Stanford

Gill Bejerano

Associate Professor of Developmental Biology, of Computer Science, of Biomedical Data Science and of Pediatrics (Genetics)

CONTACT INFORMATION

- **Alternate Contact**

  Patti Livingston - Admininstrative Associate

  Email patti.livingston@stanford.edu

  Tel 650-725-6792

Bio

BIO

The Bejerano Lab studies genome function in human and related species. We are deeply interested in the following broad questions: Mapping genome sequence (variation) to phenotype (differences) and extracting specific genetic insights from deep sequencing measurements. We take a particular interest in gene cis regulation. We use our joint affiliation to apply a combination of computational and experimental approaches. We collect large scale experimental data; write computational analysis tools; run them massively to discover the most exciting testable hypotheses; which we proceed to experimentally validate. We work in small teams, in house or with close collaborators of experimentalists and computational tool users who interact directly with our computational tool builders. Please see our research tab for more.

ACADEMIC APPOINTMENTS

- Associate Professor, Developmental Biology
- Associate Professor, Computer Science
- Associate Professor, Department of Biomedical Data Science
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Member, Editorial Board, Gene, (2007-2008)
- Technical Advisory Board, Numenta, (2008- present)

HONORS AND AWARDS

- Rector Prize & Dean’s list for undergraduate achievements., Hebrew University (1993-1996)
- Intel award for achievements., Hebrew University (1996)

- Rector Prize & Dean’s list for graduate studies achievements., Hebrew University (1997-1999)
- Rachel & Salim Banin scholarship., Hebrew University (1999)
- Best paper by a young scientist award., RECOMB conference (1999)
- Levi Eshkol graduate studies fellowship., Hebrew University (1999-2002)
- Best paper by a young scientist award., RECOMB conference (2003)
- Junior Faculty Grant, Edward Mallinckrodt, Jr. Foundation (2007-2010)
- Tomorrow's Principal Investigator, Genome Technology Magazine (2008)
- Alfred P. Sloan Fellow, Alfred P. Sloan Foundation (2008-2010)
- Young Investigator Award, Human Frontier Science Program (2008-2011)
- Searle Scholar, Searle Scholars Program (2008-2011)
- Research Grant Award, Okawa Foundation (2008)
- Fellow, David & Lucile Packard Foundation (2008-2013)
- New Faculty Fellow, Microsoft Research (2009)

PROFESSIONAL EDUCATION

- Ph.D., Hebrew University , Computer Science (2004)
- B.Sc., Hebrew University , Physics, Mathematics, Computer Science (summa cum laude) (1997)

LINKS

- Bejerano Lab: http://bejerano.stanford.edu

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

The Bejerano Lab is currently focused on the following topics:

1. Genotype - Phenotype relationships in humans.

We are developing novel methods for linking human whole genome variation with human disease and trait variation. We apply these methods to multiple datasets in the contexts of prematurity, autism, heart disease and more [20, 29, 32, 34, 36, 38, 39, 43].

2. Genotype - Phenotype relationships between mammals.

We develop novel methods to link trait evolution in the mammalian tree to whole genome evolution in over a hundred species. Application of these methods allow us to shed new light on human genome function, on human disease and on human evolution [29, 34, 35]. See our "Forward Genomics" web server.

3. Extracting genetic knowledge from high throughput genomic assays.

High throughput genomic assays are most often used to make biochemical discoveries. We develop methods to extract genetic and developmental knowledge from these assays [27, 28, 31]. Through joint work with Sue McConnell we take special interest in the developing neocortex [29, 41]. Also see our popular GREAT web server for the cis-regulatory interpretation of high throughput genomic datasets.

4. Vertebrate transcription regulation.

Much of our work relies on our strong foundations in the study of vertebrate gene regulation [9-11, 14, 15, 18, 22, 25, 27, 29-33, 35, 38-42]. See our PRISM resource of predicted transcription factor functions and COMPLEX resource for predicted transcription factor dimers and complexes. Also see our zCNE resource of conserved non-coding (likely gene regulatory) sequences in the zebrafish genome.

5. Vertebrate genome evolution.

We are extremely well versed in human and vertebrate genome evolution [9-11, 14, 17, 18, 22, 23, 25, 26, 29, 33-35, 37, 39, 40]. Notably, we discovered ultraconservation and correctly postulated that many of these elements are developmental enhancers. We also showed that mammalian ultraconserved elements evolve under extreme purifying selection, and that they are almost never lost during mammalian evolution [9, 23, 25]. We also discovered the first developmental enhancers conserved between human and protostomes [33], attempted to group human conserved non-coding DNA into paralog families [10], and studied the co-option of mobile elements into cis-regulatory roles [18, 22, 26, 41].

6. Evolutionary Developmental Biology ("evo devo").

We have done work in the field of evolutionary developmental biology [29, 33-35, 43], including a first survey of developmental enhancers (including a penile spine/ vibrissae enhancer) uniquely lost in humans [29], fueled by our deep interest in phenotype - genotype relationships.

[For links to the references and more, pleae see our lab's website]

Teaching

COURSES

2018-19

- The Human Genome Source Code: BIOMEDIN 273A, CS 273A, DBIO 273A (Win)

2017-18

- The Human Genome Source Code: BIOMEDIN 273A, CS 273A, DBIO 273A (Win)

2016-17

- A Computational Tour of the Human Genome: CS 273A (Aut)

2015-16

- A Computational Tour of the Human Genome: CS 273A (Aut)

STANFORD ADVISEES

Master's Program Advisor

Taide Ding, Zaid Nabulsi, Vishnu Shankar, Sam Shleifer, Ahmed Shuaibi, Meera Srinivasan

Doctoral Dissertation Co-Advisor (AC)

Yosuke Tanigawa

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)
- Biomedical Informatics (Masters Program)
- Cardiovascular Medicine (Fellowship Program)
- Clinical Informatics (Fellowship Program)
- Developmental Biology (Phd Program)

- Developmental-Behavioral Pediatrics (Fellowship Program)
- Genetics (Phd Program)
- Human Genetics and Genetic Counseling (Masters Program)
- Medical Genetics (Fellowship Program)
- Molecular and Genetic Medicine (Fellowship Program)
- Neonatal-Perinatal Medicine (Fellowship Program)
- Neurosciences (Phd Program)

Publications

PUBLICATIONS

- **CRISPR/Cas9 Genome Engineering in Engraftable Human Brain-Derived Neural Stem Cells.** *iScience*
  Dever, D. P., Scharenberg, S. G., Camarena, J., Kildebeck, E. J., Clark, J. T., Martin, R. M., Bak, R. O., Tang, Y., Dohse, M., Birgmeier, J. A., Jagadeesh, K. A., Bejerano, G., Tsukamoto, et al
  2019; 15: 524–35

- **Darwin: A Genomics Coprocessor** *IEEE MICRO*
  Turakhia, Y., Bejerano, G., Dally, W. J.
  2019; 39 (3): 29–37

- **S-CAP extends pathogenicity prediction to genetic variants that affect RNA splicing** *NATURE GENETICS*
  Jagadeesh, K. A., Paggi, J. M., Ye, J. S., Stenson, P. D., Cooper, D. N., Bernstein, J. A., Bejerano, G.
  2019; 51 (4): 755-+

- **LUNG DISEASE IN SYSTEMIC JIA: AN EMERGING PROBLEM LINKED WITH YOUNG AGE AND ANTI-IL-1/IL-6**
  Chen, G., Saper, V., Deutsch, G., Guillerman, R. P., Jagadeesh, K., Schulert, G., Canna, S., Lu, Y., Birgmeier, J., Leung, A., Grom, A., Bejerano, G., Davis, et al
  BMJ PUBLISHING GROUP.2019: A57

- **S-CAP extends pathogenicity prediction to genetic variants that affect RNA splicing.** *Nature genetics*
  Jagadeesh, K. A., Paggi, J. M., Ye, J. S., Stenson, P. D., Cooper, D. N., Bernstein, J. A., Bejerano, G.
  2019

- **Identification of rare-disease genes using blood transcriptome sequencing and large control cohorts.** *Nature medicine*
  Frésard, L., Smail, C., Ferraro, N. M., Teran, N. A., Li, X., Smith, K. S., Bonner, D., Kernohan, K. D., Marwaha, S., Zappala, Z., Balliu, B., Davis, J. R., Liu, et al
  2019

- **CLINPHEN EXTRACTS AND PRIORITIZES PHENOTYPES FROM MEDICAL RECORDS TO ACCELERATE GENOMIC DIAGNOSIS**
  Deisseroth, C. A., Birgmeier, J., Bodle, E. E., Kohler, J., Matalon, D., Nazarenko, Y., Genetti, C., Brownstein, C., Schmitz-Abe, K., Schoch, K., Cope, H., Signer, R., Ud, et al
  BMJ PUBLISHING GROUP.2019: 179

- **Darwin-WGA: A Co-processor Provides Increased Sensitivity in Whole Genome Alignments with High Speedup**
  Turakhia, Y., Goenka, S. D., Bejerano, G., Dally, W. J., IEEE
  IEEE.2019: 359–72

- **A sequence-based, deep learning model accurately predicts RNA splicing branchpoints.** *RNA (New York, N.Y.)*
  Paggi, J. M., Bejerano, G.
  2018

- **Independent erosion of conserved transcription factor binding sites points to shared hindlimb, vision and external testes loss in different mammals.** *Nucleic acids research*
  Berger, M. J., Wenger, A. M., Guturu, H., Bejerano, G.
  2018

- **An MTF1 binding site disrupted by a homozygous variant in the promoter of ATP7B likely causes Wilson Disease.** *European journal of human genetics : EJHG*

Chen, H. I., Jagadeesh, K. A., Birgmeier, J., Wenger, A. M., Guturu, H., Schelley, S., Bernstein, J. A., Bejerano, G.
2018

- **Phrank measures phenotype sets similarity to greatly improve Mendelian diagnostic disease prioritization.** *Genetics in medicine : official journal of the American College of Medical Genetics*
  Jagadeesh, K. A., Birgmeier, J., Guturu, H., Deisseroth, C. A., Wenger, A. M., Bernstein, J. A., Bejerano, G.
  2018

- **BIALLELIC LOSS OF FUNCTION WNT5A MUTATIONS IN AN INFANT WITH SEVERE AND ATYPICAL MANIFESTATIONS OF ROBINOW SYNDROME AND UNAFFECTED PARENTS - A NEW LOCUS FOR AUTOSOMAL RECESSIVE DISEASE**
  Bernstein, J. A., Esplin, E. E., Jagadeesh, K. A., Birgmeier, J., Homeyer, M., Guturu, H., Wenger, A. M., Bejerano, G.
  WILEY.2018: 1504

- **ClinPhen extracts and prioritizes patient phenotypes directly from medical records to expedite genetic disease diagnosis.** *Genetics in medicine : official journal of the American College of Medical Genetics*
  Deisseroth, C. A., Birgmeier, J., Bodle, E. E., Kohler, J. N., Matalon, D. R., Nazarenko, Y., Genetti, C. A., Brownstein, C. A., Schmitz-Abe, K., Schoch, K., Cope, H., Signer, R., Martinez-Agosto, et al
  2018

- **Biallelic loss-of-function WNT5A mutations in an infant with severe and atypical manifestations of Robinow syndrome.** *American journal of medical genetics. Part A*
  Birgmeier, J., Esplin, E. D., Jagadeesh, K. A., Guturu, H., Wenger, A. M., Chaib, H., Buckingham, J. A., Bejerano, G., Bernstein, J. A.
  2018; 176 (4): 1030–36

- **A screen for deeply conserved non-coding GWAS SNPs uncovers a MIR-9-2 functional mutation associated to retinal vasculature defects in human** *Nucleic Acids Research*
  Madelaine, R., Notwell, J. H., Skariah, G., Halluin, C., Chen, C. C., Bejerano, G., Mourrain, P.
  2018; 1

- **Deriving genomic diagnoses without revealing patient genomes** *SCIENCE*
  Jagadeesh, K. A., Wu, D. J., Birgmeier, J. A., Boneh, D., Bejerano, G.
  2017; 357 (6352): 692-+

- **Chitayat syndrome: hyperphalangism, characteristic facies, hallux valgus and bronchomalacia results from a recurrent c.266A > G p.(Tyr89Cys) variant in the ERF gene** *JOURNAL OF MEDICAL GENETICS*
  Balasubramanian, M., Lord, H., Levesque, S., Guturu, H., Thuriot, F., Sillon, G., Wenger, A. M., Sureka, D. L., Lester, T., Johnson, D. S., Bowen, J., Calhoun, A. R., Viskochil, et al
  2017; 54 (3): 157-165

- **Systematic reanalysis of clinical exome data yields additional diagnoses: implications for providers** *GENETICS IN MEDICINE*
  Wenger, A. M., Guturu, H., Bernstein, J. A., Bejerano, G.
  2017; 19 (2): 209-214

- **Mutations of AKT3 are associated with a wide spectrum of developmental disorders including extreme megalencephaly.** *Brain : a journal of neurology*
  Alcantara, D., Timms, A. E., Gripp, K., Baker, L., Park, K., Collins, S., Cheng, C., Stewart, F., Mehta, S. G., Saggar, A., Sztriha, L., Zombor, M., Caluseriu, et al
  2017; 140 (10): 2610–22

- **MicroRNA-9 Couples Brain Neurogenesis and Angiogenesis.** *Cell reports*
  Madelaine, R., Sloan, S. A., Huber, N., Notwell, J. H., Leung, L. C., Skariah, G., Halluin, C., Pa#ca, S. P., Bejerano, G., Krasnow, M. A., Barres, B. A., Mourrain, P.
  2017; 20 (7): 1533–42

- **M-CAP eliminates a majority of variants of uncertain significance in clinical exomes at high sensitivity.** *Nature genetics*
  Jagadeesh, K. A., Wenger, A. M., Berger, M. J., Guturu, H., Stenson, P. D., Cooper, D. N., Bernstein, J. A., Bejerano, G.
  2016

- **Chitayat syndrome: hyperphalangism, characteristic facies, hallux valgus and bronchomalacia results from a recurrent c.266A>G p.(Tyr89Cys) variant in the ERF gene.** *Journal of medical genetics*
  Balasubramanian, M., Lord, H., Levesque, S., Guturu, H., Thuriot, F., Sillon, G., Wenger, A. M., Sureka, D. L., Lester, T., Johnson, D. S., Bowen, J., Calhoun, A. R., Viskochil, et al
  2016

- **TBR1 regulates autism risk genes in the developing neocortex.** *Genome research*
  Notwell, J. H., Heavner, W. E., Darbandi, S. F., Katzman, S., McKenna, W. L., Ortiz-Londono, C. F., Tastad, D., Eckler, M. J., Rubenstein, J. L., McConnell, S. K., Chen, B., Bejerano, G.
  2016; 26 (8): 1013-1022

- **Systematic reanalysis of clinical exome data yields additional diagnoses: implications for providers.** *Genetics in medicine*
  Wenger, A. M., Guturu, H., Bernstein, J. A., Bejerano, G.
  2016

- **"Reverse Genomics" Predicts Function of Human Conserved Noncoding Elements** *MOLECULAR BIOLOGY AND EVOLUTION*
  Marcovitz, A., Jia, R., Bejerano, G.
  2016; 33 (5): 1358-1369

- **Erosion of Conserved Binding Sites in Personal Genomes Points to Medical Histories.** *PLoS computational biology*
  Guturu, H., Chinchali, S., Clarke, S. L., Bejerano, G.
  2016; 12 (2)

- **Changes in the enhancer landscape during early placental development uncover a trophoblast invasion gene-enhancer network.** *Placenta*
  Tuteja, G., Chung, T., Bejerano, G.
  2016; 37: 45-55

- **Mx1 and Mx2 key antiviral proteins are surprisingly lost in toothed whales** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Braun, B. A., Marcovitz, A., Camp, J. G., Jia, R., Bejerano, G.
  2015; 112 (26): 8036-8040

- **Characterization of TCF21 Downstream Target Regions Identifies a Transcriptional Network Linking Multiple Independent Coronary Artery Disease Loci** *PLOS GENETICS*
  Sazonova, O., Zhao, Y., Nuernberg, S., Miller, C., Pjanic, M., Castano, V. G., Kim, J. B., Salfati, E. L., Kundaje, A. B., Bejerano, G., Assimes, T., Yang, X., Quertermous, et al
  2015; 11 (5)

- **A family of transposable elements co-opted into developmental enhancers in the mouse neocortex** *NATURE COMMUNICATIONS*
  Notwell, J. H., Chung, T., Heavner, W., Bejerano, G.
  2015; 6

- **A family of transposable elements co-opted into developmental enhancers in the mouse neocortex.** *Nature communications*
  Notwell, J. H., Chung, T., Heavner, W., Bejerano, G.
  2015; 6: 6644-?

- **Microbiota modulate transcription in the intestinal epithelium without remodeling the accessible chromatin landscape.** *Genome research*
  Camp, J. G., Frank, C. L., Lickwar, C. R., Guturu, H., Rube, T., Wenger, A. M., Chen, J., Bejerano, G., Crawford, G. E., Rawls, J. F.
  2014; 24 (9): 1504-1516

- **Automated discovery of tissue-targeting enhancers and transcription factors from binding motif and gene function data.** *PLoS computational biology*
  Tuteja, G., Moreira, K. B., Chung, T., Chen, J., Wenger, A. M., Bejerano, G.
  2014; 10 (1)

- **Automated discovery of tissue-targeting enhancers and transcription factors from binding motif and gene function data.** *PLoS computational biology*
  Tuteja, G., Moreira, K. B., Chung, T., Chen, J., Wenger, A. M., Bejerano, G.
  2014; 10 (1)

- **Structure-aided prediction of mammalian transcription factor complexes in conserved non-coding elements.** *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*
  Guturu, H., Doxey, A. C., Wenger, A. M., Bejerano, G.
  2013; 368 (1632): 20130029-?

- **A Penile Spine/Vibrissa Enhancer Sequence Is Missing in Modern and Extinct Humans but Is Retained in Multiple Primates with Penile Spines and Sensory Vibrissae** *PLOS ONE*
  Reno, P. L., McLean, C. Y., Hines, J. E., Capellini, T. D., Bejerano, G., Kingsley, D. M.

2013; 8 (12)

- **Computational methods to detect conserved non-genic elements in phylogenetically isolated genomes: application to zebrafish.** *Nucleic acids research*
  Hiller, M., Agarwal, S., Notwell, J. H., Parikh, R., Guturu, H., Wenger, A. M., Bejerano, G.
  2013; 41 (15)

- **Computational methods to detect conserved non-genic elements in phylogenetically isolated genomes: application to zebrafish.** *Nucleic acids research*
  Hiller, M., Agarwal, S., Notwell, J. H., Parikh, R., Guturu, H., Wenger, A. M., Bejerano, G.
  2013; 41 (15)

- **The Enhancer Landscape during Early Neocortical Development Reveals Patterns of Dense Regulation and Co-option.** *PLoS genetics*
  Wenger, A. M., Clarke, S. L., Notwell, J. H., Chung, T., Tuteja, G., Guturu, H., Schaar, B. T., Bejerano, G.
  2013; 9 (8)

- **The enhancer landscape during early neocortical development reveals patterns of dense regulation and co-option.** *PLoS genetics*
  Wenger, A. M., Clarke, S. L., Notwell, J. H., Chung, T., Tuteja, G., Guturu, H., Schaar, B. T., Bejerano, G.
  2013; 9 (8)

- **PRISM offers a comprehensive genomic approach to transcription factor function prediction.** *Genome research*
  Wenger, A. M., Clarke, S. L., Guturu, H., Chen, J., Schaar, B. T., McLean, C. Y., Bejerano, G.
  2013; 23 (5): 889-904

- **Enhancers: five essential questions** *NATURE REVIEWS GENETICS*
  Pennacchio, L. A., Bickmore, W., Dean, A., Nobrega, M. A., Bejerano, G.
  2013; 14 (4): 288-295

- **Evolutionary biology for the 21st century.** *PLoS biology*
  Losos, J. B., Arnold, S. J., Bejerano, G., Brodie, E. D., Hibbett, D., Hoekstra, H. E., Mindell, D. P., Monteiro, A., Moritz, C., Orr, H. A., Petrov, D. A., Renner, S. S., Ricklefs, et al
  2013; 11 (1)

- **Evolutionary Biology for the 21st Century** *PLOS BIOLOGY*
  Losos, J. B., Arnold, S. J., Bejerano, G., Brodie, E. D., Hibbett, D., Hoekstra, H. E., Mindell, D. P., Monteiro, A., Moritz, C., Orr, H. A., Petrov, D. A., Renner, S. S., Ricklefs, et al
  2013; 11 (1)

- **A penile spine/vibrissa enhancer sequence is missing in modern and extinct humans but is retained in multiple primates with penile spines and sensory vibrissae.** *PloS one*
  Reno, P. L., McLean, C. Y., Hines, J. E., Capellini, T. D., Bejerano, G., Kingsley, D. M.
  2013; 8 (12)

- **Structure-aided prediction of mammalian transcription factor complexes in conserved non-coding elements.** *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*
  Guturu, H., Doxey, A. C., Wenger, A. M., Bejerano, G.
  2013; 368 (1632): 20130029-?

- **PESNPdb: A comprehensive database of SNPs studied in association with pre-eclampsia** *PLACENTA*
  Tuteja, G., Cheng, E., Papadakis, H., Bejerano, G.
  2012; 33 (12): 1055-1057

- **Hundreds of conserved non-coding genomic regions are independently lost in mammals** *NUCLEIC ACIDS RESEARCH*
  Hiller, M., Schaar, B. T., Bejerano, G.
  2012; 40 (22): 11463-11476

- **A "Forward Genomics'' Approach Links Genotype to Phenotype using Independent Phenotypic Losses among Related Species** *CELL REPORTS*
  Hiller, M., Schaar, B. T., Indjeian, V. B., Kingsley, D. M., Hagey, L. R., Bejerano, G.
  2012; 2 (4): 817-823

- **Human Developmental Enhancers Conserved between Deuterostomes and Protostomes** *PLOS GENETICS*
  Clarke, S. L., VanderMeer, J. E., Wenger, A. M., Schaar, B. T., Ahituv, N., Bejerano, G.
  2012; 8 (8)

- **A novel 13 base pair insertion in the sonic hedgehog ZRS limb enhancer (ZRS/LMBR1) causes preaxial polydactyly with triphalangeal thumb** *HUMAN MUTATION*
  Laurell, T., VanderMeer, J. E., Wenger, A. M., Grigelioniene, G., Nordenskjold, A., Arner, M., Ekblom, A. G., Bejerano, G., Ahituv, N., Nordgren, A.
  2012; 33 (7): 1063-1066

- **Coding exons function as tissue-specific enhancers of nearby genes** *GENOME RESEARCH*
  Birnbaum, R. Y., Clowney, E. J., Agamy, O., Kim, M. J., Zhao, J., Yamanaka, T., Pappalardo, Z., Clarke, S. L., Wenger, A. M., Loan Nguyen, L., Gurrieri, F., Everman, D. B., Schwartz, et al
  2012; 22 (6): 1059-1068

- **Control of Pelvic Girdle Development by Genes of the Pbx Family and Emx2** *DEVELOPMENTAL DYNAMICS*
  Capellini, T. D., Handschuh, K., Quintana, L., Ferretti, E., Di Giacomo, G., Fantini, S., Vaccari, G., Clarke, S. L., Wenger, A. M., Bejerano, G., Sharpe, J., Zappavigna, V., Selleri, et al
  2011; 240 (5): 1173-1189

- **Human-specific loss of regulatory DNA and the evolution of human-specific traits** *NATURE*
  McLean, C. Y., Reno, P. L., Pollen, A. A., Bassan, A. I., Capellini, T. D., Guenther, C., Indjeian, V. B., Lim, X., Menke, D. B., Schaar, B. T., Wenger, A. M., Bejerano, G., Kingsley, et al
  2011; 471 (7337): 216-219

- **Noninvasive Monitoring of Placenta-Specific Transgene Expression by Bioluminescence Imaging** *PLOS ONE*
  Fan, X., Ren, P., Dhal, S., Bejerano, G., Goodman, S. B., Druzin, M. L., Gambhir, S. S., Nayak, N. R.
  2011; 6 (1)

- **Human-specific loss of an androgen receptor enhancer is associated with the loss of vibrissae and penile spines** *80th Annual Meeting of the American-Association-of-Physical-Anthropologists*
  Reno, P. L., McLean, C. Y., Pollen, A. A., Bejerano, G., Kingsley, D. M.
  WILEY-BLACKWELL.2011: 252–252

- **Endangered Species Hold Clues to Human Evolution** *JOURNAL OF HEREDITY*
  Lowe, C. B., Bejerano, G., Salama, S. R., Haussler, D.
  2010; 101 (4): 437-447

- **GREAT improves functional interpretation of cis-regulatory regions** *NATURE BIOTECHNOLOGY*
  McLean, C. Y., Bristor, D., Hiller, M., Clarke, S. L., Schaar, B. T., Lowe, C. B., Wenger, A. M., Bejerano, G.
  2010; 28 (5): 495-U155

- **Dispensability of mammalian DNA** *GENOME RESEARCH*
  McLean, C., Bejerano, G.
  2008; 18 (11): 1743-1751

- **Human genome ultraconserved elements are ultraselected** *SCIENCE*
  Katzman, S., Kern, A. D., Bejerano, G., Fewell, G., Fulton, L., Wilson, R. K., Salama, S. R., Haussler, D.
  2007; 317 (5840): 915-915

- **Comparative genomic analysis using the UCSC genome browser.** *Methods in molecular biology (Clifton, N.J.)*
  Karolchik, D., Bejerano, G., Hinrichs, A. S., Kuhn, R. M., Miller, W., Rosenbloom, K. R., Zweig, A. S., Haussler, D., Kent, W. J.
  2007; 395: 17-34

- **Thousands of human mobile element fragments undergo strong purifying selection near developmental genes** *Proc. Nat?l Acad. Sci. USA*
  C.B. Lowe, G. Bejerano, D. Haussler
  2007; 104 (19): 8005-8010

- **Branch and bound computation of exact p-values** *BIOINFORMATICS*
  Bejerano, G.
  2006; 22 (17): 2158-2159

- **Identification and classification of conserved RNA secondary structures in the human genome** *PLOS COMPUTATIONAL BIOLOGY*
  Pedersen, J. S., Bejerano, G., Siepel, A., Rosenbloom, K., Lindblad-Toh, K., Lander, E. S., Kent, J., Miller, W., Haussler, D.
  2006; 2 (4): 251-262

- **The UCSC Genome Browser Database: update 2006** *NUCLEIC ACIDS RESEARCH*
  Hinrichs, A. S., Karolchik, D., Baertsch, R., Barber, G. P., Bejerano, G., Clawson, H., Diekhans, M., Furey, T. S., Harte, R. A., Hsu, F., Hillman-Jackson, J., Kuhn, R. M., PEDERSEN, et al
  2006; 34: D590-D598

- **A Distal Enhancer and an Ultraconserved Exon are Derived From a Novel Retroposon** *Nature*
  G. Bejerano, C.B. Lowe, N. Ahituv, B. King, A. Siepel, S.R. Salama, E.M. Rubin, W.J. Kent, D. Haussler
  2006; 441 (7089): 87-90

- **Forces Shaping the Fastest Evolving Regions in the Human Genome** *PLoS Genetics*
  K.S. Pollard, K.S. Pollard, S.R. Salama, B. King, A.D. Kern, T. Dreszer, S. Katzman, A.Siepel, J.S. Pedersen, G. Bejerano, R. Baertsch, K.R. Rosenbloom, J. Kent, D. Haussler
  2006; 2 (10): e168

- **Computational screening of conserved genomic DNA in search of functional noncoding elements** *NATURE METHODS*
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