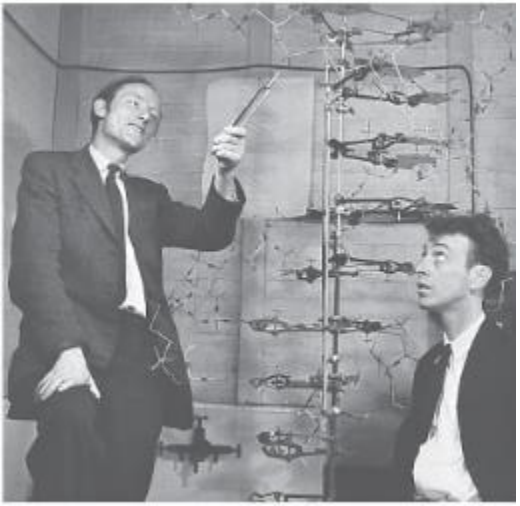
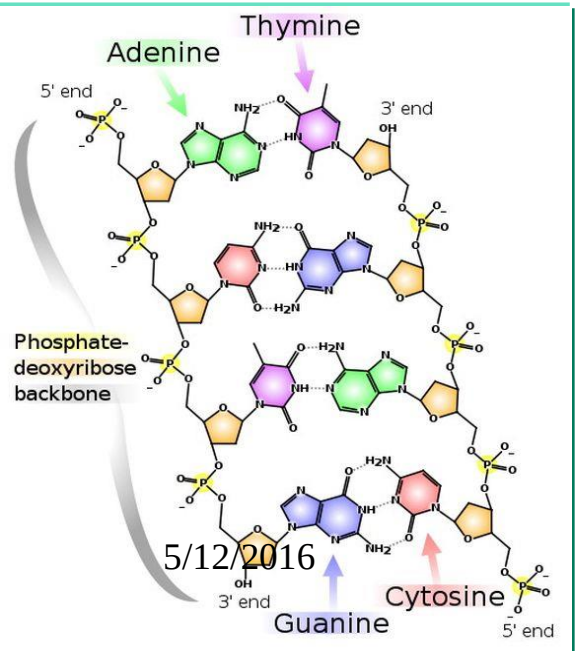
…a modell…

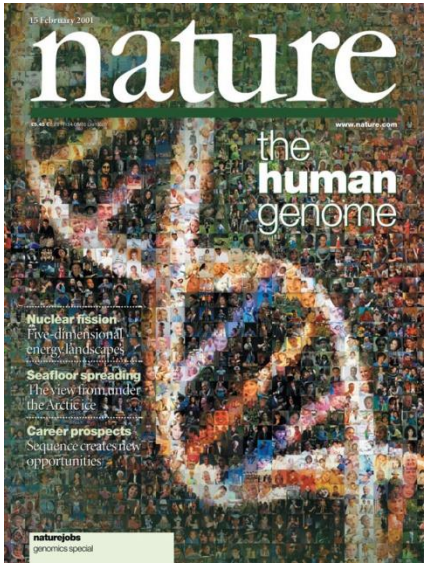


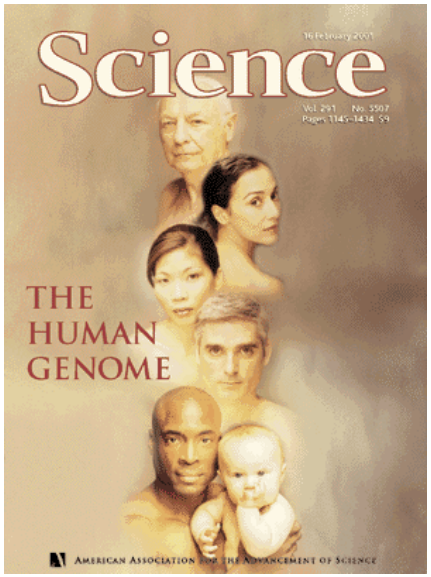
Nature 171, 737-738

1953. április 25.



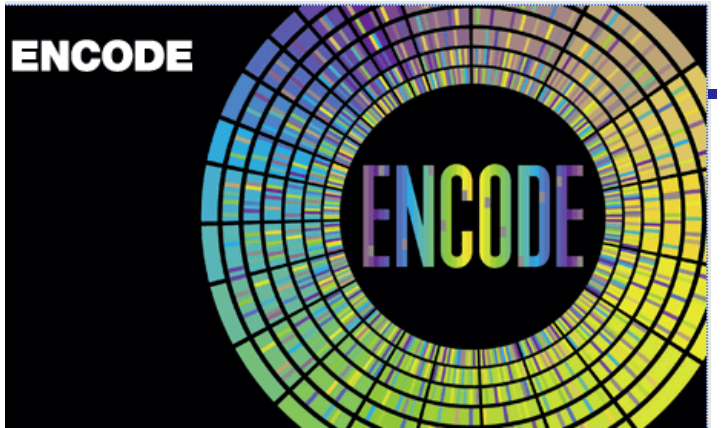
..a humán genom…





2001. február 15-16.

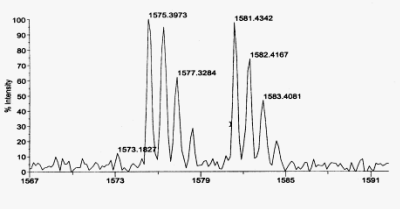
..az enciklopédia



…1000-2500-5 millió genom

2012. szeptember

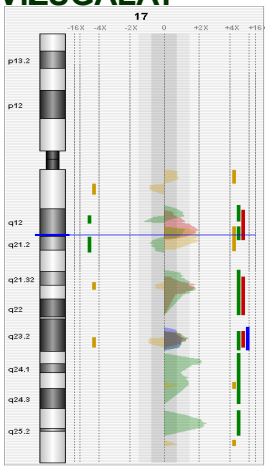
METODIKAI REPERTOIRE



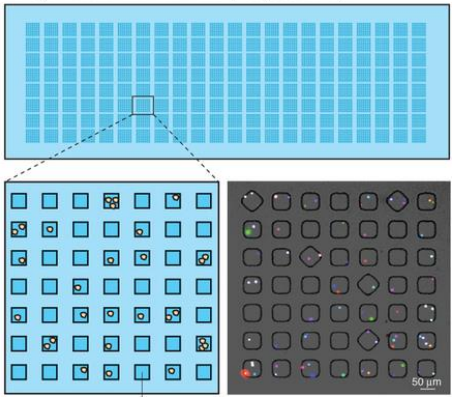
GCAATCGATCTGGTACAGTAGCTA
GCAATTGATCGGGTACATTAGCTA

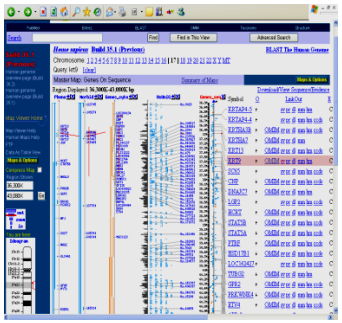
Hap-Map/ 20 millió pontmutáció

TELJES GENOM VIZSGÁLAT

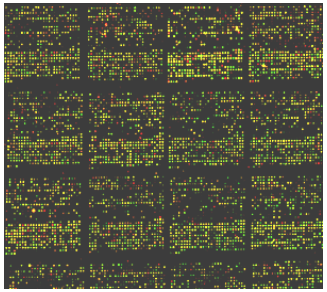


FEHÉRJE **FIZIKAI TECHNIKÁK**
Biofizika, nanofizika





Adatbázisok

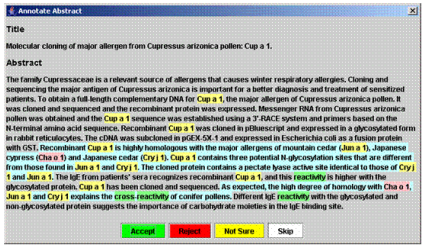


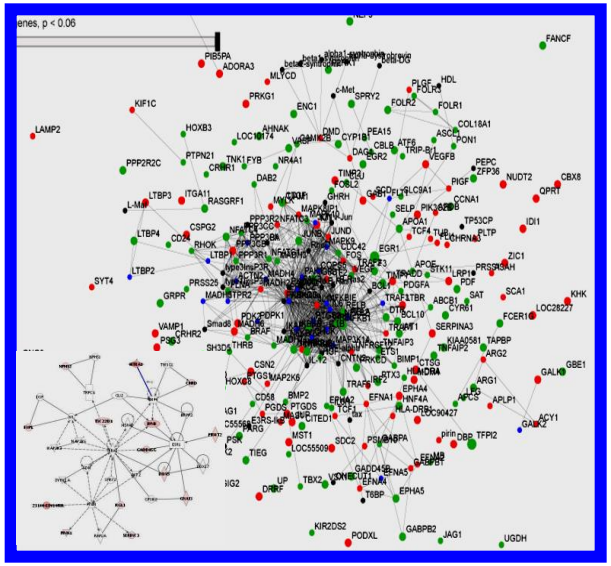
Egy sejt analitika (subnano)

EXPRESSZIÓS MICROARRAY/CHIP
NANOTECHNOLÓGIA,
Szilárd Fázisú KÉMIA

NGS

gene editing



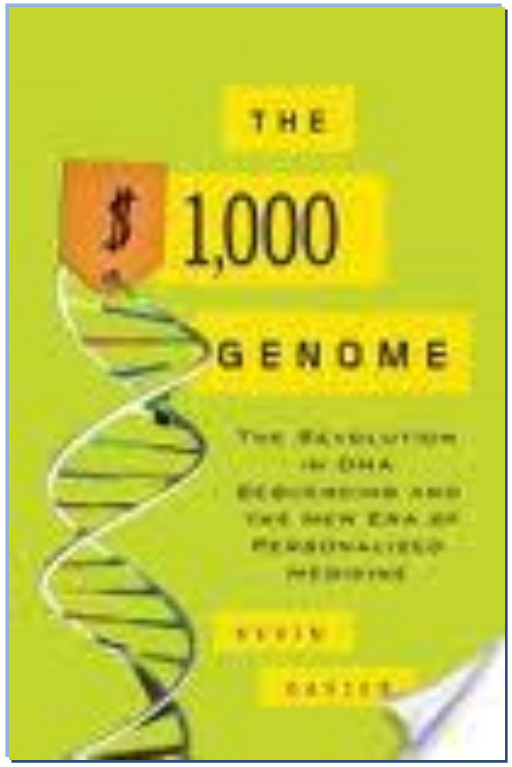


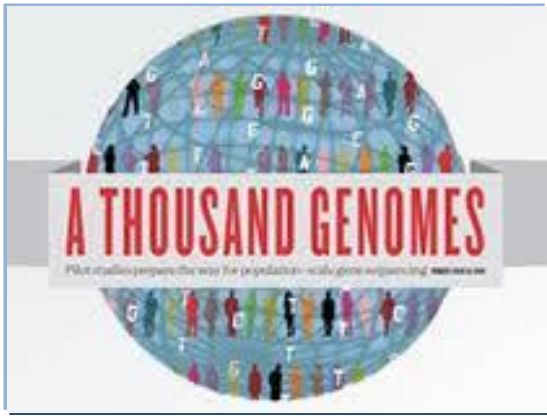
DNS „NYELVÉSZETI” ELJÁRÁSOK

ÚJ GENERÁCIÓS SZEKVENÁLÁSOK
CRISP/Cas9 gene editing rendszer

BIOINFORMATIKA
GÉNHÁLÓZATOK- ÚTVONAL ANALÍZIS

- **DNA sequence data doubled in 18 month**
- **The number of known genomes doubled in 18 month**
- **Cost of sequencing halved in 18 month**



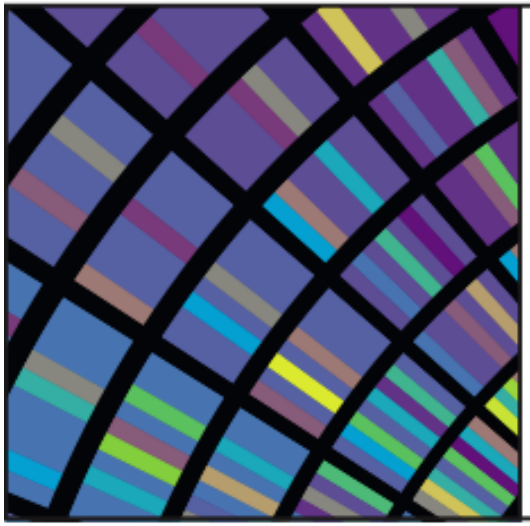


2010

1000 Genomes
A Deep Catalog of Human Genetic Variation

→ **3500 genome (2014)**

→ **5 million genome (2017)**



ENCODE

Encyclopedia of DNA Elements

nature.com/encode

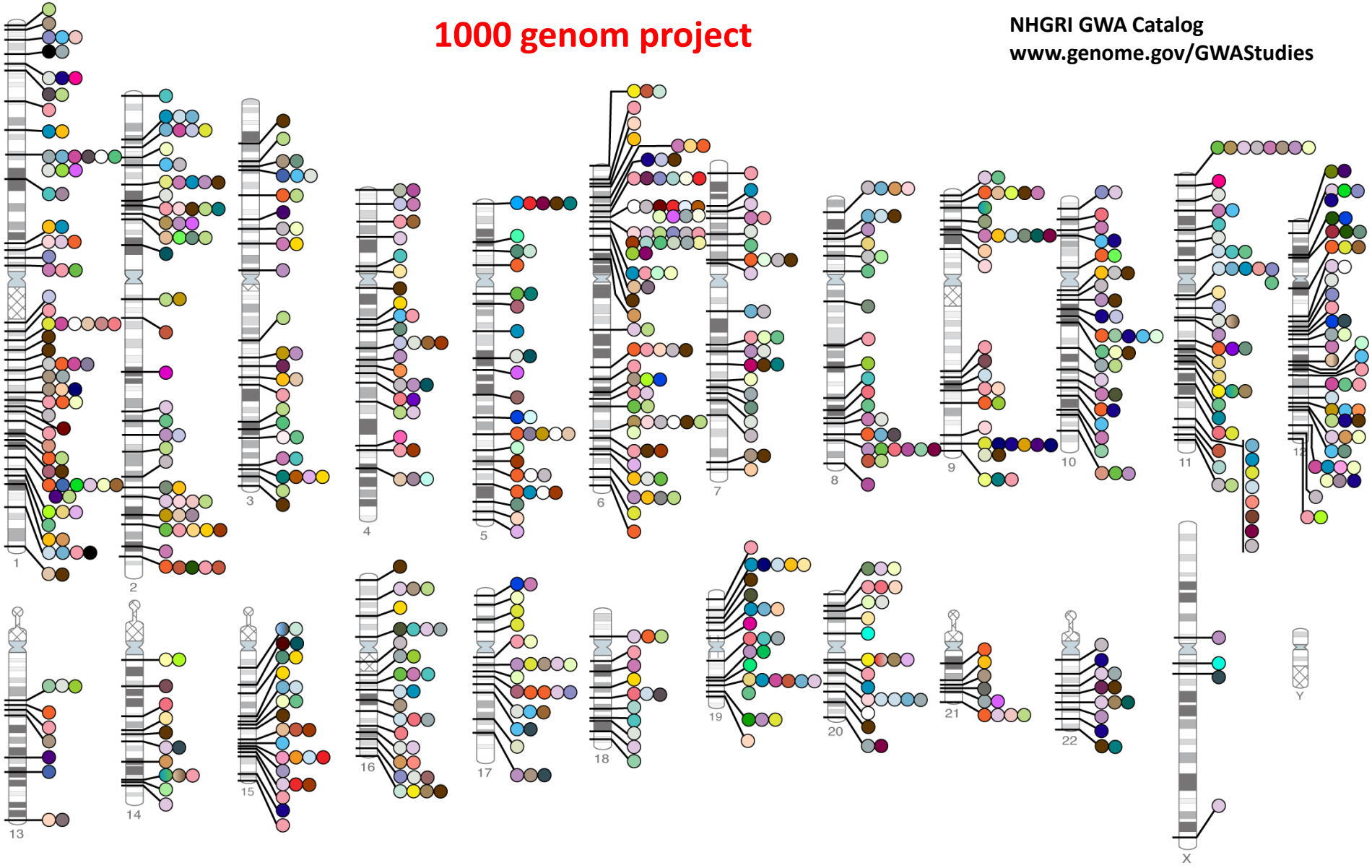
Nov 1, 2012

Scientists Release 1,000 Genomes Map of Genetic Variation

Genome-wide associations studies December, 2010
779 studies, $p \leq 5 \times 10^{-8}$ 148 markers

1000 genom project

NHGRI GWA Catalog
www.genome.gov/GWAStudies



An integrated encyclopedia of DNA elements in the human genome

The ENCODE Project Consortium*

The human genome encodes the blueprint of life, but the function of the vast majority of its nearly three billion bases is unknown. The Encyclopedia of DNA Elements (ENCODE) project has systematically mapped regions of transcription, transcription factor association, chromatin structure and histone modification. These data enabled us to assign biochemical functions for 80% of the genome, in particular outside of the well-studied protein-coding regions. Many discovered candidate regulatory elements are physically associated with one another and with expressed genes, providing new insights into the mechanisms of gene regulation. The newly identified elements also show a statistical correspondence to sequence variants linked to human disease, and can thereby guide interpretation of this variation. Overall, the project provides new insights into the organization and regulation of our genes and genome, and is an expansive resource of functional annotations for biomedical research.

A major project to sequence the genomes of 1,092 people from a range of different ethnicities has generated a detailed map of millions of genetic variations ranging from both rare and relatively common single nucleotide polymorphisms, to major chromosomal abnormalities. The results, published in Nature by the 1,000 Genomes Consortium, are being made freely available for scientists to exploit in disease-related research, and studies on the spread of genes and the genetic evolution of populations around the world. Importantly, researchers will also have access to cell lines from all 1,092 individuals.

The final map from Phase I of the project, generated from the genomes of people from 14 populations in Europe, East Asia, sub-Saharan Africa, and the Americas, includes some 38 million SNPs, 1.4 million short insertions and deletions, and more than 14,000 larger deletions. The investigators say the map includes about 98% of all those SNPs present in less than 1% of a population.

Interestingly, the results found that rare gene variants tend to be constrained within particular geographic regions, as they are more likely to arise from more recent mutations. And it's these rare genetic variants, found in less than 1% of a particular population, that are thought to contribute most to the development of some diseases. “The implication is that the interpretation of rare variants in individuals with a particular disease should be within the context of the local (either geographic or ancestry-based) genetic background,” the researchers write in their published paper, titled “An integrated map of genetic variation from 1,092 human genomes.”

Personal and population genomics of human regulatory variation

Benjamin Vernot, Andrew B. Stergachis, Matthew T. Maurano, Jeff Vierstra, Shane Neph, Robert E. Thurman, John A. Stamatoyannopoulos,[1] and Joshua M. Akey[1]

Department of Genome Sciences, University of Washington, Seattle, Washington 98195, USA

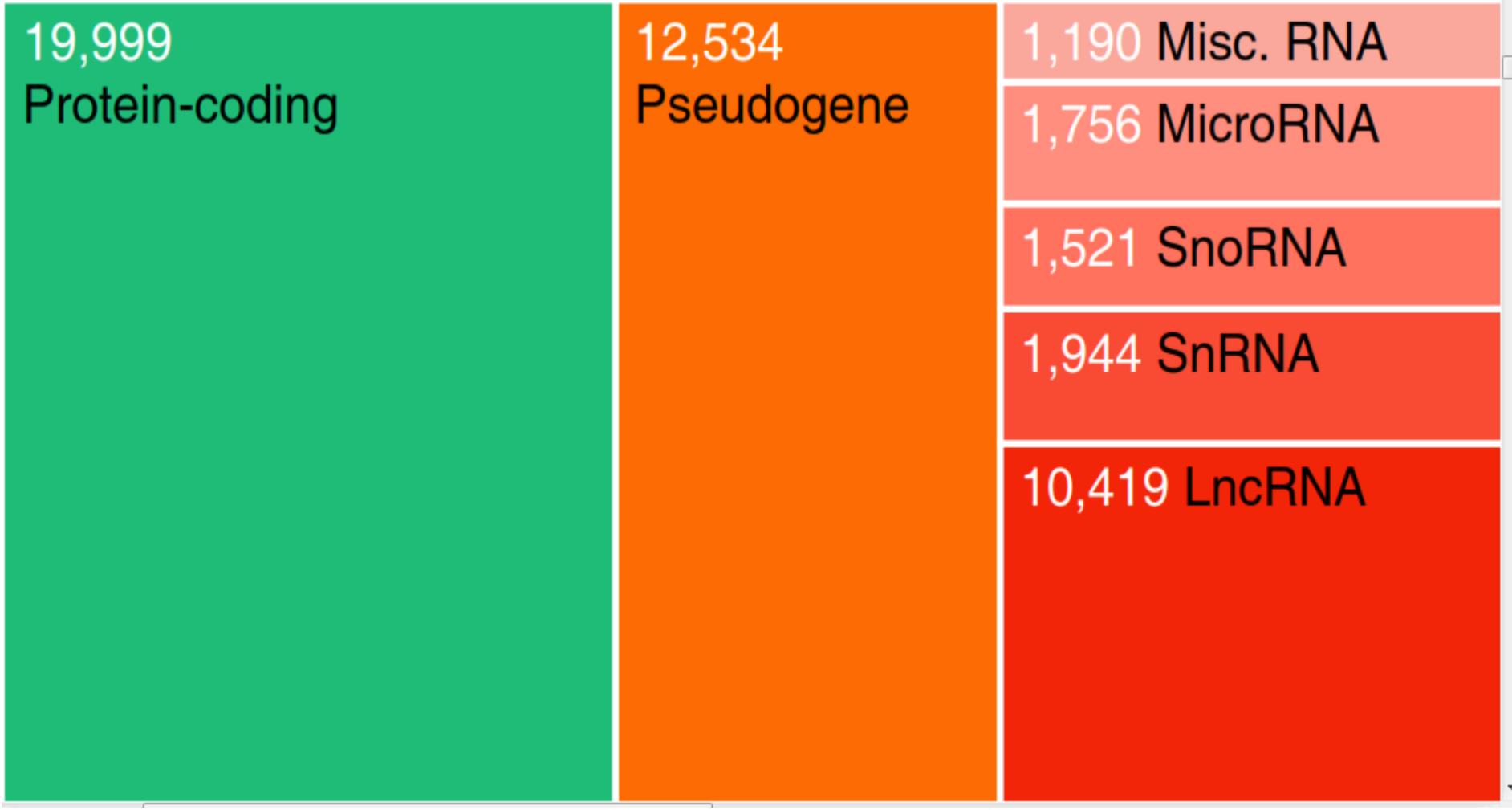
lead SNPs that are most strongly supported by functional evidence

Lead SNP score	Phenotype	PubMed ID
2a	Serum urate	20884846
2a	Crohn's disease	20570966
	Crohn's disease	18587394
2a	Waist–hip ratio	20935629
2a	Hematocrit	19862010
	Other erythrocyte phenotypes	19862010
2a	QT interval	19305408
2a	Platelet aggregation	20526338
2a	Prostate cancer	21743057
2a	Conduct disorder (symptom count)	20585324
2a	Crohn's disease	21102463
2a eQTL	Type 1 diabetes	19430480
2a	Protein quantitative trait loci	18464913
2a	Colorectal cancer	19011631
2a	Alzheimer's disease	21460840

Linking disease associations with regulatory information in the human genome

Marc A. Schaub,[1] Alan P. Boyle,[2] Anshul Kundaje,[1] Serafim Batzoglou,[1,3] and Michael Snyder[2,3,4]

[1]Department of Computer Science, Stanford University, Stanford, California 94305, USA; [2]Department of Genetics, Stanford University School of Medicine, Stanford, California 94305, USA


19,999
Protein-coding
12,534
Pseudogene
1,190 Misc. RNA
1,756 MicroRNA
1,521 SnoRNA
1,944 SnRNA
10,419 LncRNA

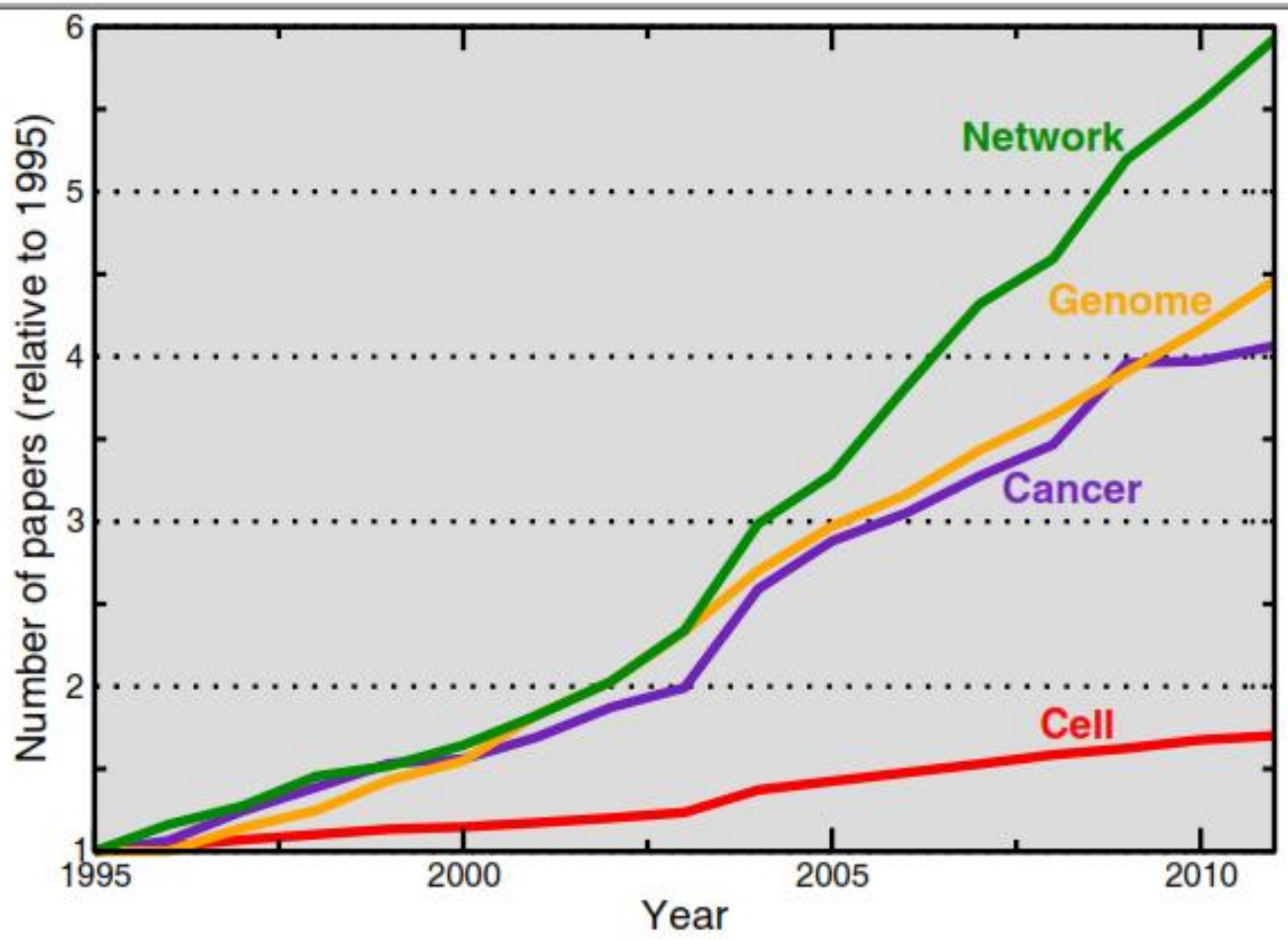
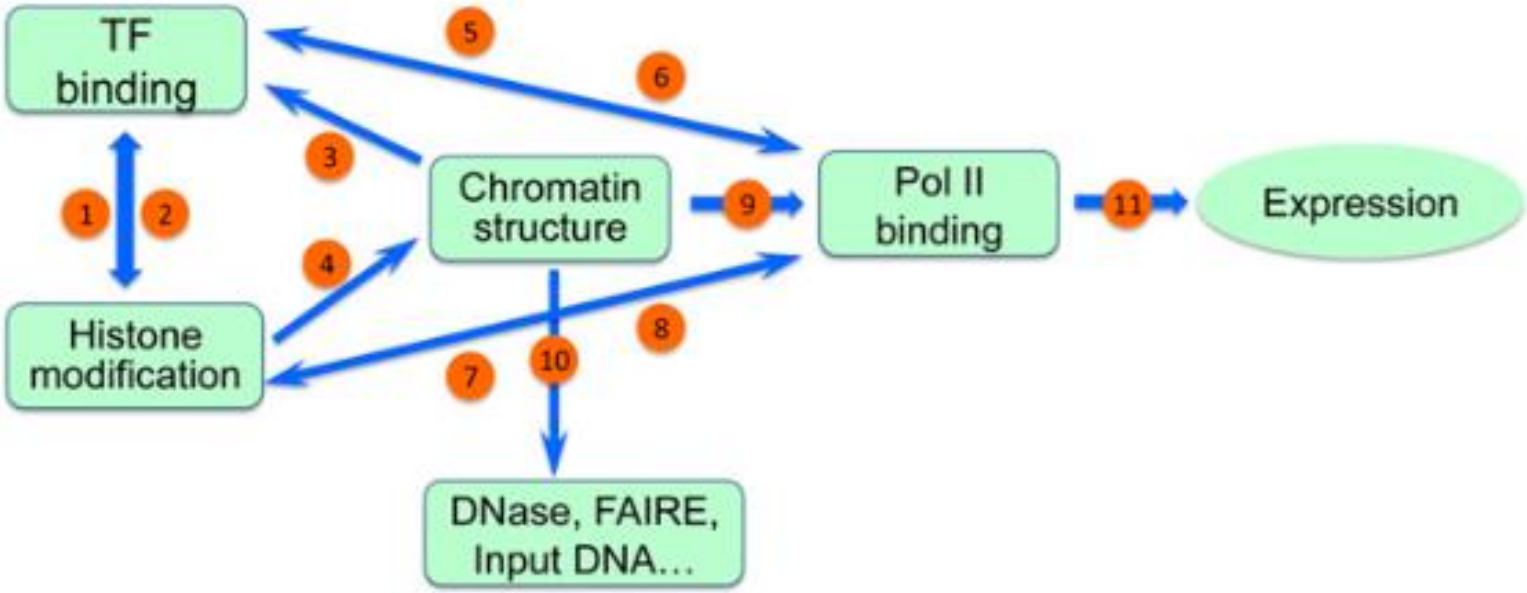


FIGURE 1 | Evolution of the number of articles in the life sciences about different topics, including networks. The data was obtained by querying the "Topic" field in the ISI Web of Science with the corresponding terms (for example, "network or networks" or "cancer"), and including publications in areas such as Biochemistry and Molecular Biology, Cell Biology, Genetics and Heredity, Neurosciences, or Pharmacology

Landscape of transcription in human cells

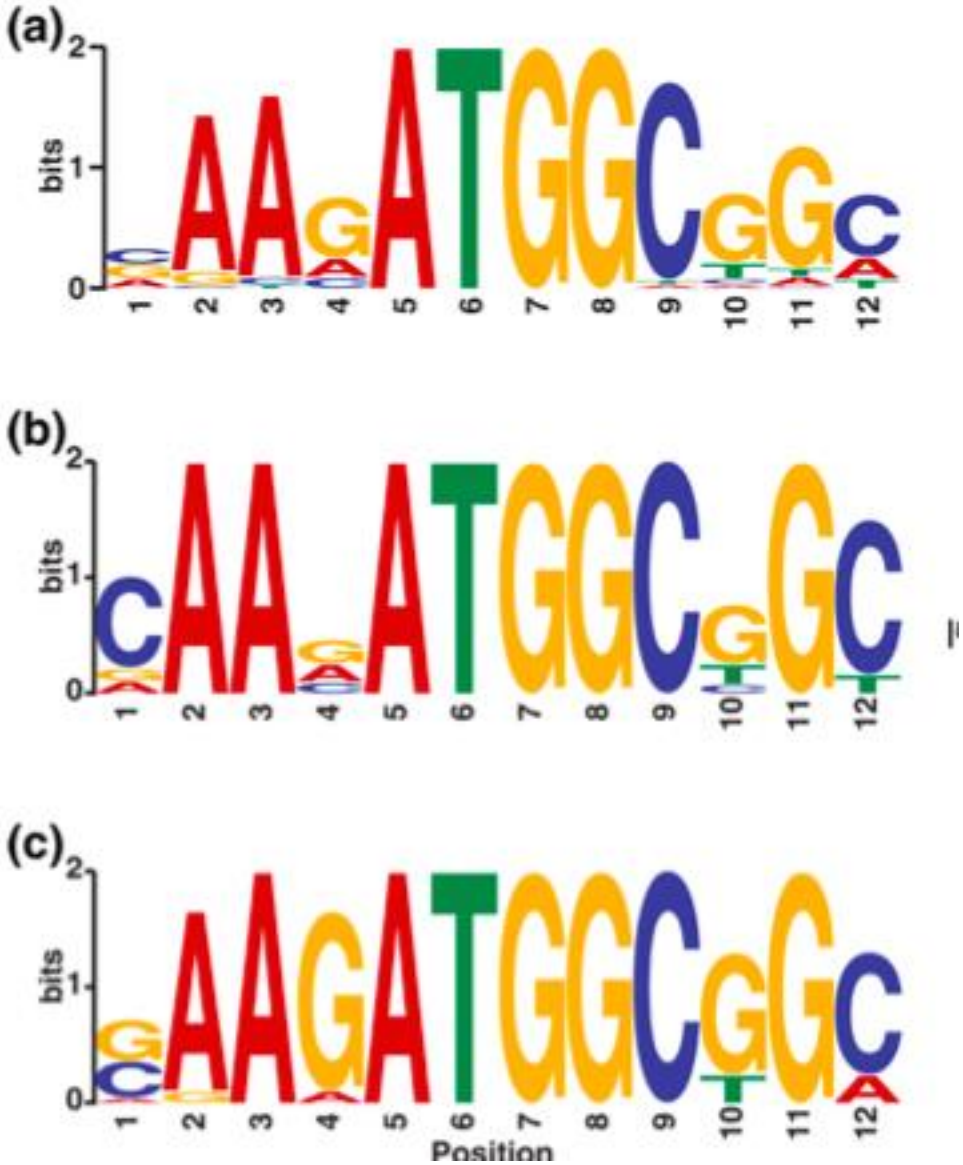
Sarah Djebali[1]*, Carrie A. Davis[2]*, Angelika Merkel[1], Alex Dobin[2], Timo Lassmann[3], Ali Mortazavi[4,5], Andrea Tanzer[1], Julien Lagarde[1], Wei Lin[2], Felix Schlesinger[2], Chenghai Xue[2], Georgi K. Marinov[4], Jainab Khatun[6], Brian A. Williams[4], Chris Zaleski[2], Joel Rozowsky[7,8], Maik Röder[1], Felix Kokocinski[9], Rehab F. Abdelhamid[3], Tyler Alioto[1,10], Igor Antoshechkin[4], Michael T. Baer[2], Nadav S. Bar[11], Philippe Batut[2], Kimberly Bell[2], Ian Bell[12], Sudipto Chakrabortty[2], Xian Chen[13], Jacqueline Chrast[14], Joao Curado[1], Thomas Derrien[1], Jorg Drenkow[2], Erica Dumais[12], Jacqueline Dumais[12], Radha Duttagupta[12], Emilie Falconnet[15], Meagan Fastuca[2], Kata Fejes-Toth[2], Pedro Ferreira[1], Sylvain Foissac[12], Melissa J. Fullwood[16], Hui Gao[12], David Gonzalez[1], Assaf Gordon[2], Harsha Gunawardena[13], Cedric Howald[14], Sonali Jha[2], Rory Johnson[1], Philipp Kapranov[12,17], Brandon King[4], Colin Kingswood[1,10], Oscar J. Luo[16], Eddie Park[5], Kimberly Persaud[2], Jonathan B. Preall[2], Paolo Ribeca[1,10], Brian Risk[6], Daniel Robyr[15], Michael Sammeth[1,10], Lorian Schaffer[4], Lei-Hoon See[2], Atif Shahab[16], Jorgen Skancke[1,11], Ana Maria Suzuki[3], Hazuki Takahashi[3], Hagen Tilgner[1]†, Diane Trout[4], Nathalie Walters[14], Huaien Wang[2], John Wrobel[6], Yanbao Yu[13], Xiaoan Ruan[16], Yoshihide Hayashizaki[3], Jennifer Harrow[9], Mark Gerstein[7,8,18], Tim Hubbard[9], Alexandre Reymond[14], Stylianos E. Antonarakis[15], Gregory Hannon[2], Morgan C. Giddings[6,13], Yijun Ruan[16], Barbara Wold[4], Piero Carninci[3], Roderic Guigó[1,19] & Thomas R. Gingeras[2,12]

92 szerző

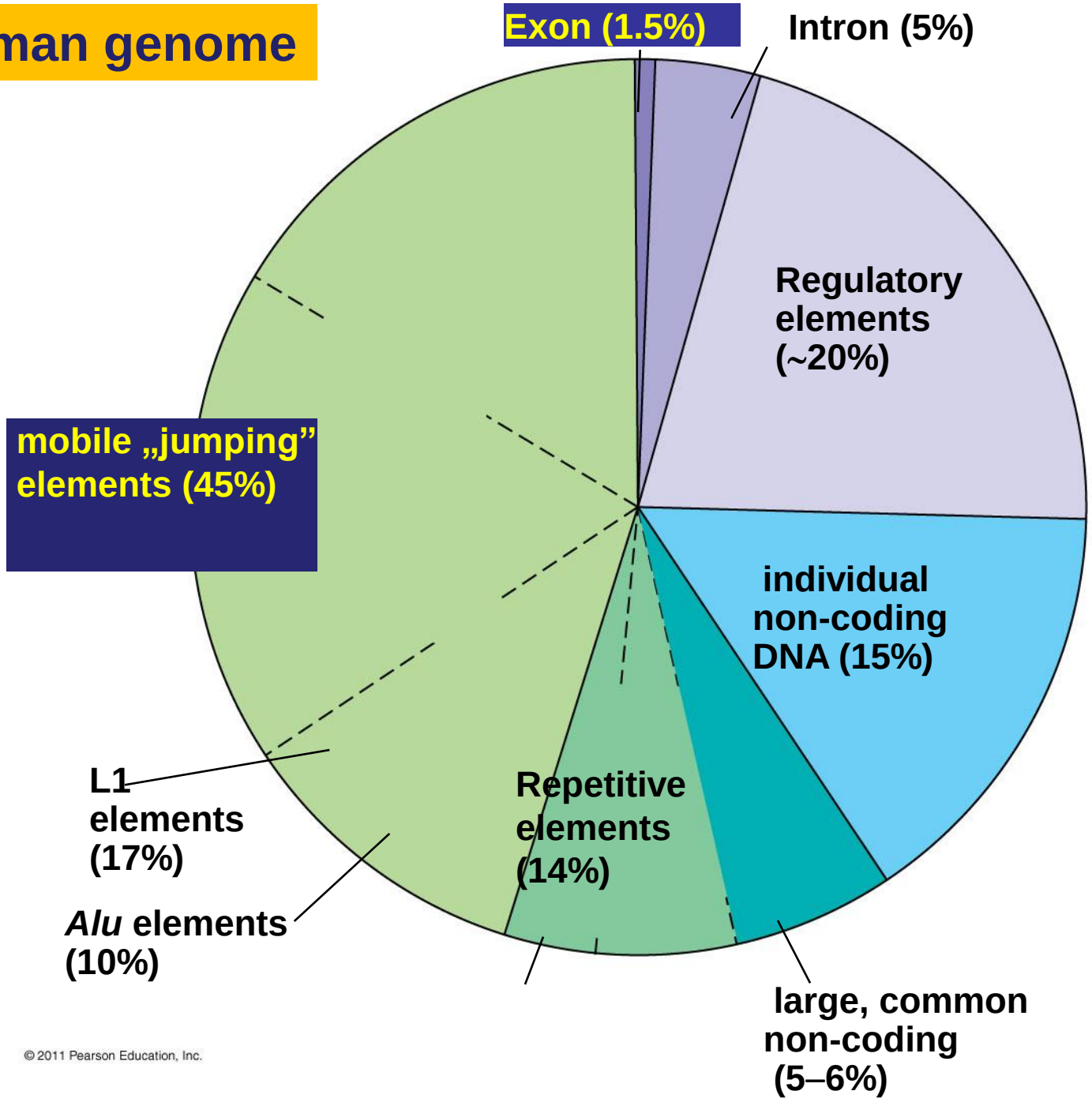


(1) Recruiting histone modifiers
(2) Recruiting TFs
(3) Accessibility
(4) Remodeling
(5) Recruiting general TFs
(6) Interacting with TFs
(7) Recruit general TFs
(8) Interacting with histone modifiers
(9) Accessibility
(10) Accessibility
(11) Transcription

Figure 8. Regulatory mechanism of TF binding, histone modification, and other chromatin features on gene expression.


(a)
(b)
(c)
bits
2
1
0
1 2 3 4 5 6 7 8 9 10 11 12
Position

The human genome



ENCODE major conclusions

- **--more than 80% of the human genome is functional**
- **--the fraction of the genome that is evolutionarily conserved through purifying selection is under 10%.**
- **--at least 80 – 10 = 70% of the genome is perfectly invulnerable to deleterious mutations, either because no mutation can ever occur in these "functional" regions, or because no mutation in these regions can ever be deleterious.**
- **"junk DNA" and "garbage DNA," are DEAD**
- **--The ENCODE results were predicted by one of its authors to necessitate the rewriting of textbooks.** 2
- **--mass-media hype, and public relations may well have to be rewritten.**

- Downloaded from http://gbe.oxfordjournals.org/

www.sciencemag.org/cgi/content/full/306/5696/636/DC2