

THE DATA CITATION INDEX^S

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Mike Takats

Thomson Reuters

April 30, 2013

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In 1955, Dr. Eugene Garfield revolutionized research with his concept of citation indexing and searching, giving birth to the **Science Citation Index®**

Web of Science is the largest citation database with approx. **900 million cited references** from 1900 to 2013

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1961



1961 Science Citation Index® revolutionizes scientific research

1974 Derwent World Patents Index® provides searchable access to patents from all technologies

1997 Web of Science™ provides seamless access to information from worldwide research journals



2001 Web of Knowledge™ provides a single research platform for journal literature, patents, chemical compounds, genetic sequencing and more



2006 ScholarOne Manuscripts Management® enables authors to create manuscripts in EndNote and seamlessly submit them for review

2007 ResearchID provides an invaluable index to accurate author identification and information

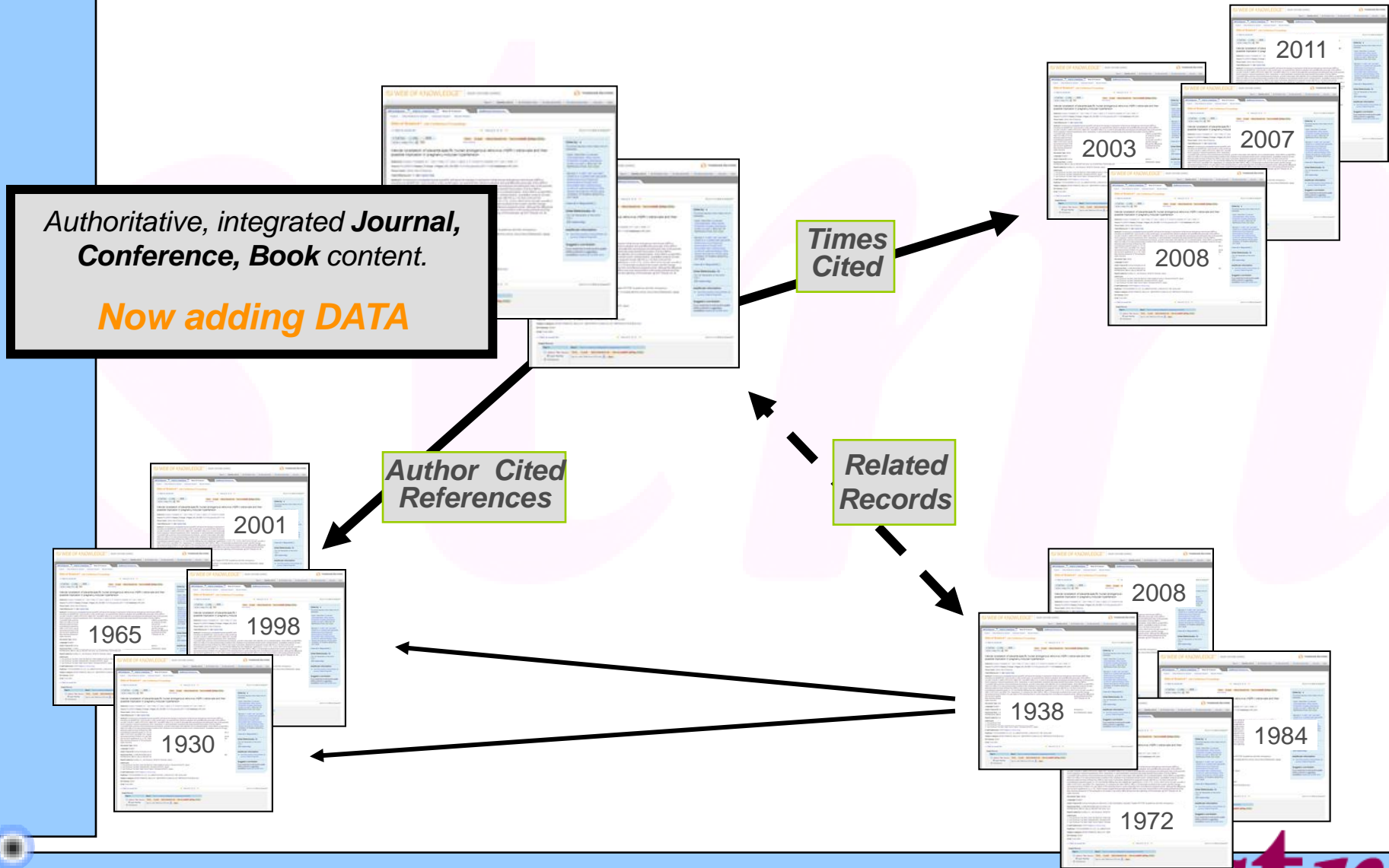
2009 Thomson Reuters launches InCites, the first ever tool to provide comprehensive, customized citation-based research evaluation on the Web

2010 Thomson Reuters undertakes massive data collection exercise, partnering with hundreds of universities worldwide in the Global Institutional Profiles Project

2011 Thomson Reuters Research In View™ helps redefine research management. The enterprise-wide solution links and standardizes data from multiple sources, connecting scholarly activity across an entire institution

2011

WEB OF KNOWLEDGE - A FULL RESEARCH PICTURE



Data Citation IndexSM : Connecting Data to the Research it Informs



Advancing Discovery, Access, Citation and Metrics
on Research Data

BENEFITS OF RESEARCH DATA SHARING



By tk-link

- Advancement of scholarship
- Verification of results
- Promotion of scholar's work

INFLUENCE OF FUNDING AGENCIES

2010 Mandate from the US National Science Foundation –

All funding proposals submitted or due on or after January 18, 2011, must include a “Data Management Plan” describing how the proposal will conform to NSF policy on the dissemination and sharing of research results.



Data elevated to “Article Status”?

January 14, 2013.. Biographical Sketch(es), has been revised to rename the “Publications” section to “Products”.... This change makes clear that products may include, but are not limited to, publications, data sets, software, patents, and copyrights.

Biosketches now include “Products”, not “Publications



IMPACT ON RESEARCH LIBRARIES

The image shows a composite of two web pages. The top page is titled "Data Management at Harvard" and features a navigation menu with items like "Overview", "Feedback", "Harvard Guidelines and Policies", "Funding Agencies Guidelines and Policies", "Publishing and Storing Your Data", "Security", and "Best Practices". The main content area is titled "Funding Agencies Guidelines and Policies" and specifically addresses the "National Science Foundation".

The bottom page is a screenshot of the Association of Research Libraries (ARL) website. The header includes the ARL logo and the text "ASSOCIATION OF RESEARCH LIBRARIES" with the URL "www.arl.org". The main article is titled "Transforming Research Libraries" and "E-Science", with a sub-heading "Guide for Research Libraries: The NSF Data Sharing Policy". The authors are listed as Patricia Hswe and Ann Holt. The article text states: "In Spring 2010, the National Science Foundation (NSF) announced that it would alter its data sharing policy to require data management plans (DMPs) in future grant proposals to the agency. The Association for Research Libraries has developed...". A sidebar on the left contains a "Planning and Visioning" section with links to "Resources for Planning and Visioning" and "Envisioning Research Library Futures: A Scenario Thinking Project". A "More on This Topic" section lists "Unpacking the NSF Requirement" and "A New Leadership Role for Libraries".

VISIBILITY OF RESEARCH DATA

Grant funding agencies

Journal publishers

Data repositories & registration agencies



WHERE DO WE START?

Discover data repositories, data studies & data sets in the context of traditional literature

Help researchers find data sets and studies and track the full impact of their research output

REPOSITORY SELECTION & EVALUATION



REUTERS/ Moham Rizza

REPOSITORY EVALUATION, SELECTION, AND COVERAGE POLICIES

FOR THE DATA CITATION INDEXSM WITHIN THOMSON REUTERS WEB OF KNOWLEDGESM

- Editorial Content
- Persistence and stability
- Thoroughness of descriptive information.
- Links from data to research literature.

Selection essay:

http://wokinfo.com/products_tools/multidisciplinary/dci/selection_essay/

CHALLENGES

Data availability

Data quality



U.S. Dept. of Justice, Bureau of Justice Statistics (1996): MURDER CASES IN 33 LARGE URBAN COUNTIES IN THE UNITED STATES, 1988. Version 1. Inter-university Consortium for Political and Social Research [distributor].

<http://dx.doi.org/10.3886/ICPSR09907.v1>

Our first data set is the Bureau of Justice Statistics "Murder Cases in 33 Large Urban Counties." This is a random sample of homicide cases drawn from prosecutors' files. The data set includes information on offender characteristics, victim characteristics and trial outcomes for 2800 murders. The 75 largest counties account for more than half of the murders in the U.S. each year. This data set brings together information on the crime, the offender, the victim, and the sentence. Such information cannot all be linked in other larger data sets such as the Uniform Crime Reporting (UCR) Data or the National Crime Victimization Survey (NCVS). Most crime

INDEXING OF RESEARCH DATA REPOSITORIES

TR takes
descriptive
metadata feed
from repository

Repository
raw metadata
is analyzed by
TR

TR adds
metadata

TR DCI records:
- data repository
- data study
- data set

Data Citation IndexSM : Connecting Data to the Research it Informs



REUTERS/Aly Song

- Almost 100 repositories covered
- Comprising >2.5 million records
- Reciprocal links to/from DCI and WoS records

Data Citation IndexSM : Connecting Data to the Research it Informs

Show Refine

Data Types

Refine

Exclude

Cancel

Sort these by: Record Count

The first 100 Data Types (by record count) are shown. For advanced refine options, use [Analyze results](#).

- | | | |
|--|---|---|
| <input type="checkbox"/> RNA (507,025) | <input type="checkbox"/> NUMERIC (1,434) | <input type="checkbox"/> TEXTUAL DATA INDIVIDUAL MICRO LEVEL (210) |
| <input type="checkbox"/> PROTEIN SEQUENCE DATA (500,413) | <input type="checkbox"/> GENOME BINDING OCCUPANCY PROFILING BY GENOME TILING ARRAY (1,108) | <input type="checkbox"/> SNP GENOTYPING BY SNP ARRAY (190) |
| <input type="checkbox"/> VECTOR DIGITAL DATA (189,171) | <input type="checkbox"/> BATHYMETRY SINGLEBEAM (841) | <input type="checkbox"/> PRESSURE (184) |
| <input type="checkbox"/> GENOMIC (105,267) | <input type="checkbox"/> NUMERIC DATA INDIVIDUAL MICRO LEVEL (755) | <input type="checkbox"/> CTD ANCILLARY (179) |
| <input type="checkbox"/> TABULAR DIGITAL DATA (89,966) | <input type="checkbox"/> GRAVITY FIELD (738) | <input type="checkbox"/> NUMERIC SURVEY DATA (174) |
| <input type="checkbox"/> RAW DATA (21,338) | <input type="checkbox"/> MAGNETIC FIELD (683) | <input type="checkbox"/> NUMERIC SUMMARY STATISTICS (162) |
| <input type="checkbox"/> MIRNA SEQUENCE DATA (18,227) | <input type="checkbox"/> EVENT TRANSACTION DATA (670) | <input type="checkbox"/> METHYLATION PROFILING BY GENOME TILING ARRAY (158) |
| <input type="checkbox"/> EXPRESSION PROFILING BY ARRAY (17,977) | <input type="checkbox"/> TEMPERATURE (662) | <input type="checkbox"/> SEISMIC REFLECTION SCS (147) |
| <input type="checkbox"/> SURVEY DATA (16,873) | <input type="checkbox"/> STRUCTURED QUESTIONNAIRE (650) | <input type="checkbox"/> TEXTUAL DATA NUMERIC DATA INDIVIDUAL MICRO LEVEL (146) |
| <input type="checkbox"/> PROCESSED DATA (16,229) | <input type="checkbox"/> BATHYMETRY SWATH (643) | <input type="checkbox"/> NUMERIC DATA ALPHA NUMERIC DATA INDIVIDUAL MICRO LEVEL (143) |
| <input type="checkbox"/> SCAN (15,302) | <input type="checkbox"/> ADMINISTRATIVE RECORDS DATA (566) | <input type="checkbox"/> GIS VECTOR DATA (141) |
| <input type="checkbox"/> NORMALIZATION (11,548) | <input type="checkbox"/> AGGREGATE DATA (558) | <input type="checkbox"/> PHENOTYPE STRAIN SURVEY (141) |
| <input type="checkbox"/> SRA (10,721) | <input type="checkbox"/> METEOROLOGICAL (534) | <input type="checkbox"/> CLINICAL DATA (131) |
| <input type="checkbox"/> PROCESSED DATA MATRIX (9,127) | <input type="checkbox"/> CENSUS ENUMERATION DATA (524) | <input type="checkbox"/> NUMERIC DATA AGGREGATE MACRO LEVEL (124) |
| <input type="checkbox"/> CURRENT ALL LINES COUNTY BASED (6,468) | <input type="checkbox"/> GENOME VARIATION PROFILING BY GENOME TILING ARRAY (488) | <input type="checkbox"/> CURRENT BLOCK GROUP STATE BASED (112) |
| <input type="checkbox"/> CURRENT AREA HYDROGRAPHY COUNTY BASED (6,468) | <input type="checkbox"/> GENOME BINDING OCCUPANCY PROFILING BY HIGH THROUGHPUT SEQUENCING (477) | <input type="checkbox"/> CURRENT BLOCK STATE BASED (112) |
| <input type="checkbox"/> TOPOLOGICAL FACES POLYGONS WITH ALL GEOCODES COUNTY BASED SHAPEFILE (6,468) | <input type="checkbox"/> NON CODING RNA PROFILING BY ARRAY (463) | <input type="checkbox"/> CURRENT CENSUS TRACT STATE BASED (112) |
| <input type="checkbox"/> CURRENT TOPOLOGICAL FACES AREA HYDROGRAPHY COUNTY BASED RELATIONSHIP FILE (6,467) | <input type="checkbox"/> BATHYMETRY (404) | <input type="checkbox"/> CURRENT COUNTY SUBDIVISION STATE BASED (112) |
| <input type="checkbox"/> CURRENT FEATURE NAMES COUNTY BASED RELATIONSHIP FILE (6,466) | <input type="checkbox"/> CONDUCTIVITY (390) | <input type="checkbox"/> CURRENT PLACE STATE BASED (112) |
| <input type="checkbox"/> ALL ROADS COUNTY BASED (6,464) | <input type="checkbox"/> EXPRESSION PROFILING BY GENOME TILING ARRAY (346) | <input type="checkbox"/> CURRENT UNIFIED SCHOOL DISTRICT STATE BASED (112) |
| <input type="checkbox"/> LINEAR HYDROGRAPHY COUNTY BASED (6,464) | <input type="checkbox"/> GENOME VARIATION PROFILING BY ARRAY (342) | <input type="checkbox"/> ICECONCENTRATION (112) |
| <input type="checkbox"/> ADDRESS RANGE FEATURE COUNTY BASED (6,442) | <input type="checkbox"/> NAVIGATION (335) | <input type="checkbox"/> PRIMARY AND SECONDARY ROADS STATE BASED (112) |
| <input type="checkbox"/> CURRENT ADDRESS RANGE FEATURE NAME COUNTY BASED RELATIONSHIP FILE (6,442) | <input type="checkbox"/> GENOME VARIATION PROFILING BY SNP ARRAY (327) | <input type="checkbox"/> DATASET (107) |
| <input type="checkbox"/> CURRENT ADDRESS RANGES COUNTY BASED RELATIONSHIP FILE (6,442) | <input type="checkbox"/> NON CODING RNA PROFILING BY HIGH THROUGHPUT SEQUENCING (321) | <input type="checkbox"/> CURRENT STATE LEGISLATIVE DISTRICT SLD UPPER CHAMBER STATE BASED (104) |
| <input type="checkbox"/> TEXT TAB SEPARATED VALUES (4,257) | <input type="checkbox"/> SIDESCAN (280) | <input type="checkbox"/> CURRENT STATE LEGISLATIVE DISTRICT SLD LOWER CHAMBER STATE BASED (100) |
| <input type="checkbox"/> OTHER IDENTIFIERS RELATIONSHIP FILE (4,161) | <input type="checkbox"/> BACKSCATTER ACOUSTIC (263) | <input type="checkbox"/> SEQUENCE DATA (100) |
| <input type="checkbox"/> NAVIGATION PRIMARY (3,691) | <input type="checkbox"/> SALINITY (254) | <input type="checkbox"/> SOUNDVELOCITY (92) |
| <input type="checkbox"/> CURRENT AREA LANDMARK COUNTY BASED (3,222) | <input type="checkbox"/> EXPRESSION PROFILING BY HIGH THROUGHPUT SEQUENCING (245) | <input type="checkbox"/> GENOME BINDING OCCUPANCY PROFILING BY ARRAY (90) |
| <input type="checkbox"/> CURRENT TOPOLOGICAL FACES AREA LANDMARK COUNTY BASED RELATIONSHIP FILE (3,222) | <input type="checkbox"/> RADIATION VISIBLE (234) | <input type="checkbox"/> NON CODING RNA PROFILING BY GENOME TILING ARRAY (89) |
| <input type="checkbox"/> CURRENT POINT LANDMARK COUNTY BASED (3,219) | <input type="checkbox"/> EXPRESSION PROFILING BY SAGE (225) | <input type="checkbox"/> TEXTUAL DATA NUMERIC DATA ALPHA NUMERIC DATA (87) |
| <input type="checkbox"/> MIXED (3,069) | <input type="checkbox"/> RADIATION INFRARED (221) | <input type="checkbox"/> ALPHA NUMERIC DATA INDIVIDUAL MICRO LEVEL (85) |
| <input type="checkbox"/> SAGE (2,531) | <input type="checkbox"/> MPSS (211) | <input type="checkbox"/> NUMERIC DATA (82) |
| <input type="checkbox"/> PROTEIN (2,362) | <input type="checkbox"/> FLUORESCENCE (210) | <input type="checkbox"/> FIELD STUDY (80) |
| <input type="checkbox"/> NUMERIC SURVEY (2,247) | | |

Refine

Exclude

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Sort these by: Record Count

Data Citation IndexSM : Connecting Data to the Research it Informs

Data Citation IndexSM

“Repository” Record – Link to the citing literature.

<< Back to results list

Record 3 of 6

Record from Data Citation IndexSM

Save to: [ENDNOTE[®] WEB](#) [ENDNOTE[®]](#) [RefWorks](#) [ResearcherID](#) more options

UniProt Knowledgebase.

Editor(s): [UniProt Consortium](#)

Source: UniProt Knowledgebase

Source URL: <http://www.uniprot.org/>

Cited References: 0

Abstract: The UniProt Knowledgebase accurate, consistent and rich annotated amino acid sequence, protein name or possible is added. This includes widely of the quality of annotation in the form

Document Type: **Repository**

Accession Number: DRCI:DATA201

Language: English

Funding:

Funding Agency

National Institutes of Health

European Commission SLING

NIH GO

Swiss Federal Office of Education and

GEN2PHEN

MICROME

NIH

Full Text Full Text Links NCBI Save to: ENDNOTE[®] WEB ENDNOTE[®] RefWorks ResearcherID more options

From protein sequences to 3D-structures and beyond: the example of the UniProt Knowledgebase

Author(s): [Hinz, U \(Hinz, Ursula\)¹](#)

Group Author(s): [UniProt Consortium](#)

Source: CELLULAR AND MOLECULAR LIFE SCIENCES Volume: 67 Issue: 7 Pages: 1049-1064 DOI: 10.1007/s00018-009-0229-6 Published: APR 2010

Times Cited: 5 (from Web of Science)

Cited References: 106 [[view related records](#)] [Citation Map](#)

Abstract: With the dramatic increase in the volume of experimental results in every domain of life sciences, assembling pertinent data and combining information from different fields has become a challenge. Information is dispersed over numerous specialized databases and is presented in many different formats. Rapid access to experiment-based information about well-characterized proteins helps predict the function of uncharacterized proteins identified by large-scale sequencing. In this context, universal knowledgebases play essential roles in providing access to data from complementary types of experiments and serving as hubs with cross-references to many specialized databases. This review outlines how the value of experimental data is optimized by combining high-quality protein sequences with complementary experimental results, including information derived from protein 3D-structures, using as an example the UniProt knowledgebase (UniProtKB) and the tools and links provided on its website (<http://www.uniprot.org/>). It also evokes precautions that are necessary for successful predictions and extrapolations.

Accession Number: WOS:000275419800003

Document Type: Review

Language: English

Author Keywords: Data flood; Annotation; Swiss-Prot; Knowledgebase; UniProtKB; Proteomics; Structural genomics; Protein 3D-structure

KeyWords Plus: DEPENDENT K+ CHANNEL; X-RAY-STRUCTURE; STRUCTURAL GENOMICS; CRYSTAL-STRUCTURE; UNIPROT; SWISS-PROT; DISORDERED PROTEINS; INTERACTOME NETWORK; ATOMIC

222886-2

5R01GM080646-04

0284GM088646-0188

Times Cited: 11

[Create Citation Alert](#)

This article has been cited 11 times in Web of Knowledge.

Hinz, Ursula. From protein sequences to 3D-structures and beyond: the example of the UniProt Knowledgebase. CELLULAR AND MOLECULAR LIFE SCIENCES, APR 2010.

Lima, Tania. HAMAP: a database of completely sequenced microbial proteome sets and manually curated microbial protein families in UniProtKB/Swiss-Prot. NUCLEIC ACIDS RESEARCH, JAN 2009.

Suzek, Baris E. UniRef: comprehensive and non-redundant UniProt reference clusters. BIOINFORMATICS, MAY 15 2007.

[\[view all 11 citing articles \]](#)

Cited References: 0

Additional information

[How to cite this Resource](#)

Times Cited: 5

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This article has been cited 5 times in Web of Knowledge.

Moro, Monica. Identification of New Hematopoietic Cell Subsets with a Polyclonal Antibody Library Specific for Neglected Proteins. PLOS ONE, APR 4 2012.

MacDonald, Justin A. Intrinsically Disordered N-Terminus of Calponin Homology-Associated Smooth Muscle Protein (CHASM) Interacts with the Calponin Homology Domain to Enable Tropomyosin Binding. BIOCHEMISTRY, APR 3 2012.

Bombarely, Aureliano. The Sol Genomics Network (solgenomics.net): growing tomatoes using Perl. NUCLEIC ACIDS RESEARCH, JAN 2011.

[\[view all 5 citing articles \]](#)

Related Records:

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“Repository” Records – information presented may vary depending upon the characteristics of the repository.

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Data Citation IndexSM

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Record 1 of 5,338

Record from Data Citation IndexSM

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GSE12195: Mutations of multiple genes deregulate the NF- κ B pathway in diffuse large B cell lymphoma.

From Repository: Gene Expression Omnibus.

Author(s): Pasqualucci, Laura; Basso, Katia

Source: Gene Expression Omnibus **Source URL:** <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE12195> (Viewed Date: 12 Dec 2011)

Published Year: 2009

Cited References: 0

Abstract: Diffuse large B-cell lymphoma (DLBCL), the most common form of lymphoma in adulthood, comprises distinct subtypes including germinal center B cell-like (GCB) and activated B cell like (ABC) DLBCL. Gene expression of its most aggressive subtype, ABC-DLBCL, is associated with constitutive activation of the NF- κ B transcription factor. The fraction of cases, it remains unclear whether NF- κ B activation in these tumors represents an intrinsic program of pathogenetic event. Here we show that >50% of ABC-DLBCL and a smaller fraction of GCB-DLBCL carry somatic mutations including negative (TNFAIP3/A20) and positive (CARD11, TRAF2, TRAF5, MAP3K7/TAK1 and TNFRSF11A/RAA20) gene, which encodes for a ubiquitin-modifying enzyme involved in termination of NF- κ B responses, is the most frequent of the patients displaying biallelic inactivation by mutations and/or deletions, suggesting a tumor suppressor role for TRAF2 and CARD11 produce molecules with significantly enhanced ability to activate NF- κ B. Thus, our results suggest that DLBCL is caused by genetic lesions affecting multiple genes, whose loss or activation may promote lymphomagenesis. We show that most ABC-DLBCL and a smaller fraction of GCB-DLBCL display germline mutations in NF- κ B pathway genes, with A20 representing the most frequently mutated gene.

Document Type: Data study

Data Type: Expression profiling by array

Accession Number: DRCL:DATA2012007000275875

Language: English

Author Keywords: Phenotypic characterization of human DLBCL

Addresses:

1. Columbia University, Institute for Cancer Genetics, 1130 St Nicholas Ave, New York, 10032, USA
2. Columbia University, Institute for Cancer Genetics, 1150 St. Nicholas Avenue, New York, 10032, USA

E-mail Address: lp171@columbia.edu; kb451@columbia.edu

Web of Science Category: Biochemistry & Molecular Biology; Genetics & Heredity

Subject Area: Biochemistry & Molecular Biology; Genetics & Heredity

Taxonomic Data:

SUPER TAXA	TAXA NOTES	Organism Classifier	Organism Name
Animalia, Chordata, Vertebrata, Mammalia, Primates	Animals, Chordates, Humans, Mammals, Primates, Vertebrates	Hominidae	Homo sapiens

Miscellaneous: Transcription; missense mutation; Gene Expression Profiling; phenotype; Tumor; B-Cell lymphoma; Germinal Center; genomics; Molecular Genetics

Associated Records: [View All]

GSM476306: Lymphoblastoid B cell line_IARC 304.	Data set	Link to External Source
GSM476290: Follicular lymphoma_FLE.14.	Data set	Link to External Source
GSM476291: Follicular lymphoma_FLE.15.	Data set	Link to External Source
GSM476279: Follicular lymphoma_FLE.03.	Data set	Link to External Source

Times Cited: 4

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This article has been cited 4 times in Web of Knowledge.

Pasqualucci, Laura. Inactivating mutations of acetyltransferase genes in B-cell lymphoma. NATURE, MAR 10 2011.

How to cite this Resource - Windows Internet Explorer

Thomson Reuters recommend citing this resource as:
Pasqualucci, Laura; Basso, Katia (2009): GSE12195: Mutations of multiple genes deregulate the NF- κ B pathway in diffuse large B cell lymphoma. Gene Expression Omnibus. <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE12195>

Cited References: 0

[How to cite this Resource](#)

[Suggest a correction](#)

If you would like to improve the quality of the data in this record, please [suggest a correction](#).

This Data Study record links to multiple Data Set records.

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Data Citation IndexSM : Connecting Data to the Research it Informs

Data Citation IndexSM

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Record 1 of 1

Record from Data Citation IndexSM

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GSM476306: Lymphoblastoid B cell line_IARC 304.

From Data study: GSE12195: Mutations of multiple genes deregulate the NF- κ B pathway in diffuse large B cell lymphoma.

Author(s): Pasqualucci, Laura; Basso, Katia

Source: Gene Expression Omnibus Source URL: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM476306> (Viewed Date: 12 Dec 2011)

Published Year: 2010

Cited References: 0

Abstract: Gene expression data from lymphoblastoid cell line.

Document Type: Data set

Data Type: RNA

Accession Number: DR0

Language: English

Addresses:

1. Columbia University, Ins
2. Columbia University, Ins

E-mail Address: lp171@

Web of Science Catego

Subject Area: Biochemis

Taxonomic Data:

SUPER TAXA

Animalia, Chordata, Vert
Primates

Method: Platform:GPL57

The screenshot shows the NCBI GEO Accession Display page for GSM476306. The page includes a search bar, navigation links, and a detailed description of the sample. The 'GEO' logo is highlighted with a red circle, and a red arrow points from the source URL in the Data Citation Index record to this logo.

Sample GSM476306	
Status	Public on Feb 01, 2010
Title	Lymphoblastoid B cell line_IARC 304
Sample type	RNA
Source name	EBV-immortalized lymphoblastoid cell line
Organism	<i>Homo sapiens</i>
Characteristics	cell type: EBV-immortalized lymphoblastoid B cell cell line: IARC 304
Treatment protocol	Cells were lysated in Trizol Reagent (Invitrogen) and frozen
Extracted molecule	total RNA
Extraction protocol	Total RNA was extracted using Trizol Reagent (Invitrogen) following the manufacturer's indications.
Label	biotin
Label protocol	Biotinylated cRNA were prepared according to the standard Affymetrix protocol from 6 ug total RNA (Expression Analysis Technical Manual, 2001, Affymetrix).
Hybridization protocol	Following fragmentation, 15 ug of cRNA were hybridized for at least 16 hr at 45C on GeneChip Human Genome Array U133Plus_2. GeneChips were washed and stained in the Affymetrix Fluidics Station 450.

Times Cited: 0

Create Citation Alert

This article has been cited 0 times in Web of Knowledge.

Cited References: 0

Additional information

How to cite this Resource

Suggest a correction


If you would like to improve the quality of the data in this record, please suggest a correction.

STM

What's next for DCI?

- ✓ More repositories and data sets
- ✓ Improving Data citation capture
- ✓ Developing new Metrics
- ✓ Continue working with industry partners to influence data citation practice

Time's Up!



About your speaker:

- Name: Mike Takats
- Company: Thomson Reuters
- Tel: +1 215 823 3712
- Email:
michael.takats@thomsonreuters.com