

Kevin A. T. Silverstein — *Curriculum Vitae*

2108 Folwell Ave, St. Paul MN 55108

612-625-0292 (work)

Cell: 651-500-6671 E-mail: kats@umn.edu

OBJECTIVE

To make significant contributions to a leading-edge bioinformatics program, collaborate with outstanding life sciences researchers, and mentor the next generation of scientists in this interdisciplinary area.

RESEARCH HIGHLIGHTS

- Broad training in cross-disciplinary computational sciences.
- Graduate work with Ken Dill, teased apart key driving forces of protein folding.
- As postdoc, lead an interdisciplinary team in the development of a publicly accessible protein family database, MetaFam, that preceded InterPro.
- In the Plant Biology Department, discovered hundreds of unannotated genes encoding proteins similar to antimicrobial peptides within plant genomes. Investigated the genome evolution and organization of these large gene families. Developed a custom Affymetrix microarray to detect the expression of these gene families, and designed novel normalization algorithms for use with these boutique arrays.
- Investigated genome organization events among highly rearranged APOBEC genes in artiodactyls.
- Characterized transposable elements among six fungal genomes.
- Developed novel NGS analysis pipelines for transposon insertion processing and annotation, detection of somatic frameshift mutations for targeting personalized tumor vaccines, and the detection of structural variants in plant and cancer genomes.
- Led the development of an NGS diagnostic pipeline currently used by Fairview Hospital for patient diagnosis of inherited disorders in the clinic.

SKILLS

- NGS analysis, gene expression, phylogenetic analysis, genome comparison, database design
- Platforms: UNIX, Windows, Mac; MySQL; PostgreSQL; Oracle; Galaxy
- Languages: Perl, R/Bioconductor, Python, Java, C++, Fortran, LISP, SQL

EDUCATION AND TRAINING

1988-1992	Rutgers University , New Brunswick, NJ. B.A. 1992. Major: Computer Science; Minor: Chemistry; Advisor: Wilma K. Olson
1989, 1990	Bellcore (now Telcordia), Piscataway, NJ. Summer Intern. Field: Computer Science; Advisor: John S. Kaminsky
1992-1997	University of California, San Francisco , San Francisco, CA. Ph.D. 1997. Field: Biophysics; Advisor: Ken A. Dill
1998-2000	University of Minnesota , Minneapolis, MN. Field: Bioinformatics; Postdoctoral Advisor: Ernest F. Retzel

PROFESSIONAL APPOINTMENTS

2000-2001	Research Associate, Academic Health Center, University of Minnesota, Minneapolis, MN
2001-2008	Research Associate, Dept. of Plant Biology, University of Minnesota, St. Paul MN (50% 2006-2008)
2003-	Member, Graduate Faculty, Plant Biological Sciences Graduate Program, University of Minnesota
2006-2012	Coordinator, Masonic Cancer Center Bioinformatics Core, University of Minnesota, Minneapolis, MN (50% 2006-2008)
2012-present	Scientific Lead, RIS program, Minnesota Supercomputing Institute, University of Minnesota, Minneapolis, MN

TEACHING EXPERIENCE

1999	Student, GRAD 8100: Innovative Teaching for Future Faculty
1999, 2004	Guest lecturer, HINF 5431: Health Informatics
2001, 2002	Guest lecturer, PIPa 5301: Plant Genomics
2003, 2004, 2006	Workshop presenter, Bioinformatics Summer Institute (BSI)
2005	Guest lecturer, PBS 8081: Current Topics in Plant Biology
2011	Invited Seminar, PIPa Seminar
2013-2016	Guest lecturer, PubH 6160: Toxicology
2014-2015	Co-Instructor, Agro 5999: Biocomputing Data Skills

AWARDS AND FELLOWSHIPS

1988	Member of the Phi Eta Sigma Honor Society (Rutgers University)
1988-1992	Edward J. Bloustein Distinguished Scholar (Rutgers University)
1988-1992	Dean's List (Rutgers University)
1991	Calm Foundation Merit Scholarship (Rutgers University)
1992	Women's League of Rutgers University Scholarship (Rutgers University)
1992	Henry Rutgers Scholar (Rutgers University)
1992	Highest Honors in Chemistry and Computer Science (Rutgers University)
1993-1996	National Science Foundation Predoctoral Fellowship (UCSF)
1996-1997	U.C. Regents Fellowship (UCSF)

MENTORING EXPERIENCE

Undergraduate students	Bioinformatics Summer Institute (BSI) co-advisor for: Andrea Carlson, Katayoun Jafari, Kate Lauer, Amber Martell Undergraduate Research Opportunities Program (UROP) advisor for: Amber Martell Directed Research (PBio 4994) advisor for: Jeremy Ragan
Graduate students	Plant Pathology Ph.D. co-advisor for: Peng Zhou Plant Biological Sciences (PBS) Ph.D. co-advisor for: Sumitha Nallu (graduated 2010), Diana Trujillo, Joseph Guhlin Veterinary Clinical Sciences M.S. committee member for: Kyra Wingate
Professional scientists	Masonic Cancer Center Coordinator, supervisor for: Aaron Sarver PhD, Flora Fan PhD, Jesse Erdmann, TaeHyun Hwang PhD, Getiria Onsongo PhD RIS MSI Lead Analyst, Interim supervisor (2013-2014) for: John Garbe, PhD, Getiria Onsongo PhD, Ying Zhang PhD, Lauren Mills, PhD, Rendong Yang, PhD, Christine Henzler, PhD.

PUBLICATIONS

1. Haymet ADJ, **Silverstein KAT**, and Dill KA. Hydrophobicity reinterpreted as 'minimization of the entropy penalty of solvation. *Faraday Discuss. Chem. Soc.* 1996:103:117-124.
2. **Silverstein KAT**, Haymet ADJ, and Dill KA. Hydrophobicity in a simple model of water: solvation and hydrogen bond energies. *Fluid Phase Equilibria.* 1998:151:83-90.
3. **Silverstein KAT**, Haymet ADJ, and Dill KA. A simple model of water and the hydrophobic effect. *J. Am. Chem. Soc.* 1998:120:3166-3175.
4. **Silverstein KAT**, Haymet ADJ, and Dill KA. Molecular model of hydrophobic solvation. *J. Chem. Phys.* 1999:111:8000-8009.
5. **Silverstein KAT**, Haymet ADJ, and Dill KA. The strength of hydrogen bonds in liquid water and around nonpolar solutes. *J. Am. Chem. Soc.* 2000:122:8037-8041.
6. **Silverstein KAT**, Kilian A, Freeman JL and Retzel EF. PANAL: an integrated resource for Protein sequence ANALysis. *Bioinformatics.* 2000:16:1157-1158. PMID:11159337.
7. **Silverstein KAT**, Dill KA and Haymet ADJ. Hydrophobicity in a simple model of water: entropy penalty as a sum of competing terms via full, angular expansion. *J. Chem. Phys.* 2001:114:6303-6314.
8. **Silverstein KAT**, Shoop E, Johnson JE, Kilian A, Freeman JL, Kunau TK, Awad IA, Mayer, M and Retzel EF. The MetaFam server: a comprehensive protein family resource. *Nucleic Acids Res.* 2001:29:49-52. PMID:11125046.
9. **Silverstein KAT**, Shoop E, Johnson JE and Retzel EF. MetaFam: A unified classification of protein families. I. Overview and statistics. *Bioinformatics.* 2001:17:249-261. PMID:11294790.
10. Shoop E, **Silverstein KAT**, Johnson JE and Retzel EF. MetaFam: A unified classification of protein families. II. Schema and query capabilities. *Bioinformatics.* 2001:17:262-271. PMID:11294791.
11. Lamblin A-F, Crow JA, Johnson JE, **Silverstein KAT**, Kunau TM, Kilian A, Benz D, Stromvik M, Endre G, VandenBosch KA, Cook DR, Young ND, and Retzel EF. MtDB: A database for personalized data mining of the model legume *Medicago truncatula* transcriptome. *Nucleic Acids Res.* 2003:31:196-201. PMID:12519981.
12. Johnson JE, Stromvik MV, **Silverstein KAT**, Crow JA, Shoop E and Retzel EF. TableView: portable genomic data visualization. *Bioinformatics.* 2003:19:1292-1293. PMID:12835275.
13. Graham MA, **Silverstein KAT**, Cannon SB and VandenBosch KA. Computational identification and characterization of novel genes from legumes. *Plant Physiol.* 2004:135:1179-1197. PMID:15266052.
14. Sherrier DJ, Taylor GS, **Silverstein KAT**, Gonzales MB and VandenBosch KA. Accumulation of extracellular proteins bearing unique proline-rich motifs in intercellular spaces of the legume nodule parenchyma. *Protoplasma.* 2005:225:43-55. PMID:15868212.
15. Graham MA, **Silverstein KAT**, Cannon SB and VandenBosch KA. Computational identification of legume-specific genes. In *Genome Exploitation: Data Mining the Genome*, edited by JP Gustafson, R Shoemaker and JW Snape. Springer Science. New York. 2005:211-225.
16. **Silverstein KAT**, Graham MA, Paape TD and VandenBosch KA. Genome organization of more than 300 defensin-like genes in *Arabidopsis*. *Plant Physiol.* 2005:138:600-610. PMID:15955924.
17. Lohar DP, Sharapova N, Endre G, Penuela S, Samac D, Town C, **Silverstein KAT** and VandenBosch KA. Transcript analysis of early nodulation events in *Medicago truncatula*. *Plant Physiol.* 2006:140:221-234. PMID:16377745.
18. **Silverstein KAT**, Graham MA, VandenBosch KA. Novel paralogous gene families with potential function in legume nodules and seeds. *Curr. Opin. Plant. Biol.* 2006:9:142-146. PMID:16459131.

19. Tesfaye M, **Silverstein KAT**, Bucciarelli B, Samac D and Vance CP. The Affymetrix Medicago GeneChip® Array is Applicable for Transcript analysis of Alfalfa (*Medicago sativa* L.). *Functional Plant Biol.* 2006;33:783-788.
20. **Silverstein KAT**, Moskal Jr. WA, Wu HC, Underwood BA, Graham MA, Town CD and VandenBosch KA. Small cysteine-rich peptides resembling antimicrobial peptides have been under-predicted in plants. *The Plant Journal.* 2007;51:262-280. PMID:17565583.
21. Graham MA, **Silverstein KAT** and VandenBosch KA. Defensin-like genes: genomic perspectives on a diverse superfamily in plants. *Crop Sci.* 2008;48:S3-S11.
22. Wingate KV, Tores SM, **Silverstein KAT**, Hendrickson JA and Rutherford MS. Expression of endogenous antimicrobial peptides in normal canine skin. *Veterinary Dermatology.* 2009;20:19-26. PMID:19037917.
23. LaRue RS, Jonsson SR, **Silverstein KAT**, Lajoie M, Bertrand D, El-Mabrouk N, Hotzel I, Andresdottir V, Smith TPL and Harris RS. The artiodactyl APOBEC3 innate immune repertoire shows evidence for a multi-functional domain organization that existed in the ancestor of placental mammals. *BMC Molecular Biology.* 2008;9:104. PMID:19017397.
24. Keng VW, Villanueva A, Chiang DY, Dupuy AJ, Ryan BJ, Matise I, **Silverstein KAT**, Sarver A, Starr TK, Akagi K, Tessarollo L, Collier LS, Powers S, Lowe SW, Jenkins NA, Copeland NG, Llovet JM and Largaespada DA. A conditional transposon-based insertional mutagenesis screen for hepatocellular carcinoma-associated genes in mice. *Nature Biotechnology.* 2009;27:264-274. PMID:19234449.
25. Starr TK, Allaei R, **Silverstein KAT**, Staggs RA, Sarver AL, Bergemann TL, Gupta M, O'Sullivan MG, Matise I, Dupuy AJ, Collier LS, Powers S, Oberg AL, Asmann YW, Thibodeau SN, Tessarollo L, Copeland NG, Jenkins NA, Cormier RT, Largaespada DA. A transposon-based genetic screen in mice identifies genes altered in colorectal cancer. *Science.* 2009;323:1747-1750. PMID:19251594.
26. Butler G, Rasmussen MD, Lin MF, Santos MA, Sakthikumar S, Munro CA, Rheinbay E, Grabherr M, Forche A, Reedy JL, Agrafioti I, Arnaud MB, Bates S, Brown AJ, Brunke S, Costanzo MC, Fitzpatrick DA, de Groot PW, Harris D, Hoyer LL, Hube B, Klis FM, Kodira C, Lennard N, Logue ME, Martin R, Neiman AM, Nikolaou E, Quail MA, Quinn J, Santos MC, Schmitzberger FF, Sherlock G, Shah P, **Silverstein KAT**, Skrzypek MS, Soll D, Staggs R, Stansfield I, Stumpf MP, Sudbery PE, Srikantha T, Zeng Q, Berman J, Berriman M, Heitman J, Gow NA, Lorenz MC, Birren BW, Kellis M, Cuomo CA. Evolution of pathogenicity and sexual reproduction in eight *Candida* genomes. *Nature.* 2009;459:657-662. PMID:19465905.
27. Cunningham JM, Oberg AL, Borralho PM, Kren BT, French AJ, Wang L, Bot BM, Morlan BW, **Silverstein KAT**, Staggs R, Zeng Y, Lamblin A-F, Hilker CA, Fan J-B, Steer CJ, Thibodeau, SN. Evaluation of a new high-dimensional miRNA profiling platform. *BMC Medical Genomics* 2009;2:57. PMID:19712457.
28. Sarver AL, French AJ, Borralho PM, Thayanithy V, Oberg AL, **Silverstein KAT**, Morlan BW, Riska SM, Boardman LA, Cunningham JM, Subramanian S, Wang L, Smyrk TC, Rodrigues CM, Thibodeau SN, Steer CJ. Human colon cancer profiles show differential microRNA expression depending on mismatch repair status and are characteristic of undifferentiated proliferative states. *BMC Cancer.* 2009;9:401. PMID:19922656.
29. Young ND, Debelle F, Oldroyd GE, Geurts R, Cannon SB, Udvardi MK, Benedito VA, Mayer KF, Gouzy J, Schoof H, Van de Peer Y, Proost S, Cook DR, Meyers BC, Spannagl M, Cheung F, De Mita S, Krishnakumar V, Gundlach H, Zhou S, Mudge J, Bharti AK, Murray JD, Naoumkina MA, Rosen B, **Silverstein KAT**, Tang H, Rombauts S, Zhao PX, Zhou P, Barbe V, Bardou P, Bechner M, Bellec A, Berger A, Bergès H, Bidwell S, Bisseling T, Choisne N, Couloux A, Denny R, Deshpande S, Dai X, Doyle JJ, Dudez AM, Farmer AD, Fouteau S, Franken C, Gibelin C, Gish J, Goldstein S, González AJ, Green PJ, Hallab A, Hartog M, Hua A, Humphray SJ, Jeong DH, Jing Y,

- Jöcker A, Kenton SM, Kim DJ, Klee K, Lai H, Lang C, Lin S, Macmil SL, Magdelenat G, Matthews L, McCarrison J, Monaghan EL, Mun JH, Najar FZ, Nicholson C, Noiro C, O'Bleness M, Paule CR, Poulain J, Prion F, Qin B, Qu C, Retzel EF, Riddle C, Sallet E, Samain S, Samson N, Sanders I, Saurat O, Scarpelli C, Schiex T, Segurens B, Severin AJ, Sherrier DJ, Shi R, Sims S, Singer SR, Sinharoy S, Sterck L, Viollet A, Wang BB, Wang K, Wang M, Wang X, Warfsmann J, Weissenbach J, White DD, White JD, Wiley GB, Wincker P, Xing Y, Yang L, Yao Z, Ying F, Zhai J, Zhou L, Zuber A, Dénarié J, Dixon RA, May GD, Schwartz DC, Rogers J, Quétier F, Town CD, Roe BA. The Medicago genome provides insights into the evolution of rhizobial symbioses. *Nature*. 2011;480:520-524. PMID:22089132.
30. Bergemann TL, Starr TK, Yu H, Steinbach M, Erdmann J, Chen Y, Cormier RT, Largaespada DA, **Silverstein KAT**. New methods for finding common insertion sites and co-occurring common insertion sites in transposon- and virus-based genetic screens. *Nucleic Acids Res*. 2012;40:3822-3833. PMID:22241771.
 31. Li Y, Hwang TH, Oseth LA, Hauge A, Vessella RL, Schmechel SC, Hirsch B, Beckman KB, **Silverstein KAT**, Dehm SM. AR intragenic deletions linked to androgen receptor splice variant expression and activity in models of prostate cancer progression. *Oncogene*. 2012;31:4759-4767. PMID:22266865.
 32. Bergerson RJ, Collier LS, Sarver AL, Been RA, Lugthart S, Diers MD, Zuber J, Rappaport AR, Nixon MJ, **Silverstein KAT**, Fan D, Lamblin AF, Wolff L, Kersey JH, Delwel R, Lowe SW, O'Sullivan MG, Kogan SC, Adams DJ, Largaespada DA. An insertional mutagenesis screen identifies genes that cooperate with Mll-AF9 in a murine leukemogenesis model. *Blood*. March 2012;119:4512-4523. PMID:22427200.
 33. Giacomelli L, Nanni V, Lenzi L, Zhuang J, Dalla Serra M, Banfield MJ, Town CD, **Silverstein KAT**, Baraldi E, Moser C. Identification and characterization of the defensin-like gene family of grapevine. *Mol Plant Microbe Interact*. 2012;25:1118-1131. PMID:22550957.
 34. O'Donnell KA, Keng VW, York B, Reineke EL, Seo D, Fan D, **Silverstein KAT**, Schrum CT, Xie WR, Mularoni L, Wheelan SJ, Torbenson MS, O'Malley BW, Largaespada DA, Boeke JD. A Sleeping Beauty mutagenesis screen reveals a tumor suppressor role for Ncoa2/Src-2 in liver cancer. *Proc Natl Acad Sci U S A*. 2012;109:E1377-E1386. PMID:22556267.
 35. Knutson TP, Daniel AR, Fan D, **Silverstein KAT**, Covington KR, Fuqua SA, Lange CA. Phosphorylated and sumoylation-deficient progesterone receptors drive proliferative gene signatures during breast cancer progression. *Breast Cancer Res*. 2012;14:R95. PMID:22697792.
 36. Pérez-Mancera PA, Rust AG, van der Weyden L, Kristiansen G, Li A, Sarver AL, **Silverstein KAT**, Grützmann R, Aust D, Rümmele P, Knösel T, Herd C, Stemple DL, Kettleborough R, Brosnan JA, Li A, Morgan R, Knight S, Yu J, Stegeman S, Collier LS, ten Hoeve JJ, de Ridder J, Klein AP, Goggins M, Hruban RH, Chang DK, Biankin AV, Grimmond SM; Australian Pancreatic Cancer Genome Initiative, Wessels LF, Wood SA, Iacobuzio-Donahue CA, Pilarsky C, Largaespada DA, Adams DJ, Tuveson DA. The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. *Nature*. 2012;486:266-270. PMID:22699621.
 37. Sarver AL, Erdman J, Starr T, Largaespada DA, **Silverstein KAT**. TAPDANCE: an automated tool to identify and annotate transposon insertion CISs and associations between CISs from next generation sequence data. *BMC Bioinformatics*. 2012;13:154. PMID:22748055.
 38. Musselman JR, Bergemann TL, Ross JA, Sklar C, **Silverstein KAT**, Langer EK, Savage SA, Nagarajan R, Krailo M, Malkin D, Spector LG. Case-parent analysis of variation in pubertal hormone genes and pediatric osteosarcoma: a Children's Oncology Group (COG) study. *Int J Mol Epidemiol Genet*. 2012;3:286-93. PMID:23205180.
 39. Li Y, Chan SC, Brand LJ, Hwang TH, **Silverstein KAT**, Dehm SM. Androgen receptor splice variants mediate enzalutamide resistance in castration-resistant prostate cancer cell lines. *Cancer*

Res. 2013 Jan 15;73(2):483-489. PMID:23117885.

40. Tesfaye M, **Silverstein KAT**, Nallu S, Wang L, Botanga CJ, Gomez SK, Costa LM, Harrison MJ, Samac DA, Glazebrook J, Katagiri F, Gutierrez-Marcos JF, Vandenbosch KA. Spatio-temporal expression patterns of Arabidopsis thaliana and Medicago truncatula defensin-like genes. *PLoS One*. 2013;8(3):e58992. PMID:23527067.
41. Nallu S, **Silverstein KAT**, Samac DA, Bucciarelli B, Vance CP, VandenBosch KA. Regulatory patterns of a large family of defensin-like genes expressed in nodules of Medicago truncatula. *PLoS One*. 2013;8(4):e60355. PMID:23573247.
42. Hwang TH, Atluri G, Kuang R, Kumar V, Starr T, **Silverstein KAT**, Haverty PM, Zhang Z, Liu J. Large-scale integrative network-based analysis identifies common pathways disrupted by copy number alterations across cancers. *BMC Genomics*. 2013 14:440. PMID:23822816.
43. Rathe SK, Johnson JE, **Silverstein KAT**, Erdmann JJ, Watson AL, Popescu FE, Ohlfest JR, Largaespada DA. MMuFLR: missense mutation and frameshift location reporter. *Bioinformatics*. 2013 29(18):2353-4. PMID:23825368.
44. Nyquist MD, Li Y, Hwang TH, Manlove LS, Vessella RL, **Silverstein KAT**, Voytas DF, Dehm SM. (2013) TALEN-engineered AR gene rearrangements reveal endocrine uncoupling of androgen receptor in prostate cancer. *Proc Natl Acad Sci U S A*. 2013 Oct 22;110(43):17492-7. PMID:24101480.
45. Zhou P, **Silverstein KAT**, Gao L, Walton JD, Nallu S, Guhlin J, Young ND. Detecting small plant peptides using SPADA (Small Peptide Alignment Discovery Application). *BMC Bioinformatics*. 2013 14:335. PMID:24256031.
46. McAloney CA, **Silverstein KAT**, Modiano JF, Bagchi A. Polymorphisms within the Telomerase Reverse Transcriptase gene (TERT) in four breeds of dogs selected for difference in lifespan and cancer susceptibility. *BMC Vet Res*. 2014 10(1):20. PMID:24423165.
47. Landman SR, Hwang TH, **Silverstein KAT**, Li Y, Dehm SM, Steinbach M, Kumar V. SHEAR: sample heterogeneity estimation and assembly by reference. *BMC Genomics*. 2014 15(1):84. PMID:24476358.
48. Nallu S, **Silverstein KAT**, Zhou P, Young ND, Vandenbosch KA. Patterns of divergence of a large family of nodule cysteine-rich peptides in accessions of Medicago truncatula. *Plant J*. 2014. PMID:24635121.
49. Costa LM, Marshall E, Tesfaye M, **Silverstein KAT**, Mori M, Umetsu Y, Otterbach SL, Papareddy R, Dickinson HG, Boutiller K, VandenBosch KA, Ohki S, Gutierrez-Marcos JF. Central cell-derived peptides regulate early embryo patterning in flowering plants. *Science*. 2014. 344(6180):168-72. PMID:24723605.
50. Zhang Y, Sun Y, Rao E, Yan F, Li Q, Zhang Y, **Silverstein KAT**, Liu S, Sauter E, Cleary MP, Li B. Fatty acid-binding protein E-FABP restricts tumor growth by promoting IFN- β responses in tumor-associated macrophages. *Cancer Res*. 2014 Jun 1;74(11):2986-98. PMID: 24713431.
51. Shah JD, Baller J, Zhang Y, **Silverstein KAT**, Xing Z, Cardona CJ. Comparison of tissue sample processing methods for harvesting the viral metagenome and a snapshot of the RNA viral community in a turkey gut. *J Virol Methods*. 2014 Dec;209:15-24. PMID: 25181646.
52. Onsongo G, Erdmann J, Spears MD, Chilton J, Beckman KB, Hauge A, Yohe S, Schomaker M, Bower M, **Silverstein KAT**, Thyagarajan B. Implementation of Cloud based next generation sequencing data analysis in a clinical laboratory. *BMC Res Notes*. 2014 May 23;7:314. PMID: 24885806.
53. Trujillo DI, **Silverstein KAT**, Young ND. Genomic Characterization of the LEED..PEEDs, a Gene Family Unique to the Medicago Lineage. *G3 (Bethesda)*. 2014 Aug 25. PMID: 25155275.

54. Yohe S, Hauge A, Bunjer K, Kemmer T, Bower M, Schomaker M, Onsongo G, Wilson J, Erdmann J, Zhou Y, Deshpande A, Spears MD, Beckman K, **Silverstein KAT**, Thyagarajan B. Clinical validation of targeted next-generation sequencing for inherited disorders. *Arch Pathol Lab Med*. 2015 Feb;139(2):204-10. PMID: 25611102.
55. Dorr C, Janik C, Weg M, Been RA, Bader J, Kang R, Ng B, Foran L, Landman SR, O'Sullivan MG, Steinbach M, Sarver AL, **Silverstein KAT**, Largaespada DA, Starr TK. Transposon Mutagenesis Screen Identifies Potential Lung Cancer Drivers and CUL3 as a Tumor Suppressor. *Mol Cancer Res*. 2015. PMID: 25995385.
56. Hargreaves ML, Shaw KM, Dobbins G, Snippes Vagnone PM, Harper JE, Boxrud D, Lynfield R, Aziz M, Price LB, **Silverstein KAT**, Danzeisen JL, Youmans B, Case K, Sreevatsan S, Johnson TJ. Clonal Dissemination of Enterobacter cloacae Harboring blaKPC-3 in the Upper Midwestern United States. *Antimicrob Agents Chemother*. 2015 Dec;59(12):7723-34. PMID: 26438492.
57. Poynter JN, Bestrashniy JR, **Silverstein KAT**, Hooten AJ, Lees C, Ross JA, Tolar J. Cross platform analysis of methylation, miRNA and stem cell gene expression data in germ cell tumors highlights characteristic differences by tumor histology. *BMC Cancer*. 2015 Oct 23;15:769. PMID:26497383.
58. Yang R, Nelson AC, Henzler C, Thyagarajan B, **Silverstein KAT**. ScanIndel: a hybrid framework for indel detection via gapped alignment, split reads and de novo assembly. *Genome Med*. 2015 Dec 7;7:127. PMID: 26643039.
59. Young ND, Zhou P, **Silverstein KAT**. Exploring structural variants in environmentally sensitive gene families. *Curr Opin Plant Biol*. 2016 Feb 5;30:19-24. PMID: 26855303.
60. Wu J, Keng VW, Patmore DM, Kendall JJ, Patel AV, Jousma E, Jessen WJ, Choi K, Tschida BR, **Silverstein KAT**, Fan D, Schwartz EB, Fuchs JR, Zou Y, Kim MO, Dombi E, Levy DE, Huang G, Cancelas JA, Stemmer-Rachamimov AO, Spinner RJ, Largaespada DA, Ratner N. Insertional Mutagenesis Identifies a STAT3/Arid1b/ β -catenin Pathway Driving Neurofibroma Initiation. *Cell Rep*. 2016 Mar 1;14(8):1979-90. PMID: 26904939.

SELECTED CONFERENCE PRESENTATIONS (Oral presentations in bold)

- Silverstein, KAT**, Haymet, ADJ, and Dill, KA. 1997. "Hydrophobicity in a simple model of water." Thirteenth Symposium on Thermophysical Properties. (Oral presentation). Boulder, Colorado, June 22-27.
- Silverstein, KAT, Shoop, E and Retzel, EF. 1999. "Analysis of protein family clusters." PAG-VII: Plant and Animal Genome VII. (Poster presentation). San Diego, California, January 17-21.
- Silverstein, KAT, Johnson, JE, Endre, G, Lamblin, A-F, Retzel, EF and VandenBosch, KA. 2002. "Automatic detection of sequence assembly errors." Fourteenth International Genome Sequencing and Analysis Conference. (Poster presentation). Boston, Massachusetts, October 2-5.
- Silverstein, KAT**, Graham, MA, Cannon, SB and VandeBosch KA. 2004. "Identification of novel legume-specific gene families: a potential source of new targets for crop improvement." PAG-XII: Plant and Animal Genome XII. (Oral presentation). San Diego, California, January 10-14.
- Silverstein, KAT, Graham, MA, Moskal Jr., WA, Wu, HC, Town, CD and VandenBosch, KA. 2005. "Small anti-microbial peptides have been grossly under-predicted among plants." 2005 Model Legume Congress. (Poster presentation). Pacific Grove, California, June 5-9.
- Silverstein, KAT**, Moskal Jr., WA, Wu, HC, Underwood, BA, Graham, MA, Town, CD and VandenBosch, KA. 2006. "Small cysteine-rich peptides resembling antimicrobial peptides have been under-predicted in plants." Ninth Computational Genomics Conference. (Oral presentation). Baltimore, Maryland, October 28-31.
- Silverstein, KAT, Moskal Jr., WA, Wu, HC, Underwood, BA, Graham, MA, Town, CD and

VandenBosch, KA. 2007. "Small cysteine-rich peptides resembling antimicrobial peptides have been under-predicted in plants." Genome Informatics Meeting. (Poster Presentation). Cold Spring Harbor, New York, November 1-5.

Silverstein, KAT, Beckman, K, Bower, M, Bunjer, K, Schomaker, M, Kemmer, T, Schimmenti, L, Yohe, S, Peterson, R, Karger, A, Roychowdhury, M and Thyagarajan, B. 2011. "Optimization of bait selection for sequence capture arrays." RECOMB 2011. (Poster Presentation). Vancouver, March 28-31.

Miller, J, Zhou, P, Mudge, J, Ramaraj, T, Walenz, B, Tiffin, P, Young, N and Silverstein, KAT. "Highly dynamic expansions of antimicrobial loci among Medicago truncatula accessions previously missed by short-read assemblies are revealed by inclusion of SMRT sequencing." Genome Informatics 2015. (Poster Presentation). Cold Spring Harbor, New York, October 28-31, 2015.

INVITED EXTERNAL SEMINARS

Silverstein, KAT. 1997. "Mercedes-Benz model of water and hydrophobicity." Invited by John Matachek, Chair, Dept. of Chemistry, Hamline University, St. Paul, MN, October 21.

Silverstein, KAT. 2004. "Panel on genetic engineering, genomics and molecular biology." Invited by Daniel Tix, Metro State University, St. Paul, MN, October 12.

Silverstein, KAT and Mitra, R. 2006. "Plant-microbe interactions: friend or foe?" Invited by Kyle Zimmer, University of St. Thomas, St. Paul, MN, February 24.

Silverstein, KAT. 2006. "Small cysteine-rich peptides resembling antimicrobial peptides have been under-predicted in plants." Invited by Tim Secott, Minnesota State University, Mankato, MN. November 10.

PATENTS

Dehm, SM, **Silverstein, KAT**, and Beckman, KB. 2014. "Composition and methods related to Prostate Cancer." Pub. No: US 2014/0206748 A1.

PEER REVIEW PARTICIPATION

- Peer-reviewed approx 2-3 papers/year for Plant Physiology, Nucleic Acids Research, Bioinformatics, BMC Plant Biology, Phytochemistry, Genetica, and Plant Cell Reports.
- Ad-hoc reviewer for UM Biofuels discovery grant (2007), USDA-ARS (2003; 2007), NSF Plant Genome Research Program (2008, 2014), and the MCC Brainstorm awards (2010).

COMMITTEES

- PBS Graduate Student Recruitment Committee (2003-4).
- MSI RIS Bioinformatics Search Committees (2010, 2011, 2012, 2013, 2016), Database Hosting Committee (2010) and Lab and Software Planning Committees (2011).
- Genome Cluster Faculty Search Committee (2014).

FUNDED GRANT AUTHORSHIP

NSF/NIH EEC-0234112 Kumar (PI)

1/01/03-8/31/06

The University of Minnesota Summer Bioinformatics Institute.

Role: Co-investigator

This institutional grant provided summer training in the field of bioinformatics for undergraduate students. Dr. Silverstein provided annual workshops and supervised undergraduate students.

NSF IOB-0516811 VandenBosch (PI)

7/01/05-6/30/09

Defensin-like Genes in Two Model Plant Species: Expression, Function and Genome Organization of a Large Gene Family.

Role: Co-investigator

This study investigated the expression, genome organization and antimicrobial activity of a large family (more than 300 genes per species) of defensin-like genes and protein products in plants.

NIH/NCI 1R01CA166474

Dehm (PI)

04/01/13-03/31/18

AR Gene Rearrangements and Androgen Receptor Signaling in Prostate Cancer

The goal of this study is to define the role of AR gene rearrangements in clinical prostate cancer progression.

Role: Co-Investigator

Aim 1: Determine the Spectrum of AR Gene Rearrangements and Splicing Alterations in Clinical CRPC

Aim 2: Define the Biological Impact of AR Gene Rearrangements and AR Splicing Alterations in CRPC

Aim 3: Establish AR Gene Rearrangements as Biomarkers of Resistance to Conventional Androgen Depletion Therapy and Next-Generation AR-Targeted Therapies.

ACS RSG 122143

Dehm (PI)

01/01/12-12/31/2015

AR Gene Structure Alterations and Prostate Cancer Progression

The goal of this proposal is to test whether rearrangements in the AR gene underlie stable and efficient synthesis of alternatively-spliced, truncated AR isoforms that can support the CRPCa phenotype in mouse xenograft models of prostate cancer progression.

Role: Co-Investigator

Aim 1: Assess rearrangements that occur in the 180kb AR locus in xenograft models of PCa progression and define the impact on AR expression.

Aim 2: Determine the mechanistic basis for constitutive, ligand-independent transcriptional activity of alternatively-spliced, truncated AR isoforms.

Aim 3: Determine the roles of full-length and alternatively-spliced AR isoforms in a model of PCa progression

NSF IOS-7137778

Young (PI)

02/15/13-01/31/16

Expanding the *Medicago truncatula* Hapmap as a Platform for Exploring the Genetics of Legume Symbioses.

This study seeks to (1) validate candidate symbiosis loci through reverse genetics, (2) discover sequence-level gene-for-gene associations between *Medicago* and *Sinorhizobium* and (3) explore structural variation and characterize the architecture and evolution of symbiosis-related gene families.

Role: Co-PI

Wrote grant sections, letters of collaboration, and arranged percent efforts for staff for 17 additional funded collaborative proposals (2009-2015).

REFERENCES

Available upon request.