

The Yale Center for Genome Analysis



A Core Research Facility at Yale's West Campus



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The first map of the human genome, announced in 2003 by Craig Venter and Francis Collins, was an astonishing accomplishment, requiring more than a decade of research, a \$3 billion investment, and the work of 900 DNA sequencing machines in laboratories around the world. Today, the Yale Center for Genome Analysis produces the equivalent of more than 3,000 complete human genomes a month, yielding a tremendous volume of information that drives research not only in human biology and medicine, but in every area of the life sciences.

This is indeed the age of genomics. The marriage of high-throughput screening technologies and bioinformatics has created a powerful and expanding paradigm for discovery. Breakthrough technologies are enabling scientists to discern life's patterns—as well as its most minute details—from a growing trove of genomic data, while powerful computational techniques open the resulting data to exacting analysis.

The Yale Center for Genome Analysis, a state-of-the-art DNA sequencing facility located at Yale's West Campus, is one of a small handful of academic laboratories in the nation equipped to support this kind of research at the cutting edge. Offering specialized services to sequence the genes and genomes of humans, animals, plants, and microbes, the Center supports wide-ranging inquiries into genetic functions and their effects. Yale researchers turn to the Center to investigate human evolution, basic cellular functions, the genetic traits of animal species, and the relationships among species in an ecosystem. Most tantalizing, scientists are also exploring the limits of biomedical knowledge for ways to diagnose and treat diseases from Alzheimer's to cancer.

Genome analysis at this scale requires a continuing investment in advanced laboratories, specialized equipment, and highly trained staff. Thanks to the acquisition of the West Campus — with its 434,000 square feet of state-of-the-art laboratory space — these resources are now available to a growing cohort of investigators at Yale and other institutions. The University is determined to sustain and expand these capabilities at the absolute cutting edge. Donor support will play an essential role in this burgeoning enterprise, not only enabling groundbreaking discovery, but also helping to secure Yale's place in the top echelon of research institutions.



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Leading science at the boundaries of disciplines

Yale's strength as a global research institution comes from its ability to mount top-ranking programs of teaching and research not just in one area, but across the physical, biological, engineering, and medical sciences. By connecting all these disciplines to advance the life sciences, Yale researchers are making dramatic progress toward answering some of life's most compelling questions.



The Center for Genome Analysis is an integral part of a larger research pipeline taking shape at West Campus in support of the life sciences, from exploration to translation to application. In addition to the Center for Genome Analysis, Yale has established core facilities for small molecule discovery, analytical chemistry, and computation. Six research institutes are coalescing around the areas of cancer biology, chemical biology, systems biology, nanobiology, energy sciences, and microbial diversity. In summer 2013, the School of Nursing relocated its 450 students, staff, and faculty members to West Campus. And in the future, supporting both the Medical

and Nursing schools, the campus may be home to medical clinics supporting state-of-the-art patient care as well as clinical trials for drug development. These interrelated cores, institutes, and activities are a natural outgrowth of Yale's multidisciplinary research culture, linking wide-ranging science departments and clinical operations.

Indeed, some of today's most exciting discoveries happen at the boundaries of traditional disciplines, blending chemistry with genetics, or biology with engineering. West Campus provides an ideal environment for this collaborative research, with the latest laboratories, equipment, and meeting spaces needed to support a vibrant research community. Already, the Center for Genome Analysis is uniting researchers in the Faculty of Arts and Sciences, the School of Engineering & Applied Science, and the School of Medicine as well as investigators from outside institutions.

Accelerating discovery with high-throughput gene sequencing

Yale has an extraordinary history and strength in the life sciences, spanning basic biology, biomedical engineering, and medicine. Work now under way at labs across the University illustrates the promise of high-throughput sequencing technologies in solving urgent problems, from the environment to the food supply to human health.

Developmental biologist **Timothy Nelson** asks how plants with just a few dozen cell types can organize themselves into robust and complicated structures. The answer, uncovered by genomics techniques, seems to lie in the regulation of gene expression as the plant matures from a seedling. Using similar methods, Nelson also hopes to augment photosynthesis in rice and other plants, developing hardy, fast-growing strains that make more efficient use of water, light, and nitrogen.

Jeffery Townsend combines math, computation, and evolutionary theory to identify mutations in the genome and determine which drive the development of cancer. Analyzing vast volumes of genetic information from tumors screened at the Center for Genome Analysis, he and his colleagues compare the tumors' genetic information to that of normal tissue in the same individual, to the genomes of similar tumors, and finally across cancer types. By determining the genetic architecture of cancer, they hope, they can help identify specific targets for novel therapies.

Geneticist **Richard Lifton** broke new ground with the first clinical diagnosis using comprehensive DNA sequencing of the protein-coding genes in the genome. This work altered the course of treatment for a dehydrated infant, thought to have kidney disease, who actually suffered from congenital diarrhea.



As director of the Center for Genome Analysis, **Dr. Shrikant Mane** leads a scientific staff of twenty-two in an effort to make highly specialized research tools available across the University. The Center is equipped with eleven high-throughput gene sequencers and a broad spectrum of microarray platforms to measure gene expression. It also boasts high-performance capabilities in computing, which are essential to warehouse and analyze the massive amounts of data generated in genome analysis. Working closely with faculty to design experiments and to analyze the findings, Mane and his team help scientists achieve the greatest impact from their work. To date, he has collaborated on projects that seek the genetic basis of autism and age-related macular degeneration; help test novel ways to repair the central nervous system; explore genes crucial to the evolution of the human brain; and look for genes involved in asthma, schizophrenia, cancer, hypertension, cardiovascular disorders, bipolar disease, kidney disease, and brain aneurysms.

Mane's work is facilitated by his many deep connections and leadership roles across campus. He is co-director of the Keck Biotechnology Resource Laboratory; director of Microarray, DNA Sequencing, and Oligonucleotide Synthesis at Keck; and one of the PIs of the Yale/National Institutes of Health Center for Mendelian Genomics.



James Noonan explores the genomic basis of what makes humans distinct from other species, and his work with gene regulatory regions is shedding new light on human diseases that have a developmental component. He has also collaborated on some of the first human-to-human genome comparisons in an effort to uncover the root causes of autism.

Through millions of years of evolution, microbes have been wildly inventive in making novel chemical compounds they can use to solve the problems posed by their environment. Biologist **Scott Strobel** hopes to apply the best of these solutions to problems facing humans today. Working with never-before-studied fungi from tropical rainforests, Strobel uses whole genome sequencing to understand his specimens – including fungi that produce volatile organic

compounds, or biofuels. Strobel is optimistic that the organisms' unusual biosynthetic pathways can be mimicked as a viable means of biofuel production.

Not content to map the genomes of a few model organisms, like *E. coli* or the mouse, **Michael Donoghue** explores life's genetic diversity among species and whole ecosystems. By comparing the DNA from plants and animals around the world and through time, Donoghue and his colleagues aim to expand our understanding of the tree of life and the mechanics of its evolution.

Jo Handelsman also takes a big-picture view as a pioneer of metagenomics, an emerging discipline that looks at the diversity of genes found in specimens across a whole ecosystem. Opening a window on a vast microbial world that was previously inaccessible, metagenomics has both theoretical and practical applications, allowing Handelsman to look for new antibiotics, for example, or to explore the genetic basis of antibiotic resistance.



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To learn more

For more information about Yale's West Campus, please visit:
www.yale.edu/westcampus

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Michael Marsland: inside back cover

Yale's West Campus is an ideal setting to connect the high-throughput sequencing of genes and genomes to new discoveries in every area of the life sciences.



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