The Danish Node

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The Danish ELIXIR node: goals and means

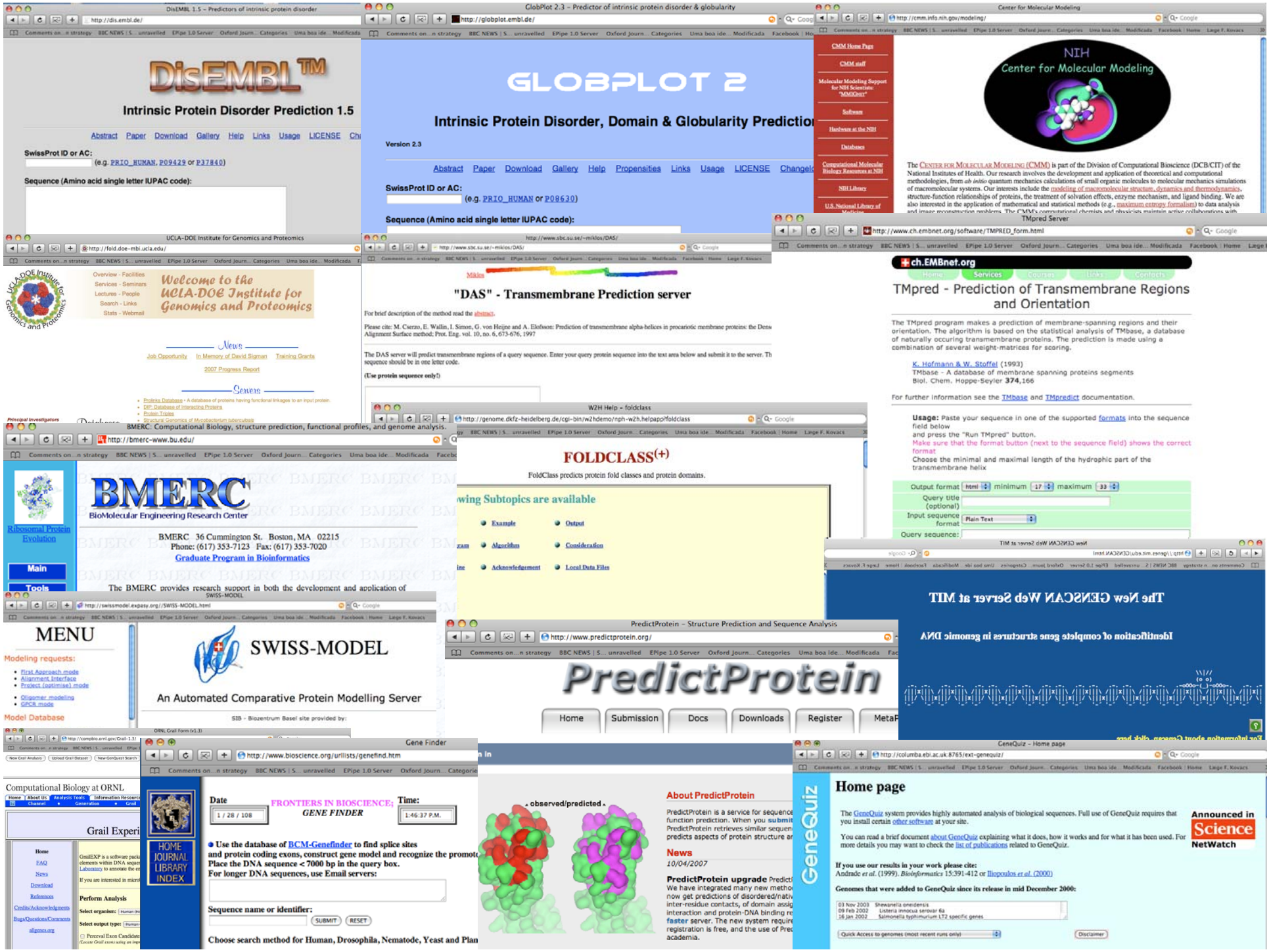
"The overall purpose of the Danish ELIXIR node on bioinformatics tool interoperability and integration is to address the main problems in tool utilization experienced currently by the life sciences community."

Three key concepts:

- Being user-centric
- Consultancy
- EU-wide partnerships

ELIXIR Denmark Node

- The Danish ELIXIR Node is coordinated by DTU, and includes CU, AU, and SDU as partners + Industry partners.
- The overall purpose of the Danish ELIXIR Node is :
  - The creation of a comprehensive tool registry
  - The provision of tools in the form preferred by users across academia and industry
  - Tool interoperability
  - Benchmarking, ensure tool sustainability through different interfaces


DisEMBL 1.5 - Predictors of intrinsic protein disorder
DisEMBL™
Intrinsic Protein Disorder Prediction 1.5
Abstract Paper Download Gallery Help Links Usage LICENSE
SwissProt ID or AC:
Sequence (Amino acid single letter IUPAC code):
GlobPlot 2.3 - Predictor of intrinsic protein disorder & globularity
GLOBPLOT 2
Intrinsic Protein Disorder, Domain & Globularity Prediction
Version 2.3
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Center for Molecular Modeling
NIH
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CMM Home Page
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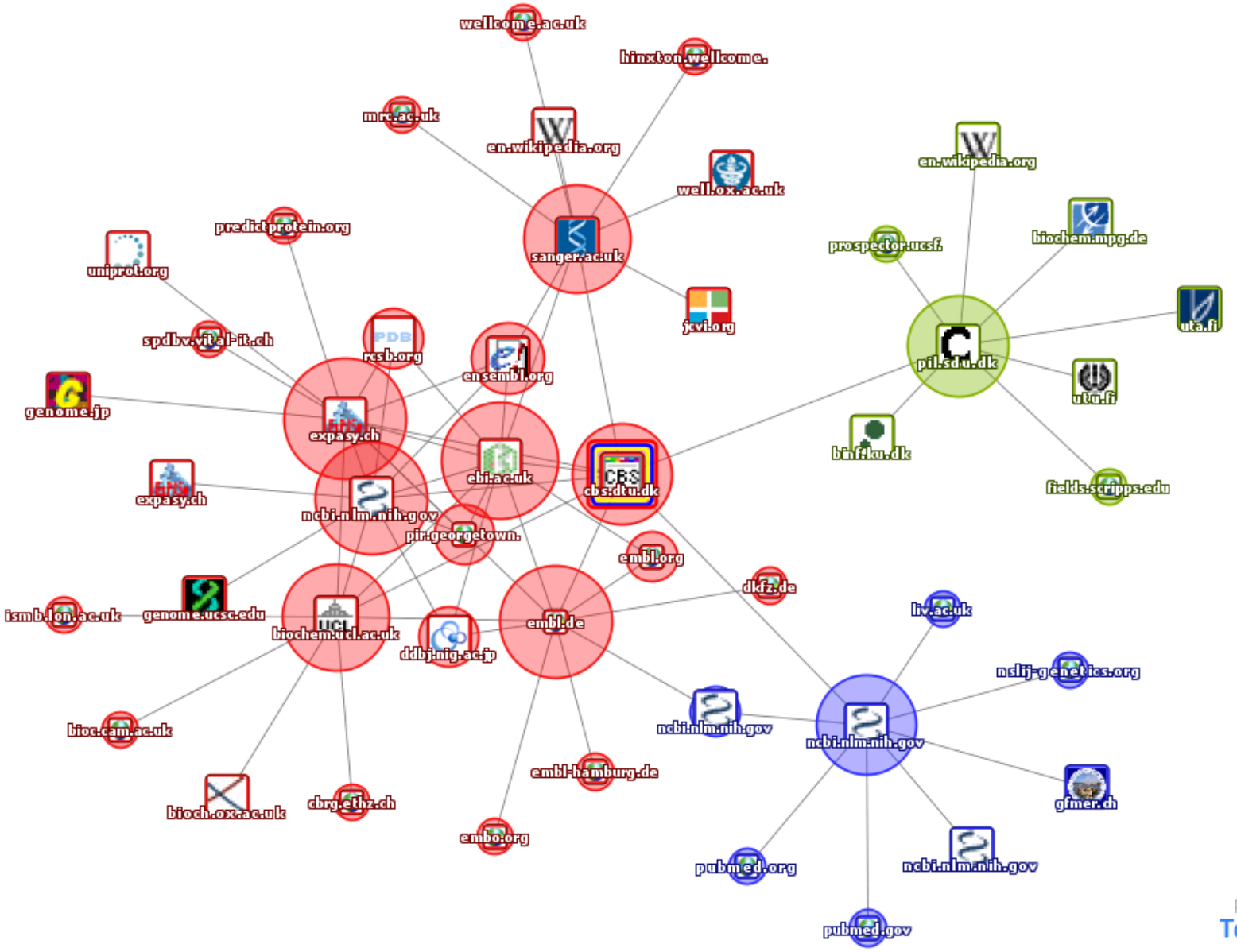
Software
Hardware at the NIH
Databases
NIH Library
The Center for Molecular Modeling (CMM) is part of the Division of Computational Bioscience (DCB/CIT) of the National Institutes of Health.
UCLA-DOE Institute for Genomics and Proteomics
Welcome to the UCLA-DOE Institute for Genomics and Proteomics
News
Servers
"DAS" - Transmembrane Prediction server
TMpred Server
ch.EMBnet.org
TMpred - Prediction of Transmembrane Regions and Orientation
The TMpred program makes a prediction of membrane-spanning regions and their orientation.
W2H Help - foldclass
FOLDCLASS(+)
FoldClass predicts protein fold classes and protein domains.
BMERC: Computational Biology, structure prediction, functional profiles, and genome analysis.
BMERC
BioMolecular Engineering Research Center
BMERC 36 Cummington St. Boston, MA 02215
Phone: (617) 353-7123 Fax: (617) 353-7020
Graduate Program in Bioinformatics
Ribosomal Protein Evolution
Main
Tools
SWISS-MODEL
MENU
Modeling requests:
First Approach mode
Alignment Interface
Project (optimise) mode
Oligomer modelling
GPCR mode
Model Database
SWISS-MODEL
An Automated Comparative Protein Modelling Server
PredictProtein - Structure Prediction and Sequence Analysis
PredictProtein
Home Submission Docs Downloads Register
The New GENSCAN Web Server at MIT
Identification of complete gene structures in genomic DNA
Computational Biology at ORNL
Grail Experi
Gene Finder
FRONTIERS IN BIOSCIENCE; GENE FINDER
Use the database of BCM-Genefinder to find splice sites
Sequence name or identifier:
SUBMIT RESET
HOME JOURNAL LIBRARY INDEX
observed/predicted
About PredictProtein
News
10/04/2007
PredictProtein upgrade
GeneQuiz - Home page
GeneQuiz
Home page
The GeneQuiz system provides highly automated analysis of biological sequences.
Announced in Science NetWatch

CBS web similarity to other players



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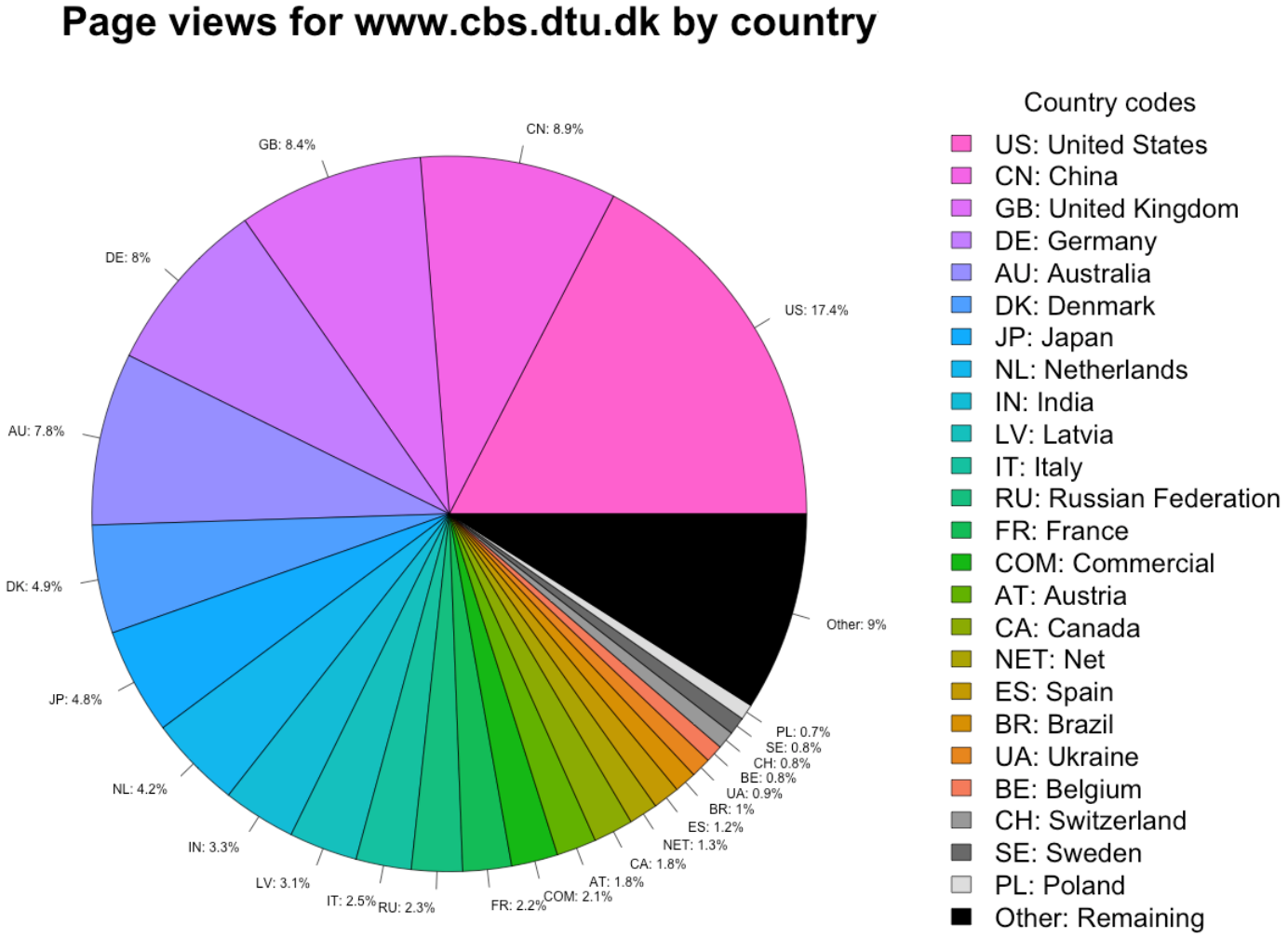
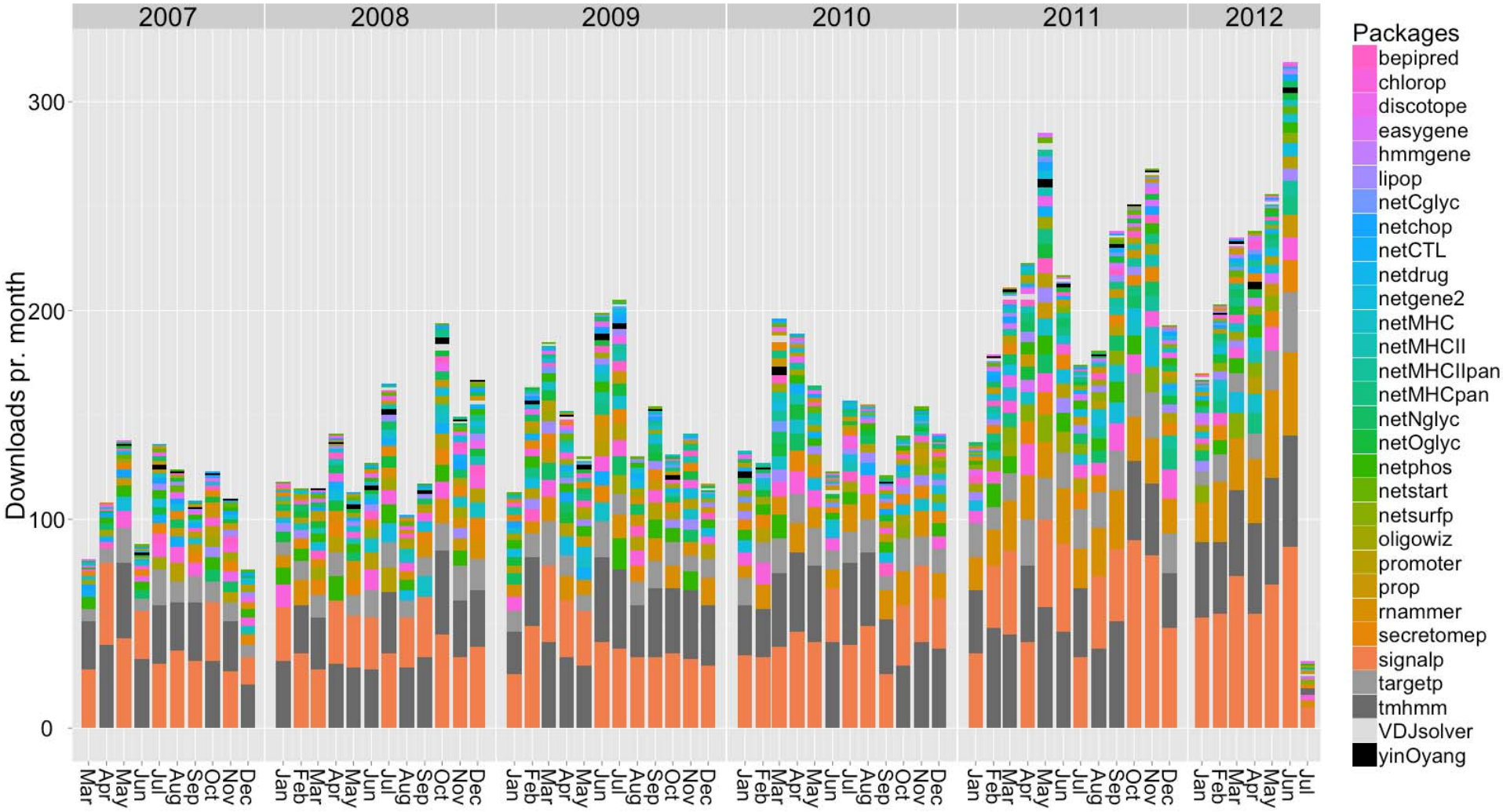
Pageviews - countries

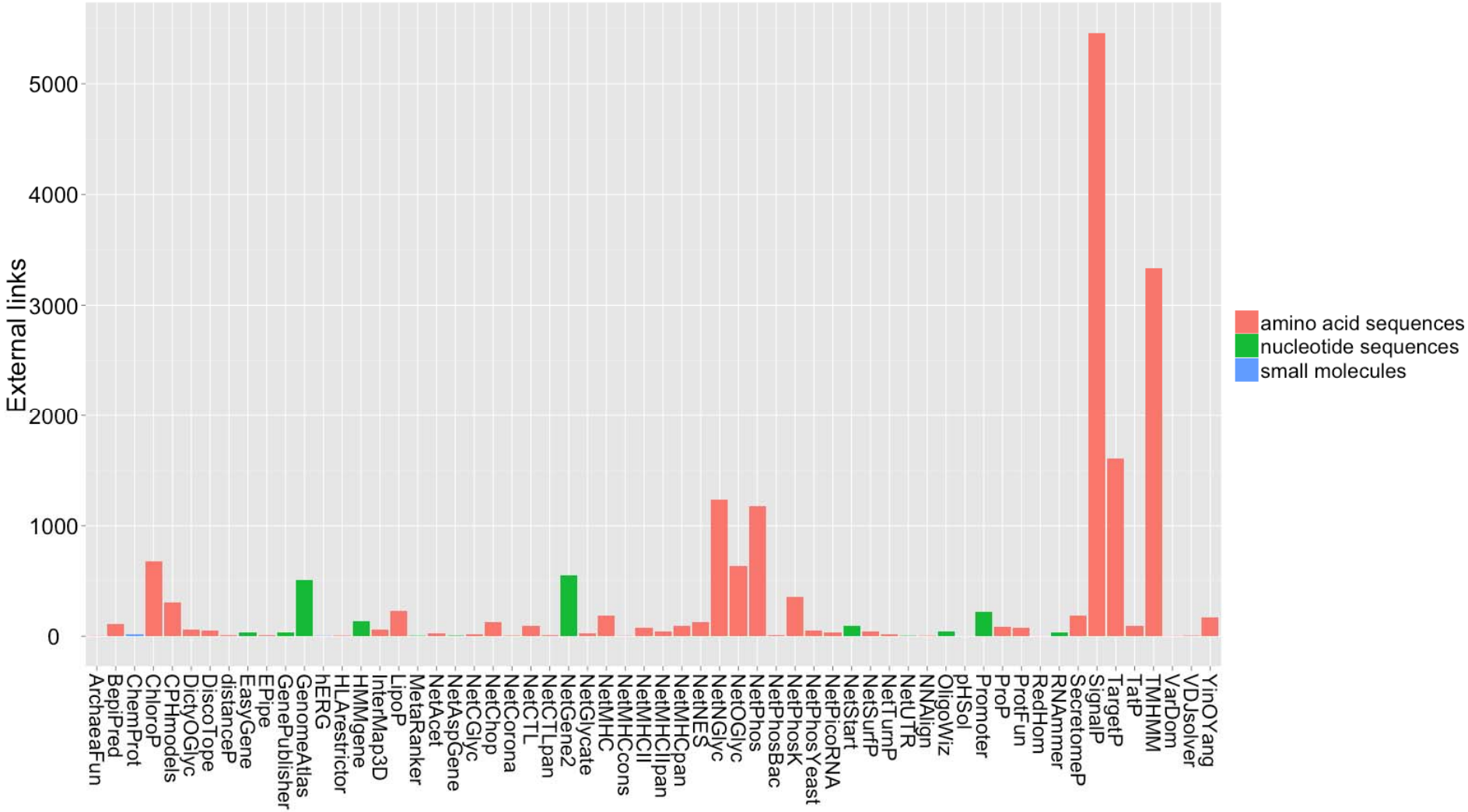


*) .gov and .edu counted as United States. Internal views not counted

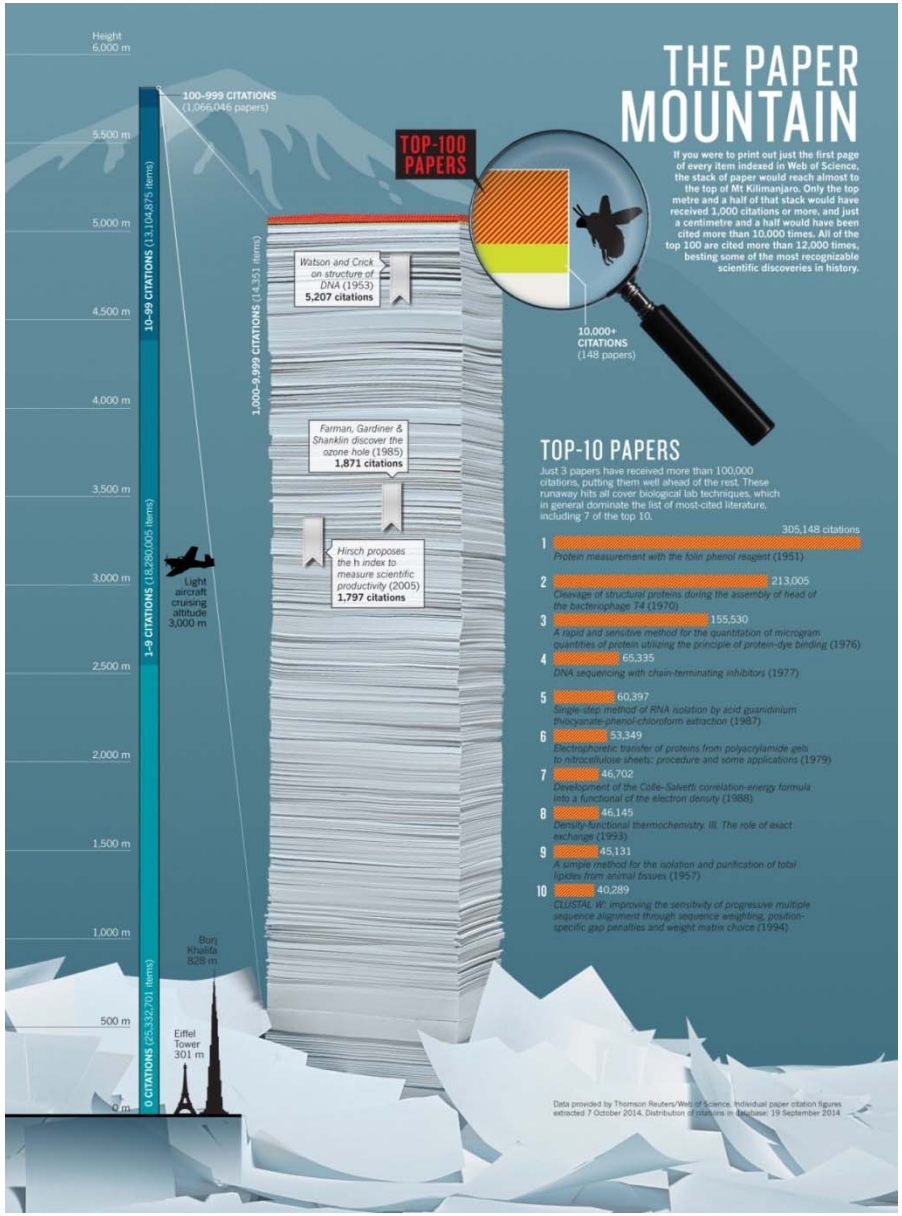
Package downloads per month

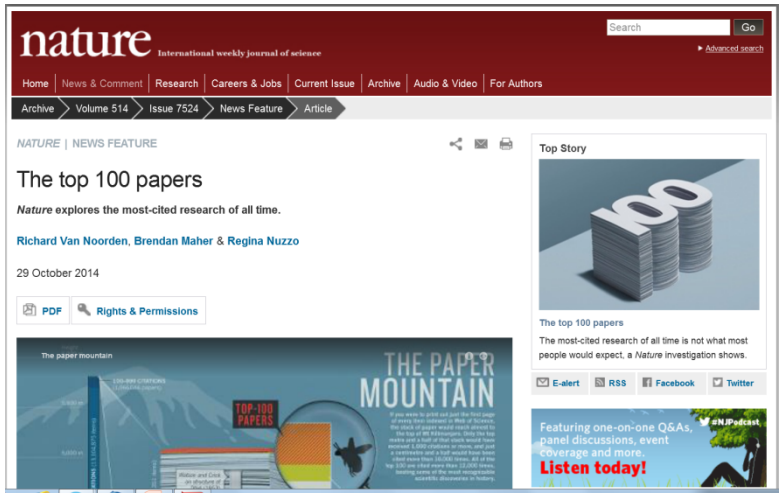


External links to www.cbs.dtu.dk



Tool benchmarking – Obsolete tools are still being cited





Tools do not always deliver on their published promises

Some old news

Biotechnology firm Amgen tried to confirm published findings related to haematology and oncology. Fifty-three papers were deemed ‘landmark’ studies describing something completely new, such as fresh approaches to targeting cancers or alternative clinical uses for existing therapeutics. Scientific findings were confirmed in only 6 (11%) cases.

COMMENT

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Many landmark findings in preclinical oncology research are not reproducible, in part because of inadequate cell lines and animal models.

Raise standards for preclinical cancer research

C. Glenn Begley and Lee M. Ellis propose how methods, publications and incentives must change if patients are to benefit.

Efforts over the past decade to characterize the genetic alterations in human cancers have led to a better understanding of molecular drivers of this complex set of diseases. Although we in the cancer field hoped that this would lead to more effective drugs, historically, our ability to translate cancer research to clinical success has been remarkably low[1]. Sadly, clinical trials in oncology have the highest failure rate compared with other therapeutic areas. Given the high unmet need in oncology, it is understandable that barriers to clinical development may be lower than for other disease areas, and a larger number of drugs with suboptimal preclinical validation will enter oncology trials. However, this low success rate is not sustainable or acceptable, and investigators must reassess their approach to translating discovery research into greater clinical success and impact.

Many factors are responsible for the high failure rate, notwithstanding the inherently difficult nature of this disease. Certainly, the limitations of preclinical tools such as inadequate cancer-cell-line and mouse models[2] make it difficult for even ▸

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REPRODUCIBILITY OF RESEARCH FINDINGS

Preclinical research generates many secondary publications, even when results cannot be reproduced.

Journal impact factor	Number of articles	Mean number of citations of non-reproduced articles*	Mean number of citations of reproduced articles
>20	21	248 (range 3–800)	231 (range 82–519)
5–19	32	169 (range 6–1,909)	13 (range 3–24)

Results from ten-year retrospective analysis of experiments performed prospectively. The term ‘non-reproduced’ was assigned on the basis of findings not being sufficiently robust to drive a drug-development programme.
*Source of citations: Google Scholar, May 2011.

Dimensions the Registry will address