aim at both GPCRs and other molecular targets. "We also need to identify those individuals who, based on their tumor’s molecular profile, are most likely to respond to these therapeutic combinations," says Grandis.

Learning even more about GPCR structure is "one key to developing more effective cancer drugs," says Benovic, who worked with Kobilka in the Lefkowitz lab in the 1980s. Many GPCRs, including CXCR4, normally activate signaling through both G-protein-dependent and arrestin-dependent pathways, but certain ligands can selectively trigger a particular pathway. These biased ligands, he says, may prove to be more effective drugs.

**Privacy Protection in Whole-Genome Sequencing**

Scientists, physicians, and ethicists alike agree that current laws and regulations don’t offer sufficient privacy protection for the vast amounts of personal data now available through whole-genome sequencing (WGS). To address this issue, the Presidential Commission for the Study of Bioethical Issues recently released a 154-page report, *Privacy and Progress in Whole Genome Sequencing*, which lays out a number of recommendations to improve present practices.

The report recommends strong protection of whole-genome data and data security while maintaining data-sharing opportunities to advance research. A primary facet of these protections focuses on individuals, who should be assured that medical professionals will consider their needs. To that end, the commission advises “robust and understandable informed consent procedures,” noting that WGS findings will likely reveal information that has implications for the future health of each patient and his or her relatives.

The second aspect of privacy protection is in information technology, which should be tailored to protect sensitive biomedical information, given the public’s concern about identify theft and other forms of information misuse. The final facet is policy-level protection, meaning that institutions should have a system in place for secure handling of WGS data.

Cancer geneticist Charis Eng, MD, PhD, chair and founding director of the Genomic Medicine Institute of the Cleveland Clinic Foundation, praises the discussions around privacy and security detailed in the report. However, she notes that it doesn’t specifically address genetic counseling, which is vital when it comes to disclosing sensitive information.

As she points out, genetic information specific to a study’s goals is shared with patients. But what about incidental findings? “When we ask patients if they want to know everything, most of them don’t,” says Eng. “But if we find something that is life threatening, like a **BRCA1** mutation, we are obligated to tell them.” That’s the type of information that should be delivered to a patient by a genetic counselor—but kept secure and private from others, says Eng.

**NIH Boosts Single-Cell Analysis Tools**

Until recently, scientists were limited in their ability to study individual cells, including those that might drive tumor growth. Now converging advances in high-throughput sequencing, proteomics, molecular imaging, and other technologies make it increasingly possible to investigate single cells in their native microenvironments.

In October, the NIH announced a plan to invest $90 million in the Single Cell Analysis Program (SCAP), funding short- and long-term research aimed at developing the tools and methods scientists need to study individual cells in cancer and other biologic contexts.

“The goal is to help scientists answer questions about how single cells behave and interact with a lot more precision than they have now,” says Jennifer Couch, PhD, chief of the Structural Biology and Molecular Applications Branch in the Division of Cancer Biology at the National Cancer Institute (NCI).

Promising technologies supported by the program, Couch says, include new types of reverse transcription polymerase chain reaction that reveal the influence of morphology on gene expression in individual cells within intact tissues; new sensors that detect intra- and extracellular variations in acidity, which can affect tumor growth; a technology that tracks the immune response of single cells in live animals; an automated high-throughput assay for predicting the metastatic and drug response potential of pancreatic cancer cells; and a high-throughput assay for looking at the genetic heterogeneity of single cancer cells in tissue.

According to Couch, these SCAP efforts generate entirely new views of cell heterogeneity. “They mark a significant advance from studies of isolated cells or measurements in bulk tissues,” she says. “Cells express genes differently when they’re in their native environment than they do when they’re in cultures. With these approaches, we’ll be able to build more accurate signaling networks and get to a better understanding of how cells communicate with each other.”

While the SCAP applies to a range of disciplines, Couch and her NCI colleague Randy Knowlton, PhD, a program director also in the Division of Cancer Biology, note that the emerging technologies are often applied first to studies of cancer, many with clear clinical promise.

For more news on cancer research, visit Cancer Discovery online at http://CDnews.aacrjournals.org.