Genomics, the NIH, and Health Informatics

Betsy L. Humphreys, MLS Deputy Director, NLM



NIH – Present at the creation of ...

- Genomics
- Health/Medical/Biomedical Informatics
 - -1964 − NLM: MEDLARS (\rightarrow MEDLINE \rightarrow PubMed)
 - 1966 NCI: Computer-assisted analysis of oligonucleotides
 - 1972 NLM: Informatics training
- Beginning of convergence
 - 1988 NCBI established by law at NLM;
 Office of Human Genome Research

established by NIH Director





Research/Healthcare Benefits of EHRs = Rationale for Common Standards = Perpetual Informatics R&D Agenda

- Research data captured as a by-product of patient care
- More rapid translation of research findings into improved patient care & public health
- Best evidence delivered to patients & health professionals when, where, & how needed



Do more of what works, e.g.,

- Rapid release of research data, standards, results in public, maintained, connected databases
- Standardization & "analysis" at the data source to reduce cost, improve quality
 - e.g., NISO Z39.96 JATS: Journal Article Tag Suite
- Use/improvement of existing standards for clinical research & genetics
 - e.g., SNOMED CT, LOINC, RxNorm, HL7
- New standards ONLY when needed, e.g., RefSeqGene
- Investigator-initiated informatics research
 - e.g., Personally-controlled health records, flexible anonymization techniques, explaining probability, NLP





New IHTSDO Policy Facilitates Inclusion of SNOMED CT Terms and Identifiers in International Research Databases, Other Health IT Standards

Copenhagen, Denmark: January 28th, 2011.

International Genetic Databases to be early beneficiary

The International Health Terminology Standards Development Organisation (IHTSDO) has announced a new policy to enable free use of English-language SNOMED CT terms and identifiers in international research databases, in complementary health IT standards, and in other projects and resources available worldwide. The new policy allows SNOMED CT to serve as a standard vocabulary for key data elements and value sets in international resources that accept input from - and are used in – both IHTSDO Member and non-Member countries.





A service of the U.S. National Library of Medicine | National Institutes of Health



UMLS Terminology Services

UTS Home **Applications** SNOMED CT

Resources

Downloads

Documentation

UMLS Home @

Welcome »

Request a License

Get a DVD

News/Announcements

Training

Welcome to the UTS

The UMLS Terminology Services (UTS) allows you to:

- Reguest a UMLS Metathesaurus License and create a UTS account
- Search and display content from UTS Applications including:
 - Metathesaurus Browser
 - Semantic Network Browser
 - SNOMED CT Browser
- Download data files including:
 - UMLS Knowledge Sources
 - RxNorm weekly and monthly updates
 - SNOMED CT
 - CORE Problem List and Route of Administration Subsets of SNOMED CT
- Query data remotely via Web Services (see API Documentation)
- Complete UMLS Annual Report and SNOMED CT® Affiliate Reports

Copyright| Privacy| Accessibility| Freedom of Information Act| National Institutes of Health| Health & Human Services

















Sign In | Sign Up | Contact



Search NCBI

Search



The Genetic Testing Registry (GTR) is currently in development, with a projected launch in the latter part of 2011. Once operational, GTR will provide access to information about genetic tests for inherited and somatic genetic variations, including newer types of tests such as arrays and multiplex panels. GTR information about tests primarily will be based on voluntary data submissions by test developers and manufacturers.

A key part of the GTR development process has been engagement with stakeholders—such as genetic test developers, test kit manufacturers, health care providers, patients, researchers, and relevant federal agencies—for their insights on critical data elements to include in the database and the best ways to display test information. Further information about that is available on NIH's GTR policy website, at http://oba.od.nih.gov/GTR/gtr_intro.html; the policy website includes background information, FAQs, Federal Register notices, public comments on the June 11, 2010 Request for Information, a transcript of the November 2, 2010 public meeting, and other information.

The GTR design is continuing to evolve based on feedback from advisory groups, stakeholders and other interested parties. However, it is sufficiently developed that NCBI is making available working documents about the design for further comment. Please see the README file for context and explanations of the other documents.

Send a comment

Files Available for Download

README	pdf Word	text
GTR Design Considerations	pdf Word	text
Proposed GTR Field Definitions	pdf Word	text
GTR Test Example files		zip
GTR Test Example Display (Screen Sho	ots)	pdf
GTR Submission XML Example		xml



Office of Biotechnology Activities

r Genetics, Health, Society

Help Sitemap Contact us

Search

Printer Friendly Page

http://oba.od.nih.gov/GTR/gtr_intro.html/

Genetic Testing Registry



A service of the U.S. National Library of Medicine NIH National Institutes of Health

Home About MedlinePlus Site Map FAQs Contact Us

|--|

Health Topics

Drugs & Supplements Videos & Cool Tools



GO

MedlinePlus Connect: Linking Electronic Health Records (EHRs) to MedlinePlus Health Information

Overview

MedlinePlus Connect is a free service of the National Library of Medicine (NLM) and the National Institutes of Health (NIH). This service allows electronic health record (EHR) systems to easily link users to MedlinePlus, an authoritative up-to-date health information resource for patients, families and health care providers.

How it Works

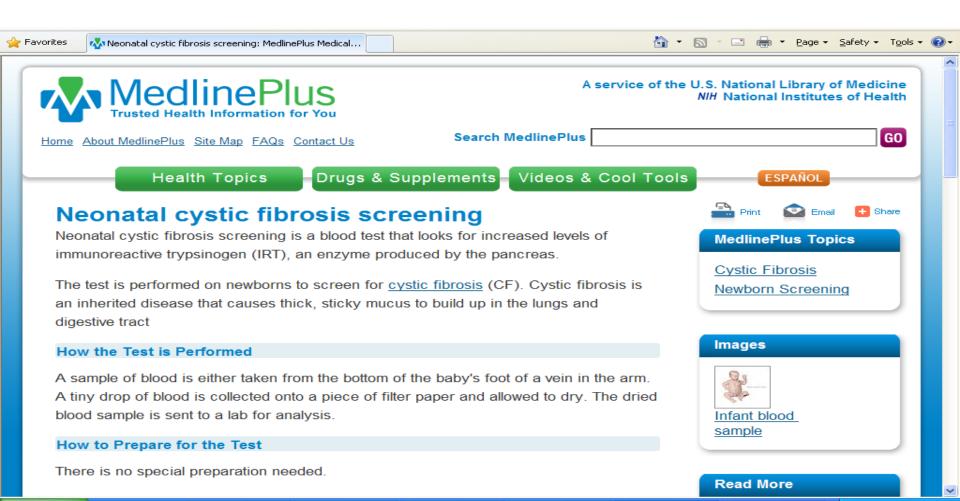
MedlinePlus Connect accepts requests for information on diagnoses (problem codes) and medications. It is available as a Web application or a Web service.



NATIONAL LIBRARY OF MEDICINE, NATIONAL INSTITUTES OF HEALTH, HEALTH AND HUMAN SERVICES

COMING SOON: Lab test links in MedlinePlus Connect

LOINC:3067-6 Trypsinogen I Free [Mass/volume] in Serum or Plasma ↓





Home Search Study Topics Glossary

Search

Full Text View

Tabular View

No Study Results Posted

Related Studies

Effects of CYP2B6 Genetic Polymorphisms on Efavirenz Pharmacokinetics

This study is ongoing, but not recruiting participants.

First Received on November 27, 2007. Last Updated on May 25, 2010 History of Changes

Sponsor:	Indiana University
Collaborator:	National Institutes of Health (NIH)
Information provided by:	Indiana University
ClinicalTrials.gov Identifier:	NCT00668395

Purpose

 To see how the liver breaks down efavirenz by an enzyme called CYP2B6. It is suggested that when Efavirenz is taken repeatedly it may increase the amount of CYP2B6 in your liver and thus speed up your liver's ability to get rid of efavirenz from your body. This may render efavirenz and other medications ineffective.



CLCNKA (Ka Renal Chloride Channel[CIC-Ka]) Polymorphism Effects on Hypertrophy Regression

This study is not yet open for participant recruitment.

Verified on January 2011 by Washington University School of Medicine

First Received on January 10, 2011. Last Updated on January 19, 2011 History of Changes

Sponsor:	Washington University School of Medicine
Collaborator:	University of Pennsylvania
Information provided by:	Washington University School of Medicine
ClinicalTrials.gov Identifier:	NCT01275352

Purpose

This study will consist of middle-aged Caucasian non-failing subjects with high blood pressure who are homozygous for a gene that confers increased risk of developing heart failure, the Glycine 83 variant of the Ka renal chloride channel (CIC-Ka Gly/Gly 83), or middle-aged Caucasian non-failing hypertensive subjects who lack the heart failure risk gene, the wild-type Arginine 83 Ka renal chloride channel (CIC-Ka Arg/Arg 83). Subjects on standard therapy for high blood pressure with an angiotensin converting inhibitor (ACEI) or angiotensin recenter blocker (APR) will be randomized to additional treatment with enforcement



