CARVER COLLEGE OF MEDICINE CURRICULUM VITAE

Terry A Braun

May 2017

I. EDUCATIONAL AND PROFESSIONAL HISTORY

A. List of institutions attended (earliest to most recent)

1993	BS (Electrical Engineering) - University of Iowa, Iowa City, Iowa, United States
1995	MS (Electrical and Computer Engineering) - University of Iowa, Iowa City, Iowa, United States
2001	PhD (Genetics) - University of Iowa, Iowa City, Iowa, United States

B. Employment History

1992 - 1993	Research Assistant University of Iowa, Iowa City, Iowa, United States
1990 - 1993	Electrical Engineer Rockwell Collins, Cedar Rapids, Iowa, United States
1993 - 1999	Teaching Assistant University of Iowa, Iowa City, Iowa, United States
2012 - Present	Secondary Appointment: ECE (0%) University of Iowa
2002 - 2007	Assistant Professor, University of Iowa
2007 - 2017	Associate Professor, University of Iowa
2009 - Present	Adjunct Associate Research Professor, Cell, Biology & Anatomy University of North Texas Eye Research Institute
2002 - Present	Director, Coordinated Laboratory for Computational Genomics University of Iowa, Iowa City, Iowa, United States
2004 - Present	Senior Scientific Advisor / Board of Directors / Founder Biotech company, bioinformatics software: Bio::Neos
2014 - Present	Director of Bioinformatics PhD, MS and PhD Certificate Programs Iowa Graduate Program in Informatics
2016 - Present	Senior Bioinformatics Consultant, Biotech company, cancer therapies: Immortagen

C. Honors, Awards, Recognitions, Outstanding Achievements

2003	John Pappajohn New Ventures Business Plan Competition - John Pappajohn
2004	Huber E Storer Business Plan Competition - Huber E Storer

II. TEACHING

A. Teaching assignments

Classroom, Seminar, Teaching Laboratory

2003	Bioinformatics Techniques. Developed new course: Bioinformatics Techniques. Covers topics on development tools for bioinformatics (full semester)
2004	Bioinformatics Techniques (full semester)
2004	Engineering Problem Solving II. (Introduction to C Programming for Engineers) (full semester)
2004	Genetics and Quantitative Physiology. Course organizer. Co-instructor with Dr. David Wilder. (full semester)
2005	Genetics and Quantitative Physiology. Co-instructor: Dr. Madhavan Raghavan. (full semester)
2006	Bioinformatics Techniques. (full semester)
2006	Engineering and Problem Solving II. (full semester)
2006	Special Topics in Genetics (full semester) Co-instructor Peter Nagy
2007	Bioinformatics Techniques. (full semester)
2007	Engineering and Problem Solving II. (full semester)
2008	Bioinformatics Techniques. (full semester)
2008	Engineering and Problem Solving II. (full semester)
2009	Software Design (full semester)
2009-Present	Engineering and Problem Solving II. Course Coordinator.
2009	Genetic Analysis of Biological Systems (2 lectures).
2010	Engineering and Problem Solving II. Spring, this course was "flipped," with students performing daily, small, "hands-on" programming assignments in-class. (full semester)
2010	Genetic Analysis of Biological Systems (2 lectures).
2010	Human Molecular Genetics (2 lectures).
2011	Practical Bioinformatics. One of 6 lecturers.
2011	Bioinformatics Tools Survey. Week-long intensive course, meets 8 hours per day for 5 days. University of North Texas.
2011	Engineering and Problem Solving II. (full semester)
2011	Practical Bioinformatics (1 lecture).
2012	Engineering Problem Solving II (full semester).
2012	BME Freshman Forum (full semester).
2013	Practical Bioinformatics. (One of 6 lectures)
2014	BioImaging and Bioinformatics (1/2 semester)
2014	Engineering Problem Solving II. (full semester)

2014	Practical Bioinformatics. (One of 6 lecturers)
2014	Bioinformatics Tools Survey. Week-long intensive course, meets 8 hours per day for 5 days. University of North Texas
2015	Bioinformatics Techniques. Course reorganized to contain modern next generation sequencing algorithms. (full semester)
2015	Engineering Problem Solving II. (full semester)
2015	Computational Genomics. Course reorganized to use next-generation sequencing tools, and Univ of Iowa compute cluster (full semester)
2015	Practical Bioinformatics. (One of 6 lectures)
2015	Engineering Problem Solving II. (full semester)
2016	Computational Genomics (full semester)
2016	Practical Bioinformatics. (One of 6 lectures)
2017	BME First Year Forum (full semester)
2017	Practical Bioinformatics (One of 6 lectures).
2017	Computation Genomics (full semester)

B. Student Supervision (* indicates chair of the committee)

Graduate Student Research Supervision and Advising - PhD

2003 - 2004	Rong Guo - BME PhD Left school, personal hardship.
2002 - 2006	Annie Chiang - Genetics Program, PhD (Co-advisor). Comparative and Integrative Genomic Approach Toward Disease Gene Discovery: Application to Bardet-Biedl Syndrome
2009 - 2012	*Adam DeLuca - BME, PhD - Computational methods for efficient exome sequencing-based genetic testing.
2015	Mike Hector - BME, MS/PhD - Left Program
2011 - 2015	*Alex Wagner - Genetics Program, PhD. Novel exon prediction with RNA sequencing.
2016	Tyler Marrs -- IGPI, PhD -- Left program

BME = Biomedical Engineering, EE = Electrical and Computer Engineering, IGPI = Iowa Graduate Program in Informatics. MS = Master's of Science Degree, PhD = Doctor of Philosophy Degree

Graduate Student Research Supervision and Advising - MS

2002 - 2003	*Steven Davis - EE, MS - Tools for, and Evaluation of, a Computer-based Genetic Mutation Screening System.
2004 - 2007	*Michael Smith - EE, MS - Computational Integration of Heterogeneous Data to Prioritize Candidate Disease Genes
2004 - 2005	*Brian O'Leary - EE MS - Optimizing Analytical Models for Efficient Genetic Mutation Screening.

2004 - 2005	*Jared Bischof - EE MS - Computational Identification of Pseudogenes for Predicting Gene Conversion and Molecular Mechanisms for Disease.
2004 - 2006	*Mushtaq Ali - BME MS - A Computational and Statistical Analysis System for Expression Arrays.
2004 - 2006	*Matthew Kemp - EE, MS - Computational Methods for SNPlex Genotyping and Copy Number Variation Detection.
2005 - 2006	Adrienne Brown BME MS - Left Program
2007 - 2009	*Adam DeLuca - BME, MS - Automated Sequence Analysis Pipeline (ASAP)
2007 - 2008	Aristee Harris - BME -- Left Program
2007 - 2008	Michael Jones - BME - Left Program
2011	*Amy Munson - BME MS (non thesis)
2014	*Tyson Fuller - BME, MS (non-thesis)
2013 - 2014	* Sean Ephraim - BME, MS. Design and Application of Methods for Curating Genetic Variation Databases.
2014 - 2016	*Andrea Hallier - BME, MS. Variant-curation and Database Instantiation (Variant-CADI): An integrated software system for the automation of collection, annotation and management of variations in clinical genetic testing.
2016 - present	*Rob Marini - Bioinformatics IGPI, MS
2016 - present	*Jonathon Tessmann - BME, MS

Graduate Student Committees - PhD

2006	Rani Kalari - BME, PhD. Computational approach to identify deletions or duplications in a gene
2007	Teyana Nosenk - Biology, PhD. Chromalveolate genome evolution.
2009	Ahmed Moustafa - Genetics, PhD. Evolutionary and Functional Genomics of Photosynthetic Eukaryotes
2010	Anna Williford - Biology, PhD. Local Effects of Limited Recombination in Drosophila.
2010	Jessica Skeie, BME, PhD. Chroidal Endothelial Cell Activation in Age-related Macular Degneration.
2010	Jinlu Cai, - Genetics, PhD. Coex-Rank: An approach for microarray combined analysis -- applications to PPARgamma related datasets
2010	Kishore Nannapaneni, BME, PhD. Design of a Bioinformatics System for Insertional Mutagenesis Analysis and Its Application to Sleeping Beauty.
2011	Abe Sheffield - Genetics, PhD
2013	Ramesh Ratnappan - Biology, PhD
2013	Farah Alul - Biology, PhD. Investigation of genetic factors associated with complex pregnancy and neonatal disorders.

2013	John Ma - Genetics, PhD.
2014	Xitize Chamling - Genetics, PhD. Identification and characterization of CEP131 as a novel BBSOME interacting Protein
2014	Kyle Taylor - EE, PhD. Machine learning approaches for predicting gentoype form phenotype and a novel clustering technique for subgenotype discovery: An application to inherited deafness.
2015	Scott Whitmore - Genetics, PhD.
2017	Long Gao, BME, PhD
Present	Mary Wilson, IGPI
Present	Wes Goar, Genetics
Present	Nikale Pettie, Biology
Present	Brendan Hodis, BME
2013 - present	Samantha Atkinson - Bioinformatics IGPI, PhD (academic advisor)
Present	Hernan Bernabe, BME
Present	Jin-Young Koh, BME
Present	Tanner Koomar, Genetics

Graduate Student Committees - MS

2005	Jesse Walters
2009	Ryan Smith
2009	Katie Cribben
2012	Corey Goodman
2013	Amanda DeHoedt
2015	Adam Dupuy
2015	Donghai Dai
2016	Gen Shinozaki

Undergraduate Research and Project Supervision

2003	Kimberly Ma, Maureen Jacobson, Catherine Crouch, A web-crawler for protein sequence and OMIM mutations.
2005	Daniel Smart, PrimerViewerLite for IDT
2012	Derek Hornberg, Steven Schulte, Stephen Badding, Low Vision and rapid serial visual presentation (RSVP).
2015	Andrea Hallier, Interactive protocol and interface for collecting up-to-date records For disease-associated genetic variations.
2015	Christopher Winters, Grant Beteulius, Zac DeSalvo, Rimas Lapinas, Design of an Economical Low Vision Reader Using Commercial Touch Pads
2016	Jonathan Tessmann, Genome analysis for identifying germline and somatic mutations in cancer

2016 - 2017	Matthew Andress -- Deafness Variation Database development (research)
2016 - Present	Matthew Jack -- Electronic Stone Rounds (research)
2016 - Present	Dylan Green, and Spencer Van Dorn -- Low-vision Enhancement Optoelectronic (LEO) Belt. https://iq.intel.com.au/technology-brings-spatial-awareness-to-the-visually-impaired/

III. SCHOLARSHIP/PROFESSIONAL PRODUCTIVITY

A. Publications or creative works (most recent to earliest)

Peer-reviewed papers

Genomics of Vision in Humans

1. Stone, Andorf, Whitmore, DeLuca, Giacalone, Streb, **Braun**, Mullins, Scheetz, Sheffield, Tucker. Clinically Focused Molecular Investigation of 1000 Consecutive Families with Inherited Retinal Disease. Journal of Ophthalmology (**Accepted for publication**). 2017

2. Bax NM, Sangermano R, Roosing S, Thiadens AA, Hoefsloot LH, van den Born LI, Phan M, Klevering BJ, Westeneng-van Haaften C, **Braun TA**, Zonneveld-Vrieling MN, de Wijs I, Mutlu M, Stone EM, den Hollander AI, Klaver CC, Hoyng CB, Cremers FP. Heterozygous deep-intronic variants and deletions in ABCA4 in persons with retinal dystrophies and one exonic ABCA4 variant. Human mutation. 2015; 36(1):43-7. PubMed [journal] PMID: 25363634

3. Whitmore SS, Wagner AH, DeLuca AP, Drack AV, Stone EM, Tucker BA, Zeng S, **Braun TA**, Mullins RF, Scheetz TE. Transcriptomic analysis across nasal, temporal, and macular regions of human neural retina and RPE/choroid by RNA-Seq. Experimental eye research. 2014; 129:93-106. NIHMSID: NIHMS640738 PubMed [journal] PMID: 25446321, PMCID: PMC4259842

4. Burnight ER, Wiley LA, Drack AV, **Braun TA**, Anfinson KR, Kaalberg EE, Halder JA, Affatigato LM, Mullins RF, Stone EM, Tucker BA. CEP290 gene transfer rescues Leber congenital amaurosis cellular phenotype. Gene Therapy. 2014; 21(7):662-72. NIHMSID: NIHMS631361 PubMed [journal] PMID: 24807808, PMCID: PMC4188442

5. **Braun TA**, Mullins RF, Wagner AH, Andorf JL, Johnston RM, Bakall BB, Deluca AP, Fishman GA, Lam BL, Weleber RG, Cideciyan AV, Jacobson SG, Sheffield VC, Tucker BA, Stone EM. Non-exomic and synonymous variants in ABCA4 are an important cause of Stargardt disease. Human molecular genetics. 2013; 22(25):5136-45. PubMed [journal] PMID: 23918662, PMCID: PMC3842174

6. Tucker BA, Mullins RF, Streb LM, Anfinson K, Eyestone ME, Kaalberg E, Riker MJ, Drack AV, **Braun TA**, Stone EM. Patient-specific iPSC-derived photoreceptor precursor cells as a means to investigate retinitis pigmentosa. eLife. 2013; 2:e00824. PubMed [journal] PMID: 23991284, PMCID: PMC3755341

7. Wagner AH, Taylor KR, DeLuca AP, Casavant TL, Mullins RF, Stone EM, Scheetz TE, **Braun TA**. Prioritization of retinal disease genes: an integrative approach. Human mutation. 2013; 34(6):853-9. NIHMSID: NIHMS457105 PubMed [journal] PMID: 23508994, PMCID: PMC4509594

8. Wagner AH, Anand VN, Wang WH, Chatterton JE, Sun D, Shepard AR, Jacobson N, Pang IH, Deluca AP, Casavant TL, Scheetz TE, Mullins RF, **Braun TA**, Clark AF. Exon-level expression profiling of ocular tissues. Experimental eye research. 2013; 111:105-11. NIHMSID: NIHMS456381 PubMed [journal] PMID: 23500522, PMCID: PMC3664108

9. Scheetz TE, Fingert JH, Wang K, Kuehn MH, Knudtson KL, Alward WL, Boldt HC, Russell SR, Folk JC, Casavant TL, **Braun TA**, Clark AF, Stone EM, Sheffield VC. A genome-wide association study for primary open angle glaucoma and macular degeneration reveals novel Loci. PloS one. 2013; 8(3):e58657. PubMed [journal] PMID: 23536807, PMCID: PMC3594156

10. Whitmore SS, **Braun TA**, Skeie JM, Haas CM, Sohn EH, Stone EM, Scheetz TE, Mullins RF. Altered gene expression in dry age-related macular degeneration suggests early loss of choroidal endothelial cells. Molecular vision. 2013; 19:2274-97. PubMed [journal] PMID: 24265543, PMCID: PMC3834599

11. Mahajan VB, Skeie JM, Bassuk AG, Fingert JH, **Braun TA**, Daggett HT, Folk JC, Sheffield VC, Stone EM. Calpain-5 mutations cause autoimmune uveitis, retinal neovascularization, and photoreceptor degeneration. PLoS genetics. 2012; 8(10):e1003001. PubMed [journal] PMID: 23055945, PMCID: PMC3464205

Genomics of Deafness in Human

12. Ephraim, Azaiez, Black-Ziegelbein, Booth, Crone, Casavant, **Braun**, Smith. The Deafness Variation Database: A Comprehensive Open-Source Platform for the Analysis, Classification and Distribution of Genetic Variants Related to Hearing Loss. American journal of human genetics. 2017 (**Pending** review and acceptance).

13. Taylor KR, Booth KT, Azaiez H, Sloan CM, Kolbe DL, Glanz EN, Shearer AE, DeLuca AP, Anand VN, Hildebrand MS, Simpson AC, Eppsteiner RW, Scheetz TE, **Braun TA**, Huygen PL, Smith RJ, Casavant TL. Audioprofile Surfaces: The 21st Century Audiogram. Ann Otol Rhinol Laryngol. 2016 May;125(5):361-8. doi: 10.1177/0003489415614863. Epub 2015 Nov 3. PubMed PMID: 26530094; PubMed Central PMCID: PMC4821702.

14. Ephraim SS, Anand N, DeLuca AP, Taylor KR, Kolbe DL, Simpson AC, Azaiez H, Sloan CM, Shearer AE, Hallier AR, Casavant TL, Scheetz TE, Smith RJ, **Braun TA**. Cordova: web-based management of genetic variation data. Bioinformatics (Oxford, England). 2014; 30(23):3438-9. PubMed [journal] PMID: 25123904, PMCID: PMC4296146

15. Shearer AE, Eppsteiner RW, Booth KT, Ephraim SS, Gurrola J 2nd, Simpson A, Black-Ziegelbein EA, Joshi S, Ravi H, Giuffre AC, Happe S, Hildebrand MS, Azaiez H, Bayazit YA, Erdal ME, Lopez-Escamez JA, Gazquez I, Tamayo ML, Gelvez NY, Leal GL, Jalas C, Ekstein J, Yang T, Usami S, Kahrizi K, Bazazzadegan N, Najmabadi H, Scheetz TE, **Braun TA**, Casavant TL, LeProust EM, Smith RJ. Utilizing ethnic-specific differences in minor allele frequency to recategorize reported pathogenic deafness variants. American journal of human genetics. 2014; 95(4):445-53. PubMed [journal] PMID: 25262649, PMCID: PMC4185121

16. Shearer AE, Black-Ziegelbein EA, Hildebrand MS, Eppsteiner RW, Ravi H, Joshi S, Guiffre AC, Sloan CM, Happe S, Howard SD, Novak B, Deluca AP, Taylor KR, Scheetz TE, **Braun TA**, Casavant TL, Kimberling WJ, Leproust EM, Smith RJ. Advancing genetic testing for deafness with genomic technology. Journal of medical genetics. 2013; 50(9):627-34. NIHMSID: NIHMS527553 PubMed [journal] PMID: 23804846, PMCID: PMC3887546

17. Taylor KR, Deluca AP, Shearer AE, Hildebrand MS, Black-Ziegelbein EA, Anand VN, Sloan CM, Eppsteiner RW, Scheetz TE, Huygen PL, Smith RJ, **Braun TA,** Casavant TL. AudioGene: predicting hearing loss genotypes from phenotypes to guide genetic screening. Human mutation. 2013; 34(4):539-45. NIHMSID: NIHMS489320 PubMed [journal] PMID: 23280582, PMCID: PMC3753227

18. Eppsteiner RW, Shearer AE, Hildebrand MS, Taylor KR, Deluca AP, Scherer S, Huygen P, Scheetz TE, **Braun TA**, Casavant TL, Smith RJ. Using the phenome and genome to improve genetic diagnosis for deafness. Otolaryngology--head and neck surgery : official journal of American Academy of Otolaryngology-Head and Neck Surgery. 2012; 147(5):975-7. NIHMSID: NIHMS472449 PubMed [journal] PMID: 22785243, PMCID: PMC3694170

19. Eppsteiner RW, Shearer AE, Hildebrand MS, Deluca AP, Ji H, Dunn CC, Black-Ziegelbein EA, Casavant TL, **Braun TA**, Scheetz TE, Scherer SE, Hansen MR, Gantz BJ, Smith RJ. Prediction of cochlear implant performance by genetic mutation: the spiral ganglion hypothesis. Hearing research. 2012; 292(1-2):51-8. NIHMSID: NIHMS404315 PubMed [journal] PMID: 22975204, PMCID: PMC3461332

Vision Genomics in Model Organisms

20. Bermudez JY, Webber HC, Brown B, **Braun TA**, Clark AF, Mao W. A Comparison of Gene Expression Profiles between Glucocorticoid Responder and Non-Responder Bovine Trabecular Meshwork Cells Using RNA Sequencing. PLoS One. 2017 Jan 9;12(1):e0169671. doi: 10.1371/journal.pone.0169671. eCollection 2017. PubMed PMID: 28068412; PubMed Central PMCID: PMC5222504.

21. Sharma TP, McDowell CM, Liu Y, Wagner AH, Thole D, Faga BP, Wordinger RJ, **Braun TA**, Clark AF. Optic nerve crush induces spatial and temporal gene expression patterns in retina and optic nerve of BALB/cJ mice. Molecular neurodegeneration. 2014; 9:14. PubMed [journal] PMID: 24767545, PMCID: PMC4113182

22. Kim BJ, **Braun TA**, Wordinger RJ, Clark AF. Progressive morphological changes and impaired retinal function associated with temporal regulation of gene expression after retinal ischemia/reperfusion injury in mice. Molecular neurodegeneration. 2013; 8:21. PubMed [journal] PMID: 23800383, PMCID: PMC3695831

Genomics for Other Diseases

23. Breen ME, Gaynor SC, Monson ET, de Klerk K, Parsons MG, **Braun TA**, DeLuca AP, Zandi PP, Potash JB, Willour VL. Targeted Sequencing of FKBP5 in Suicide Attempters with Bipolar Disorder. PLoS One. 2016 Dec 28;11(12):e0169158. doi: 10.1371/journal.pone.0169158. eCollection 2016. PubMed PMID: 28030643; PubMed Central PMCID: PMC5193409.

24. Brownstein CA, Beggs AH, Homer N, Merriman B, Yu TW, Flannery KC, DeChene ET, Towne MC, Savage SK, Price EN, Holm IA, Luquette LJ, Lyon E, Majzoub J, Neupert P, McCallie D Jr, Szolovits P, Willard HF, Mendelsohn NJ, Temme R, Finkel RS, Yum SW, Medne L, Sunyaev SR, Adzhubey I, Cassa CA, de Bakker PI, Duzkale H, Dworzyński P, Fairbrother W, Francioli L, Funke BH, Giovanni MA, Handsaker RE, Lage K, Lebo MS, Lek M, Leshchiner I, MacArthur DG, McLaughlin HM, Murray MF, Pers TH, Polak PP, Raychaudhuri S, Rehm HL, Soemedi R, Stitziel NO, Vestecka S, Supper J, Gugenmus C, Klocke B, Hahn A, Schubach M, Menzel M, Biskup S, Freisinger P, Deng M, Braun M, Perner S, Smith RJ, Andorf JL, Huang J, Ryckman K, Sheffield VC, Stone EM, Bair T, Black-Ziegelbein EA, **Braun TA**, Darbro B, DeLuca AP, Kolbe DL, Scheetz TE, Shearer AE, Sompallae R, Wang K, Bassuk AG, Edens E, Mathews K, Moore SA, Shchelochkov OA, Trapane P, Bossler A, Campbell CA, Heusel JW, Kwitek A, Maga T, Panzer K, Wassink T, Van Daele D, Azaiez H, Booth K, Meyer N, Segal MM, Williams MS, Tromp G, White P, Corsmeier D, Fitzgerald-Butt S, Herman G, Lamb-Thrush D, McBride KL, Newsom D, Pierson CR, Rakowsky AT, Maver A, Lovrečić L, Palandačić A, Peterlin B, Torkamani A, Wedell A, Huss M, Alexeyenko A, Lindvall JM, Magnusson M, Nilsson D, Stranneheim H, Taylan F, Gilissen C, Hoischen A, van Bon B, Yntema H, Nelen M, Zhang W, Sager J, Zhang L, Blair K, Kural D, Cariaso M, Lennon GG, Javed A, Agrawal S, Ng PC, Sandhu KS, Krishna S, Veeramachaneni V, Isakov O, Halperin E, Friedman E, Shomron N, Glusman G, Roach JC, Caballero J, Cox HC, Mauldin D, Ament SA, Rowen L, Richards DR, San Lucas FA, Gonzalez-Garay ML, Caskey CT, Bai Y, Huang Y, Fang F, Zhang Y, Wang Z, Barrera J, Garcia-Lobo JM, González-Lamuño D, Llorca J, Rodriguez MC, Varela I, Reese MG, De La Vega FM, Kiruluta E, Cargill M, Hart RK, Sorenson JM, Lyon GJ, Stevenson DA, Bray BE, Moore BM, Eilbeck K, Yandell M, Zhao H, Hou L, Chen X, Yan X, Chen M, Li C, Yang C, Gunel M, Li P, Kong Y, Alexander AC, Albertyn ZI, Boycott KM, Bulman DE, Gordon PM, Innes AM, Knoppers BM, Majewski J, Marshall CR, Parboosingh JS, Sawyer SL, Samuels ME, Schwartzentruber J, Kohane IS, Margulies DM. An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. Genome biology. 2014; 15(3):R53. PubMed [journal] PMID: 24667040, PMCID: PMC4073084

Cancer Genomics

25. Keck, Breheny, **Braun**, Darbro, Li, Dillon, Bellizzi, O'Dorisio, Howe. Gene Expression Changes in Small Bowel Neuroendocrine Tumors Associated with Progression to Metastases. (Accepted, Pending revision. Surgery). 2017

26. Sherman SK, Maxwell JE, Qian Q, Bellizzi AM, **Braun TA**, Iannettoni MD, Darbro BW, Howe JR. Esophageal cancer in a family with hamartomatous tumors and germline PTEN frameshift and SMAD7 missense mutations. Cancer genetics. 2015; 208(1-2):41-6. NIHMSID: NIHMS651699 PubMed [journal] PMID: 25554686, PMCID: PMC4355394

27. Levy MA, Freymann JB, Kirby JS, Fedorov A, Fennessy FM, Eschrich SA, Berglund AE, Fenstermacher DA, Tan Y, Guo X, Casavant TL, Brown BJ, **Braun TA**, Dekker A, Roelofs E, Mountz JM, Boada F, Laymon C, Oborski M,

Rubin DL. Informatics methods to enable sharing of quantitative imaging research data. Magnetic resonance imaging. 2012; 30(9):1249-56. NIHMSID: NIHMS382195 PubMed [journal] PMID: 22770688, PMCID: PMC3466343

Additional Publications (Ordered by date):

28. Walters JD, Bair TB, **Braun TA**, Scheetz TE, Robinson JP, Casavant TL. Validation of computational prediction of horizontal gene transfer events—XenoCluster. The Journal of Supercomputing. 2011. Vol 57, Number 2, 141-150.

29. Hildebrand MS, Morín M, Meyer NC, Mayo F, Modamio-Hoybjor S, Mencía A, Olavarrieta L, Morales-Angulo C, Nishimura CJ, Workman H, Deluca AP, Del Castillo I, Taylor KR, Tompkins B, Goodman CW, Schrauwen I, Wesemael MV, Lachlan K, Shearer AE, **Braun TA**, Huygen PL, Kremer H, Van Camp G, Moreno F, Casavant TL, Smith RJ, Moreno-Pelayo MA. DFNA8/12 caused by TECTA mutations is the most identified subtype of nonsyndromic autosomal dominant hearing loss. Hum Mutat. 2011 Jul;32(7):825-34. doi: 10.1002/humu.21512. Epub 2011 Jun 7. PubMed PMID: 21520338.

30. Davis L, Meyer K, Schindler E, Beck J, Rudd D, Grundstad AJ, Scheetz T, **Braun T**, Fingert J, Kwon WA, Folk J, Russell S, Wassink T, Sheffield V, Stone E. Copy Number Variations (CNVs) and Primary Open Angle Glaucoma (POAG). Invest Ophthalmol Vis Sci. 2011 Feb 10. [Epub ahead of print] PubMed PMID: 21310917.

31. Meyer KJ, Davis LK, Schindler EI, Beck JS, Rudd DS, Grundstad AJ, Scheetz TE, **Braun TA**, Fingert JH, Alward WL, Kwon YH, Folk JC, Russell SR, Wassink TH, Stone EM, Sheffield VC. Genome-wide analysis of copy number variants in age-related macular degeneration. Hum Genet. 2011 Jan;129(1):91-100. Epub 2010 Oct 28. PubMed PMID: 20981449.

32. Walters JD, Bair TB, **Braun TA**, Scheetz TE, Robinson JP, Casavant TL. Multi-granularity Parallel Computing in a Genome-Scale Molecular Evolution Application. J Supercomput. 2009 Jan 1;5698:49-59.

33. Shankar, S. P., Carelli, V., **Braun, T. A**., Taylor, C. M., Abdulkawy, H., King, T. M., Daiger, S. P., Salomao, S. R., Sadun, A. A., Stone, E. M. "Evidence for genetic heterogeneity of X-linked modifier loci in Leber Hereditary Optic Neuropathy (LHON)." Ophthalmic Genet. 2008. March 29:17-24.

34. O'Leary, B. M., Davis, S. G., Smith, M. F., Brown, B., Kemp, M. B., Almabrazi, H., Grundstad, J. A., Burns, T., Andorf, J., Leontiev, V., Clark, A. F., Sheffield, V. C., Casavant, T. L., Scheetz, T. E., Stone, E. M., **Braun, T. A.** "Transcript Annotation Prioritization and Screening System (TrAPSS) for Mutation Screening." J. Bioinform. Comput. Biol. Vol 5, No. 6 (2007) 1155-1172.

35. Scheetz, T. E., Kim, K-Y. A., Swiderski, R.E., Philp, A. R., **Braun, T. A.**, Knudtson, K. L., Dorrance, A. M., DiBona, G. F., Huang, J., Casavant, T. L., Sheffield, V. C., Stone, E. M. "Regulation of gene expression in the mammalian eye and its relevance to eye disease." Proc Natl Acad Sci USA, 2006 Sep 26;103(39):14429-34.

36. Chiang, A. P., Beck, J. S., Yen, H-J., Tayeh, M. K., Scheetz, T. E., Swiderski, R. E., Nishimura, D. Y., **Braun, T. A**., Kim, K-Y. A., Huan, J., Elbedour, K., Carmi, R., Slusarski, D. C., Casavant, T. L., Stone, E. M. and Sheffield, V. C. "Homozygosity mapping with SNP arrays identifies TRIM32, an E3 ubiquitin ligase, as a Bardet-Biedl syndrome gene (BBS11)." Proc Natl Acad Sci USA, 103(16): 6287-6298, 2006.

37. Steely, H. T., Dillow, G. W., Grundstad, J., **Braun, T. A**., Casavant , T. L., McCartney, M. D., Clark, A. F. "Protein expression in a transformed trabecular meshwork cell line: proteome analysis." Molecular Vision, 12:372-83, 2006.

38. Bischof, J. M., Chiang, A. P., Scheetz, T. E., Stone E. M., Casavant, T. L., Sheffield, V. C., **Braun, T. A.** "Genome-wide identification of pseudogenes capable of disease-causing gene conversion." Human Mutation 27(6), 542-552, 2006.

39. **Braun, T. A.,** Shankar, S. P., Davis, S., O'Leary, B., Scheetz, T. E., Clark, A. F., Sheffield, V. C., Casavant, T. L., Stone, E. M. "Prioritizing Regions of Candidate Genes for Efficient Mutation Screening." Human Mutation 27(2), 195-200, 2006.

40. Sibenaller, Z. A. , Etame, A. B., Ali, M. M., Barua, M., **Braun, T. A.**, Casavant, T. L., Ryken, T. C. “Genetic characterization of commonly used glioma cell lines in the rat animal model system.” Neurosurg Focus 19, 4: Oct 15, 2005

41. Walters, J. D., Casavant, T. L., Robinson, J. P., Bair, T. B., **Braun, T. A.**, Scheetz, T. E. “XenoCluster: A Grid Computing Approach to Finding Ancient Evolutionary Genetic Anomalies.” Lecture Notes in Computer Science. Volume 3603, p. 355. 2005.

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Conference papers (3 or more reviewers):

1. DeLuca, Adam P.; Wagner, Alex H.; Taylor, Kyle R.; Faga, Ben; Thole, David; Sheffield, Val C.; Stone, Edwin M.; Casavant, Thomas L.; Scheetz, Todd E.; **Braun, Terry A.** "Sequencing and disease variation detection tools and techniques," Computer Systems and Applications (AICCSA), 2011 9th IEEE/ACS International Conference on , vol., no., pp.80-83, 27-30 Dec. 2011

2. Taylor, Kyle R.; DeLuca, Adam P.; Goodman, Corey W.; Tompkins, Bruce W.; Scheetz, Todd E.; Hildebrand, Michael S.; Huygen, Patrick L. M.; Smith, Richard J. H.; **Braun, Terry A.**; Casavant, Thomas L.; , "AudioGene: Computer-based prediction of genetic factors involved in non-syndromic hearing impairment," Computer Systems and Applications (AICCSA), 2011 9th IEEE/ACS International Conference on , vol., no., pp.75-79, 27-30 Dec. 2011

3. Trivedi, N., Pedretti, K. T., **Braun, T. A.**, Scheetz, T. E., Casavant, T. L. “Alternative parallelization strategies in EST clustering.” International Proceedings of Parallel Computing Technologies. Nizhni Novgorod, Russia, September 15-19, 2003.

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6. **Braun, T. A.**, Scheetz, T. E., Casavant, T. L., Munn, K., J., Sheffield, V. C., Stone, E. M. “A Web-based System for Robust Genotype Gathering and Storage." High Performance Networking and Computing, Amsterdam, April 1999.

7. Nishimura, D., Scheetz, T. E., Birkett, C. L., **Braun, T. A.**, Sheffield, V. C., Casavant, T. L., Soares, M. B. “A Program for Rat Gene Discovery and Mapping." 1998 Human Genome and Sequencing Meeting, Cold Spring Harbor Laboratory, Long Island, NY, May 1998.

8. Scheetz, T. E., Birkett, C. L., **Braun, T. A**., Nishimura, D., Sheffield, V. C., Soares, M. B., Casavant, T. L. “Informatics for Preparation of EST Reads in a Mixed-Tissue cDNA Library Setting." 1998 Human Genome and Sequencing Meeting, Cold Spring Harbor Laboratory, Long Island, NY, May 1998.

9. **Braun, T. A.**, Scheetz, T. E., Casavant, T. L., Munn, K. J., Sheffield, V. C., Stone, E. M. “A Web-based System for Robust Genotype Gathering and Storage." Human Genome Organization (HUGO-98) Abstract Proceedings, Torino, Italy, March 1998, p. 8.

10. Casavant, T. L., Munn, K. J., **Braun, T. A**., Scheetz, T. E., Sheffield, V. C., Stone, E. M. “Informatics for Preparation of EST Reads in a Mixed-Tissue cDNA Library Setting." 1997 Human Genome and Sequencing Meeting, Abstract and Computer Demonstration, Cold Spring Harbor Laboratory, Long Island, NY, May 1997, p. 99.

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12. Casavant, T. L., **Braun, T. A.**, Munn, K. J., Scheetz, T. E., Sheffield, V. C., Stone, E. M., Kusiak, D., Cross, G. J., Galvez, J. G. “Choosing an Operating System for Genomic-Scale Mapping and Sequencing." Human Genome Organization (HUGO-97) Abstract Proceedings, Toronto, March 1997, p. 7.

13. Dietz, R. D., Casavant, **T. L., Braun**, T. A., Scheetz, T. E., Andersland, M. S. “Modeling the Impact of Run-Time Uncertainty on Optimal Computation Scheduling Using Feedback." 1997 International Conference on Parallel Processing, Bloomington, IL, August 1997, pp. 481-488.

14. Dietz, R. D., Casavant, T. L., Andersland, M. S., **Braun, T. A.**, Scheetz, T. E. “The Use of Feedback in Scheduling Parallel Computation." 2nd Aizu International Symposium on Parallel Algorithm/Architecture Synthesis, Aizu-Wakamatsu, Japan, March, 1997, pp. 124-132.

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18. Scheetz, T. E., B**raun, T. A.**, Casavant, T. L., Gannon, J. A., Andersland, M. S., Dietz, R. D. “Effectiveness of software trace recovery techniques for current parallel architectures." Proceedings of the 1995 International Conference on High Performance Computing, New Delhi, India, Dec. 1995.

Abstract or Poster Reviewed by Three or More Reviewers

1. Bermudez J, Webber HC, Brown B, **Braun T**, Clark AF, Mao W. Differential gene expression between trabecular meshwork cells of glucocorticoid responder and non-responder bovine eyes, Investigative Ophthalmology & Visual Sciences. 2016 May 4;57(ARVO Annual Meeting. Seattle, WA):[Abstract Number: 4703 - Poster D0188].

2. **Braun TA**, Deluca AP, Hildebrand MS, Taylor KR, Shearer AE, Sloan C, Casavant TL, Smith RJ. Combining Phenotypes with Next-generation Sequencing for Genetic Testing in Patients with Deafness. Human Gene Variation Society. San Francisco, CA. Sept 9-10, 2011.

3. **T.A. Braun**, A.P. DeLuca, N. Anand, K. Taylor, J. Bogaard, B. Faga, T.E. Scheetz, T. L. Casavant1, V.C. Sheffield, and E.M. Stone. Automated Sequence Analysis Pipeline (ASAP) for Genetic Testing. ARVO. Fort Lauderdale, FL. May, 2009.

4. Hakeem Almabrazi, Bart Brown, Jason Grundstad, Mathew Kemp, Michael Smith, John Ritchison, Thomas Casavant, Todd Schettz, **Terry Braun**. "TrAPSS to accelerate Idnetification of cancer causing mutations." Sixth Annual Joint Bioinformatics Symposium. Iowa State University, Ames, Iowa. July 13-14, 2006.

5. Michael Smith, **Terry Braun**, Todd Scheetz, Thomas Casavant. "CLiPH: A system for Prioritizing candidate gene lists." Sixth Annual Joint Bioinformatics Symposium. Iowa State University, Ames, Iowa. July 13-14, 2006.

6. Mushtaq Ali, Todd Scheetz, Thomas Casavant, **Terry Braun**. "A computational and Statistical Analysis System for Expression Arrays." Sixth Annual Joint Bioinformatics Symposium. Iowa State University, Ames, Iowa. July 13-14, 2006.

7. Thomas Bair, Todd Scheetz, Nathan Schultz, Thomas Casavant, **Terry Braun**. "Using network properties of a large complex data-set to evaluate the correlation of gene expression from a large microarray experiment." Sixth Annual Joint Bioinformatics Symposium. Iowa State University, Ames, Iowa. July 13-14, 2006. (Presentation)

8. Annie Chiang, **Terry Braun**, Val Sheffield, Thomas Casavant. "Phylogenetic profile of human disease genes." Sixth Annual Joint Bioinformatics Symposium. Iowa State University, Ames, Iowa. July 13-14, 2006. (Presentation)

9. Krishna Kalari, **Terry Braun**, Edwin Stone, Val Sheffield, Thomas Casavant, Todd Scheetz. "Computational and machine learning approach to prioritize deletion or duplication candidates in genes." Sixth Annual Joint Bioinformatics Symposium. Iowa State University, Ames, Iowa. July 13-14, 2006.

10. Henry Keen, John Beck, Thomas Wassink, **Terry Braun**, Todd Scheetz, Edwin Stone, Val Sheffield, Thomas Casavant. "Computational analysis of large-scale array-based genotyping of pooled DNA samples." Presentation. Sixth Annual Joint Bioinformatics Symposium. Iowa State University, Ames, Iowa. July 13-14, 2006.

11. Matthew Kemp, **Terry Braun**, Jason Grundstad, Rod Philp, Thomas Casavant, Edwin Stone. "Functional Assay Designer: A theoretical Approach to Assay Workflow." Sixth Annual Joint Bioinformatics Symposium. Iowa State University, Ames, Iowa. July 13-14, 2006.

12. Brian O'Leary, Steve Davis, Todd Scheetz, Val Sheffield, Edwin Stone, Thomas Casavant, **Terry Braun**. "Optimization and evaluation of high-throughput mutation screening." 2005 Genome Informatics Conference, Cold Spring Harbor, Laboratories, NY, October 28-November 1, 2005.

13. Jared Bischof, Todd Scheetz, Thomas Casavant, Edwin Stone, Val Sheffield, **Terry Braun**. "Pseudogene Identification and Prediction of Gene Conversion." 2005 Genome Informatics Conference, Cold Spring Harbor, Laboratories, NY, October 28-November 1, 2005.

14. **Terry Braun**, Brian O'Leary, Steve Davis, Michael Smith, Hakeem Almabrazi, Bart Brown, John Ritchison, Suma Shankar, Todd Scheetz, Val Sheffield, Edwin Stone, Thomas Casavant. "Analysis of 1,924 disease genes for evaluating utility of functional sequence annotation for mutation screening." American Society for Human Genetics. Salt Lake City, Utah, October 25-29, 2005.

15. **Terry Braun**, Brian O'Leary, Todd Scheetz, Thomas Casavant. "Optimization of mutation screening strategies." 2004 Genome Informatics Conference, Welcome Trust Genome Campus, Hinxton, UK, September 21-26, 2004.

16. **Terry Braun**, Brian O'Leary, Todd Scheetz, Thomas Casavant. "A machine Learning Approach to Optimizing Annotation Parameters in the PAR Algorithm." ISU/UI Joint Symposium in Bioinformatics. Ames, IA. August 6, 2004.

17. **Terry Braun**, Todd Scheetz, Hakeem Abdulkawy, Bart Brown, Steve Davis, Matt Kemp, Brian O'Leary, John Ritchison, Mike Smith, Suma Shankar, Abe Clark, Val Sheffield, Edwin Stone, Thomas Casavant. "Inferring Pathogenicity to Prioritize Candidate Disease-Causing Sequence Variations." Association for Research in Vision and Ophthalmology. Fort Lauderdale, FL. April 25-29, 2004.

18. **Terry Braun**, Todd Scheetz, Hakeem Abdulkawy, Bart Brown, Steve Davis, Brian O'Leary, John Ritchison, Rhett Sutphin, Suma Shankar, Val Sheffield, Edwin Stone, Thomas Casavant. "Quantitatively prioritizing candidate disease gene sequences using annotation." American Society for Human Genetics, Los Angeles, CA, October, 2003.

19. **T.A. Braun**, T.E. Scheetz, H. Abdulkawy, B. Brown, S. Davis, B. O'Leary, J. Ritchison, S. Shankar, V.C. Sheffield, E.M. Stone, T.L. Casavant , "A Quantitative Prioritization Approach to Predict Potential Mutations for Disease Gene Screening," 2003 Genome Informatics Conference, Cold Spring Harbor Laboratories, NY, May 2003.

20. **T.A. Braun**, T.E. Scheetz, H. Abdulkawy, B. Brown, S. Davis, B. O'Leary, J. Ritchison, S. Shankar, V.C. Sheffield, E.M. Stone, T.L. Casavant , "GeneScreen: Automated knowledge discovery for high-throughput disease gene mutation screening," 2002 Genome Informatics Conference, Wellcome Trust Genome Campus, Hinxton, UK, September 2002.

21. T.E Scheetz, **T.A. Braun**, K.T. Pedretti, C.A. Roberts, N.L. Robinson, A.J Gavin, B. O'Learu, N. Trivedi, J. Walters, N. Winokur, J.P. Robinson, V.C. Sheffield, M.B. Soares, T.L. Casavant, "CAEPA: An Online, Integrated Bulk EST Sequence Processing and Annotation Pipeline," 2001 Genome Informatics Conference, Wellcome Trust Genome Campus, Hinxton, UK, August 2001.

22. T.E. Scheetz, G. Beck, B. Berger, C.L. Birkett, E.A. Black, M.F. Bonaldo, R.C. Braun**, T.A. Braun**, R. Brown, K. Crouch, M. Donahue, G. Doonan, J. Gardiner, B. Johnson, S. Kaliannan, R. Kincaid, V. Miljokovic, K.J. Munn, D. Nishimura, K.T. Pedretti, C. Roberts, C. Smith, L.H. Stier, T.L. Casavant, V.C. Sheffield, and M. Bento Soares, "A Program For Rat Gene Discovery," 1999 Human Genome and Sequencing Meeting, Cold Spring Harbor Laboratory, Long Island, NY, May 1999.

23. D. Nishimura, T.E. Scheetz, C.L. Birketkt, **T.A. Braun**, V.C. Sheffield, T.L. Casavant and M.B. Soares, "A Program for Rat Gene Discovery and Mapping," 1998 Human Genome and Sequencing Meeting, Cold Spring Harbor Laboratory, Long Island, NY, May 1998.

24. T.E. Scheetz, C.L. Birkett, **T.A. Braun**, D. Nishimura, V.C. Sheffield, M.B. Soares and T.L. Casavant, "Informatics for Preparation of EST Reads in a Mixed-Tissue cDNA Library Setting," 1998 Human Genome and Sequencing Meeting, Cold Spring Harbor Laboratory, Long Island, NY, May 1998.

25. **T.A. Braun**, T.E. Scheetz, T.L. Casavant, K.J. Munn, V.C. Sheffield and E.M. Stone, "A Web-based System for Robust Genotype Gathering and Storage," HUGO-98 Abstract Proceedings, Torino, Italy, March 1998, p. 8.

26. T.L. Casavant, **T.A. Braun**, K.J. Munn, T.E. Scheetz, V. Sheffield, E.M. Stone, D. Kusiak, G. Cross and J.J. Galvez, "An Integrated Environment for the Support of Gene Hunting," 1997 Human Genome Meeting, March 1997, Toronto, Canada, p. 7 (abstract).

27. T.L. Casavant, **T.A. Braun**, K.J. Munn, T.E. Scheetz, V. Sheffield, E.M. Stone, D. Kusiak, G. Cross and J.J. Galvez, "Choosing an Operating System for Genomic-Scale Mapping and Sequencing," 1997 Human Genome Meeting, March 1997, Toronto, Canada, p. 7 (abstract).

28. T.L. Casavant, K.J. Munn, **T.A. Braun**, T.E. Scheetz, V. Sheffield, E.M. Stone, "GenoMap: A Portable, Network-Based Gene-Mapping System," 1997 Human Geome and Sequencing Meeting, Abstract and Computer Demonstration, Cold Spring Harbor, NY, May 1997.

B. Areas of Research Interest

STATEMENT OF RESEARCH OBJECTIVES.
I have been involved in the application of high-performance computing technologies to the challenges of disease gene identification. My efforts, in collaboration of members of the College of Medicine, have involved the design of novel techniques utilizing software and algorithms to analyze genomic sequence and descriptive data (annotation). This includes utilization of high-throughput technologies, such as next-generation sequencing, expression microarrays, SNP chips, and exon arrays, for the purposes of prioritizing genes and sub-regions of genes for mutation discovery. These tools are actively being applied to identify disease-causing inherited eye diseases, hearing loss and cancer.

C. Grants (Total Direct Costs)

Current

O'dorisio, S. (PI), Braun, T. (Co-Principal). "Specialized Programs of Research Excellence (SPORE) in Human Cancer - Neuroendocrine Tumors," Sponsored by NCI, $7,553,702. (2015 - 2020).

Braun, T. (Co-Principal), Howe (Co-Principal). "Project 3: A genomic approach to improved diagnosis and treatment of neuroendocrine tumors," NCI. $957,275. (2015 - 2020).

Buatti (PI), Braun, T. A. (Co-Investigator). "Quantitative Imaging to Assess Response in Cancer Therapy Trials," Sponsored by NIH, $4,350,326 (April 1, 2009 - 2021).

Weiner (PI), Braun, T. (Co-Investigator), "Specialized Programs of Research Excellence (SPORE) in Human Cancer", NCI, $19,685,504, (2006-2021)

Braun, T. (Co-Principal), Smith (Co-Principal). Optimizing Genetic Testing for Deafness for Clinical Diagnostics, NIH, $3,833,506. (2011-2021)

Leslie, K. (PI), Braun, T. (Co-Investigator), Targeted Therapy for Endometrial Cancer, NIH, $2,776,707. (2013-2018)

Pending

Brogden, K. (PI), Braun, T. (Co-Investigator), "Cell genomics and biomarkers influence PD-L1 immunotherapy responses in HNSCC." $355,268. NIH

Mao, W. (PI), Braun, T. (Co-PI), "Cross-talk between TGF-beta and Wnt pathways in the trabecular meshwork." $74,837. NIH

Henry, M. (PI), Braun, T. (Co-Investigator), "Generation and Testing of Patient -Derived Xenograft Models." $750,000 NIH.

Clark, A. (PI), Braun, T. (Co-Investigator), "Glucocorticoids Ocular Hypertension and Glaucoma." $40,127.97. NIH

Completed

Sheffield, V. (PI), Braun, T. A. (Co-Investigator), "Complex Mechanisms in Bardet-Biedl Syndrome Retinopathy," Sponsored by NIH, $974,298. (January 1, 2013 - January 1, 2016).

Cornell (PI), Braun, T. A. (Co-Principal), "Transcription factors in the neural crest gene regulatory network," Sponsored by NSF, $822,962. (January 1, 2012 - January 1, 2017).

Clark (PI), Braun, T. A. (Co-Principal), "Identification of genes responsible for glucocorticoid-induced glaucoma," Sponsored by NIH, $44,302. (2013 - 2016).

Mao, W. (PI), Braun, (Co-Investigator), "Identification of Genes Responsible for Glucocorticoid-induced Glaucoma," Sponsored by NIH, $407,851.71 . (2011 - 2012).

Monick, M. (PI), Braun, T. (Co-Investigator). "Cigarette Smoking Alters the Genomic Tone of Alveolar Macrophages," Sponsored by NIH. $269,000. (2011-2012).

Clark (PI), Braun, T. (Co-Investigator), "University of North Texas Health Science Center VISION (Traumatic Eye Injury in Mouse) Modeling of eye injury, evaluation of protective compounds and analysis of gene expression and pathways.," Sponsored by DOD, $407,851. (2010 - 2011).

Stone (PI), Braun, T. (Co-Investigator), "Molecular Genetics of Age Related Macular Degeneration. Bioinformatics for candidate disease gene screening and expression analysis," Sponsored by NIH, $1,020,245, (September 1, 2010 - May 31, 2013).

Weiner, G. (PI), Braun, T., (Co-Investigator), "ARRA: Cancer Center Support Grant (CCSG) Administrative Supplement –Bioinformatics," Sponsored by NIH/NCI, $199,082. (2009 - 2011).

Braun, T. (Co-Principal), Mullins, R. F. (Co-Principal), "University of Iowa/Alcon Retinal Disorders Genomics Collaboration," Sponsored by Alcon, $351,095. (2009 - 2012).

Wassink (PI), Braun, T. (Co-Investigator), "ARRA: Genetic Determinants of Brain Structure and Disease Risk in Schizophrenia", NIH. $529,727 (2009-2010).

Braun, T. (Principal Investigator), "cancer Biomedical Informatics Grid (caBIG): Document and Training Strategic Level Working Group," Sponsored by NIH/NCI, $14,184 (2008 - 2010).

Braun, T. (PI), Casavant, T. (Co-PI). "University of Iowa/Alcon Gene Mutation Identification Collaboration," Sponsored by Alcon, $1,175,719 (2007 - 2011).

Sheffield, V. (PI), Braun, T. (Co-Investigator), "Interdisciplinary Approach to Retinal Disease Gene Identification.," Sponsored by NIH, $1,843,235. (June 1, 2007 - May 31, 2012).

Sheffield (PI), Braun, T. (Co-Investigator), "Molecular Genetics of Glaucoma," Sponsored by NIH, $1,690,456. (April 1, 2006 - March 30, 2011).

Braun, T. (Principal Investigator), "cancer Biomedical Informatics Grid (caBIG): Data Sharing and Intellectual Capital Strategic Level Working Group," Sponsored by NIH/NCI, $100,322. (2005 - 2010).

Stone, E. (PI), Braun, T. (Co-PI), "University of Iowa/Alcon Macular Degeneration Genomics Collaboration," Sponsored by Alcon, $1,253,417 (2004 - 2009).

Stone, E. M. (PI), Braun, T. (Co-Investigator). "Fibulin-Associated Age-Related Macular Degeneration," Sponsored by NEI, $247,194. (2006 - 2007).

Braun, T. (PI), Casavant, T. L. (Co-Principal), "cancer Biomedical Informatics Grid (caBIG): Strategic Planning Strategic Level Working Group," Sponsored by NIH/NCI, $144,500 (2004 - 2008).

Braun, T. (Principal Investigator), "cancer Biomedical Informatics Grid (caBIG): Integrative Cancer Research Working Group," Sponsored by NIH/NCI, $66,380.00 (2004 - 2007).

Wassink (PI), Braun, (Co-Investigator), "A Novel Approach for Finding Genes in Autism," Sponsored by NIH, $659,416. (2003 - 2006).

Braun, T. (Principal Investigator), "cancer Biomedical Informatics Grid (caBIG): Integrative Cancer Research – TrAPSS System Design and Implementation," Sponsored by NIH/NCI, $164,184. (2004 - 2006).

Braun, T. (Principal Investigator), "cancer Biomedical Informatics Grid (caBIG): Clinical Trials Management Systems Working Group," Sponsored by NIH/NCI, $53,707 (2004 - 2007).

Braun, T. (Principal Investigator), "cancer Biomedical Informatics Grid (caBIG): Clinical Trials Management Systems Working Group," Sponsored by NIH/NCI, $53,707 (2004 - 2007).

D. Presentations

Invited Lectures/Guest Speaker

2001 February 8	University of Iowa Dept. of Biomedical Engineering Graduate Seminar, University of Iowa. *"What's in a Genome? (for an Engineer)."* Braun, Terry.
2002 April 6	Iowa State University and. *"GeneScreen: a Multifaceted System for High-throughput Disease Gene Prioritization and Mutation Identification."* Braun, Terry.
2002 October 10	Department of Biomedical Engineering, University of Iowa. Graduate Student Seminar. *"TrAPSS: Transcript Annotation Prioritization and Screening System: Automated Knowledge Discovery for High-throughput Disease Gene Mutation Screening."* Braun, Terry.
2002 October 17	Biomedical Engineering Student Society, Department of Biomedical Engineering, University of Iowa. *"TrAPSS: Transcript Annotation Prioritization and Screening System: The Human Genome and Mutation Identification."* Braun, Terry.
2003 February 19	Center for Bioinformatics and Computational Biology Seminar. *"Automated Knowledge Discovery for Accelerated Mutation."* Braun, Terry.
2003 April 15	University of Iowa, Holden Comprehensive Cancer Center. *"Predicting Mutation Potential for Disease Gene Screening."* Braun, Terry.
2003 April 26	Iowa State University and University of Iowa Joint Bioinformatics Workshop. *"Predicting Deleterious Mutations for Disease Gene Screening."* Braun, Terry.
2004 August 24	caBIG Integrative Cancer Research (ICR), National Cancer Institute. *"Standards for Translational Research: A Developers.* Braun, Terry.

2004 October 28	Information and Health at Iowa. *"TrAPSS - Knowledge Discovery for Disease Gene Mutation Discovery."* Braun, Terry.
2004 November 9	ISU Engineering Faculty Symposium. *"Bioinformatics for High-Throughput Disease Gene Mutation."* Braun, Terry.
2005 May 3	caBIG -- Integrative Cancer Research, Face-to-face, Translational Research. *"Integrated Cancer Research Face-to-Face Translational."* Braun, Terry.
2005 May 7	LSU. *"TrAPSS: a System for High-Throughput Disease Gene Mutation Screening."* Braun, Terry.
2005 July 19	Iowa- Iowa State Joint Bioinformatics Symposium. *" Mapping Expression as Phenotype in Mammalian Eye."* Braun, Terry.
2005 August 16	Ophthalmology Morning Rounds. *"Techniques for Pseudogene Identification and Prediction of Gene Conversion."* Braun, Terry.
2006 January 6	Neurosurgery Research Conference. *"Bioinformatics for Mutation Screening -- Making Sense out of Missense and Nonsense."* Braun, Terry.
2006 January 26	Integrative Cancer Research Face-to-face. *"Transcript Annotation Prioritization and Screening System (TrAPSS): Live Demo."* Braun, Terry.
2006 March 22	Holden Comprehensive Cancer Center Lecture Forum. *"Iowa Neuroendocrine Database – Lessons Learned from the CPDB."* Braun, Terry.
2006 April 3	The cancer Biomedical Informatics Grid. *"Transcript Annotation Prioritization and Screening System – TrAPSS: A developer's perspective."* Braun, Terry.
2006 April 3	NIH Special Session, American Association for Cancer Research (AACR). *"Transcript Annotation Prioritization and Screening System – TrAPSS: Meet the Expert."* Braun, Terry.
2006 April 10	Technology Demonstration, caBIG Annual Meeting. *"Transcript Annotation Prioritization and Screening System – TrAPSS: Screening Deleted Subtelomeric Regions."* Braun, Terry.
2007 February 9	keynote bioinformatics talk, Association for Ocular Pharmacology and Therapeutics. *"Bioinformatic Resources Applied to Inherited Eye Diseases."* Braun, Terry.
2007 May	Special session on Genetics., Association for Vision and Research in Ophthalmology (ARVO). *"Collaborative Phenotype Database (CPDB)."* Braun, Terry.
2010 March	Cancer Genomics and Cell Biology Program. *"Integrating bioinformatics with cancer research – the new HCCC Bioinformatics Shared Resource (BSR) Core."* Braun, Terry.
2014.	*"Phenotypes and Exome Sequencing for Mutation Screening: Vision and Hearing Loss."* University of Wisconsin -- BigTen Speaker Exchange
2017.	*"Using Phenotypes to Narrow the Search for Disease-causing Variants: Tools to Support Clinical Genetic Testing for Hearing Loss and Other Inherited Diseases."* University of Maryland -- BigTen Speaker Exchange.

Conference Presentations/Seminars

2001 October 16	American Society of Human Genetics. *"Applying computational methods to search genomic sequence to identify candidate disease genes and novel sequence.* Braun, Terry.

Patents

2009	Single nucleotide polymorphisms and genes associated with age-related macular degeneration. WO 2011053774 A1
2004	Bardet-Biedl susceptibility gene and uses thereof. US 7332591 B2

IV. SERVICE

A. Professional Service, Offices/Positions/Roles Held in Professional Organizations

Other Professional Service

National

Study Section

2006	Grant review for National Human Genomics Research Institute (NHGRI). DNA, Cell-line, and tissue repository.
2006	Contract review for National Heart, Lung, and Blood Institute (NHLBI). (Center for Inherited Disease Research (CIDR) High Throughput Genotyping Contract -- RFP NHBLI-HG-07-06
2007	Study section for Brain Disorders and Clinical Neurosciences, Small Business Visual Systems, National Institute of Health. 7 grants reviewed
2007	Study section for Brain Disorders and Clinical Neurosciences (BDCN-F), National Institute of Health. Bethesda, MD. 8 grants reviewed
2007	Study section for Brain Disorders and Clinical Neurosciences, National Institute of Health. 1 grant reviewed.
2007	Study section co-chairman for Brain Disorders and Clinical Neurosciences (BDCN-F), National Institute of Health. Georgetown DC. 6 grants reviewed
2008	Study section for Brain Disorders and Clinical Neurosciences (BDCN-F), National Institute of Health. Washington DC. 8 grants reviewed
2008	Study section for Emerging Technology and Training in Neurosciences (ETTN). Washington DC. 5 grants reviewed
2009	Study section for Brain Disorders and Clinical Neurosciences (BDCN), NIH. Washington DC. 3 grants reviewed.
2011	Grant review for National Human Genomics Research Institute (NHGRI). DNA, Cell-line, and tissue repository.
2011	Study section for National Cancer Institute (NCI). Cancer Target Discovery and Development. 6 grants reviewed
2011	Study section for National Eye Institute (NEI). Genomic Research Grant on Integrative Data Analysis for Vision Research. 3 grants reviewed.
2013	Study section for Veterans Affairs - Gulf War Illness Bioinformatics
2014	Study section for NIDCR. Targeting Co-dependent Molecular Pathways in Oral Cancer
2015	NCI Special Emphasis Panel Exploratory/Developmental Research Grant Program/Small Grants
2016	NIH Study Section, Special Emphasis Hearing and Genetics
2017	NIH Study Section, Genetics and Molecular Mechanisms

Journal Papers Reviewed

Cancer Research. 06/01/2017: Papers reviewed: 1

Bioinformatics. 05/15/2017: Papers reviewed: 1

Cancer Research. 02/22/2017: Papers reviewed: 1

Bioinformatics. 07/11/2016: Papers reviewed: 1

Bioinformatics. 04/22/2016: Papers reviewed: 1

Bioinformatics. 12/14/2015: Papers reviewed: 1

Stem Cells Translational Medicine. 04/01/2015: Papers reviewed: 1

Bioinformatics. 06/20/2014. Papers reviewed: 1

Genome Medicine. 06/13/2013. Papers reviewed: 1

Bioinformatics. 07/24/2012. Papers reviewed: 1

Genome Research. 01/20/2012. Papers reviewed: 1

Bioinformatics. 07/07/2011. Papers reviewed: 1

ACS/IEEE International Conference on Computer Systems and Applications (AICCSA), 06/27/2011. Papers reviewed: 3

Bioinformatics. 01/14/2011. Papers reviewed: 1

Human Mutations. 12/15/2010. Papers reviewed: 1

Bioinformatics. 09/27/2010. Papers reviewed: 1

Bioinformatics. 08/19/2010. Papers reviewed: 1

Investigative Ophthalmology and Visual Science. 05/03/2010. Papers reviewed: 1

Bioinformatics. 01/28/2010. Papers reviewed: 1

PLoS Computational Biology. 12/02/2009. Papers reviewed: 1

Human Mutation. 05/29/2009. Papers reviewed: 1

Human Mutation. 2/04/2009. Papers reviewed: 1

Bioinformatics. 09/21/2008. Papers reviewed: 1

Bioinformatics. 08/14/2008. Papers reviewed: 1

Bioinformatics. 07/11/2008. Papers reviewed: 1

BMC Bioinformatics 5/09/2008. Papers reviewed: 1

Human Mutation, 1/14/2008. Papers reviewed: 1

Bioinformatics, 3/19/2007. Papers reviewed: 1

American Journal of Human Genetics, 01/20/2007. Papers reviewed: 1

Bioinformatics, 01/15/2007. Papers reviewed: 1

Genome Research, 10/04/2005. Papers reviewed: 1

Mammalian Genome, 05/01/2005. Papers reviewed: 1

The Journal of Biological Chemistry, 03/2005. Papers reviewed: 1

Investigative Ophthalmology and Visual Science, 01/2005. Papers reviewed: 1

Genome Research, 10/2003. Papers reviewed: 1

CSB, 2004. Papers reviewed: 9

University

2014 - Present	Iowa Graduate Program in Bioinformatics, Director
2016 - Present	Holden Comprehensive Cancer Center, Bioinformatics Shared Resource Core, Director
2015 - Present	Holden Comprehensive Cancer Center, NET SPORE Bioinformatics Core, Director

B. University, College, Department Service

University Service

2003	VP for Research Biological Sciences Review Committee, Officer, Vice President
2004	VP for Research Biological Sciences Funding Program, 3 grants reviewed, Officer, Vice President
2005	VP for Research Carver Scientific Research Initiative Grants, Officer, Vice President
2005 - 2007	Bioinformatics recruitment committee College of Engineering, member
2006 - 2007	Bioinformatics Committee, Genetics Program, Member
2007 - 2011	Genetics Program, Recruiting Committee, Member
2007	VP for Research Biological Sciences Review Committee, Officer, Vice President
2009 - 2012	Bioinformatics Training Grant, Admissions Committee, Member
2013 - 2014	Informatics Initiative Curriculum Committee, Member
2009 - 2011	9.Bioinformatics Training Grant, Admissions Committee, Member
2010 - 2011	Biosciences Admissions Committee, Member
2011 - 2014	Biosciences Admissions Liaison for BME
2016 - Present	College of Engineering, Curriculum Committee
2006	VP for Research Biological Sciences Funding Program, 5 grants reviewed, Officer, Vice President
2013 - Present	Iowa Institute of Human Genetics, Member
2014 - Present	Informatics Initiative Services Committee, Member
2015 - Present	Wynn Institute for Vision Research, Member

Collegiate Service

2016 - Present	College of Engineering, Curriculum Committee, Member

Department Service

2002 - 2003	BME, Strategic Planning Committee, member
2002 - 2003	Bioinformatics EFA Committee member, Member
2002 - 2003	Strategic Planning Committee member, Member
2004 - 2005	BME, Undergraduate Committee member, Member

2005	Curriculum Development Committee, Quantitative Modeling in Biomedical Engineering, Micro Biotechnology, BME Fundamentals, and Quantitative Physiology, Member
2005	Faculty Secretary
2005	BME, Curriculum Development Committee, Quantitative Modeling in Biomedical Engineering, Micro Biotechnology, BME Fundamentals, and Quantitative Physiology, Fall 2005, Member
2010 - 2011	BME Undergraduate Committee, Member
2011 - 2012	BME Graduate Committee, Member
2006 - 2007	Genetics Program, Bioinformatics Committee, Member
2004 - 2010	Undergraduate Committee member, Member
2010	Strategic Planning Committee member, Member
2007 - 2011	Genetics Program, Recruiting Committee, Member
2010 - 2011	Biosciences Admissions Committee
2010 - 2011	BME Undergraduate Committee
2013 - 2015	BME Faculty Recruitment Committee Bioinformatics, Chair
2011 - Present	BME Graduate Committee
2016 - Present	BME, Curriculum Committee, Member