NCBI News, January 2013

First NCBI Blog Post Highlights New PubReader For PMC Articles

Thursday, January 31, 2013

The first post to the *NCBI Insights* blog focuses on the recently launched PubReader view for full-text articles in PubMed Central.

The PubReader makes full-text research papers not only more readable but also more portable. Any article that is available in full-text HTML in PubMed Central is viewable in the PubReader format. The PubReader code is freely available to developers via GitHub.

Read about it here: http://ncbiinsights.ncbi.nlm.nih.gov/2013/01/29/new-pubreader-view-for-full-text-articles.

Now Available: NCBI Insights Blog!

Monday, January 28, 2013

The new *NCBI Insights Blog* was created to provide an insider's perspective, help our users better understand us and our resources, explore issues of scientific interest that drive our resource development, and demonstrate how you can use our resources to help enhance your research.
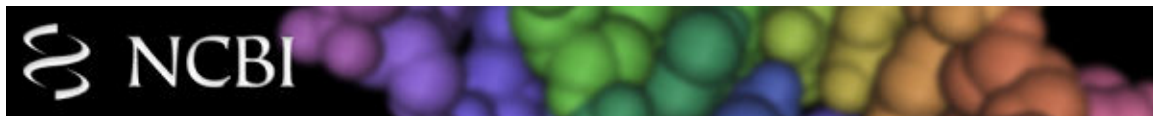
We will post articles in four categories:

- *NCBI Explained* - provides an insider's perspective on our resources and policies to help you better understand us and avoid some common misconceptions and misunderstandings.
- *What's New* - introduces our new and updated resources and include specific examples that demonstrate how you can use these to enhance your research.
- *Quick Tips & Tricks* - explains hows to perform specific tasks using our website. Selected topics will be chosen based on questions you have asked and suggestions you have provided.

- *Science Features* - explores current topics in science and demonstrate how you can find relevant data or resources on our website for further exploration.

This blog is a complement to our existing education and outreach efforts, such as News and Social Media publicity, Webinar and Workshop training programs, and Help Desk user support.

Be sure to check in to the *NCBI Insights Blog* every week or so and let us know what you think!

~300,000 ChemAxon Structures are now in PubChem

Wednesday, January 23, 2013

Just over 300,000 structures from ChemAxon's chemicalize.org database are now available in PubChem, including approximately 62,000 novel structures. All structures have links back to chemicalize.org data pages which list predicted data including pKa, logP/D, names and identifiers, and much more.

The announcement from ChemAxon provides additional details.

Genetic Testing Registry Records will list Molecular Pathology CPT Codes

Thursday, January 17, 2013

Under a recent agreement with the American Medical Association (AMA), the National Institute of Health's Genetic Testing Registry (GTR) now integrates the AMA's Current Procedural Terminology (CPT) codes for molecular pathology tests into records describing genetic test information by providers.

The addition of the molecular pathology CPT codes, along with SNOMED CT, LOINC, and IHTSDO clinical terminology, further enhances GTR's interoperability with electronic medical records and laboratory information management systems.

Come to the NCBI Discovery Workshops on February 4 & 5!

Wednesday, January 16, 2013

Spaces are still available for the free, 2-day Discovery Workshops to be held on the NIH Campus. Each hands-on session emphasizes a different set of NCBI resources using specific examples to highlight important features of the resources and tools and to demonstrate how to accomplish common tasks.

Now in GenBank: Flu Sequences from the Current Influenza Season

Tuesday, January 15, 2013

The U.S. Naval Health Research Center, San Diego and the U.S. Air Force School of Aerospace Medicine's Epidemiology Laboratory Service recently sequenced 46 influenza A and B viruses and has released them in GenBank.

The sequences were collected through their global surveillance programs as recently as November 2012 and represent the only human flu sequences of the current season available in GenBank. The sequences have GenBank accession numbers CY131965-CY131967 and CY130158-CY130200.

According to CDC, the U.S. is seeing an early flu season this year; 47 states have reported widespread flu for the first week in 2013, and the State of New York has declared an influenza emergency. The timely release of influenza sequences is important for researchers trying to understand the viruses circulating in the US and is critical for vaccine development. Additional sequences are expected later this week. The US military's fast action in releasing these invaluable data sets an exceptional example of data sharing for the influenza research community.
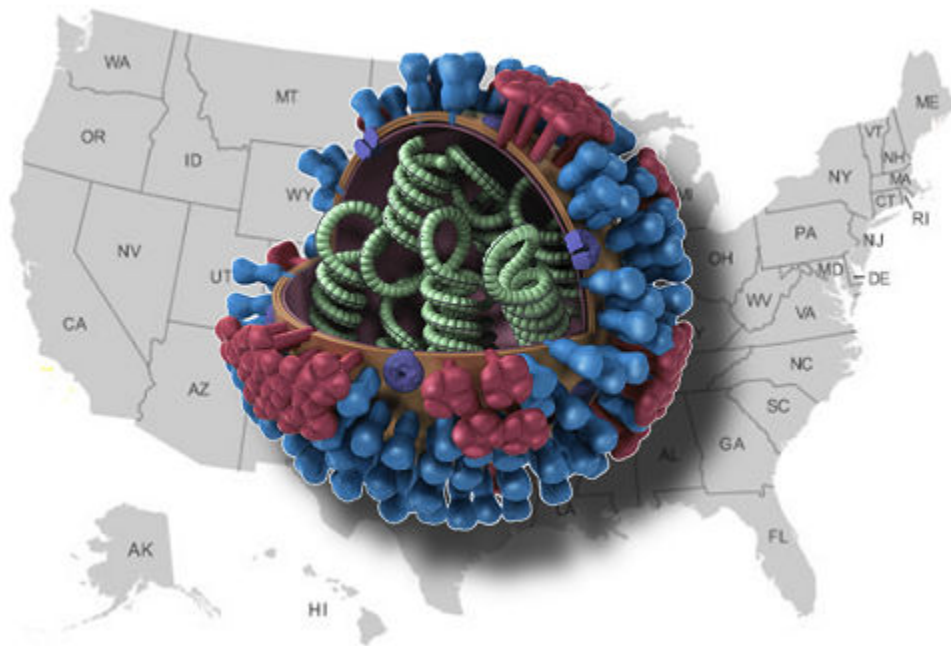
NIH Online Magazine features NCBI Researcher Teresa Przytycka

Tuesday, January 15, 2013

NIH's Intramural Research Program's online magazine, "Research in Action," has published a feature story on Teresa M. Przytycka, Ph.D. and her research team entitled "Algorithms for Life."

Dr. Teresa Przytycka is a Senior Investigator and Head of the Algorithmic Methods in Computational and Systems Biology Section in NCBI's Computational Biology Branch. For more information on her research and team, please see her Lab's webpage and a YouTube video made to accompany the NIH online magazine's article:

RefSeq Release 57 is Available for FTP

Monday, January 14, 2013

The complete RefSeq release 57 contains 34,169,407 records including 3,267,605 RNAs, and 27,845,459 proteins from 21,415 different organisms.

See the Release statistics file or Release notes for more information.

Please note that this update includes information from dbSNP Build 137, and includes incremental updates for human records.

In addition, in the first quarter of 2013 the bacterial RefSeq collection has been expanded to include more microbial genomes that represent complete or draft assemblies from novel microbial isolates as well as clinical and population samples. As part of this expansion, bacterial RefSeq genomes will be re-annotated to increase consistency across this dataset.

A New Eukaryotic Genome Annotation Status Page Keeps Researchers Informed

Thursday, January 10, 2013

Researchers often wonder "What's the status of a new build or annotation for my organism's genome?" You can now find out on the new Eukaryotic Annotation Status Page.

New Rat Genome Available in the MapViewer

Wednesday, January 09, 2013

The new *Rattus norvegicus* genome build (5.1) and annotation release (103) are now available in the MapViewer. Also, check out the Genome page listing additional information and BioProjects for the Norway Rat.

The NCBI Eukaryotic Genome Annotation Status Page. This new webpage explains the rationale for "Which genomes are annotated?", and lists "Recently completed annotation runs" and "Annotation runs in progress" along with links to the data and Assembly statistics.
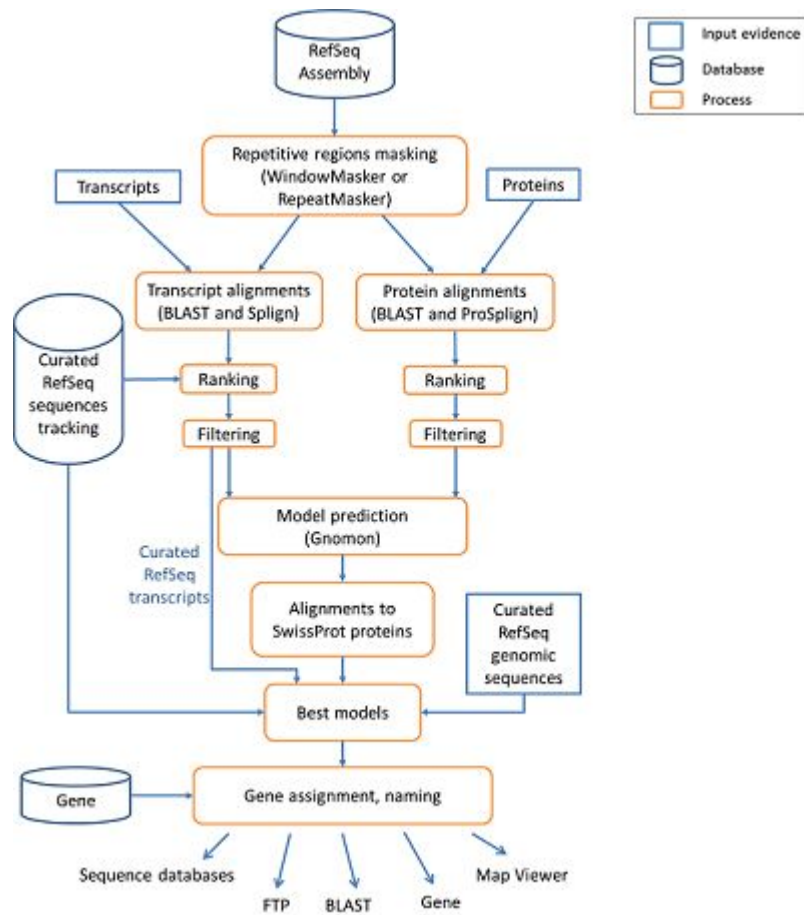
The NCBI Eukaryotic Genome Annotation Pipeline. This process provides content for various NCBI resources including Nucleotide, Protein and Genome databases, the BLAST sequence similarity algorithm, and the MapViewer genome browser. For more information, see the Eukaryotic Genome Annotation Process page.