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NCBI News, March 2010

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New Databases and Tools

Genetic Testing Registry

NIH has created the Genetic Testing Registry (GTR) that will provide access to information about the availability, validity, and usefulness of genetic tests. The NIH Office of the Director is overseeing the project. NCBI is responsible for developing the registry, expected to be fully ready in 2011. A press release with more information about GTR (www.nih.gov/news/health/mar2010/od-18.htm) and a preliminary GTR Website (www.ncbi.nlm.nih.gov/gtr/) are now available.

NCBI on Facebook and Twitter

NCBI updates and news are now on Facebook at "National Center for Biotechnology Information" and on Twitter at twitter.com/NCBI.

Bookshelf

Eighteen new reports are now on the NCBI Bookshelf in the collection of NIH-funded reports from the National Academies. To view these and other books go to: www.ncbi.nlm.nih.gov/sites/entrez?db=Books.

Microbial Genomes

Twenty-two finished microbial genomes were added to the NCBI databases during February. The original sequence data files submitted to GenBank/EMBL/DDBJ are on the FTP site: ftp.ncbi.nih.gov/genbank/genomes/Bacteria/. The RefSeq provisional versions of these genomes are also available: ftp.ncbi.nih.gov/genomes/Bacteria/.

GenBank News

GenBank release 176.0 is available on the NCBI Web Service and FTP site. The current release incorporates sequence data as of February 19, 2010. Release notes containing detailed information are available on the FTP site: ftp.ncbi.nlm.nih.gov/genbank/gbrel.txt.

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Updates and Enhancements

My NCBI Update

PubMed search results can now be customized using My NCBI through the new Result Display Settings option. For detailed information, see the NLM Technical Bulletin article: www.nlm.nih.gov/pubs/techbull/ma10/ma10_pm_results.html

E-utility Usage Policy

The requirement announced in December 2009 that all E-utilities requests must contain non-null values for both the "&email" and "&tool" parameters has been relaxed somewhat for limited use of the service. The revised policy is described in detail in the E-utilities help manual on the Bookshelf.

BLAST Release 2.2.23

BLAST version 2.2.23 of the stand-alone application is now available. Users are encouraged to move to the BLAST+ applications available at ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/. The BLAST+ programs supplant the legacy C toolkit BLAST package and will be the focus of future development. Specific enhancements for this release can be found on the BLAST News page.

RefSeq

RefSeq Release 40 is now available through the Entrez system and can be downloaded from the FTP site (ftp.ncbi.nlm.nih.gov/refseq/release). This full release incorporates genomic, transcript, and protein data available as of March 7, 2010. It includes 13,853,798 records from 10,291 different species and strains. Changes since the last release can be found in the release notes (ftp.ncbi.nlm.nih.gov/refseq/release/release-notes/RefSeq-release40.txt). More information on the RefSeq project is available on the RefSeq Homepage (www.ncbi.nlm.nih.gov/RefSeq/).

Exhibits

NCBI will exhibit at the American Association for Cancer Research annual meeting held April 17-21 in Washington, D.C.

Announce Lists and RSS Feeds

Eighteen topic-specific mailing lists are available which provide email announcements about changes and updates to NCBI resources including dbGaP, BLAST, GenBank, and Sequin. The various lists are described on the Announcement List summary page: www.ncbi.nlm.nih.gov/Sitemap/Summary/email_lists.html. For information on receiving updates about the *NCBI News*, please see: www.ncbi.nlm.nih.gov/About/news/announce_submit.html.

Twelve RSS feeds are now available from NCBI including news on PubMed, PubMed Central, NCBI Bookshelf, LinkOut, HomoloGene, UniGene, and NCBI Announce. Please see: www.ncbi.nlm.nih.gov/feed/.

Users can also keep up-to-date on changes, improvements and enhancements of NCBI resources on Facebook and Twitter: twitter.com/NCBI.

Send comments and questions about NCBI resources to: info@ncbi.nlm.nih.gov, or call 301-496-2475 between the hours of 8:30 a.m. and 5:30 p.m. EST, Monday through Friday.