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# NCBI News, April 2014

## Coffee Break tutorial: The promise of PCSK9

*Thursday, April 24, 2014*

The latest Coffee Break tutorial explores PCSK9, an enzyme that plays a major regulatory role in cholesterol homeostasis, and the cholesterol-lowering drugs that target it. This Coffee Break also includes a video exploration of ClinicalTrials.gov.

## New NCBI Insights Blog: Sequence updates in human genome assembly GRCh38

*Wednesday, April 23, 2014*

The latest NCBI Insights blog post explores just one of the many changes and improvements introduced by the newest human reference genome released in December 2013, GRCh38.

## HomoloGene release 68 now available

*Tuesday, April 22, 2014*

HomoloGene release 68 is now available on Homologene! In this release, genome annotation was updated for 19 organisms, the number of HomoloGene groups increased to 44,233, and one organism, Xenopus tropicalis, was added. Release 68 is also available on the FTP site.

HomoloGene is an NCBI resource that identifies and clusters homologous genes, transcripts and proteins for selected eukaryotes.

## Milestone: NCBI's Taxonomy database contains over 300,000 species with formal scientific names!

*Friday, April 18, 2014*

NCBI's Taxonomy database has now surpassed 300,000 individual records of species with formal scientific names. The majority of these represent eukaryotic organisms. While worldwide estimates of prokaryotic and viral species number in the millions or tens of millions, very few have been formally described, isolated, or are able to be cultured. However, the Taxonomy database contains listings for nearly all of the prokaryotes and viruses that have been described.

The Taxonomy database, created in 1991, is a standard nomenclature and classification repository that includes organism names and taxonomic lineages for each of the sequences represented in the International Nucleotide Sequence Database Collaboration (INSDC).

## GenBank release 201.0 is now available via FTP

*Thursday, April 17, 2014*

Release 201.0 (4/13/2014) has 171,744,486 non-WGS, non-CON records containing 159,813,411,760 base pairs of sequence data. In addition, there are 143,446,790 WGS records containing 621,015,432,437 base pairs of sequence data.

During the 60 days between the close dates for GenBank Releases 200.0 and 201.0, the non-WGS/non-CON portion of GenBank grew by 1,869,618,589 base pairs and by 620,737 sequence records. During the same period, 2,046,345 records were updated; an average of 44,451 non-WGS/non-CON records per day were added and/or updated. Between releases 200.0 and 201.0, the WGS component of GenBank grew by 29,636,733,893 base pairs and by 3,720,995 sequence records.

The total number of sequence data files increased by 18 with this release. The divisions are as follows:

- BCT: 15 new files, now a total of 133
- CON: 4 new files, now a total of 246
- ENV: 2 new files, now a total of 69
- EST: 1 new file, now a total of 476
- GSS: 1 new file, now a total of 285
- MAM: 1 new files, now a total of 9
- PLN: 1 new file, now a total of 68
- VRL: 2 new files, now a total of 31

For downloading purposes, please keep in mind that the GenBank flatfiles are approximately 625 GB (sequence files only). ASN.1 data are approximately 527 GB.

More information about GenBank Release 201.0 and coming changes are available in the release notes.

## Enterococci: From commensals to leading causes of drug resistant infection on Bookshelf

*Tuesday, April 15, 2014*

"*Enterococci*: From commensals to leading causes of drug resistant infection" (Michael S Gilmore, Don B Clewell, Yasuyoshi Ike, and Nathan Shankar, editors; Boston: Massachusetts Eye and Ear Infirmary; 2014), a comprehensive text aiming to advance the understanding of *Enterococci* is free to access on the NCBI Bookshelf. This book has been compiled from peer-reviewed content contributed by leaders in the *Enterococcus* research community, and will be regularly updated on the Bookshelf.

*Enterococci* are an ancient and highly evolved genus of bacteria that were first described 115 years ago. They adapted to survive in a range of extreme environments, and thrive inside the gastrointestinal tracts of many species, including humans. In the human gut, commensal enterococci act in harmony with other microbes to do good gastric deeds, such as helping with digestion and crowding out harmful microbes.

However, *Enterococci* have continued to evolve to have more harmful roles. About 40 years ago, new traits in *E. faecalis* and *E. faecium* propelled these microbes to become the leading cause of multidrug-resistant, hospital-acquired infections. In addition, *Enterococci* can spread their new traits for antibiotic resistance to other pathogens, such as *Staphylococcus aureus*.

To date, there are over 40 distinct species of *Enterococcus*. Understanding the appearance of new strains of antibiotic-resistant enterococci, some of which feature new resistance mechanisms, is key to finding a solution to multidrug resistance.

## CCDS release 16 for mouse now public in Gene

*Monday, April 14, 2014*

The Consensus Coding Sequence (CCDS) update for Mus musculus annotation release 104 released last week is now reflected in Gene. This update adds 803 new CCDS IDs and 97 genes into the mouse CCDS set. CCDS release 16 includes a total of 23,880 CCDS IDs that correspond to 20,079 GeneIDs. For more information, visit the CCDS homepage.

## New on the Bookshelf: The Art and Politics of Science, a memoir by Dr. Harold Varmus

*Thursday, April 10, 2014*

Dr. Harold Varmus's memoir, The Art and Politics of Science (W.W. Norton and Company, New York; 2009), is now freely available on the NCBI Bookshelf.

In this book, he chronicles his path from a graduate student in English literature at Harvard to co-recepient of the Nobel Prize for cellular origin of retroviral oncogenes, to director of the National Institutes of Health, to President and CEO of Memorial Sloan-Kettering Cancer Center.

## Coffee Break tutorial: Brown fat and obesity

*Tuesday, April 01, 2014*

The latest Coffee Break tutorial discusses EHMT1, an enzyme responsible for brown fat production, and its possibility as a target for new obesity treatments.

The tutorial includes a discussion of recent research on brown fat cells, EHMT1$^{adipo}$ knockout mice, and a video exploration of ClinVar, PubMed, and Bookshelf.