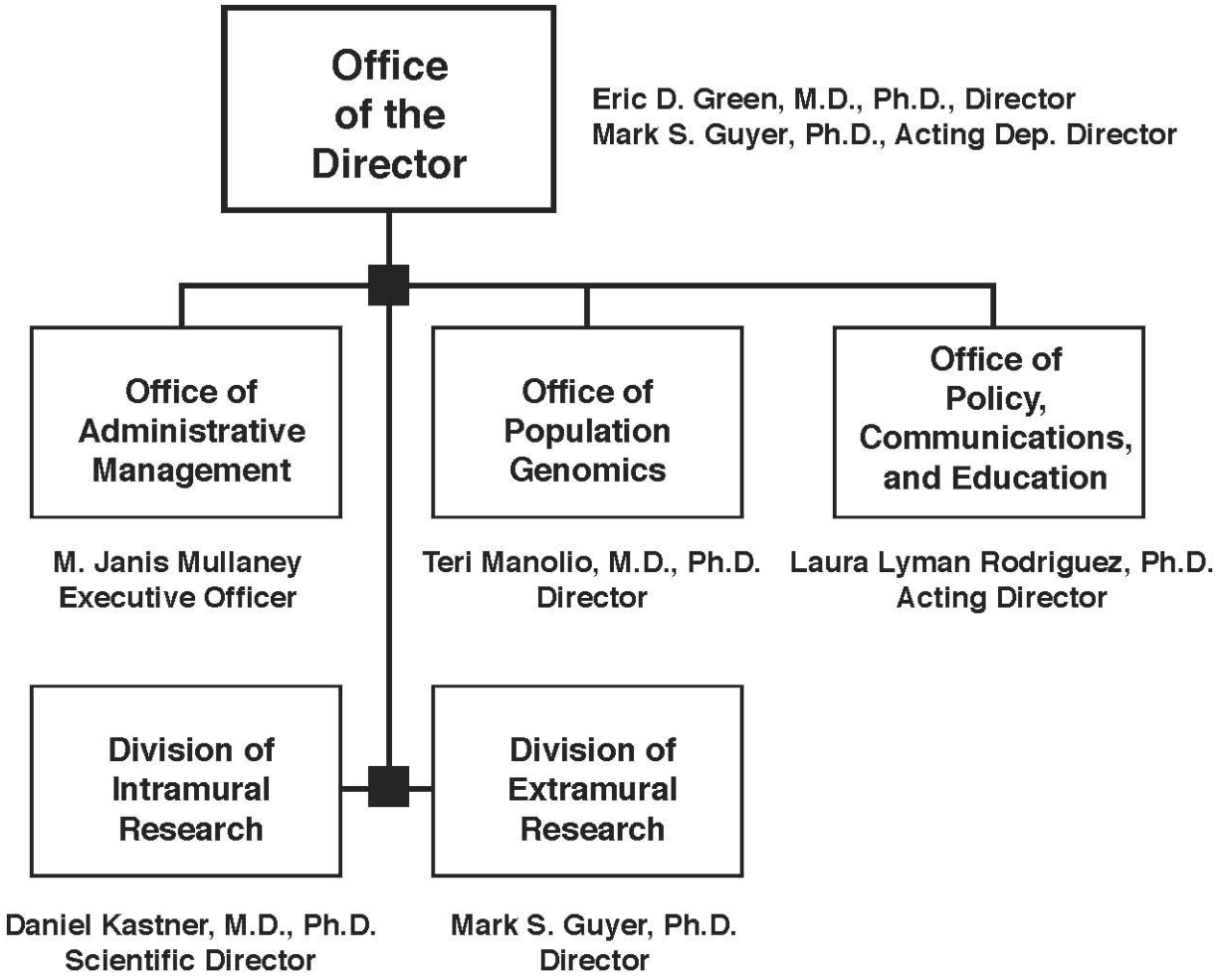
DEPARTMENT OF HEALTH AND HUMAN SERVICES

NATIONAL INSTITUTES OF HEALTH

National Human Genome Research Institute

FY 2012 Budget Page No.

NATIONAL HUMAN GENOME RESEARCH INSTITUTE
Organizational Structure



NATIONAL INSTITUTES OF HEALTH

National Human Genome Research Institute

For carrying out section 301 and title IV of the Public Health Services Act with respect to human genome research $524,807,000.

NATIONAL INSTITUTES OF HEALTH
National Human Genome Research Institute

Amounts Available for Obligation [1]
(Dollars in Thousands)

Source of Funding	FY 2010 Actual	FY 2011 CR	FY 2012 PB
Appropriation	516,028	516,028	524,807
Type 1 Diabetes	0	0	0
Rescission	0	0	0
Supplemental	0	0	0
Subtotal, adjusted appropriation	516,028	516,028	524,807
Real transfer under Director's one-percent transfer authority (GEI)	8,192	0	0
Real transfer under Secretary's one-percent transfer authority	(77)	0	0
Comparative Transfers to NLM for NCBI and Public Access	(152)	(439)	0
Comparative transfer under Director's one-percent transfer authority (GEI)	(8,192)	0	0
Comparative transfer under Secretary's one-percent transfer authority		0	0
Subtotal, adjusted budget authority	515,799	515,589	524,807
Unobligated balance, start of year	0	0	0
Unobligated balance, end of year	0	0	0
Subtotal, adjusted budget authority	515,799	515,589	524,807
Unobligated balance lapsing	(12)	0	0
Total obligations	515,787	515,589	524,807

[1] Excludes the following amounts for reimbursable activities carried out by this account:
FY 2010 - $62,595 FY 2011 - $63,002 FY 2012 - $90,073
Excludes $117 in FY 2010, $171 in FY 2011, and $145 in FY 2012 for royalties.

NATIONAL INSTITUTES OF HEALTH

National Human Genome Research Institute

Budget Mechanism - Total [1/]

(Dollars in Thousands)

MECHANISM	FY 2010 Actual		FY 2011 CR		FY 2012 PB		Change vs. FY 2010	
	No.	Amount	No.	Amount	No.	Amount	No.	Amount
Research Grants								
Research Projects								
Noncompeting	156	$106,696	141	$79,090	155	$81,456	(1)	($25,240)
Administrative Supplements	*19*	6,267	*26*	21,106	*26*	20,660	*7*	14,393
Competing:								
Renewal	15	10,579	19	13,720	19	13,546	4	2,967
New	55	19,178	70	24,871	68	24,555	13	5,377
Supplements	0	0	0	0	0	0	0	0
Subtotal, Competing	70	$29,757	89	$38,591	87	$38,101	17	$8,344
Subtotal, RPGs	226	$142,720	230	$138,787	242	$140,217	16	($2,503)
SBIR/STTR	29	$10,962	23	$10,564	23	$10,763	(6)	($199)
Research Project Grants	255	$153,682	253	$149,351	265	$150,980	10	($2,702)
Research Centers								
Specialized/Comprehensive	27	$163,722	32	$168,647	32	$170,333	5	$6,611
Clinical Research	0	1,242	0	0	0	0	0	(1,242)
Biotechnology	20	40,408	15	37,040	15	37,410	(5)	(2,998)
Comparative Medicine	0	0	0	0	0	0	0	0
Research Centers in Minority Institutions	0	700	0	0	0	0	0	(700)
Research Centers	47	$206,072	47	$205,687	47	$207,743	0	$1,671
Other Research								
Research Careers	4	$623	4	$620	4	$626	0	$3
Cancer Education	0	0	0	0	0	0	0	0
Cooperative Clinical Research	0	0	0	0	0	0	0	0
Biomedical Research Support	0	0	0	0	0	0	0	0
Minority Biomedical Research Support	0	0	0	0	0	0	0	0
Other	15	922	25	1,587	25	1,603	10	681
Other Research	19	$1,545	29	$2,207	29	$2,229	10	$684
Total Research Grants	321	$361,299	329	$357,245	341	$360,952	20	($347)
Research Training	FTTPs		FTTPs		FTTPs			
Individual Awards	12	$549	17	$904	17	$936	5	$387
Institutional Awards	166	8,044	171	8,304	171	8,595	5	551
Total Research Training	178	$8,593	188	$9,208	188	$9,531	10	$938
Research & Development Contracts	11	$16,829	12	$19,560	12	$23,453	1	$6,624
(SBIR/STTR)	*0*	*$21*	*0*	*$21*	*0*	*$21*	*0*	*$0*
	FTEs		FTEs		FTEs		FTEs	
Intramural Research	255	$104,140	256	$104,140	256	$105,181	1	$1,041
Research Management and Support	83	24,938	84	25,436	84	25,690	1	752
Construction		0		0		0		0
Buildings and Facilities		0		0		0		0
Total, NHGRI	338	$515,799	340	$515,589	340	$524,807	2	$9,008

1/ All items in italics are "non-adds"; items in parenthesis are subtractions

Major Changes in Fiscal Year 2012 Budget Request

Major changes by budget mechanism and/or budget activity detail are briefly described below. Note that there may be overlap between budget mechanism and activity detail and these highlights will not sum to the total change for the FY 2012 budget request for NHGRI, which is $9.0 million more than the FY 2010 Actual, for a total of $524.8 million.

Medical Sequencing (+$4.7 million; total $71.0 million): Translating the fruits of the Human Genome Project into medical practice remains a high priority for NHGRI and NIH. Combined with ever-decreasing sequencing costs, the additional $4.734 million provided will increase the proportion of the Institute's sequencing program to support new opportunities to apply genomic tools to the study of human disease.

Large-scale Sequencing (Non-Medical) (-$3.1 million; total $11.9 million): This decrease in non-medical sequencing represents a continuing reprioritization of research funding at NHGRI towards clinical applications of genomic research. The decrease is balanced both by an increase in medical sequencing as well as ever-decreasing sequencing costs.

NATIONAL INSTITUTES OF HEALTH
National Human Genome Research Institute
Summary of Changes
(Dollars in Thousands)

FY 2010 Actual				**$515,799**
FY 2012 Estimate				**524,807**
Net change				**$9,008**
	2012 Estimate		**Change from FY 2010**	
CHANGES	**FTEs**	**Budget Authority**	**FTEs**	**Budget Authority**
A. Built-in:				
1. Intramural Research:				
a. Annualization of January 2010 pay increase		$34,895		$210
b. January FY 2012 pay increase		34,895		0
c. One less day of pay (n/a for 2011)		34,895		(135)
d. Payment for centrally furnished services		16,361		165
e. Increased cost of laboratory supplies, materials, and other expenses		53,925		527
Subtotal				$767
2. Research Management and Support:				
a. Annualization of January 2010 pay increase		$11,007		$66
b. January FY 2012 pay increase		11,007		0
c. One less day of pay (n/a for 2011)		11,007		(42)
d. Payment for centrally furnished services		791		11
e. Increased cost of laboratory supplies, materials, and other expenses		13,892		133
Subtotal				$168
Subtotal, Built-in				$935

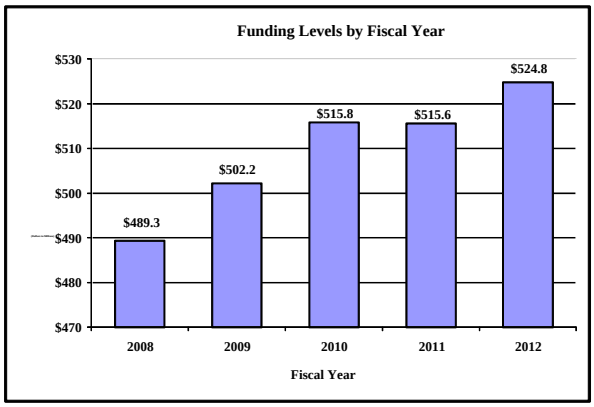
NATIONAL INSTITUTES OF HEALTH
National Human Genome Research Institute

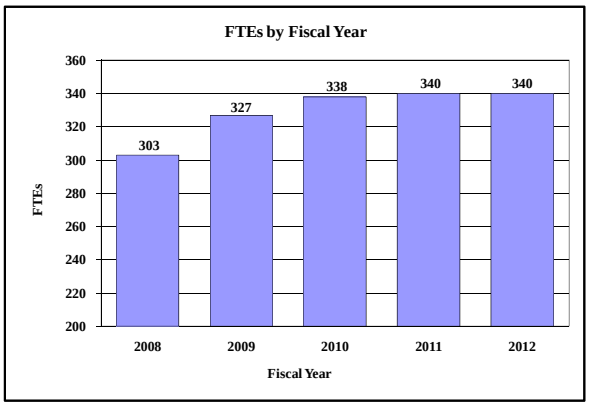
Summary of Changes--continued

CHANGES	2012 Estimate		Change from FY 2010	
	No.	**Amount**	**No.**	**Amount**
B. Program:				
1. Research Project Grants:				
a. Noncompeting	155	$102,116	(1)	($10,847)
b. Competing	87	38,101	17	8,344
c. SBIR/STTR	23	10,763	(6)	(199)
Total	265	$150,980	10	($2,702)
2. Research Centers	47	$207,743	0	$1,671
3. Other Research	29	2,229	10	684
4. Research Training	188	9,531	10	938
5. Research and development contracts	12	23,453	1	6,624
Subtotal, Extramural		$242,956		$9,917
	FTEs		FTEs	
6. Intramural Research	256	$105,181	1	$274
7. Research Management and Support	84	25,690	1	584
8. Construction		0		0
9. Buildings and Facilities		0		0
Subtotal, program		524,807		$8,073
Total changes	340		2	$9,008

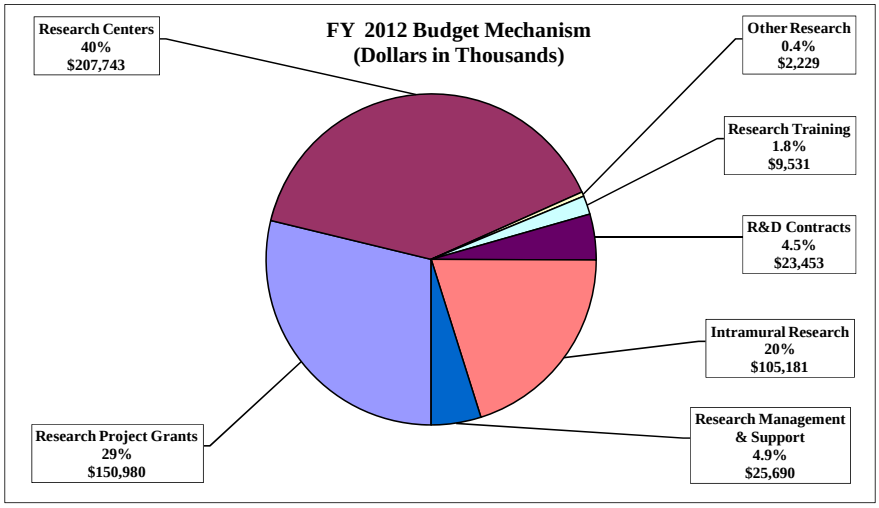
Budget Graphs

History of Budget Authority and FTEs:

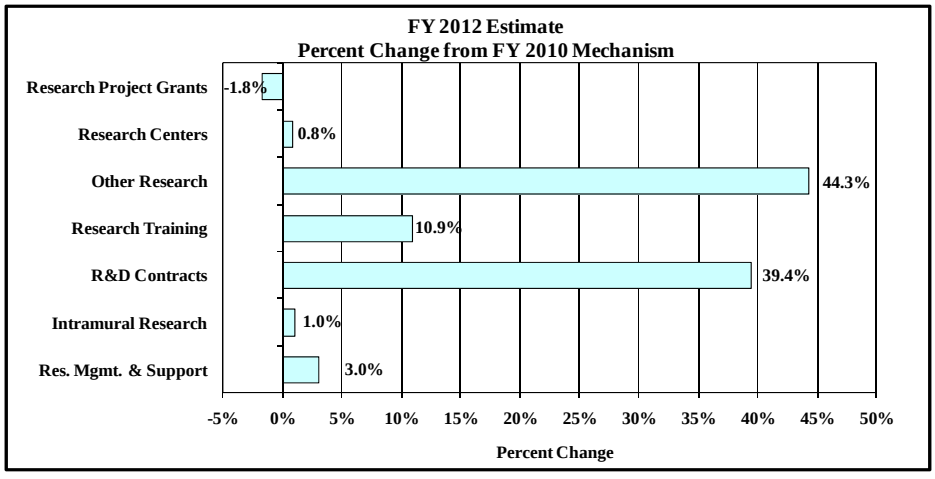




Distribution by Mechanism:



Change by Selected Mechanism:



NATIONAL INSTITUTES OF HEALTH
National Human Genome Research Institute
Budget Authority by Activity
(Dollars in thousands)

	FY 2010 Actual		FY 2011 CR		FY 2012 PB		Change vs. FY 2010	
Extramural Research	**FTEs**	**Amount**	**FTEs**	**Amount**	**FTEs**	**Amount**	**FTEs**	**Amount**
Detail:								
Basic Genomics								
Large-scale Sequencing								
Comparative Genomic Sequencing		$15,066		$15,066		$11,934		-$3,132
Medical Sequencing		66,246		66,246		70,980		4,734
The Cancer Genome Atlas		34,111		34,111		34,783		672
Genomic Function		55,554		55,554		56,648		1,094
Genomic Variation		20,328		20,328		20,728		400
Computational Genomics		49,260		49,260		50,230		970
Technology Development		43,699		43,699		44,560		861
Other Basic Genomics		62,111		61,403		62,931		820
Translational Genomics		21,581		21,581		22,006		425
ELSI		18,765		18,765		19,135		370
Subtotal, Extramural		$386,721		$386,013		$393,936		$7,215
Intramural Research	255	$104,140	256	$104,140	256	$105,181	1	$1,041
Research Management & Support	83	$24,938	84	$25,436	84	$25,690	1	$752
TOTAL	338	$515,799	340	$515,589	340	$524,807	2	$9,008

NATIONAL INSTITUTES OF HEALTH
National Human Genome Research Institute

Authorizing Legislation

	PHS Act/ Other Citation	U.S. Code Citation	2011 Amount Authorized	FY 2010 Estimate	2012 Amount Authorized	FY 2012 PB
Research and Investigation	Section 301	42§241	Indefinite	$515,799,000	Indefinite	$524,807,000
National Human Genome Research Institute	Section 401(a)	42§281	Indefinite		Indefinite	
Total, Budget Authority				$515,799,000		$524,807,000

NATIONAL INSTITUTES OF HEALTH
National Human Genome Research Institute

Appropriations History

Fiscal Year	Budget Estimate to Congress	House Allowance	Senate Allowance	Appropriation
2003	$458,182,000	$458,182,000	$468,037,000	$468,037,000
Rescission				($3,042,000)
2004	$478,072,000	$478,072,000	$482,372,000	$482,222,000
Rescission				($3,149,000)
2005	$492,670,000	$492,670,000	$496,400,000	$492,670,000
Rescission				($4,062,000)
2006	$490,959,000	$490,959,000	$502,804,000	$490,959,000
Rescission				($4,910,000)
2007	$482,942,000	$482,942,000	$486,315,000	$486,491,000
Rescission				$0
2008	$484,436,000	$493,996,000	$497,031,000	$495,434,000
Rescission				($8,655,000)
Supplemental				$2,589,000
2009	$487,878,000	$504,603,000	$501,411,000	$502,367,000
Rescission				$0
2010	$509,594,000	$520,311,000	$511,007,000	$516,028,000
Rescission				$0
2011	$533,959,000		$533,127,000	
Rescission				
2012	$524,807,000			

Justification of Budget Request

National Human Genome Research Institute

Authorizing Legislation: Section 301 and title IV of the Public Health Service Act, as amended.

Budget Authority (BA):

	FY 2010 Actual	FY 2011 Continuing Resolution	FY 2012 Budget Request	FY 2012 + / - FY 2010
BA	$515,799,000	$515,589,000	$524,807,000	+$9,008,000
FTE	338	340	340	+2

Program funds are allocated as follows: Competitive Grants/Cooperative Agreements; Contracts; Direct Federal/Intramural and Other.

Director's Overview

In 2010, Dr. Eric Green, the new Director of the National Human Genome Research Institute (NHGRI), concluded an extensive strategic planning process that culminated in the early 2011 publication of a vision for the most cutting-edge opportunities in genomics over the next decade. Building upon a solid foundation of knowledge, the new strategic vision describes a path from the Human Genome Project (HGP) to the development of new diagnostics, therapies, and clinical practices, and the eventual widespread adoption of genomic medicine. Achieving the goals laid out in the strategic plan will involve funding research across a continuum, from basic genomics to the application of genomic medicine to improving human health.

Biology of Genomes: Since completion of the HGP, NHGRI-funded research has moved the field of genomics forward, building upon our understanding of the 'functional parts' of the human genome. The ENCylopedia Of DNA Elements (ENCODE) program is successfully generating a wealth of data about the human genome's functional elements (such as those that turn genes on and off), which are critical for understanding the perturbations in biological pathways that manifest in disease.

New Centers of Excellence in Genome Science will combine cutting-edge genomics research to accelerate discoveries with training programs that focus on traditionally underrepresented groups. These programs are designed to increase multi-disciplinary research and education in the field of genomics, thereby reinvigorating the biomedical research community— both key NIH initiatives (Technologies to Accelerate Discovery, New Investigators, New Ideas).

A consequence of the dramatic increase in DNA sequencing capacity, and the resulting increase in the volume of electronic genomic data generated, is the urgent need for new tools and strategies for managing large amounts of genomic data and for innovative methodologies to analyze large genomic data sets. This need is a high priority for the NHGRI Computational Biology Program, and is consistent with the NIH initiative, "Technologies to Accelerate Discovery." Each human genome consists of 6 billion DNA bases, which is ~200 GB of sequence information per individual. Since there are a large number of participants typically

included in a research study and there are an ever-increasing number of studies that generate genome sequence data, the NHGRI program is actively seeking to address the substantial bottleneck in available computational capacity that represents an acute challenge for the field.

Genomics and Disease: The Cancer Genome Atlas, a project conducted in conjunction with the National Cancer Institute (NCI), is revealing new insights into the biological mechanisms underlying different cancers. NHGRI aims to replicate those successes in the NHGRI Medical Sequencing Program, bringing similar strategies to common, genetically complex diseases as well as rare, genetically simpler diseases. In fact, studies of this kind are already generating exciting results. NHGRI-funded researchers recently sequenced and then compared the genomes of four members of a family in which both children are afflicted with Miller syndrome, a malformation disorder. In this way, the scientists were able to identify the genetic cause of this disease rapidly, something that had eluded research efforts until now. Discovering the genetic causes of these diseases reveals possible avenues for therapies, an important step in translating basic science into new and better treatments— another of NIH's priorities as laid out in the initiative "Re-engineering the Therapeutic Development Pipeline."

The Human Heredity and Health in Africa (H3Africa) Project, funded through the NIH Common Fund, is led by NHGRI scientists, and aims to establish similarly robust projects for studying diseases that are important to people living in Africa and, indirectly, in America. H3Africa will generate extensive data about genetic variation in African populations, where there is greater genetic diversity than anywhere else on the planet, and then facilitate the growth of genomics infrastructure and training to empower local researchers to address health challenges through genomics-based strategies.

Importantly, many NHGRI programs do not just sequence DNA, but also analyze phenotypic and environmental information that is fundamental to understanding genomic data in a broader functional context. In line with NIH initiatives to apply high-throughput technologies (Technologies to Accelerate Discovery) and to increase translational research (Re-engineering the Therapeutic Development Pipeline), the NHGRI-administered NIH Chemical Genomics Center (NCGC) has been partnering with sister agencies such as the U.S. Environmental Protection Agency, providing technical expertise to screen commonly used chemicals for potential health effects; this aids their decision-making processes and their ability to achieve their missions. A concrete example of this has been NCGC working with federal partners in the response to the Gulf oil spill, conducting toxicological analysis on the dispersants in use, and informing EPA and other agencies in their deliberation on safe exposure levels for workers as well as the safety of seafood from the affected area.

Unlike rare diseases, which are more often the result of a mutation(s) in one gene or an area of the genome, common diseases (such as diabetes and cardiovascular disease) are the result of a complex interplay among genes, behavior, and the environment. As such, teasing out the inherited components of common diseases has been extraordinarily challenging; however, research efforts across NHGRI’s portfolio are applying genomic technologies in new and powerful ways to do just that. For instance, the NHGRI ClinSeq program is exploring the clinical strategies that will be needed for widespread medical sequencing. As sequencing costs continue to decrease, these tools will be integrated into clinical care. A vivid example of NIH’s work to apply genomic strategies to translational research questions, ClinSeq recently sequenced the first

whole genome of a patient with cardiovascular disease, revealing the cause of his family's history of heart disease.

Genomics and Medicine: While full deployment of genomic medicine is one of the key longer-term goals for genomics and NHGRI, work in this area already is beginning to have an effect in the clinic. For instance, pharmacogenomic strategies are now being used in the treatment of cancer. Testing breast cancer patients for *Her2* gene mutations or colorectal cancer patients for *KRAS* gene mutations to establish whether a particular drug will be effective are examples of effective genomic-based clinical steps that are already saving patients' lives. This also obviates the need for costly but ineffective drug treatments, which supports the NIH initiative "Enhancing the Evidence Base for Health Care Decisions" to use science to inform healthcare cost analyses.

Genomics and Clinical Care: Ultimately, informing clinical care using genomics is the central long-term goal of NHGRI, and research efforts in this area are already being pursued. The Electronic Medical Records and Genomics (eMERGE) Network is a multi-center effort to combine genomic techniques and electronic medical records to improve patient care. The emphasis now is on translating scientific findings from genome-wide association studies into new and better treatments for disease, but the lessons learned will be applicable to implementing genomic medicine down the road, aiding NIH in its goal of using science to enable healthcare reform ("Enhancing the Evidence Base for Health Care Decisions").

Full realization of the potential of genomic medicine will require a multi-pronged approach that includes not only basic science advances, but also health applications research, the education of health professionals and the public, and the continued engagement with issues relevant to society through our Ethical, Legal, and Social Implications (ELSI) program. NHGRI's programs described above, as well as our other innovative basic, translational, clinical, and educational efforts, will all be leveraged to ensure that the promise of genomic medicine can and will benefit the health of the nation.

Overall Budget Policy: The FY 2012 request for NHGRI is $524.8 million, an increase of $9.0 million or +1.8 percent over the FY 2010 Actual level. NHGRI is increasing funding for Medical Sequencing while proportionally decreasing funding for Comparative Genomics Sequencing. This will allow NHGRI to devote a larger proportion of the overall large-scale sequencing effort in FY 2012 to projects directed toward understanding disease.

Funds are included in R&D contracts to reflect NHGRI's share of NIH-wide funding required to support several trans-NIH initiatives, such as the Therapies for Rare and Neglected Diseases program, the Basic Behavioral and Social Sciences Opportunity Network (OppNet), and support for a new synchrotron at the Brookhaven National Laboratory. For example, each IC that will benefit from the new synchrotron will provide funding to total NIH's commitment to support this new technology--$10 million. NIH will provide an increase of four percent for stipends levels under the Ruth L. Kirschstein National Research Service Award training program to continue efforts to attain the stipend levels recommended by the National Academy of Sciences. This will build on the two percent increase in stipend levels for FY 2011. Stipend levels were largely flat for several years, and the requested increase will help to sustain the development of a highly qualified biomedical research workforce.

Program Descriptions and Accomplishments

Comparative Genome Sequencing: NHGRI's comparative genome sequencing program performs genome sequencing on many different organisms to better our understanding of how the human genome functions. By comparing the genome sequences of humans with those of both closely and distantly related organisms, we are able to identify regions of similarity and difference. Such studies reveal regions of the genome that have been preserved throughout evolution, inferring that these regions serve critical biological functions. Conversely, rigorous study of regions that have changed substantially during evolution can reveal sequences that confer human-specific functions. This work provides insights about the structure, function, and evolution of human genes and can point to new paths for combating human disease. Currently, the genomes of more than 200 organisms either have been sequenced or are being sequenced using NHGRI funding. Among these include livestock such as the cow and chicken genomes, data from which can have a direct benefit to food production and food safety. Ongoing sequencing targets include non-human primates and other mammals; fungi, including multiple strains of yeast; and other disease-causing organisms, such as parasites and their host vectors. NHGRI funds this work largely through three major sequencing centers that are world renowned for their cost-effective, high-quality work.

Budget Policy: The FY 2012 budget estimate for Comparative Genomic Sequencing is $11.9 million, a decrease of $3.1 million or 20.8 percent below the FY 2010 Actual level. The activity in Comparative Genomic Sequencing will continue NHGRI's signature efforts to generate the genomic sequence data from many sources. These data represent a key resource that, along with other data sets such as those from the ENCODE and modENCODE projects (see below), are needed to reveal the functional components of the human genome. However, as the sequences of additional organisms accumulate, NHGRI needs to add fewer new ones. This allows the Institute to continue its on-going reprioritization and expand the Medical Sequencing and The Cancer Genome Atlas components of the NHGRI large-scale sequencing program (see below). The total amount of NHGRI spending on large-scale sequencing will remain constant. The reprioritization will allow the Institute to devote a larger proportion of the overall large-scale sequencing effort in FY 2012 to projects directed toward understanding disease.

Medical Sequencing: Initiated in 2006, NHGRI's medical sequencing program funds the application of new DNA sequencing technologies in clinical settings, in order to gain a more complete understanding of the genetics and genomics of human diseases. The medical sequencing program supports a number of studies to identify the genes responsible for relatively rare disorders and to identify genetic variants associated with a range of common diseases, including diabetes, breast cancer, cardiovascular disease, schizophrenia, and autism. Some of these projects are being done in collaboration with other NIH institutes. In FY2012, the NHGRI sequencing program will add two new projects, one focused on single gene disorders (Mendelian Disorders Genome Centers) and one on the use of genomic sequencing in the clinic (Clinical Sequencing Exploratory Research Projects).

Budget Policy: The FY 2012 budget estimate for Medical Sequencing is $71.0 million, an increase of $4.7 million or 7.1 percent over the FY 2010 Actual level. Medical sequencing continues to be an area of growth for NHGRI. With large-scale sequencing now completely transitioned to the next-generation sequencing instruments, many new opportunities have been

created to apply genomic tools to the study of human disease and the application of that information to the development of new approaches to disease management. In FY 2012, NHGRI will continue to increase the proportion of its Large-Scale Sequencing program funds that support the Medical Sequencing component, and initiate new aspects of medical sequencing. Many of the new opportunities will be pursued in collaboration with other NIH ICs.

Portrait of a Program: Medical Sequencing

FY 2010 Level: [$66.3 million]
FY 2012 Level: [$71.0 million]

Change: [+$4.7 million]

Having sequenced the human genome (and the genomes of a number of other organisms to aid in understanding how the human genome sequence confers functional information), NHGRI is intensifying its focus on applying DNA sequencing to elucidate the genomic basis of human disease. While approaches vary, this is, in general, accomplished by obtaining and comparing sequence information from many (sometimes thousands) of individuals with and without a disease (e.g., Alzheimer's, autism, and cardiovascular disease), and looking for sequence differences (or variants) that correlate with that disease. Though the variants usually do not directly reveal the underlying cause of the disease, they do provide significant clues about the gene(s) that could be involved, and provide significant direction for follow-up study. As a group, such studies provide basic information about important questions, such as whether variants for common disease are more likely to reside in genes or outside of genes (e.g., regulatory sequence), or whether the frequency of a disease in the population is due to many different rare variants in the same gene or pathway or to fewer more common variants.

The opportunity for extremely productive medical sequencing projects is now provided by the significant gains in sequencing efficiency (lower cost) that have occurred over the last five years, and the development of computational infrastructure and analysis methods that can handle the massive amounts of sequence data being generated by such studies. Both the technology and the informatics/analysis development are far from optimized at this point, and a significant aim of the medical sequencing program is to drive their ongoing optimization so that such studies become more routine and efficient.

NHGRI is pursuing this opportunity in three ways. Additional medical sequencing targets are being added to the large-scale genome sequencing program, joining those already ongoing in autism, diabetes/metabolic disease, cancer, cardiovascular disease, macular degeneration, and several other diseases. In 2011 two significant initiatives will begin: one focused on rare disease (aimed at setting up a program for more efficiently identifying the molecular basis for all such disorders) and another focused on applying genome sequencing to clinical practice, the latter is important both for improving our understanding of genetic disease and for establishing genome sequencing as a routine clinical tool.

The Cancer Genome Atlas: All cancers are diseases of the genome, as they result from DNA mutations and epigenetic changes that lead to uncontrolled cell growth. The Cancer Genome Atlas (TCGA) is a collaborative program of NHGRI and the National Cancer Institute to develop a comprehensive catalog of the many genomic alterations that occur in each major type of cancer and to provide these data rapidly to the research community. Taking advantage of recent advances in technologies for studying genomes (in particular sequencing genomes), tumor and matched normal tissue samples can be analyzed for gene mutations, chromosomal rearrangements, copy-number variation, gene-expression alteration, and changes in epigenetic modifications. In its pilot phase, TCGA met several objectives, most importantly the demonstration of the feasibility and value of comprehensively analyzing the genomes of specific tumor types. TCGA's first undertaking, which focused on brain cancer, demonstrated in FY 2009

the technical feasibility and potential clinical utility of large-scale, multi-dimensional analysis of cancer genomes. Comprehensive characterization of ovarian cancer, the second tumor type completed by TCGA, is opening new avenues of research for the diagnosis and treatment of this devastating disease. TCGA has now initiated projects on colon and rectal cancers, breast cancer, melanoma, bladder cancer, prostate cancer, stomach cancer, and several others.

Budget Policy: The FY 2012 budget estimate for TCGA is $34.8 million, an increase of $672 thousand or 2.0 percent over the FY 2010 Actual level. Now in its full-scale production phase, the TCGA effort will be generating enormous amounts of data that will change the face of cancer research. The increase in FY 2012 will allow NHGRI to build upon advances made using ARRA funding in 2009-2010.

Genomic Function: NHGRI supports research to identify and characterize the function of all parts of genomes and to understand their biological relevance. The major activities in this area are the ENCODE and modENCODE projects. ENCODE (ENCyclopedia of DNA Elements) is a research consortium organized by NHGRI designed to take advantage of new analytical technologies, including next-generation DNA sequencing, for identifying all of the functional coding and non-coding (e.g., regulatory) elements in the human genome. The full-scale ENCODE effort has been so successful that the National Advisory Council for Human Genome Research advised NHGRI to extend the program for an additional year (FY2011) to take advantage of the high rate of data production (more than 2000 experiments performed). The results of these experiments are being analyzed and promise to lead to new ways of thinking about the biology of the human genome and, in combination with the results from a number of other NHGRI and NIH projects, will lead to an enhanced understanding of human disease. As understanding the genomes of other 'model' organisms can also give important insights into the structure and function of the human genome, the Model Organism ENCODE (modENCODE) Project extends the ENCODE approach to two models that are widely used in biomedical research: the fruit fly and the round worm. The modENCODE data are providing important insights into the biology of these organisms, which serve as valuable tools for comparative studies aimed at understanding human biology. Two papers published in Science at the end of 2010 document the significant discoveries made in the modENCODE project. The current versions of the ENCODE and modENCODE projects will be completed in FY2011 and the National Advisory Council for Human Genome Research is currently considering a proposal for FY2012 to continue the Institute's large-scale efforts in functional genomics by improving the technology to analyze gene regulation and to develop methods for high-throughput biological validation of the results of ENCODE and modENCODE.

Budget Policy: The FY 2012 budget estimate for Genomic Function is $56.6 million, an increase of $1.1 million or 2.0 percent over the FY 2010 Actual level. Activity in Genomic Function will remain essentially constant, maintaining the proportion of the NHGRI extramural budget devoted to this area. This can be done because the use of next-generation sequencing technology has resulted in a significant increase in the amount of data generated without an increase in cost. The Institute also will continue to fund meritorious investigator-initiated applications submitted in response to announcements that encourage new technologies and new approaches to the analysis of genomic function.

Genomic Variation: Despite the fact that two individuals' genomes differ by less than one percent, these differences underlie distinct traits that range from the benign (such as hair or eye color) to disease (such diabetes, cancer, Alzheimer's, and heart disease). NHGRI began the comprehensive cataloging of human genetic variation by leading the International HapMap Project, which captured the common patterns of genetic variation, specifically the single-letter variations in our genome's alphabet known as single-nucleotide polymorphisms (SNPs). To get a more detailed description of human genetic variation, the 1,000 Genomes Project is sequencing the genomes of approximately 2,500 people from around the world to produce an updated map of the human genome that will provide a view of biomedically relevant DNA variants at a very high resolution. As with other major genomic reference projects, data from the 1,000 Genomes Project are rapidly being made available to the worldwide scientific community through freely accessible public databases. In addition, larger scale genomic variants—'structural variants' involving a few thousand to more than a million letters—are now known to be a significant cause of disease. Important information about human structural variation will come out of the 1,000 Genomes Project, as well as from a number of investigator-initiated research projects funded by NHGRI.

Budget Policy: The FY 2012 budget estimate for Genomic Variation is $20.7 million, an increase of $400 thousand or 2.0 percent over the FY 2010 Actual level. Activity in Genomic Variation will remain essentially constant, maintaining the proportion of the NHGRI extramural budget devoted to this area. The primary emphasis within this program will continue to be on the full-scale implementation of the 1000 Genomes Project. New directions will include the analysis of the role of variation in understanding gene expression. The Institute also will continue to fund meritorious investigator-initiated applications submitted in response to announcements that encourage new technologies and new approaches to the analysis of genetic variation, and the role that genetic variation plays in the determination of human disease, disease susceptibility, and environmental sensitivities.

Computational Genomics: New genomic methods, such as next-generation DNA sequencing technologies, are driving the generation of prodigious amounts of data; each whole genome sequence is around 250 GB, the size of a large laptop hard drive, and studies can involve hundreds or thousands of samples. The need to correlate these data with other biological and clinical data has led to an explosion in the amount and complexity of data associated with genomic studies. As such, the effort required to manage genomic data and make them available to the entire scientific community is increasing significantly. Therefore, NHGRI is supporting the development of new technologies and analytical approaches for working with the enormous amount of data generated by large-scale genomic studies and how to make such large data sets available to the broad research community. The increasing volume of data necessitates a new and stronger emphasis on data management and analysis strategies. Additional work is also needed for analyzing individual genomes and for understanding the relationship between genetic variation and disease. NHGRI will continue its support for genomic databases because these are essential resources that link biological data to genome sequence information and are utilized worldwide to accelerate biomedical research. NHGRI will also continue to encourage investigator-initiated research to develop robust software tools to improve the utility of these genomic databases and the ability to analyze genomic data.

Budget Policy: The FY 2012 budget estimate for Computational Genomics is $50.2 million, an increase of $970 thousand or 2.0 percent over the FY 2010 Actual level. Activity in Computational Genomics will remain essentially constant, maintaining the proportion of the NHGRI extramural budget devoted to this area. Effort will be directed to increasing the efficiency of data storage and distribution mechanisms, as the amount of data that needs to be processed has increased significantly with the introduction of next-generation sequencing and other new genomic technologies. In FY 2012, NHGRI will continue its support for the essential biomedical research resource represented by genomic databases. The Institute also will continue to fund meritorious investigator-initiated applications submitted in response to announcements that encourage new technologies and new approaches to the rapidly emerging issue of public access to large genomic datasets.

Technology Development: The mission of NHGRI's technology development program is to make DNA sequencing and other genomic analyses faster and more cost-effective for use in medical research and eventually, in the provision of health care. The cost of DNA sequencing has fallen dramatically, by a factor of more than 100, over the past decade, and it continues to fall. This cost reduction is due in large part to research supported by NHGRI. The ability to sequence an individual's genome inexpensively will not only further biomedical research, but also eventually enable health care professionals to tailor diagnosis, treatment, and prevention strategies to each person's unique genetic profile. After the completion of the Human Genome Project, NHGRI continued to support the development of new genomic technologies, and in 2004 started a program to reduce DNA sequencing costs within five years from approximately $10 million for a human genome sequence to $100,000. In 2009, that goal was exceeded. In doing so, NHGRI funded 17 teams of investigators who worked toward those goals, several of whom also participated in private sector efforts with similar goals. But at $100,000 per human genome, DNA sequencing is not yet into the realm of a diagnostic technology, so NHGRI is continuing its sequencing technology development efforts. Currently, the majority of effort is focused on achieving another 100-fold reduction in cost, which would bring the cost of sequencing a human genome to $1,000 or less. A total of 27 groups of investigators are actively supported to work toward that goal, including 10 new or extended awards made in FY 2010 to accelerate progress. NHGRI also leads the Department's High Priority Performance Goal to reduce the cost of a fully-loaded genome sequence to $15,000 by the end of FY 2012. The reduction of sequencing costs will be enabled through incremental improvements in the latest platforms at the NHGRI-funded large scale DNA sequencing centers.
Examples of other genomic technology investments include single-cell genomic analysis, which is of great interest to understand biological mechanisms in all cells, and particularly in cancer, and to learn how to control and analyze large numbers of individual DNA molecules to build maps that complement sequence information.

Budget Policy: The FY 2012 budget estimate for Technology Development is $44.6 million, an increase of $861 thousand or 2.0 percent over the FY 2010 Actual level. NHGRI will continue in FY 2011 its ground-breaking efforts to reduce the cost of DNA sequencing so that this technology, which has increasingly become central to biomedical research, can become a widely disseminated research tool and, beyond that, a tool for clinical application and individual healthcare. The Institute also will continue to fund meritorious investigator-initiated applications submitted in response to announcements that encourage the development of new technologies for biomedical and translational research.

Other Basic Genomics: Multi-investigator, interdisciplinary research teams that can create, use, and expand the data sets and technologies developed by the Human Genome Project (and by genomic efforts since the end of the HGP) are crucial to develop new and innovative research projects, and to foster the wider application of genomic methods to the study of human biology and disease. Started in FY 2001, the NHGRI Centers of Excellence in Genomic Science (CEGS) program supports the formation of such teams, and provides focal points across the country to provide education and training about genomic research opportunities to more than a hundred aspiring young investigators, including members of groups traditionally under-represented in science. In FY 2010, NHGRI announced a grant to establish one new CEGS focused on how differences in gene sequences between individuals relate to disease. Nine previously funded CEGS are continuing their research. Although CEGS is the largest single program in basic genomics, significant funding is devoted to individual investigator grants.

Budget Policy: The FY 2012 budget estimate for Other Basic Genomics is $62.9 million, an increase of $820 thousand or 1.3 percent over the FY 2010 Actual level. In FY 2012, NHGRI will continue to support the CEGS program in its efforts to stimulate highly innovative research approaches that will substantially advance genomic approaches to the study of a biological problem, and to foster the wider application of comprehensive, high-throughput genomics methods to the study of human biology and disease. The Institute will also continue to fund meritorious investigator-initiated applications that will increase the ability of genomics to have a major impact on the progress of biomedical and translational research.

Translational Genomics: With the exception of rare diseases caused by variations in single genes, most human diseases arise from a very complex interplay between genetic factors and environmental exposures. Therefore, DNA variation and external factors acting 'on' the genome must all be considered in diagnosing and treating patients. Understanding this interplay will change approaches to health care, allowing not only more accurate predictions of disease, but, ultimately, individually based disease prevention and treatment. In FY 2010, the Genes, Environment, and Health Initiative (GEI) program took the first steps in identifying key genetic variants associated with specific diseases and using that information in clinical research. A one-year, fast track FY 2010 GEI project is aimed at identifying all the genetic variants, even those that are quite rare, in genomic regions found associated with specific diseases. This effort will involve extensive genome sequencing in large numbers of individuals. Another important program, the Electronic Medical Records and Genomics (eMERGE) Network, is described below in more detail as a program portrait. In FY 2008, NHGRI initiated a four-year project to measure disease-implicated gene variants in well-characterized populations to gain a better understanding of how specific genetic variants act to influence the risk of diabetes, heart disease, cancer, and other common diseases. Scientists have already discovered more than 800 genetic variants associated with over 150 diseases and clinical traits, such as cancer, cholesterol levels, and lipid levels. In FY 2009, NHGRI initiated a major new program to identify genetic variants associated with treatment response using genetic association studies in randomized clinical trials.

Budget Policy: The FY 2012 budget estimate for Translational Genomics is $22.0 million, an increase of $425 thousand or 2.0 percent over the FY 2010 Actual level. Activity in Translational Genomics will remain essentially constant, maintaining the proportion of the NHGRI extramural budget devoted to this area. NHGRI will continue in FY 2012 to support this area of research as the combination of advances in genomics with cutting-edge approaches to population studies

remains of very high programmatic interest as an important strategy for addressing problems of human health. The Institute also will continue to fund meritorious investigator-initiated applications, and to collaborate with other NIH Institutes/Centers in the area of translational genomics.

Portrait of a Program: eMERGE

FY 2010 Level: [$4.3 million]
FY 2012 Level: [$8.7 million]

Change: [+$4.4 million]

Increasing the adoption of electronic health records is now a national priority, offering the potential to improve patient health and reduce health care costs. Biorepositories, also known as biobanks, are facilities that store and maintain tissue samples and other biospecimens for use in research. The Electronic Medical Records and Genomics (eMERGE) Network is an NHGRI-led effort in which participating sites that have existing DNA biorepositories and electronic medical records integrate the two (linking each specific DNA sample to the corresponding patient's electronic medical record), and then to use those resources to explore the relationship between genetic variation and common human traits.

Since the generation of the first human genome sequence ten years ago, researchers have uncovered many gene variants that are associated with disease through studies that analyze both genomic and phenotypic information (physical traits, disease symptoms, and so forth) to search of associations. These studies often require a great investment of both time and money. eMERGE aims to advance the efficiency of this approach. Specifically, a patient's medical record already contains much of the phenotypic data of interest to researchers, and being able to integrate these data with genomic data offers the promise of greatly improving the efficiency of identifying relevant genetic and genomic links to disease.

The first phase of the eMERGE project involves the efforts of five leading medical research institutions across the country (Group Health Cooperative of the University of Washington, Marshfield Clinic, Mayo Clinic, Northwestern University, and Vanderbilt University). These groups are investigating a number of diseases, including dementia, cataracts, cardiovascular disease, asthma, diabetes, and arrhythmia. In addition to studying the genotype-phenotype relationships within these diseases, the eMERGE investigators are looking at the ethical, social, and legal issues involved with incorporating genomic data into electronic medical record data for both research and patient care.

The second phase of the eMERGE project involves expanding the number of phenotypes being captured from 14 to at least 40, and increasing the number and diversity of both patients and sites. This phase also seeks to develop approaches and tools that will have a direct impact on improving patient care. Examples include (but will not be limited to) identifying patients that are at a very high genetic risk for a given condition and then alerting their clinicians to the need for increased surveillance or preventative care; and identifying pharmacogenetically important variants in patients that ought to be taken into account by their care providers (choosing the correct dosage of a particular therapy and avoiding drugs that have a high likelihood of adverse effects). Sharing expertise and experience both within and outside eMERGE will continue to be a key goal, with the intent of improving the methodology for genomic research with biorepositories and their incorporation into medical care in general.

Ethical, Legal, and Social Implications: As the use of genetic and genomic technologies in translational and clinical research studies continues to increase, the importance of addressing the societal implications of this work grows as well. NHGRI addresses such issues through its Ethical, Legal, and Social Implications (ELSI) Research Program and through public consultation and community engagement activities that identify and respond to culturally

specific concerns. It is also important to provide participating communities opportunities for input into the design and conduct of genetic and genomic research. One important component of the ELSI Research Program is the Centers of Excellence in ELSI Research (CEERs) program. These CEERs, modeled on the successful CEGS program, have a number of aims: creating the kinds of multi-disciplinary approaches needed to study the ethical, legal, and social issues that are raised by progress in genomic science; using those approaches to conduct ELSI research to inform the development of research, health, and public policies and practices; and importantly to train the next generation of ELSI researchers. Four CEERs were originally established in FY 2004; in FY 2008, two new centers were funded. Center sites now include Case Western Reserve University, Duke University, University of Pennsylvania, Stanford University, University of North Carolina, and University of Washington. In FY 2010, three of the four original CEERS were competitively renewed, and the fourth center was funded at a reduced level as it transitions to independent support. In addition, two new three-year Exploratory Centers were funded at the Oregon Health & Science University and Columbia University. NHGRI-funded ELSI researchers have been studying a wide range of research questions, from public attitudes towards genetic testing and research, including direct-to-consumer testing, to the impact of gene patents on the development of new diagnostic tests.

Budget Policy: The FY 2012 budget estimate for ELSI is $19.1 million, an increase of $370 thousand or 1.97 percent over the FY 2010 Actual level. The ELSI budget is legislatively mandated at 5.0 percent of the total NHGRI extramural budget. In FY 2012, NHGRI will continue to support the ELSI research program in its efforts to anticipate and address the social, legal, and ethical issues that will arise from new information about the human genome and the genetic contribution to human disease, and new approaches to applying that information to the improvement of human health.

Intramural Research: Researchers within NHGRI's Division of Intramural Research continue to identify and characterize the genetic components of both rare and common diseases. NHGRI research groups have recently identified a number of genetic variants that increase an individual’s susceptibility to specific diseases, such as diabetes, attention deficit hyperactivity disorder (ADHD), and lung cancer. NHGRI's researchers also have identified genes that are responsible for a number of debilitating developmental disorders, such as microcephaly, and have made significant advances in understanding the underlying mechanisms responsible for proper development of the overall body plan of vertebrates. NHGRI Intramural investigators plan to continue expanding their collective focus on translational research in FY 2012. One such study focuses on the microbial communities (microbiomes) of the skin and nose in patients with atopic dermatitis (eczema) and immunodeficiency syndromes. The goal of this program is to characterize the microorganisms that live on (or in) the human body, so that appropriate, targeted therapies can be developed to treat diseases caused by these microbes. As part of this project, the *Staphylococcus* genome will be sequenced to begin to understand how certain strains of this pathogenic bacterium become drug-resistant. Meanwhile, two NHGRI Intramural clinical genomics initiatives have reached a mature and productive stage. The first, called ClinSeq, is a pilot study aimed at developing the technologic and procedural infrastructure to facilitate large-scale genome sequencing in a clinical research setting. The second, called Multiplex, is a large, multi-disciplinary research project aimed at understanding patients’ reactions to genetic susceptibility testing for common health conditions. Both of these studies have already provided valuable insights into how these kinds of genomic approaches can be used towards advancing

personalized medicine, thereby improving the health of individuals. The NIH Undiagnosed Diseases Program, a clinical research program to study patients with mysterious conditions that have long eluded diagnosis, is now in full stride; more than 2,350 inquires have already been evaluated for potential participation and over 100 patients have been admitted into the program.

Budget Policy: The FY 2012 budget estimate for Intramural Research is $105.2 million, an increase of $1.0 million or 1 percent over the FY 2010 Actual level. This increase will facilitate growth in three major areas: (1) The addition of physician-scientists to strengthen the Institute's translational and clinical research programs. The increase also includes continued growth of our flagship intramural clinical genomics projects ClinSeq and growth to support the Undiagnosed Diseases Program; (2) Continued acquisition and implementation of 'next-generation' technologies for performing large-scale DNA sequencing. Genomics continues to see major growth in terms of new methods for obtaining very large amounts of DNA sequence data at lower costs. The NHGRI Intramural Program will continue to implement these powerful new DNA sequencing technologies in FY 2012. This requires substantial expansion of computational infrastructure as well as increased bioinformatics and computational staffing. Note that these new technologies are increasingly being applied to clinical research projects; and (3) Continued growth of a trans-disciplinary program to explore the skin's microbiome—all of the genomes of the microbes that inhabit human skin. This effort will help to define the delicate balance between our own cells and the millions of bacteria and other single-celled microbes that live on the skin's surface, one of the body's first lines of defense against illness and injury.

Research Management and Support: The NHGRI Office of the Director, part of the RMS program, oversees the operation of the Institute and includes a number of component parts. Major ongoing initiatives for which the Office of the Director provides key leadership and financial support include National DNA Day, the U.S. Surgeon General's Family History Initiative, community genomics programs, and the development of genetics education resources for health professionals. Through these activities, the Office of the Director supports a suite of innovative communications tools to convey the NIH and NHGRI messages to the public and the media. DNA Day is an annual opportunity to educate students about genetics and genomics and to use this cutting-edge field to spark their interest in science. The U.S. Surgeon General's Family History Initiative is a coordinated multi-agency effort to encourage all American families to learn more about their family health history and to employ it in preventive health care. To expand the initiative's reach and public benefit, NHGRI continues to collaborate across federal agencies to enhance the family history tool's capabilities and to engage in demonstration projects to develop evidence regarding the tool's utility, including as part of electronic health records. Projects to promote the public's awareness of and participation in the initiative will also be pursued. NHGRI’s leadership role in instigating the development, pilot testing, and dissemination of an interdisciplinary web-based genetics educational resources, known as G2C2 (http://www.g-2-c-2.org), is creating stronger and deeper relationships with those developing the educational standards for all health care professionals.

Budget Policy The FY 2012 budget estimate for research management and support is $25.7 million, an increase of $752 thousand or 3.0 percent over the FY 2010 Actual level. In FY 2012, NHGRI plans to continue to develop ongoing initiatives for which the Office of the Director provides leadership and financial support. Such programs within the Office of Policy, Communication, and Education include National DNA Day, the U.S. Surgeon General's Family History Initiative, and outreach and informational resources for the general public and health

professionals through community and web-based activities. In addition, NHGRI is enhancing the Risk Management Program, which includes business process reengineering, setting up new procedures and tools to ensure our continued prudent use of RMS funds. RMS funds will be used to continue funding the activities mentioned above to support the infrastructure that allows NHGRI to pursue and achieve its mission.

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National Human Genome Research Institute

Budget Authority by Object
(Dollars in Thousands)

	FY 2010 Actual	FY 2012 PB	Increase or Decrease
Total compensable workyears:			
Full-time employment	338	340	2
Full-time equivalent of overtime and holiday hours	1	1	0
Average ES salary	$173,633	$173,633	$0
Average GM/GS grade	12.1	12.1	0.0
Average GM/GS salary	$97,322	$97,322	$0
Average salary, grade established by act of July 1, 1944 (42 U.S.C. 207)	$98,170	$101,137	$2,967
Average salary of ungraded positions	135,464	135,464	0

	OBJECT CLASSES	FY 2010 Actual	FY 2012 Estimate	Increase or Decrease
	Personnel Compensation:			
11.1	Full-time permanent	$15,210	$15,367	$157
11.3	Other than full-time permanent	14,299	14,409	110
11.5	Other personnel compensation	750	759	9
11.7	Military personnel	575	597	22
11.8	Special personnel services payments	5,050	5,085	35
	Total, Personnel Compensation	**$35,884**	**$36,217**	**$333**
12.0	Personnel benefits	$9,034	$9,114	$80
12.2	Military personnel benefits	576	581	5
13.0	Benefits for former personnel	0	0	0
	Subtotal, Pay Costs	**$45,494**	**$45,912**	**$418**
21.0	Travel and transportation of persons	$2,203	$2,245	$42
22.0	Transportation of things	206	211	5
23.1	Rental payments to GSA	2	2	0
23.2	Rental payments to others	21	23	2
23.3	Communications, utilities and miscellaneous charges	486	500	14
24.0	Printing and reproduction	46	48	2
25.1	Consulting services	1,182	1,392	210
25.2	Other services	18,227	18,690	463
25.3	Purchase of goods and services from government accounts	57,616	62,835	5,219
25.4	Operation and maintenance of facilities	579	595	16
25.5	Research and development contracts	2,684	4,476	1,792
25.6	Medical care	893	904	11
25.7	Operation and maintenance of equipment	2,295	2,308	13
25.8	Subsistence and support of persons	0	0	0
25.0	**Subtotal, Other Contractual Services**	**$83,476**	**$91,200**	**$7,724**
26.0	Supplies and materials	$9,561	$9,685	$124
31.0	Equipment	4,411	4,497	86
32.0	Land and structures	0	0	0
33.0	Investments and loans	0	0	0
41.0	Grants, subsidies and contributions	369,892	370,483	591
42.0	Insurance claims and indemnities	0	0	0
43.0	Interest and dividends	1	1	0
44.0	Refunds	0	0	0
	Subtotal, Non-Pay Costs	**$470,305**	**$478,895**	**$8,590**
	Total Budget Authority by Object	**$515,799**	**$524,807**	**$9,008**

Includes FTEs which are reimbursed from the NIH Common Fund for Medical Research

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Salaries and Expenses
(Dollars in Thousands)

OBJECT CLASSES	FY 2010 Actual	FY 2012 PB	Increase or Decrease
Personnel Compensation:			
Full-time permanent (11.1)	$15,210	$15,367	$157
Other than full-time permanent (11.3)	14,299	14,409	110
Other personnel compensation (11.5)	750	759	9
Military personnel (11.7)	575	597	22
Special personnel services payments (11.8)	5,050	5,085	35
Total Personnel Compensation (11.9)	**$35,884**	**$36,217**	**$333**
Civilian personnel benefits (12.1)	$9,034	$9,114	$80
Military personnel benefits (12.2)	576	581	5
Benefits to former personnel (13.0)	0	0	0
Subtotal, Pay Costs	**$45,494**	**$45,912**	**$418**
Travel (21.0)	$2,203	$2,245	$42
Transportation of things (22.0)	206	211	5
Rental payments to others (23.2)	21	23	2
Communications, utilities and miscellaneous charges (23.3)	486	500	14
Printing and reproduction (24.0)	46	48	2
Other Contractual Services:			
Advisory and assistance services (25.1)	1,182	1,392	210
Other services (25.2)	18,227	18,690	463
Purchases from government accounts (25.3)	44,912	45,897	985
Operation and maintenance of facilities (25.4)	579	595	16
Operation and maintenance of equipment (25.7)	2,295	2,308	13
Subsistence and support of persons (25.8)	0	0	0
Subtotal Other Contractual Services	**$67,195**	**$68,882**	**$1,687**
Supplies and materials (26.0)	$9,561	$9,685	$124
Subtotal, Non-Pay Costs	$79,718	$81,594	$1,876
Total, Administrative Costs	**$125,212**	**$127,506**	**$2,294**

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Details of Full-Time Equivalent Employment (FTEs)

OFFICE/DIVISION	FY 2010 Actual			FY 2011 CR			FY 2012 PB		
	Civilian	Military	Total	Civilian	Military	Total	Civilian	Military	Total
Office of the Director	12		12	12		12	12		12
Office of Administrative Management	22		22	22		22	22		22
Office of Policy, Communications and Educatio	11		11	11		11	11		11
Division of Intramural Research	248	7	255	249	7	256	249	7	256
Division of Extramural Research	37	1	38	38	1	39	38	1	39
Total	330	8	338	332	8	340	332	8	340
Includes FTEs which are reimbursed from the NIH Common Fund for Medical Research									
FTEs supported by funds from Cooperative Research and Development Agreements	0	0							0

FISCAL YEAR	Average GS Grade
2008	12.1
2009	12.1
2010	12.1
2011	12.1
2012	12.1

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National Human Genome Research Institute

Detail of Positions

GRADE	FY 2010 Actual	FY 2011 CR	FY 2012 PB
Total, ES Positions	2	2	2
Total, ES Salary	347,265	347,265	347,265
GM/GS-15	28	28	28
GM/GS-14	15	15	15
GM/GS-13	49	49	49
GS-12	51	52	52
GS-11	15	15	15
GS-10	3	3	3
GS-9	8	8	8
GS-8	20	20	20
GS-7	2	2	2
GS-6	0	0	0
GS-5	0	0	0
GS-4	0	0	0
GS-3	1	1	1
GS-2	0	0	0
GS-1	0	0	0
Subtotal	192	193	193
Grades established by Act of July 1, 1944 (42 U.S.C. 207):			
Assistant Surgeon General	0	0	0
Director Grade	4	4	4
Senior Grade	3	3	3
Full Grade	1	1	1
Senior Assistant Grade	0	0	0
Assistant Grade	0	0	0
Subtotal	8	8	8
Ungraded	138	139	139
Total permanent positions	202	203	203
Total positions, end of year	340	342	342
Total full-time equivalent (FTE) employment, end of year	338	340	340
Average ES salary	173,633	173,633	173,633
Average GM/GS grade	12.1	12.1	12.1
Average GM/GS salary	97,322	97,322	97,322

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New Positions Requested

	FY 2012		
	Grade	**Number**	**Annual Salary**
Senior Staff Scientist	Title 42	1	$171,000
Program Policy Analyst	GS-12	1	88,000
Total Requested		2	