Thom, 2018, Anthony French
10. Heather Zannit. (ongoing), Matt Silva
11. Lena Dang (ongoing), Josh Swamidass
12. Dana King (ongoing), Barak Cohen
13. Aura Ferreira (ongoing), Gautam Dantas
14. Yanzel Nunez (ongoing), Linda Pike
15. Arshag Mooradian (ongoing), Jason Held

Staff

1. Katherine Schaberg, Research Technician II (2012-current)
2. Jeremy Buck, Research Technician II (July 1, 2018-current)
3. Monalisa Munsu, visiting Ph.D. student, Univ. of Iowa Applied Math, (May-July 2017)
4. Matthew Matlock, Scientific Programmer 0.5FTE (July 2012-March 2013)

Outreach

1. GRC Moving and Shaking (2x1.5hr session for Junior High): Fold-X: Crowdsourcing protein folding (2012-2015)
2. GLiTCH Summer Camp (2 x 1.5hr module for Junior High): Computer science helps solve biological problems (2013)

3. INSPIRE workshop (3 hour module 6th grade): Networks and algorithms in biology and society (2014)
4. Society of Women Engineers (5x30min module High School): Networks and algorithms in biology and society (2014)
5. STEAM Day (6x10min for Elementary in Kirkwood School District): Jellyfish, Plants, and Cells - Oh My.

Administrative responsibilities Washington University in St. Louis:

Current

1. Graduate Admissions Committee, Biochemistry, Biophysics, and Structural Biology (2017)
2. BMES student chapter, Faculty Advisor, (2016-Present)
3. Graduate Committee, Department of Biomedical Engineering, Member (2016-Present)
4. Graduate Admissions Committee, Department of Biomedical Engineering, Member (2016-Present)

Past

1. JSEAS Steering Committee, School of Engineering and Applied Science (2015-2017)
2. Masters in Engineering Committee, Department of Biomedical Engineering, Member (2015-Fall 2017)
3. Undergrad Research Programs (Amgen, BioMedRAP) Selection Committee (2017)
4. JCUBES (Undergraduate research journal club) Faculty Advisor, (2015-2016)
5. Graduate Admissions, Department of Biomedical Engineering, Member (2012-2015, 2017-)
6. Graduate Committee, Department of Biomedical Engineering, Member (2014-2015, 2017-)
7. Faculty Search Committee, Department of Biomedical Engineering, Member (2014)
8. Undergraduate Committee, Department of Biomedical Engineering, Member (2015-2016)

Internal Review Work (Washington University in St. Louis)

1. University Strategic Research Alliance, 2012
2. Siteman Cancer Center, 2015, 2016

Diversity and Inclusion (Washington University in St. Louis)

1. Provost's Bring Your Own Idea: Co-awardee for Faculty Bookclub on Stereotype threat Spring 2014-Fall 2015
2. iTEACH Symposium Workshop Lead: "Understanding and Mitigating Stereotype Threat", January 2016

Software Products and Intellectual Property (all software links available from naegle.wustl.edu)

1. OpenEnsembles: An open-source Python package for ensemble clustering. Under active development and available to the public.
2. ASPEN: An open-source package for the reconstruction of evolutionary trees.
3. Partial SDP identification from alignments or ensembles of alignments.
4. "Kinase toolkit for the production of phosphorylated proteins". Provisional patent filed September 2016, Continuation in Part September 2017.
5. *ProteomeScoutAPI*: An easy API for access to ProteomeScout database downloads.
6. *ProteomeScout*: A universal resource for protein visualization, protein features, and analysis of post-translational modifications. A former version of this web-based tool existed as ptmscout.mit.edu
 - a. Statistics: ProteomeScout: 15,589 visits (11,749 visitors), 75,293 page views, 4.83 pages/session (April 2013 – November 2017).
7. PTMScout: 4,523 visits (2,827 visitors), average duration of visit 3 minutes (January 2010-January 2014). This resource now redirects to ProteomeScout.
8. *MCAM: Multiple Clustering Analysis Methodology*. A Matlab-based software package implementing ensemble clustering. Download frequency has not been tracked.