



- p.265 Presidential reading list: Vanegar Bush (1945): Science, The Endless Frontier & The War Against Disease
- p269-270: Ising model quantum computing
- p.286&321: Friedkin, Belief systems dynamics
- p. 298: Metastasis casts a NET, *Sci. Transl. Med.* 8, 361ra38 (2016)
- p. 336: Convergent evolution (hemoglobin) based on unpredictable molecular underpinnings
- p. 354: M. Mishto: HLA class I peptides are proteasome-spliced peptides



- **p. 15: Gene-environment interplay, generate a new genetic disease ? predicting traits from genomic sequence?**
- **p. 26 Guardian of the genome: combat cancer by propping up mutated p53**
- **p. 36: MIF in parthanatos**
- **p. 64: Yosef & Aviv Regev, REVIEW: Genomic dissection of the effect of cellular environment on immune response**
- **p.118: Chromatin: New methods map genomic structure**



- p. 7: Genomics data access: openSNP, DNA.LAND, Promethease, GEDmatch, Genome Mate Pro, NY Genome Center Seeq app, MyGene2
- p.18: Psychiatry needs more mathematics: human connectome project, brain circuitry
- p. 93: Olfactory receptor pseudo-pseudogenes: pseudogenes with PTC (Premature Stop Codon) could nevertheless be functional due to read-through



- **S1-S20: Parkinson Outlook**
- **p. 462-3 & 514-518: precision timing in synthetic gene circuit, repressilator**
- **p.467 & 471: deep neural reasoning, hybrid computing using a neural network with external memory**
- **p 533: Intron evolution mechanisms, nucleosome sized exons (147 bp ??)**



- p. 322 Epichaperome and cancer
- p. 329-335 design of hyperstable constrained peptides, David Baker, ROSETTA
- p. 344-49 Stuart Schreiber: diversity synthesis of antimalarial inhibitors
- p 378-82 renewed model of pancreatic cancer evolution based on genome rearrangement patterns
- p. 392: endothelium regulates tissue-resident macrophages



- p. 140, p 154-157: reassess links between mutations and disease, ExAC, human knockouts
- p 183-192 in vitro and ex vivo strategies for intracellular delivery
- p 201-06: The Simons Genome diversity project: 300 genomes from 142 diverse populations
- p. 243-247: De novo assembly and phasing of a Korean genome
- p. 248-252: GWAS for birth weight and adult disease, > 150.000 individuals !
- p. 265-271: new chromatin domains determine pathogenicity of genomic duplications, Hi-C and 4C-seq
- p 275-277: The dark side of the human genome