NCBI News, October 2016

November 9th webinar: PubMed for Clinicians

Friday, October 28, 2016

On November 9th, NLM staff will show health care professionals how to search PubMed for the most relevant and recent literature, explore specific clinical research areas, set up email alerts, an dmore.

Date and time: Wednesday, November 9, 2016 1:00 PM - 2:00 PM EST

Registration URL: http://bit.ly/2feyobc

After registering for the webinar, you will receive a confirmation email with information about attending the webinar. After the live presentation, the webinar will be uploaded to the NCBI YouTube channel. Any related materials will be accessible on the Webinars and Courses page; you can also learn about future webinars on this page.

NLM In Focus blog profiles Dr. Kim Pruitt, NCBI staff scientist

Tuesday, October 25, 2016

The inaugural article in NLM In Focus's new series on NLM scientists features Kim Pruitt, PhD. Dr. Pruitt is a staff scientist at NCBI; she heads the Reference Sequence Database, better known as RefSeq.
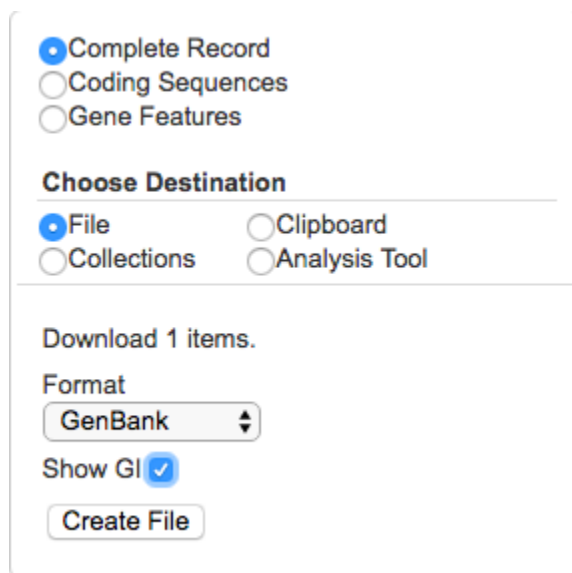
In the article, Dr. Pruitt shares her career trajectory as well as pearls of wisdom for young scientists.

Genome Workbench 2.11.0 now available

Friday, October 21, 2016

The latest version of Genome Workbench includes a number of new features, fixes and improvements like an improved ProSplign tool, improvements to Graphical Sequence View and new documentation for using Tree View and other processes.

For a full list of changes, please see the Genome Workbench release notes.

Figure 1. Revised Send dialog in sequence databases. After choosing "File" as the destination, a new checkbox labeled "Show GI" will appear. When checked, the downloaded data will contain GI numbers as in the past. When unchecked, flat file (GenBank, GenPept) and FASTA formats will not display GI numbers.

GI numbers will be removed from sequence record presentations

Monday, October 17, 2016

As announced in March 2016, NCBI is now in the process of removing GI numbers from the presentations of nucleotide and protein sequence records. The affected presentations are the (default) flat file (GenBank and GenPept) views, along with FASTA views. NCBI will be releasing these changes on or soon after October 17, 2016.

For web presentations, please see the previous announcement for examples of the new formats. If you would like to obtain formats that include GI numbers, there will be an option in the "Send" menu that allows you to download the former presentations. Once you select "File" as the destination, a "Show GI" checkbox will appear and will be checked by default. When this box is checked, the downloaded data will contain GI numbers as in the past.

These changes also affect presentations obtained using the E-utility EFetch. By default, the new flat file and FASTA presentations will no longer contain GI numbers, just like those obtained on the web. To obtain presentations that include GI numbers, simply add the parameter & showgi to your EFetch URL and set its value to 1: https://eutils.ncbi.nlm.nih.gov/entrez/eutils/efetch.fcgi?db=nuccore&id=AF123456.2&rettype=gb&showgi=1.

New YouTube video: NCBI Staff at ASHG 2016

Monday, October 17, 2016

The newest video on the NCBI YouTube channel is a recording of the October 5th NCBI Minute, which provides a quick overview of NCBI activities at this year's upcoming meeting related to ClinVar, dbGaP, GRCh38 and other topics. In this video, you'll find out why NCBI goes to scientific meetings and how ASHG attendees benefit from having NCBI at ASHG.

NCBI staff members will be at Exhibit booth 521, where attendees can get answers and provide input for the future development of NCBI human genome resources.

Subscribe to the NCBI YouTube channel to receive alerts about new videos ranging from quick tips to full webinar presentations.

October 26th NCBI Minute: New BLAST Databases Provide Cleaner Results

Tuesday, October 11, 2016

On October 26th, NCBI staff will introduce two new BLAST databases: the RefSeq Representative Genomes database and the Model Organisms or Landmark protein database.

Date and time: Wednesday, October 26, 2016 12:00 PM - 12:30 PM EDT

Registration URL: http://bit.ly/2di8d0i

The RefSeq Representative Genomes database contains the NCBI-selected Reference and Representative Genome nucleotide assemblies. The Model Organisms or Landmark protein database contains proteomes from 27 well-characterized model organisms from diverse taxonomic groups.

After registering, you will receive a confirmation email with information about attending the webinar. After the live presentation, the webinar will be uploaded to the NCBI YouTube channel. Any related materials will be accessible on the Webinars and Courses page; you can also learn about future webinars on this page.

Multiple Sequence Alignment Viewer 1.1 is now available

Thursday, October 06, 2016

The NCBI Multiple Sequence Alignment Viewer (MSA Viewer) has recently been updated. This new version has an improved rendering mechanism for displaying projected features, improved navigation over gaps in alignment, and improved security and compatibility with HTTPS protocols. A full list of new features, improvements, and bug fixes is available in the MSA Viewer release notes.

The NCBI MSA Viewer is a graphical display for the multiple alignments of nucleotide and protein sequences.

NLM presents "Insider's Guide" webinar on E-utilities and PubMed on October 19th

Thursday, October 06, 2016

On Wednesday, October 19, 2016, the U.S. National Library of Medicine (NLM) will present "Insider's Guide to Accessing NLM Data: Welcome to E-utilities for PubMed".

Date and time: Wednesday, October 19, 2016, 2-3 PM EDT

Registration URL: http://bit.ly/2dHKTdy

Join us for the first in the Insider's Guide series of webinars about more powerful and flexible ways of accessing NLM data, starting with an introduction to the Application Programming Interfaces (APIs) for PubMed and other NCBI databases.

This series is geared toward librarians and other information specialists who have experience using PubMed via the traditional web interface, but now want to dig deeper. For more information about the first webinar, visit the registration page.

For more information about the Insider's Guide courses, visit the class page.

Questions? Contact NLM.

CCDS release 20 for human now public in Gene

Tuesday, October 04, 2016

Consensus Coding Sequence (CCDS) release 20 compares NCBI's *Homo sapiens* annotation release 108 to Ensembl's release 85, and is now available in Gene. This update adds 1,158 new CCDS IDs and 98 genes into the human CCDS set. CCDS release 20 includes a total of 32,524 CCDS IDs that correspond to 18,892 GeneIDs.