Paul Gilna, B.Sc., Ph.D.

Director, BioEnergy Science Center (BESC)
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Education and Training

- Blackrock College Dublin Ireland. Leaving Certificate, 1974
- University College Dublin, Ireland. Bachelor of Science (Hons.) Pharmacology, 1979
- University College Dublin, Ireland. Ph.D., Pharmacology, 1984
- Graduate of LANL Phase I (1992) and Phase II (1994) management training courses
- Graduate of LANL Leadership Institute, May 2000
- Graduate of LANL Director's Development Program, Dec 2004

Citizenship: United States (Naturalized in Aug 2000)

Work Experience

Oak Ridge National Laboratory:

Director, BioEnergy Science Center (BESC)

Mar 2010 to present

Lead a $135 million basic and applied research project underlying the development of more cost effective transformation of biomass products into biofuels. The research focuses on understanding and overcoming the difficulty in converting cellulosic, or woody, products into sugars, which are in turn fermented into biofuels. BESC includes 20 research partners from other national laboratories, universities, and private corporations. BESC is in turn a partner with two other centers, the Joint BioEnergy Institute at the Lawrence Berkeley National Laboratory and the Great Lakes Bioenergy Research Center at the University of Wisconsin. Together, these institutes are funded from a total investment of $420 million over 5 years from the Department of Energy's Office of Science, Office of Biology and Environmental Research.

University of California, San Diego:

Executive Director, Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis (CAMERA)

May 2006 to Mar 2010

Recruited to take leadership position in running $24M investment from Gordon & Betty Moore Foundation to develop cyberinfrastructure for marine microbial metagenomics research. Responsible for partnership between UCSD and the J.Craig Venter Institute to develop database and web-based toolset to serve growing community of metagenomic data researchers. In one year of public operation, project currently supports over 2500 users in over 50 countries accessing systems commissioned at UCSD for data download and data analysis. Primarily

responsible for interface between project and research community as well as primary point of contact for management oversight with Moore Foundation staff. As primary external POC, have interacted with Federal agencies, the National Academy and other philanthropic groups (e.g., the Gates Foundation) in strategic planning exercises.

Los Alamos National Laboratory, Bioscience Division:

Division Leader (Acting)

Apr 2005 to Jan 01, 2006

Step in at request of Associate Director to steward B division through search period. Manage and Lead a 300-person division with approx $60M budget focused largely on basic and applied research targeted at detecting and preventing threat of naturally occurring or deliberately released infectious agents. Responsible line manager for operations envelope of division, including safety and security.

Los Alamos National Laboratory, Bioscience Division:

Center Leader, Center for Human Genome Studies (CHGS)

Jul 2001 to May 2006

Step in at request of Division Leader to steward Center for Human Genome Studies through leadership and mission transition. Work with CHGS, JGI and DOE staff to transition remainder of Chromosome 16 sequencing to Stanford sequencing center and develop capacity for microbial sequence finishing. Develop strategic plan for CHGS that positions capability to contribute to Division missions and integrates capability with related genomics and bioinformatics capabilities in Division. Manage budget, personnel and safety and security. Continue to act as champion for Genomic Science capability and participate as member of B-DO management team. Continue to provide programmatic input on BER and NIH activities. Place strong focus on re-building partnership between JGI-LANL and JGI-Walnut Creek as well as partnership between JGI capability and other capabilities within B Division and LANL. Provide program development and program management leadership and support to LANL staff involved in execution of, or proposals to NIH and DOE Office of Biology and Environmental Research programs. Interact with staff at DOE headquarters and NIH campus on program execution issues. Provide information to LANL staff on programmatic opportunities and drivers in the federal funding domain. Coordinate strategic development activities within B division, act as thrust coordinator for series of B Division strategic thrusts, assist and facilitate thrust leaders in strategic planning and implementation of thrusts.

Los Alamos National Laboratory, Bioscience Division:

Resource Manager, Michelson Resource

May 2000 to Dec 2000

Manage one of four units in 300 person newly formed Bioscience Division. In addition serve as coordinator for Division Strategic Science Thrusts--six specific areas targeted for growth in the 3-5 year timeframe. As RM, principal responsibility is to facilitate science and ensure vitality of Division's science capabilities. Responsibilities include facilitation of core science program development and project execution; act as champion for capability and infrastructure development needs; develop workforce plan for division; management of human resources,

including career development, conflict resolution, communication and formal processes of performance appraisal; line responsibility for budget, safety and security. Roles of Thrust Coordinator include mentoring thrust leaders in program development, steward and integrator of thrust strategic plans, and activities; integration of thrust capability, workforce and infrastructure needs with workforce plan; development of internal information management system to aid thrust leaders in strategic decision-making.

National Science Foundation, Biology Directorate:

Program Director for Computational Biology and Database Activity Programs

Jan 1998 to Jul 2000

Manage Database Activities Program and Computational Biology Program (later merged to become Biological Databases & Informatics Program) in Division of Biological Infrastructure; coordinate peer review process for proposals received to both programs, design public solicitations for proposals, make decisions on appropriate awards totaling ~$10M each year. Participate as bioinformatics point of contact in design, development and execution of cross-foundational funding programs in information technology, e.g. Plant Genome, Knowledge and Distributed Intelligence, Information Technology for the 21st Century (later ITR). Liaise with other funding agencies (DOE, NIH, USDA, NASA) in bioinformatics. Principal, federal, steward for Protein Databank transition. Represent NSF bioinformatics interests on Joint US-EU task force on scientific collaboration.

Los Alamos National Laboratory, LANSCE and Energy Research Program Directorate:
Program Manager for Biology and Environmental Research Programs

Oct 1994 to Jan 1998

Based in Los Alamos directorate responsible for all institutional activities funded by DOE Office of Energy Research: manage a ~$20M portfolio of Los Alamos activities in molecular and cellular biology, microbiology, genomics, bioinformatics, structural biology, chemistry, analytical instrumentation, biotechnology or biomedical technology, as well as applications of atmospheric chemistry and computer modeling in the study of global climate change. Conduct institutional strategic planning for biosciences.

Los Alamos National Laboratory, Theoretical Biology and Biophysics (T-10):

Group Leader (acting)

Jan 1993 to Oct 1994

Lead one of nation's premier theoretical biology research groups consisting of ~70 staff members, post doctoral and graduate students, technicians and clerical staff of diverse scientific backgrounds, including mathematics, biophysics, medicine, computer science, immunology and molecular biology. Administer annual budget of ~$6M, and assist in acquisition of new or continuing funds from NIH, DOE, and DOD. Serve on Sen. P. Domenici task force to design and commission National Center for Genome Resources.

Los Alamos National Laboratory, Theoretical Biology and Biophysics (T-10):
GenBank Staff Member from Nov 1988; Co-PI, Mar 1992-Sep 1994. (re-formulated as DOE-supported GSDB, Aug 1993).

Lead Biology component of and subsequently (as co-director) full operation of the international genetic sequence databank, GenBank. Established vision for turning around a two-year delay between data acquisition and public release to 24hr turnaround based on establishment of direct data submissions paradigm. Develop an external curator program to increase quality and depth of data.

University of Chicago, Ben May Institute:
Postdoctoral Fellow
Dec 1984 to Nov 1988
Work performed under Dr. Geoffrey Greene. Research results include successful isolation, sequencing and expression of human estrogen and progesterone receptor proteins, published in *Science*; development of cell transfection techniques at institute; some experience in cell culture techniques, antibody preparation and application in biomedical diagnostics (hER antibodies currently used in routine breast cancer diagnosis); establishment of a bioinformatics capability at U. Chicago.

University College Galway, Ireland:

Postdoctoral Fellow

Jan 1983 to Jan 1985. (Includes EMBO Short Term Postdoctoral Fellowship at *Laboratoire de Genetic et Molecular Endrocrinologie, Strasbourg, France*. 1984.)

Worked with Prof. Frank Gannon (now head of the European Molecular Biology Organization, EMBO) to learn basic techniques of molecular biology. Development and successful employment of monoclonal antibody based technologies of clone detection in phage lambda libraries. Worked in Prof. Pierre Chambon's labs to develop cDNA cloning in lambda phage vectors.

University College Dublin, Ireland:
Postgraduate Fellow
Oct 1979 to Jan 1983
Completed research work on PhD thesis, "Estrogens, TRH and prolactin secretion in the rat," National University of Ireland (thesis submitted and awarded in 1984).

Honors/Awards/Memberships

- Journal editor for *DNA Sequence*
- Journal Reviewer for Nucleic Acids Research (2008)
- Journal editor for *Genomics*
- Grants reviewer for NSF, DOE (SBIR), DoD-DARPA, DoD-ONR, EJLB Foundation
- DOE Bioenergy Research Centers Review team (2008)
- Member of NSF/OBER review committees for Protein DataBank (PDB)
- Member of task force for National Center for Genome Resources (NCGR)
- Member of DOE/OBER BioInformatics Strategy group
- Member of NIH Office of Scientific Integrity panel on data sharing and release
- Member of CODATA international task group on biological macro-molecules
- Member of LANL-LANSCE/ER BioSciences strategy group
- LANL Distinguished Performance Award-Genbank Team, 1992

- ComputerWorld/Smithsonian Inst. Award (GenBank), 1992
- Member of US-EU Task Force on Biotechnology Research, 1998-2000
- Member of DOE/OBER Bioinformatics Proposal Peer-Review Panel, 2001
- Member of The Arabidopsis Information Resource (TAIR) Advisory Body
- Member of the NIH/NCRR National Biomedical Computation Resource Advisory Body, UC San Diego
- Member of NSF Plant Genome project Site Review Committee 2000-2004
- Member, NSF Information Technology Research (ITR) Proposal Review Panel, 2002
- Member, NSF Biological Databases and Informatics (BDI) Proposal Review Panel, 2000, 2001, 2002
- Member, DOE Biology and Environmental Research Advisory Committee (BERAC), Sub-committee on BioDefense (June 2002)
- Member, National Academy Review panel on Data Release Policy, 2004

REPRESENTATIVE PUBLICATIONS

Gilna, P. (1984). Ph.D. Thesis: Estrogens, TRH and prolactin secretion in the rat. National University of Ireland.

Gilna, P., Collins, D., Greene, G.L. and Gannon, F. (1984). A strategy for the cloning of the human estrogen receptor gene: optimization of an immunodetection system for use in the screening of a cDNA library. *Biochem Soc Trans*, **12**:486.

Gannon, F., Jeltsch, J.M., Bloch, J., Krust, A., Garnier, J.M., Bornert, J.M. and Gilna, P. (1986). Characterization of the expression of conalbumin and ovalbumin sequences cloned into the PstI site of pBR322. *Ann NY Acad Sci*, **469**:18.

Greene, G.L., Gilna, P., Waterfield, M., Baker, A., Hort, Y. and Shine, J. (1986). Sequence and expression of human estrogen receptor complementary DNA. *Science*, **231**:1150.

Gilna, P. and Martin, F. (1986). The effect of oestriol and tamoxifen on oestradiol induced prolactin secretion in anaesthetised rats. *Acta Endocrinol*, **112**:71.

Burks, C., *et al.* (1989). GenBank: Current status and future directions. *Methods Enzymol*, **183**:3.

Gilna, P., Tomlinson, L. J., and Burks, C. (1989). Submission of nucleotide sequence data to GenBank. *J Gen Microbiol*, **135**:1779.

Greene, G. L., Gilna, P., and Kuschner, G. (1989). Estrogen and progesterone receptor analysis and action in breast cancer. In: Breast Cancer Immunodiagnosis and Immunotherapy (R. L. Ceriani, Editor). New York: Plenum.

Greene, G.L., Bettuzzi, and Gilna, P. (1989). Molecular aspects of estrogen and progesterone receptor structure and function in breast cancer. *Proc Am Assoc Can Res*, **30**:656.

Bettuzzi, S., Hiipakka, R. A., Gilna, P., and Liao, S. T. (1989). Identification of an androgen repressed mRNA in rat ventral prostate as coding for sulfated glycoprotein 2 by cDNA cloning and sequence analysis. *Biochem J*, **257**:293.

Burks, C., Cassidy, M., Cinkosky, M.J., Cumella, K.E., Gilna, P., Hayden, J. E-D., Keen G.M., Kelley T.A., Kristofferson, D., Ryals, J. (1991). GenBank. *Nucleic Acids Res*, **19**:2221-2225.

Cinkosky, M.J., Fickett, J.W., Gilna, P., and Burks, C. (1991). Electronic Data Publishing and GenBank. *Science*, **252**(5010) 1273-1277.

Burks, C., Cinkosky, M.J., and Gilna, P. (1992). Decades of Nonlinearity: The Growth of DNA Sequence Data. *Los Alamos Science*, **20**:254-257.

Cinkosky, M.J., Fickett, J.W., Gilna, P., and Burks, C. (1992). Electronic Data Publishing in GenBank. *Los Alamos Science*, **20**:270.

Burks, C., Cinkosky, M.J., Fischer, W.M., Gilna, Paul, Hayden, J. E-D., Keen G.M., Kelley, T.A., Kristofferson, D., Lawrence, J. (1992). GenBank. *Nucleic Acids Res*, **20**:2065-2069.

Martin, J.; Han, *et al.* (2004). The sequence and analysis of Duplication-rich human chromosome 16. *Nature* 432, 988-994.

Han, C. *et al*. (2006). Pathogenomic Sequence Analysis of Bacillus cereus and Bacillus thuringiensis Isolates Closely Related to Bacillus anthracis. *J Bacteriol*, Vol. 188(9) 3382-3390.

Maeder, D.L. *et al.* (2006). The Methanosarcina barkeri Genome: Comparative Analysis with Methanosarcina acetivorans and Methanosarcina mazei Reveals Extensive Rearrangement within Methanosarcinal Genomes, *J Bacteriol*, Vol. 188(22) 7922-7931.

Challacomb, J.F., *et al.* (2007). The Complete Genome Sequence of Bacillus thuringensis AL Hakam. *J Bacteriol*, Vol. 189(9) 3680-3681.

Beckstrom-Sternberg S.M., Auerbach R.K., Godbole S., Pearson J.V., Beckstrom-Sternberg J.S., *et al*. (2007). Complete Genomic Characterization of a Pathogenic A.II Strain of *Francisella tularensis* Subspecies *tularensis*. *PLoS ONE* 2(9): e947. doi:10.1371/journal.pone.0000947

Seshadri, R., Kravitz ,S.A., Smarr, L., Gilna, P., Frazier, M. (2007). CAMERA: A Community Resource for Metagenomics *PLoS Biol* 5(3): e75.

Xie, G. *et al*. (2007). Genome Sequence of the Cellulolytic Gliding Bacterium Cytophaga hutchinsonii. *Appl Environ Microbiol*, Vol. 73(11) 3536-3546.

Chistoserdova, L. *et al*. (2007). Genome of Methylobacillus flagellatus, Molecular Basis for Obligate Methylotrophy, and Polyphyletic Origin of Methylotrophy. *J Bacteriol*, Vol. 189(11) 4020-4027.

Beckstrom-Sternberg, S.M. *et al*., (2007). Complete Genomic Characterization of a Pathogenic A.II Strain of Francisella tularensis Subspecies tularensis. *PLoS ONE*, 2(9): e947.

Gilbert, J. *et al*., (2008). Detection of Large Numbers of Novel Sequences in the Metatranscriptomes of Complex Marine Microbial Communities. *PLoS ONE*, 3(8): e3042.

Smarr, L. *et al*., (2009). Building an OptIPlanet collaboratory to support microbial

metagenomics. *Future Generation Computer Systems*, 25(2) 124-131.

Huang, Y., Gilna, P., Li, W. (2009). Identification of ribosomal RNA genes in metagenomic fragments**.** *Bioinformatics*, Vol. 25(10) 1338-1340.

Brown, S.D., Klingeman, D.M., Johnson, C.M., Clum, A., Aerts, A., Salamov, A., Sharma, A., Zane, M., Barry, K., Grigoriev, I.V., Davison, B.D., Lynd, L.R., Gilna, P., Hau, H., Hogsett, D.A., Froehlich, A.C., (2013). Genome sequences of industrially relevant Saccharomyces cerevisiae Strain M3707, isolated from a sample of distillers yeast and four haploid derivatives. *Genome Announcements*, 1(3).

Gilna, P. (2013). Cellulosic Biofuels. *Science Omega Review Europe* **02**:84-85, 2013.

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Kyrpides, N.C., et al., (2014). Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. *PLOS ONE*, 12(8):e1001920.