David C. Schwartz, Professor

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1999- Present	Professor of Chemistry, Professor of Genetics; University of Wisconsin-Madison, USA
2003-Present	Current & Founding Director; Genomic Sciences Training Program
1989-1999	Assistant/Associate Prof. of Chemistry; Adjunct Assoc. Prof. of Biochemistry, Adjunct Assistant. Prof. of Computer Science; New York University, New York, NY, USA
1985-1989	Staff Associate (PI position) Carnegie Institution of Washington, Dept. of Embryology (John Hopkins University), Baltimore, MD, USA
1985 PhD	Chemistry; Columbia University, New York, NY, USA
1976 BA	Hampshire College, Amherst, MA, USA

Research Interests:

Highly integrated systems for discovery via single molecules, genome fabrication, human/cancer genomics, structural variation, fluidics

Selected Publications:

1. Calle-Casteñeda S., Winden E., Vasquez-Echeverri A., Schickling M., Browning E., Hernandez Ortiz JP, and **Schwartz DC**, Gel-Stacks gently confine or reversibly immobilize arrays of single DNA molecules for manipulation and study, ***Biotechniques,* 2024**, 76(6):285-289.
2. **Schwartz, DC**, Biophysics and the Genomic Sciences, ***Biophysical Journal***, **2019** 3495(19) 30627-7
3. Krerowicz, SJW, Hernandez-Ortiz, JP, and **Schwartz, DC,** Microscale Objects via Restructuring of Large, Double-Stranded DNA Molecules. **ACS Appl. Matter Interfaces, 2018** 10(48): 41215-41223
4. Kounovsky-Shafer, K., Hernandez-Ortiz, J.P., Potamousis, K., Tsvid, G., Place, M., Ravindran, P. Jo, K., Zhou, S., Odijk, T., de Pablo, JJ, and **Schwartz, DC,** Electrostatic Confinement and Manipulation of DNA Molecules for Genome Analysis, ***Proc. Nat'l. Acad. Sci. USA***, 2017, Dec 19; 114(51): 13400-13405

5. Gupta, A., Place, M., Goldstein, S., Sarkar, D., Zhou, S., Potamousis, K., Kim, J., Flanagan, C., Li, Y., Newton, M.A., Callander, N.S., Hematti, P., Bresnick, E.H., Ma, J., Asimakopoulos, F., and **Schwartz, DC**, Single molecule analysis reveals widespread structural variation and clonal evolution in multiple myeloma, ***Proc. Nat'l. Acad. Sci. USA, 2015,*** 112 (25): 7689-94
6. Teague, B., Waterman, M.S., Goldstein, S., Potamousis, K., Zhou, S., Reslewic, S., Sarkar, D., Valouev, A., Churas, C., Kidd, J.M., Kohn, S., Runnhein, R., Lamers, C., Forrest, D., Newton, M.A., Eichler, EE, Kent-First, M., Surti, U., Livny, M., and **Schwartz, DC,** High-resolution human genome structure by single molecule analysis. ***Proc. Nat'l. Acad. Sci. USA, 2010***, 107: 10848-10853
7. **Schwartz, DC** and Cantor, CR, Separation of yeast chromosome-sized DNAs by pulsed field gradient gel electrophoresis, ***Cell,*** **1984,** 37: 67-75

"GenSyn": A Cycle for Serial Assembly of Very Large DNA Molecules

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Abstract

The "GenSyn" system provides direct, cell-free, and validated assembly of large DNA constructs, pivotal for applications in synthetic biology and genome engineering. By leveraging the unique properties of large DNA molecules, GenSyn offers a complementary and synergistic approach to traditional cell-based DNA assembly methods. The system comprises: i) solid support binding approaches supporting chemical and enzymatic processes; ii) shear-free fluidic operations; iii) new methods for enhancing hybridization/ligation yields and iv) validations at the single molecule level. The GenSyn devices are designed for gentle fluidic operations supporting assembly and image analysis of large DNA constructs by epifluorescence microscopy. The first step in the GenSyn synthesis cycle is hybridization of DNA molecules to a support featuring oligonucleotides covalently bound to a derivatized glass surface. The hybridization and ligation steps are optimized using physical and chemical manipulations. CRISPR modified large DNAs are used as coupler molecules, supporting GenSyn cycles. Overall cycle performance metrics (coupling yields as a function of cycle number, molecule breakage, reagent retention, timings and enzymatic activity) are assessed in ways that inform and are guided by computer models.