

Erich M. Schwarz

## Erich Marquard Schwarz

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Google Scholar ranking: h-index, 25; i10-index, 31.

### Education:

A.B. in Biochemical Sciences *cum laude*, 1986. Harvard University, Cambridge, MA.

Ph.D. in Molecular Biology, 1995. California Institute of Technology, Pasadena, CA.  
Thesis: *Calx*, a sodium-calcium exchanger of *Drosophila melanogaster*. Advisor: Seymour Benzer.

Wellcome Genome Campus Advanced Course, June 19-24, 2016. Hinxton, UK.  
Topic: Practical aspects of small molecule discovery: at the interface of biology, chemistry, and pharmacology.

### Research experience:

Research assistant (with Dr. David Eisenberg), 1982-1983. Molecular Biology Institute, University of California, Los Angeles, CA.

Honors undergraduate thesis (with Dr. Matthew Meselson), 1985-1986. Dept. of Biochemistry and Molecular Biology, Harvard University, Cambridge, MA.

Graduate student (with Dr. Seymour Benzer), 1986-1995. Division of Biology, California Institute of Technology, Pasadena, CA.

Postdoctoral fellow (with Dr. Martin Chalfie), 1995-2000. Department of Biological Sciences, Columbia University, New York, NY.

Associate Biologist (with Dr. Paul Sternberg), 2000-2012. Division of Biology, California Institute of Technology, Pasadena, CA.

Senior Research Associate, 2012-2016. Department of Molecular Biology and Genetics, Cornell University, Ithaca, NY.

Research Scientist, 2016-2017. Department of Molecular Biology and Genetics, Cornell University, Ithaca, NY.

Assistant Research Professor, 2017-present. Department of Molecular Biology and Genetics, Cornell University, Ithaca, NY.

### Grants:

NIH/NIAID R21 1R21AI111173-01A1, \$149,484 projected (co-PI; 37% effort). 5/2015-4/2017.  
*Harnessing transcriptomics to identify and test novel hookworm vaccine targets.*

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NIH/NIGMS P40 5P40OD010440, \$38,750 (subcontract from Prof. A. Rougvie, U. Minn.). 2/2016-5/2016. *Caenorhabditis Genome Center*.

Moore Foundation Grant No. 4551, \$100,000 (subcontract from Prof. C.T. Brown, UC Davis). 11/2014-12/2015. *Infrastructure for data intensive biology*.

NIH/NIAID R01 7R01AI056189-11, \$12,950 (subcontract from Prof. R.V. Aroian, U. Mass. Worcester). 1/2015-5/2015. *B. thurigiensis crystal proteins as powerful next-generation anthelmintics*.

### Fellowships and academic honors:

Chancellor's and Regent's Scholarships, University of California, 1980.

Harvard College Scholarship, Harvard College, 1985.

Lucille P. Markey Charitable Trust Fellowship, 1986-1990.

National Research Service Award Predoctoral Fellowship, 1986-1990.

Beckman Institute Research Grant, 1992-1993.

American Cancer Society Postdoctoral Fellowship, 1995-1998.

Honorary Research Fellow, Faculty of Veterinary Science, University of Melbourne, 2011-2019.

### Key research articles, 2013-2018:

Yin, D., Schwarz, E.M.<sup>††</sup>, Thomas, C.G., Felde, R.L., Korf, I.F., Cutter, A.D., Schartner, C.M., Ralston, E.J., Meyer, B.J., and Haag, E.S.<sup>††</sup> (2018). Rapid genome shrinkage in a self-fertile nematode reveals sperm competition proteins. *Science* 359, 55-61.

Schwarz, E.M.<sup>†</sup>, Hu, Y., Antoshechkin, I., Miller, M.M., Sternberg, P.W., and Aroian, R.V. (2015). The genome and transcriptome of the zoonotic hookworm *Ancylostoma ceylanicum* identify infection-specific gene families. *Nat. Genet.* 47, 416-422.

Jex, A.R., Nejsum, P., Schwarz, E.M., Hu, L., Young, N.D., Hall, R.S., Korhonen, P.K., Liao, S., Thamsborg, S., Xia, J., Xu, P., Wang, S., Scheerlinck, J.-P.Y., Hofmann, A., Sternberg, P.W., Wang, J., and Gasser, R.B. (2014). Genome and transcriptome of the porcine whipworm *Trichuris suis*. *Nat. Genet.* 46, 701-706.

Schwarz, E.M.\*, Korhonen, P.K.\*, Campbell, B.E.\*, Young, N.D.\*, Jex, A.R., Jabbar, A., Hall, R.S., Mondal, A., Howe, A.C., Pell, J., Hofmann, A., Boag, P.R., Zhu, X.Q., Gregory, T.R., Loukas, A., Williams, B.A., Antoshechkin, I., Brown, C.T., Sternberg, P.W., and Gasser, R.B. (2013). The genome and developmental transcriptome of the strongylid nematode *Haemonchus contortus*. *Genome Biol.* 14, R89.

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<sup>††</sup>Co-corresponding author.

\*Equal contribution.

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### Other research articles:

Hsueh, Y.P., Gronquist, M.R., Schwarz, E.M., Nath, R.D., Lee, C.H., Gharib, S., Schroeder, F.C., and Sternberg, P.W. (2017). Nematophagous fungus *Arthrobotrys oligospora* mimics olfactory cues of sex and food to lure its nematode prey. *eLife* 6, e20023.

Wang, H., Liu, J., Gharib, S., Chai, C.M., Schwarz, E.M., Pokala N., and Sternberg, P.W. (2017). cGAL, a temperature-robust GAL4-UAS system for *Caenorhabditis elegans*. *Nat. Methods* 14, 145-148.

Schwarz, E.M. and Roeder, A.H.K. (2016). Transcriptomic effects of the cell cycle regulator LGO in *Arabidopsis* sepals. *Front. Plant Sci.* 7, 1744.

Lockhead, D., Schwarz, E.M., O'Hagan, R., Bellotti, S., Krieg, M., Barr, M.M., Dunn, A.R., Sternberg, P.W., and Goodman, M.B. (2016). The tubulin repertoire of *Caenorhabditis elegans* sensory neurons and its context-dependent role in process outgrowth. *Mol. Biol. Cell* 27, 3717-3728.

Nath, R.D., Chow, E.S., Wang, H., Schwarz, E.M., and Sternberg, P.W. (2016). *C. elegans* stress-induced sleep emerges from the collective action of multiple neuropeptides. *Curr. Biol.* 26, 2446-2455.

Liu, Z., Shi, H., Szymczak, L.C., Aydin, T., Yun, S., Conostas, K., Schaeffer, A., Ranjan, S., Kubba, S., Alam, E., McMahon, D.E., He, J., Shwartz, N., Tian, C., Plavskin, Y., Lindy, A., Dad, N.A., Sheth, S., Amin, N.M., Zimmerman, S., Liu, D., Schwarz, E.M., Smith, H., Krause, M.W., and Liu, J. (2015). Promotion of bone morphogenetic protein signaling by tetraspanins and glycosphingolipids. *PLoS Genet.* 11, e1005221.

Puckett Robinson, C., Schwarz, E.M., and Sternberg, P.W. (2013). Identification of DVA interneuron regulatory sequences in *Caenorhabditis elegans*. *PLoS ONE* 8, e54971.

Schwarz, E.M.\*, Kato, M.\*, and Sternberg, P.W. (2012). Functional transcriptomics of a migrating cell in *Caenorhabditis elegans*. *Proc. Natl. Acad. Sci. U.S.A.*, 109, 16246-16251.

Jex, A.R., Liu, S., Li, B., Young, N.D., Hall, R.S., Li, Y., Yang, L., Zeng, N., Xu, X., Xiong, Z., Chen, F., Wu, X., Zhang, G., Fang, X., Kang, Y., Anderson, G.A., Harris, T.W., Campbell, B.E., Vlaminc, J., Wang, T., Cantacessi, C., Schwarz, E.M., Ranganathan, S., Geldhof, P., Nejsun, P., Sternberg, P.W., Yang, H., Wang, J., Wang, J., and Gasser, R.B. (2011). *Ascaris suum* draft genome. *Nature*, 479, 529-533.

Mortazavi, A.\*, Schwarz, E.M.\*, Williams, B., Schaeffer, L., Wold, B.J., and Sternberg, P.W. (2010). Scaffolding a *Caenorhabditis* nematode genome with RNA-seq. *Genome Res.*, 20, 1740-1747.

Kuntz, S.G., Schwarz, E.M., DeModena, J.A., De Buyscher, T., Trout, D., Shizuya, H., Sternberg, P.W., and Wold, B.J. (2008). Multigenome DNA sequence conservation identifies Hox cis-regulatory elements. *Genome Res.* 18, 1955-1968.

Locke, C.J., Williams, S.N., Schwarz, E.M., Caldwell, G.A., and Caldwell, K.A. (2006). Genetic interactions among cortical malformation genes that influence susceptibility to convulsions in *C. elegans*. *Brain Res.* 1120, 23-34.

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Graciet, E., Hu, R.-G., Piatkov, K., Rhee, J.H., Schwarz, E.M., and Varshavsky, A. (2006). Aminoacyl-transferases and the N-end rule pathway of prokaryotic/eukaryotic specificity in a human pathogen. *Proc. Natl. Acad. Sci. U.S.A.* *103*, 3078-3083.

Schwarz, E.M. and Benzer, S. (1997). *Calx*, a Na-Ca exchanger gene of *Drosophila melanogaster*. *Proc. Natl. Acad. Sci. U.S.A.* *94*, 10249-10254.

Hryshko, L.V., Matsuoka, S., Nicoll, D.A., Weiss, J.N., Schwarz, E.M., Benzer, S., and Philipson, K.D. (1996). Anomalous regulation of the *Drosophila* Na<sup>+</sup>-Ca<sup>2+</sup> exchanger by Ca<sup>2+</sup>. *J. Gen. Physiol.* *108*, 67-74.

Rutledge, B.J., Mortin, M.A., Schwarz, E., Thierry-Mieg, D., and Meselson, M. (1988). Genetic interactions of modifier genes and modifiable alleles in *Drosophila melanogaster*. *Genetics* *119*, 391-397.

Eisenberg, D., Schwarz, E., Komaromy, M., and Wall, R. (1984). Analysis of membrane and surface protein sequences with the hydrophobic moment plot. *J. Mol. Biol.* *179*, 125-142.

\*Equal contribution.

#### **Review articles, database articles, commentaries, and book chapters:**

Schwarz, E.M. (2017). Evolution: a parthenogenetic nematode shows how animals become sexless. *Curr. Biol.* *27*, R1060–R1080.

Gasser, R.B., Schwarz, E.M., Korhonen, P.K., and Young, N.D. (2016). Understanding *Haemonchus contortus* better through genomics and transcriptomics. *Adv. Parasitol.*, *93*, 519-567.

Albertin, C.B., Bonnaud, L., Brown, C.T., Crookes-Goodson, W.J., da Fonseca, R.R., et al. (2012). Cephalopod genomics: a plan of strategies and organization. *Stand. Genomic Sci.*, *7*, 175-188.

Yook, K., Harris, T.W., Bieri, T., Cabunoc, A., Chan, J., et al. (2012). WormBase 2012: more genomes, more data, new website. *Nucleic Acids Res.* *40*, D735-D741.

Harris, T.W., Antoshechkin, I., Bieri, T., Blasiar, D., Chan, J., et al. (2010). WormBase: a comprehensive resource for nematode research. *Nucleic Acids Res.* *38*, D463-D467.

Rogers, A., Antoshechkin, I., Bieri, T., Blasiar, D., Bastiani, C., et al. (2008). WormBase 2007. *Nucleic Acids Res.* *36*, D612-D617.

Gene Ontology Consortium (2008). The Gene Ontology project in 2008. *Nucleic Acids Res.* *36*, D440-D444.

Bieri, T., Blasiar, D., Ozersky, P., Antoshechkin, I., Bastiani C., et al. (2007). WormBase: new content and better access. *Nucleic Acids Res.* *35*, D506-D510.

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Schwarz, E.M., Antoshechkin, I., Bastiani, C., Bieri, T., Blasiar, D., et al. (2006). WormBase: better software, richer content. *Nucleic Acids Res.* *34*, D475-D478.

Schwarz, E.M. and Sternberg, P.W. (2006). Searching WormBase for information about *Caenorhabditis elegans*. *Current Protocols in Bioinformatics*, Unit 1.8.

Schwarz, E.M. (2005). Genomic classification of protein-coding gene families. *WormBook*, ed. The *C. elegans* Research Community. <<http://dx.doi.org/10.1895/wormbook.1.29.1>>.

Chen, N., Harris, T.W., Antoshechkin, I., Bastiani, C., Bieri, T., et al. (2005). WormBase: a comprehensive data resource for *Caenorhabditis* biology and genomics. *Nucleic Acids Res.* *33*, D383-D389.

Harris, M.A., Clark, J., Ireland, A., Lomax, J., Ashburner, M., et al. (2004). The Gene Ontology (GO) database and informatics resource. *Nucleic Acids Res.* *32*, D258-D261.

Harris, T.W., Chen, N., Cunningham, F., Tello-Ruiz, M., Antoshechkin, I., et al. (2004). WormBase: a multi-species resource for nematode biology and genomics. *Nucleic Acids Res.* *32*, D411- D417.

Harris, T.W., Lee, R., Schwarz, E., Bradnam, K., Lawson, D., et al. (2003). WormBase: a cross-species database for comparative genomics. *Nucleic Acids Res.* *31*, 133-137.

Goodman, M.B. and Schwarz, E.M. (2003). Transducing touch in *Caenorhabditis elegans*. *Annu. Rev. Physiol.* *65*, 429-452.

Schwarz, E.M., Stein, L.D., and Sternberg, P.W. (2002). *Caenorhabditis elegans* databases. *Current Genomics* *3*, 111-119.

Stein, L., Mangone, M., Schwarz, E., Durbin, R., Thierry-Mieg, J., Spieth, J., and Sternberg (2001). WormBase: network access to the genome and biology of *Caenorhabditis elegans*. *Nucleic Acids Res.* *29*, 82-86. (Author list corrected in <http://dx.doi.org/10.1093/nar/29.4.0>.)

Schwarz, E. and Benzer, S. (1999). The recently reported NI $\beta$  domain is already known as the Calx- $\beta$  motif. *Trends Biochem. Sci.* *24*, 260.

### Peer review:

Academic Editor for *PeerJ*.

Refereed manuscripts for *ACS Chemical Neuroscience*, *BMC Evolutionary Biology*, *BMC Genomics*, *Cell Reports*, *Current Biology*, *Experimental Parasitology*, *G3*, *Genes*, *Genetics*, *Genome Biology*, *Genome Biology and Evolution*, *Genome Research*, *International Journal for Parasitology*, *Journal of Helminthology*, *Journal of Nematology*, *JoVE*, *Molecular and Cellular Probes*, *Nature Communications*, *Nature Genetics*, *Nucleic Acids Research*, *Parasites and Vectors*, *PLoS Neglected Tropical Diseases*, *PLoS ONE*, *RNA*, *Scientific Data*, and *Scientific Reports*.

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### Talks:

Schwarz, E.M. (2017). Assembling and biologically interpreting nematode genomes. Institute of Molecular Biology, September 26, 2017. Academia Sinica, Taipei, Taiwan.

Schwarz, E.M., Yoshimura, J., Ichikawa, K., Shoura, M., Artiles, K.L., Gabdank, I., Wahba, L., Smith, C.L., Edgley, M.L., Rougvie, A.E., Fire, A.Z., and Morishita, S. (2017). De-completing the *C. elegans* genome. 21st International *C. elegans* Meeting, June 21-25, 2017. University of California, Los Angeles.

Schwarz, E.M. (2017). PacBio-based *Caenorhabditis* genomes. 21st International *C. elegans* Meeting, June 21-25, 2017. University of California, Los Angeles.

Schwarz, E.M., Yin, D., Schartner, C.M., Ralston, E.J., Koutsovoulos, G., Stevens, L., Chandrasekar, S., Blaxter, M., Sternberg, P.W., Meyer, B.J., and Haag, E.S. (2016). Characterizing genome shrinkage in hermaphroditic *Caenorhabditis* with third-generation genome sequences having near-chromosomal contiguity. Evolution of *Caenorhabditis* and Other Nematodes, March 30-April 2, 2016. Cold Spring Harbor Laboratory.

Schwarz, E.M. (2016). Using nematode genomics to decipher parasitism and conserved unknown genes. [1] Department of Nematology, January 7, 2016. University of California, Riverside. [2] Department of Biology and Biotechnology, November 8, 2016. Worcester Polytechnic Institute, Worcester, Massachusetts.

Schwarz, E.M., Kim, S.J., Huang, X., Nath, R.D., Ghosh, S., and Sternberg, P.W. (2015-2016). Using *C. elegans* to discover functions of conserved unknown human genes. [1] BEACON Congress, August 15-18, 2015. Michigan State University, East Lansing, Michigan. [2] Genome Center, September 17, 2015. University of California, Davis. [3] Paul W. Sternberg Symposium, August 25, 2016. California Institute of Technology, Pasadena, California.

Schwarz, E.M. (2015). Improving *Caenorhabditis* genome assembly with long read data. 20th International *C. elegans* Meeting, June 24-28, 2015. University of California, Los Angeles. Cited by M. Blaxter in GSA Genes to Genomes blog, "Guest post: The new genomic world of wild worms", August 13, 2015.

Schwarz, E.M., Hu, Y., Antoshechkin, I., Miller, M.M., Sternberg, P.W., and Aroian, R.V. (2015). The genome of *Ancylostoma ceylanicum*: distinguishing possible immunological decoys from possible drug and vaccine targets in a model hookworm. 20th International *C. elegans* Meeting, June 24-28, 2015. University of California, Los Angeles.

Schwarz, E.M. (2015). Genomics of nematode parasites of pigs, sheep, and other animals: towards understanding human immune modulation. Plant and Animal Genome XXIII Conference, January 10-14, 2015, San Diego, California.

Schwarz, E.M., Hu, Y., Antoshechkin, I., Miller, M.M., Aroian, R.V., and Sternberg, P.W. (2013-2014). Genome and transcriptome of the zoonotic hookworm *Ancylostoma ceylanicum*. [1] Infectious Disease Genomics & Global Health, October 16-18, 2013. Wellcome Trust Genome Campus, Hinxton,

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Cambridge, United Kingdom. [2] Evolutionary Biology of *Caenorhabditis* and other Nematodes, June 14-17, 2014. Wellcome Trust Genome Campus, Hinxton, Cambridge, United Kingdom. [3] American Society of Tropical Medicine and Hygiene, 63rd Annual Meeting, November 2-6, 2014. New Orleans, Louisiana.

Schwarz, E.M., Campbell, B.E., Young, N.D., Howe, A., Pell, J., Hall, R.S., Wang, J., Wang, J., Yang, H., Brown, C.T., Gasser, R.B., and Sternberg, P.W. (2012). Characterizing the genome of *Haemonchus contortus* through pre-filtering reads on graph structure. Evolution of *Caenorhabditis* and Other Nematodes, April 3-6, 2012. Cold Spring Harbor Laboratory.

Schwarz, E.M. (2011). The genomes of gonochoristic versus hermaphroditic *Caenorhabditis* species. 18th International *C. elegans* Meeting, June 22-26, 2011. University of California, Los Angeles.

Schwarz, E.M. (2011). Next-generation worm transcriptomes and genomes. [1] Weill Institute, Cornell University, April 20, 2011. [2] University of California, San Diego, May 5, 2011.

Schwarz, E.M., Gasser, R.B., Mortazavi, A., Williams, B.A., Antoshechkin, I., Campbell, B.E., Young, N.D., Jex, A.R., Cantacessi, C., Hall, R.S., and Sternberg, P.W. (2010). Next-generation genome and transcriptome of *Haemonchus contortus*. XIIth International Congress of Parasitology, August 15-20, 2010. Melbourne, Australia.

Schwarz, E.M. (2010). Using WormBase to decipher parasitic nematode genomes. XIIth International Congress of Parasitology, August 15-20, 2010. Melbourne, Australia.

Schwarz, E.M., Mortazavi, A., Williams, B., Schaeffer, L., Antoshechkin, I., Wold, B.J., and Sternberg, P.W. (2010). Scaffolding a de novo genome of *Caenorhabditis* sp. 3 PS1010 with RNA-seq. Evolutionary Biology of *Caenorhabditis* and Other Nematodes, June 5-8, 2010. Wellcome Trust Genome Campus, Hinxton, Cambridge, United Kingdom.

Schwarz, E.M., Kato, M., and Sternberg, P.W. (2010). A transcriptome of the migrating postembryonic *C. elegans* linker cell. The Biology of Genomes, May 11-15, 2010. Cold Spring Harbor Laboratory.

Schwarz, E.M. and *Caenorhabditis* Genome Analysis Consortium (2009). The genomes of gonochoristic versus hermaphroditic *Caenorhabditis* species. 17th International *C. elegans* Meeting, June 24-28, 2009. University of California, Los Angeles.

Schwarz, E.M. (2008). Genomes and transcriptomes of *Caenorhabditis*. Department of Microbiology & Molecular Genetics, November 11, 2008. Michigan State University, East Lansing, Michigan.

Schwarz, E.M., Mortazavi, A., Kuntz, S.G., Saldanha, A.J., Shapiro, B.E., Wold, B.J., and Sternberg, P.W. (2007). Cis-regulatory analysis of four *Caenorhabditis* genomes. 16th International *C. elegans* Meeting, June 27-July 1, 2007. University of California, Los Angeles.

Schwarz, E.M. (2006). WormBase: meeting specific biological needs with general bioinformatics tools. American Phytopathological Society, August 1, 2006. Quebec City, Canada.

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Schwarz, E.M., Mortazavi, A., Kuntz, S.G., Saldanha, A.J., DeModena, J.A., Fu, D., De Buysscher, T., Shizuya, H., Roden, J.C., Wold, B.J., and Sternberg, P.W. (2006). Cis-regulatory analysis of three *Caenorhabditis* genomes. [1] The Biology of Genomes, May 10-14, 2006. Cold Spring Harbor Laboratory. [2] EMBO Workshop on the Study of Evolutionary Biology With *Caenorhabditis elegans* and Related Species, May 23-26, 2006. Instituto Gulbenkian de Ciencia, Oeiras, Portugal.

Schwarz, E.M. (2006). WormBase: how we (try to) support biology and genomics for an entire (small) animal. [1] Department of Biological Sciences, February 3, 2006. California State Polytechnic University, Pomona. [2] Department of Biology, April 14, 2006. California State University, San Bernardino.

Schwarz, E.M. and WormBase Consortium (2005). WormBase, a comprehensive resource for *C. elegans* bioinformatics. 15th International *C. elegans* Meeting, June 25-29, 2005. University of California, Los Angeles.

Schwarz, E.M., Sternberg, P.W., and WormBase Consortium (2004). The state of the WormBase: 2004. West Coast *C. elegans* Meeting, August 21-24, 2004. University of California, Santa Barbara.

Schwarz, E.M., DeModena, J.A., Moon, E., De Buysscher, T., Mullaney, N., Shizuya, H., Wold, B.J., and Sternberg, P.W. (2003). Comparative analysis of cis-regulatory sequences using four *Caenorhabditis* species. 14th International *C. elegans* Meeting, June 29-July 3, 2003. University of California, Los Angeles.

### **Workshops and discussion sections:**

Ran the following workshops and discussion sections at *C. elegans* meetings:

Bioinformatics, 2002 and 2004 West Coast meetings (UC San Diego and UC Santa Barbara);

WormBase, 2005, 2007, and 2009 International meetings (UC Los Angeles);

Evolution and Genomics [co-chair], 2009 International meeting (UC Los Angeles);

N-Genomes, 2013 International meeting (UC Los Angeles).

Ran a discussion section on analysis of multiple *Caenorhabditis* genomes at the CSHL Evolution of *Caenorhabditis* and Other Nematodes meeting, 2012.

### **Teaching experience:**

Guest lecturer, July 2017. Analyzing Next-Generation Sequencing Data course (<http://angus.readthedocs.org>), University of California Davis. Described third-generation sequencing of *Caenorhabditis* genomes (*C. elegans*, *C. nigoni*, *C. tropicalis*, and *C. wallacei*), and future prospects for genome analysis.

Guest lecturer, June 2011-2013 and August 2015. Analyzing Next-Generation Sequencing Data course (<http://angus.readthedocs.org>), Kellogg Biological Station, Michigan State University, MI. Described next-generation sequencing of *Caenorhabditis angaria* PS1010, *Haemonchus contortus*, and *Ancylostoma ceylanicum*, transcriptomics of migrating linker cells in *Caenorhabditis elegans*, and future prospects for genome analysis.



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Lecturer, "Molecular and Cellular Bases of Host-Microbes Interactions: Genomics and Sequencing", May 26-29, 2014. Institute of Molecular Biology, National Academy of Sciences, Yerevan, Armenia. Described introductory Unix, and discussed next-generation genomics analyses of two mammalian-parasitic nematodes (the hookworm *Ancylostoma ceylanicum* and the African eye worm *Loa loa*).

Guest lecturer, "Advanced Genetics", Spring 2001. California Institute of Technology, Pasadena, CA. Summarized the state of bioinformatics for advanced undergraduates.

Teaching assistant, "Behavioral Biology". Winters of 1990-1992. California Institute of Technology, Pasadena, CA. Wrote and graded examinations for the course.

Teaching assistant, "Introduction to Molecular Biology". Winters of 1988-1989. Partially graded all final examinations; ran and graded a student laboratory; prepared materials for the molecular biology section of all student laboratories.

Teaching assistant, "Organismic Biology". Winter 1987. Ran and graded a student laboratory.

### **Social media and outreach:**

Twitter: @ErichMSchwarz.

Career Day, March 4, 2008. "Molecular biology: how and why (or why not) to work in it." Loyola High School, Los Angeles, CA.

NIH Minority Outreach Program, April 15, 2005. "WormBase: how we (try to) support biology and genomics for an entire (small) animal." University of New Mexico, Albuquerque, New Mexico.