

NHGRI SEQUENCING UPDATE
as of 4/23/04*

ORGANISM	SEQUENCING CENTER(S)	# TRACES IN TRACE REPOSITORY	#DRAFT / #FINISHED BASES	OTHER INFORMATION
MOUSE , <i>Mus musculus</i>	BI/MIT, WUGSC, & Sanger	80,247,457 traces	1,874,306 kb draft 1,434,512 kb finished	Representatives of the Mouse Genome Sequencing Consortium met in March to discuss the finishing of the mouse genome. The current target for completion of the mouse genome is December 2005.
RAT , <i>Rattus norvegicus</i>	BCM-HGSC	40,003,287 traces	5,066,182 kb draft 40,078 kb finished	The Rat Genome Sequencing Project Consortium published the genome sequence and comparative analysis of the Brown Norway rat in the April 1, 2004 issue of Nature.
BOVINE , <i>Bos taurus</i>	BCM-HGSC	6,321,510 traces		The Bovine Genome Sequencing Project Advisory Committee meets monthly by telephone to discuss project progress and strategy.
CAENORHABDITIS REMANEI	WUGSC	1,421,855 traces		
CHICKEN , <i>Gallus gallus</i>	WUGSC	11,748,752 traces		The first assembly of the chicken genome was released on March 1, 2004
CHIMPANZEE , <i>Pan troglodytes</i>	WUGSC & BI/MIT	32,828,375 traces		The sequencing centers and collaborators are working to analyze the chimp genome sequence and prepare a manuscript on the draft assembly. The WUGSC is also achieving deeper sequencing coverage of the chimpanzee genome.
DOG , <i>Canis familiaris</i>	BI/MIT	36,345,477 traces		
DROSOPHILA ANANASSAE	Agencourt	159,207 traces		
DROSOPHILA PSEUDOOBSCURA	BCM-HGSC	2,640,686 traces		First freeze assembly of <i>D. pseudoobscura</i> in August 2003.
DROSOPHILA SIMULANS	WUGSC	1,119,009 traces		
DROSOPHILA VIRILIS	Agencourt	2,523,378 traces		
DROSOPHILA YAKUBA	WUGSC	2,060,963 traces		
HONEYBEE , <i>Apis mellifera</i>	BCM-HGSC	3,214,004 traces		Assembly version 1.1 released in January 2004
OPOSSUM, LABORATORY , <i>Monodelphis domestica</i>	BI/MIT	21,828,540 traces		
PLANARIAN , <i>Schmidtea mediterranea</i>	WUGSC	1,832,308 traces		
RHESUS MACAQUE , <i>Macaca mulatta</i>	Agencourt, BCM-HGSC, JCVJTC	6,668,757 traces		
SEA URCHIN , <i>Strongylocentrotus purpuratus</i>	BCM-HGSC	8,022,776 traces		
FUNGAL GENOME INITIATIVE	BI/MIT			
<i>Aspergillus nidulans</i>		623,573 traces		13X Genome Assembly released Feb 2003
<i>Aspergillus terreus</i>		4,608 traces		
<i>Coccidioides immitis</i>		529,589 traces		
<i>Coprinus cinereus</i>		711,671 traces		10X Genome Assembly released July 2003
<i>Cryptococcus neoformans</i> Serotype A		456,006 traces		11X Genome Assembly released June 2003
<i>Rhizopus oryzae</i>		770,467 traces		
<i>Ustilago maydis</i>		338,592 traces		10X Genome Assembly released July 2003

* There are a number of organisms that have been designated "High Priority" for sequencing but have not entered an NHGRI-supported sequencing pipeline as of 4/23/04. These organisms include:

Caenorhabditis japonica, *Caenorhabditis n. sp.* CB5161, *Candida guilliermondii*, *Candida lusitanae*, *Candida tropicalis*, *Chaetornium globosum*, *Cryptococcus neoformans* Serotype B, *Drosophila erecta*, *Drosophila grimshawi*, *Drosophila mojavensis*, *Drosophila persimilis*, *Drosophila sechellia*, *Drosophila willistoni*, *Gasterosteus aculeatus*, *Histoplasma capsulatum*, *Lodderomyces elongisporus*, *Ornithorhynchus anatinus*, *Oxytricha trifallax*, *Pneumocystis carinii* (human and mouse), *Podospora anserina*, *Saccharomyces cerevisiae* RM11-1A, *Saccoglossus kowalesvskii*, *Tetrahymena thermophila*, *Tribolium castaneum*, *Unicinocarpus reesii*