CURRICULUM VITAE

David Paull Hill, Ph.D
Mouse Genome Informatics
The Jackson Laboratory
600 Main Street
Bar Harbor, ME 04609-1500
Tel: 207-288-6430

EMPLOYMENT

Bioinformatics Scientist, 2006-present
Gene Ontology Consortium/Mouse Genome Informatics
The Jackson Laboratory
- Co-manage the biological content of The Gene Ontology (GO).
- Coordinate the activities of computer scientists and biologists to maintain biologically accurate and logically rigorous ontologies.
- Work with scientific experts to convert current scientific understanding into a computable format.
- Drive significant advances in the development of GO, including the introduction of new relationship types, relationship links between ontologies, introduction of 'cross-products', use of automated QC procedures, and expansion of the ontology in areas of developmental, physiological and cellular biology.
- Annotate details of mouse gene roles using GO and primary scientific literature.

Senior Scientific Curator, 2005-2006
Gene Ontology Consortium/Mouse Genome Informatics
The Jackson Laboratory
- Annotated details of mouse gene roles using GO and primary scientific literature.
- Co-designed automated pipelines for the assignment of mouse transcripts to GO terms.
- Trained new biocurators in the use of GO for gene product annotation.

Scientific Curator, 1998-2005
Mouse Genome Informatics
The Jackson Laboratory
- Annotated expression data of mouse genes using primary scientific literature and mouse anatomy ontologies.
- Coordinated and QC assured the download of SwissProt sequence data into The Mouse Genome Informatics resource.

Technical Services Scientist
Roche Applied Science, 1997-1998
- Led the Apoptosis and Cell Proliferation Reagent Team.
- Answered technical queries about the entire line of biochemical products sold by Roche.
- Worked with product managers and marketing staff to design marketing materials used in the sales of biochemical products.
- Trained account managers in the scientific aspects of cell proliferation, apoptosis and real-time PCR products.
- Performed marketing 'road shows' at academic and industrial institutions, illustrating the utility of apoptosis and cell proliferation reagents.
- Served as the scientific representative for Roche at major scientific meetings.

EDUCATION

Postdoctorate, 1994-1997
Indiana University School of Medicine, Indianapolis IN
Project Title: Retinoic acid induced differentiation of neuroblastoma cells as a model for neuronal
 Differentiation
Lab PI: Kent Robertson, M.D., Ph.D

Assistant Scientist, 1992-1994
Indianapolis VA Hospital, Indianapolis, IN

Postdoctorate, 1989-1992
Mt. Sinai Hospital Research Institute, Toronto, ON Canada
Project: Large-scale gene-trap screening for developmentally regulated genes in the mouse
Lab PI: Janet Rossant, Ph.D.

Postdoctorate, 1989
Indiana University, Bloomington IN
Project: Characterization of a paternal-effect embryonic-lethal mutation in *Caenorhabditis elegans*
Lab PI: Susan Strome, Ph.D.

Doctor of Philosophy, 1985-1988
Indiana University, Bloomington Indiana
Major: Molecular, Cellular, and Developmental Biology
Minor: Neurophysiology
Thesis: An analysis of the generation of cell differences in early *Caenorhabditis elegans* embryos
Advisor: Susan Strome, Ph.D.

Graduate Student, 1983-1985
Indiana University, Bloomington Indiana
Project: Analysis of the genomic structure of a developmentally regulated gene in sea urchins and
its regulation in cultured isolated blastomeres of sea urchin embryos
Advisor: William H. Klein, Ph.D. (Dr. Klein moved away from Indiana University in 1985)

Embryology Program, 1984
Marine Biological Laboratories, Woods Hole, MA
Project: Evolutionary study of a calcium-binding protein in various species of echinoderms

Bachelor of Science *cum laude*, 1979-1983
University of Rochester, Rochester, NY
Major: Molecular Genetics
Project: Analysis of the expression of developmentally regulated genes in animalized and
vegetalized sea urchin embryos by *in situ* hybridization
Advisor: Robert C. Angerer, Ph.D.

TEACHING EXPERIENCE

Assistant Instructor (Cell Biology), Indiana University   1987
Trained several Graduate Students, Summer Students and Technicians 1983-1997
Mentor at the 1st Gene Ontology Annotators Workshop, Cambridge, UK 2004
Mentor at the 3rd Gene Ontology Annotators Workshop, Palo Alto, CA   2006
Assistant Aikido Instructor: The Indiana Aikikai   1997
Aikido Instructor (Fukushidoin): The Ellsworth Aikikai   1998-present

HONORS, GRANTS AND FELLOWSHIPS

Graduate *cum laude* in Molecular Genetics, University of Rochester 1983
College Scholar, University of Rochester 1979-1980
Hanley Scholar, University of Rochester 1981
Boch National Scholar, University of Rochester 1982-1983
Indiana University Fellow, Indiana University 1983-1984
NIH Predoctoral Fellow, Marine Biological Laboratory 1984
NIH Predoctoral Fellow, Indiana University 1984-1987
Institute for Molecular and Cellular Biology Fellow, Indiana University 1988-1989
University Fellow, Indiana University 1988-1989
Postdoctoral Fellow, Medical Research Council of Canada 1989-1992
Yondan (4th degree black belt), United States Aikido Federation Current

OTHER SCIENTIFIC APPOINTMENTS

Meeting Organizing Committee:
International Biocuration Meeting, Berlin, Germany, April 2009
International Biocuration Meeting, San Jose, California October 2007

Reviewer: Proceedings of the National Academy of Sciences of the USA
Bioinformatics
Genome Research
Nature Biotechnology
Nucleic Acids Research
BMC Bioinformatics
Bioinformatics

PAPERS, REVIEWS AND BOOK CHAPTERS

Alam-Faruque Y, **Hill DP**, Dimmer EC, Harris MA, Foulger RE, Tweedie S, Attrill H, Howe DG, Thomas SR, Davidson D, Woolf AS, Blake JA, Mungall CJ, O'Donovan C, Apweiler R, Huntley RP. (2014) Representing Kidney Development Using the Gene Ontology. **PLoS One.** 9(6):e99864.

Huntley RP, Harris MA, Alam-Faruque Y, Blake JA, Carbon S, Dietze H, Dimmer EC, Foulger RE, **Hill DP**, Khodiyar VK, Lock A, Lomax J, Lovering RC, Mutowo-Meullenet P, Sawford T, Van Auken K, Wood V, Mungall CJ. (2014) A Method for Increasing Expressivity of Gene Ontology Annotations Using a Compositional Approach. **BMC Bioinformatics.** 15:155.

Roncaglia P, Martone ME, **Hill DP**, Berardini TZ, Foulger RE, Imam FT, Drabkin H, Mungall CJ, Lomax J. (2013) The Gene Ontology (GO) Cellular Component Ontology: Integration with SAO (Subcellular Anatomy Ontology) and Other Recent Developments. **J Biomed Semantics.** 4(1):20.

Tripathi S, Christie KR, Balakrishnan R, Huntley R, **Hill DP**, Thommesen L, Blake JA, Kuiper M, Lægreid A. (2013) Gene-ontology Annotation of Sequence-specific DNA Binding Transcription Factors: Setting the Stage for a Large-scale Curation Effort. **Database (Oxford).** bat062.

Hill DP, Adams N, Bada M, Batchelor C, Berardini TZ, Dietze H, Drabkin HJ, Ennis M, Foulger RE, Harris MA, Hastings J, Kale NS, de Matos P, Mungall CJ, Owen G, Roncaglia P, Steinbeck C, Turner S, Lomax J. (2013) Dovetailing Biology and Chemistry: Integrating the Gene Ontology with the ChEBI Chemical Ontology. **BMC Genomics.** 14:513.

Gene Ontology Consortium. (2013) Gene Ontology Annotations and Resources. **Nucleic Acids Res.** 41(Database issue):D530-5.

Gene Ontology Consortium. (2012) The Gene Ontology:Enhancements for 2011. **Nucleic Acids Res.** 40(Database issue):D559-64.

Khodiyar VK, **Hill DP**, Howe D, Berardini TZ, Tweedie S, Talmud PJ, Breckenridge R, Bhattarcharya S, Riley P, Scambler P, Lovering RC. (2011) The Representation of Heart Development in the Gene Ontology **Dev Biol.** 354(1):9-17.

Mungall CJ, Bada M, Berardini TZ, Deegan J, Ireland A, Harris MA, **Hill DP**, Lomax J. (2010). Cross-Product Extensions of the Gene Ontology. **J. Biomed. Inform.** 44(1):80-6.

Alterovitz G, Xiang M, **Hill DP**, Lomax J, Liu J, Cherkassky M, Mungall C, Harris MA, Dolan ME, Blake JA, Ramoni MF. (2010). Ontology Engineering. **Nature Biotechnol.** 28(2):128-30.

The Gene Ontology Consortium. (2010). The Gene Ontology in 2010: extensions and refinements. **Nucleic Acids Res**. 38:D331-5.

Hill DP, Berardini TZ, Howe DG, Van Auken KM. (2009). Representing Ontogeny Through Ontology: A Developmental Biologist's Guide to The Gene Ontology. **Mol Reprod. Dev**. 77(4):314-29.

Dowell, KG, McAndrews-Hill MS, **Hill DP**, Drabkin HJ, Blake JA. (2009). Integrating Text Mining into the MGI Biocuration Workflow **Database (Oxford)**. Bap019.

Reference Genome Group of the Gene Ontology Consortium. (2009). The Gene Ontology's Reference Genome Project: a unified framework for functional annotation across species. **PLoS Comput Biol.** Jul;5(7).

Feltrin E, Campanaro S, Diehl AD, Ehler E, Faulkner G, Fordham J, Gardin C, Harris M, **Hill D**, Knoell R, Laveder P, Mittempergher L, Nori A, Reggiani C, Sorrentino V, Volpe P, Zara I, Valle G, Deegan J Nee Clark. (2008). Muscle research and gene ontology: New standards for improved data integration. **BMC Med Genomics.** Jan 29;2(1):6.

Howe D, Costanzo M, Fey P, Gojobori T, Hannick L, Hide W, **Hill DP**, Kania R, Schaeffer M, St Pierre S, Twigger S, White O, Yon Rhee S. (2008). Big Data: The Future of Biocuration. **Nature.** Sep 4;455(7209):47-50.

Taşan M, Tian W, **Hill DP**, Gibbons FD, Blake JA, Roth FP. (2008). An en masse phenotype and function prediction system for Mus musculus. **Genome Biol.** 9 Suppl 1:S8.

Peña-Castillo L, Tasan M, Myers CL, Lee H, Joshi T, Zhang C, Guan Y, Leone M, Pagnani A, Kim WK, Krumpelman C, Tian W, Obozinski G, Qi Y, Mostafavi S, Lin GN, Berriz GF, Gibbons FD, Lanckriet G, Qiu J, Grant C, Barutcuoglu Z, **Hill DP**, Warde-Farley D, Grouios C, Ray D, Blake JA, Deng M, Jordan MI, Noble WS, Morris Q, Klein-Seetharaman J, Bar-Joseph Z, Chen T, Sun F, Troyanskaya OG, Marcotte EM, Xu D, Hughes TR, Roth FP. (2008). A critical assessment of Mus musculus gene function prediction using integrated genomic evidence. **Genome Biol.** 2008;9. Suppl 1:S2.

Hill DP, Smith B, McAndrews-Hill MS, Blake JA. (2008). Gene Ontology annotations: what they mean and where they come from. **BMC Bioinformatics.** Apr 29;9 Suppl 5:S2.

McCarthy FM, Wang N, Magee GB, Nanduri B, Lawrence ML, Camon EB, Barrell DG, **Hill DP**, Dolan ME, Williams WP, Luthe DS, Bridges SM, Burgess SC. (2006). AgBase: a functional genomics resource for agriculture. **BMC Genomics**. Sep 8;7(1):229.

Maeda N, Kasukawa T, Oyama R, Gough J, Frith M, Engstrom PG, Lenhard B, Aturaliya RN, Batalov S, Beisel KW, Bult CJ, Fletcher CF, Forrest AR, Furuno M, **Hill D**, Itoh M, Kanamori-Katayama M, Katayama S, Katoh M, Kawashima T, Quackenbush J, Ravasi T, Ring BZ, Shibata K, Sugiura K, Takenaka Y, Teasdale RD, Wells CA, Zhu Y, Kai C, Kawai J, Hume DA, Carninci P, Hayashizaki Y. (2006). Transcript annotation in FANTOM3: mouse gene catalog based on physical cDNAs. **PLoS Genet**. 2(4):e62.

Carninci P, Kasukawa T, Katayama S, Gough J, Frith MC, Maeda N, Oyama R, Ravasi T, Lenhard B, Wells C, Kodzius R, Shimokawa K, Bajic VB, Brenner SE, Batalov S, Forrest AR, Zavolan M, Davis MJ, Wilming LG, Aidinis V, Allen JE, Ambesi-Impiombato A, Apweiler R, Aturaliya RN, Bailey TL, Bansal M, Baxter L, Beisel KW, Bersano T, Bono H, Chalk AM, Chiu KP, Choudhary V, Christoffels A, Clutterbuck DR, Crowe ML, Dalla E, Dalrymple BP, de Bono B, Della Gatta G, di Bernardo D, Down T, Engstrom P, Fagiolini M, Faulkner G, Fletcher CF, Fukushima T, Furuno M, Futaki S, Gariboldi M, Georgii-Hemming P, Gingeras TR, Gojobori T, Green RE, Gustincich S, Harbers M, Hayashi Y, Hensch TK, Hirokawa N, **Hill D**, Huminiecki L, Iacono M, Ikeo K, Iwama A, Ishikawa T, Jakt M, Kanapin A, Katoh M, Kawasawa Y, Kelso J, Kitamura H, Kitano H, Kollias G, Krishnan SP, Kruger A, Kummerfeld SK, Kurochkin IV, Lareau LF, Lazarevic D, Lipovich L, Liu J, Liuni S, McWilliam S, Madan Babu M, Madera M, Marchionni L, Matsuda H, Matsuzawa S, Miki H, Mignone F, Miyake S, Morris K, Mottagui-Tabar S, Mulder N, Nakano N, Nakauchi H, Ng P, Nilsson R, Nishiguchi S, Nishikawa S, Nori F, Ohara O, Okazaki Y, Orlando V, Pang KC, Pavan WJ, Pavesi G, Pesole G, Petrovsky N, Piazza S, Reed J, Reid JF, Ring BZ, Ringwald M, Rost B, Ruan Y, Salzberg SL, Sandelin A, Schneider C, Schonbach C, Sekiguchi K, Semple CA, Seno S, Sessa L, Sheng Y, Shibata Y, Shimada H, Shimada K, Silva D, Sinclair B, Sperling S, Stupka E, Sugiura K, Sultana R, Takenaka Y, Taki K, Tammoja K, Tan SL, Tang S, Taylor MS, Tegner J, Teichmann SA, Ueda HR, van Nimwegen E, Verardo R, Wei CL, Yagi K, Yamanishi H, Zabarovsky E, Zhu S, Zimmer A, Hide W, Bult C, Grimmond SM, Teasdale RD, Liu ET, Brusic V, Quackenbush J, Wahlestedt C, Mattick JS, Hume DA, Kai C, Sasaki D, Tomaru Y, Fukuda S, Kanamori-Katayama M, Suzuki M, Aoki J, Arakawa T, Iida J, Imamura K, Itoh M, Kato T, Kawaji H, Kawagashira N, Kawashima T, Kojima M, Kondo S, Konno H, Nakano K, Ninomiya N, Nishio T, Okada M, Plessy C, Shibata K, Shiraki T, Suzuki S, Tagami M, Waki K, Watahiki A, Okamura-Oho Y, Suzuki H, Kawai J, Hayashizaki Y; FANTOM Consortium; RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group). (2005). The transcriptional landscape of the mammalian genome. **Science.** 309(5740):1559-63.

Drabkin HJ, Hollenbeck C, **Hill DP**, Blake JA. (2005). Ontological visualization of protein-protein interactions. **BMC Bioinformatics.** 6(1):29.

Harris MA, Clark J, Ireland A, Lomax J, Ashburner M, Foulger R, Eilbeck K, Lewis S, Marshall B, Mungall C, Richter J, Rubin GM, Blake JA, Bult C, Dolan M, Drabkin H, Eppig JT, **Hill DP**, Ni L, Ringwald M, Balakrishnan R, Cherry JM, Christie KR, Costanzo MC, Dwight SS, Engel S, Fisk DG, Hirschman JE, Hong EL, Nash RS, Sethuraman A, Theesfeld CL, Botstein D, Dolinski K, Feierbach B, Berardini T, Mundodi S, Rhee SY, Apweiler R, Barrell D, Camon E, Dimmer E, Lee V, Chisholm R, Gaudet P, Kibbe W, Kishore R, Schwarz EM, Sternberg P, Gwinn M, Hannick L, Wortman J, Berriman M, Wood V, de la Cruz N, Tonellato P, Jaiswal P, Seigfried T, White R; Gene Ontology Consortium. (2004). The Gene Ontology (GO) database and informatics resource. **Nucleic Acids Res.** 32:D258-61.

Hill DP, Begley DA, Finger JH, Hayamizu TF, McCright IJ, Smith CM, Beal JS, Corbani LE, Blake JA, Eppig JT, Kadin JA, Richardson JE, Ringwald M. (2004). The Mouse Gene Expression Database (GXD): updates and enhancements. **Nucleic Acids Res.** 32:D568-D571.

Baldarelli RM, **Hill DP,** Blake JA, Adachi J, Furuno M, Bradt D, Corbani LE, Cousins S, Frazer KS, Qi D, Yang L, Ramachandran S, Reed D, Zhu Y, Kasukawa T, Ringwald M, King BL, Maltais LJ, McKenzie LM, Schriml L, Maglott D, Church D, Pruitt K, Okazak Y, Hayashizaki Y, Eppig JT, Richardson JE, Kadin JA, Bult CJ. (2003). Connecting sequence and biology in the laboratory mouse. **Genome Res.** 13(6B):1505-19.

Kasukawa T, Furuno M, Nikaido I, Bono H, Hume DA, Bult C, **Hill DP,** Baldarelli R, Gough J, Kanapin A, Matsuda H, Schriml LM, Hayashizaki Y, Okazaki Y, Quackenbush J. (2003). Development and evaluation of an automated annotation pipeline and cDNA annotation system. **Genome Res.** 13(6B):1542-51.

Kawasawa Y, McKenzie LM, **Hill DP**, Bono H, Yanagisawa M; RIKEN GER Group; GSL Members. (2003). G protein-coupled receptor genes in the FANTOM2 database. **Genome Res.** 13(6B):1466-77.

Schriml LM, **Hill DP,** Blake JA, Bono H, Wynshaw-Boris A, Pavan W, Ring BZ, Beisel K, Setou M, Okazaki Y, Hayashizaki Y. (2003). Human disease genes and their cloned mouse orthologs: exploration of the FANTOM2 cDNA data set. **Genome Res.** 13(6b):1496-1500.

Hill DP, Blake JA, Richardson JE, Ringwald M. (2002). Extension and Integration of the Gene Ontology (GO): Combining GO Vocabularies With External Vocabularies. **Genome Res.** 12:1982-1991.

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. (2002). Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. **Nature.** 420:563-573.

Hill DP, Davis AP, Richardson JE, Corradi JP, Ringwald M, Eppig JT, Blake JA. (2001). Strategies for Biological Annotation of Mammalian Systems: Implementing Gene Ontologies in Mouse Genome Informatics. **Genomics.** 74: 121-128.

Hill, DP. (2001). Using the Gene Ontology Vocabularies for Functional Annotation of Mammalian Gene Products. In "How to make the best use of the decoded genomic information (Japanese)" pp. 11-17, Tokyo Kaguka Dozin CO., LTD., Tokyo, Japan.

Ringwald M, Eppig JT, Begley DA, Corradi JP, McCright IJ, Hayamizu TF, **Hill DP,** Kadin JA, Richardson JE. (2001). The Mouse Gene Expression Database (GXD). **Nucleic Acids Res.** 29:98-101.

Gene Ontology Consortium. (2001) Creating the gene ontology resource: design and implementation. **Genome Res.** 11:1425-1433.

The RIKEN Genome Exploration Research Group Phase II Team and **the FANTOM Consortium**. (2001). Functional annotation of a full-length mouse cDNA collection. **Nature.** 409: 685-690.

Gene Ontology Consortium. (2000). Gene Ontology: tool for the unification of biology. **Nature Genet.** 25: 25-29.

Robertson KA, **Hill DP**, Kelley MR, Tritt R, Crum B, Van Epps S, Srour E, Rice S, Hromas R. (1998). The myeloid zinc finger gene (MZF-1) delays retinoic acid-induced apoptosis and differentiation in myeloid leukemia cells. **Leukemia.**12(5):690-8.

Hill, DP, Robertson, KA. (1998). Differentiation of LA-N-5 neuroblastoma cells into cholinergic neurons: methods for differentiation, immunohistochemistry and reporter gene introduction. **Brain Res Brain Res Protoc.** Mar;2(3):183-90.

Hill, DP, Robertson, KA. (1997). Characterization of the cholinergic neuronal differentiation of the human neuroblastoma cell line LA-N-5 after treatment with retinoic acid. **Brain Res Dev Brain Res.** Aug 18;102(1):53-67.

Robertson KA, **Hill DP**, Xu Y, Liu L, Van Epps S, Hockenbery DM, Park JR, Wilson TM, Kelley MR. (1997). Down-regulation of apurinic/apyrimidinic endonuclease expression is associated with the induction of apoptosis in differentiating myeloid leukemia cells. **Cell Growth Differ.** 1997 Apr;8(4):443-9.

Wurst W, Rossant J, Prideaux V, Kownacka M, Joyner A, **Hill DP**, Guillemot F, Gasca S, Cado D, Auerbach A, *et al.* (1995). A large-scale gene-trap screen for insertional mutations in developmentally regulated genes in mice. **Genetics.** Feb;139(2):889-99.

Gasca S, **Hill DP**, Klingensmith J, Rossant J. (1995). Characterization of a gene trap insertion into a novel gene, cordon-bleu, expressed in axial structures of the gastrulating mouse embryo. **Dev Genet.** 17(2):141-54.

Hill DP, Wurst W. (1993). Gene and enhancer trapping: mutagenic strategies for developmental studies. **Curr Top Dev Biol.** 28:181-206.

Hill DP, Wurst W. (1993). Screening for novel pattern formation genes using gene trap approaches. **Methods Enzymol.** 1993;225:664-81.

Hill DP, Strome S. (1990). Brief cytochalasin-induced disruption of microfilaments during a critical interval in 1-cell C. elegans embryos alters the partitioning of developmental instructions to the 2-cell embryo. **Development.** Jan;108(1):159-72.

Hill DP, Shakes DC, Ward S, Strome S. (1989). A sperm-supplied product essential for initiation of normal embryogenesis in Caenorhabditis elegans is encoded by the paternal-effect embryonic-lethal gene, spe-11. **Dev Biol.** 136(1):154-66.

Hill, DP., Strome, S., and Radice, G. (1989). The cytoskeleton in development. In "Cytoplasmic organization in development" (G.M. Malacinski, editor), McGraw Hill, New York.

Strome S, **Hill DP. (**1988). An analysis of the role of microfilaments in the establishment and maintenance of asymmetry in Caenorhabditis elegans zygotes. **Dev Biol.** 125(1):75-84.