Stanford

Alexander Eckehart Urban

Assistant Professor of Psychiatry and Behavioral Sciences (Major Laboratories and Clinical Translational Neurosciences Incubator) and of Genetics

NIH Biosketch available Online

Bio

ACADEMIC APPOINTMENTS

- Assistant Professor, Psychiatry and Behavioral Sciences
- Assistant Professor, Genetics
- Member, Bio-X
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Wu Tsai Neurosciences Institute

PROFESSIONAL EDUCATION

- PhD, Yale University , Molecular, Cellular and Developmental Biology (2007)

LINKS

- Urban Lab web site: http://urbanlab.stanford.edu
- Google Scholar: http://scholar.google.com/citations?user=IGyIeMsAAAAJ&hl=en
- NCBI myBibliography: https://www.ncbi.nlm.nih.gov/myncbi/collections/bibliography/44935252/

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

I have over a decade’s worth of experience in developing and applying high-throughput and high-resolution genomics analysis tools and procedures, in particular in the context of studying genomic sequence variation in brain development and function.

I have been involved on numerous occasions in using a large-scale and high-throughput setup for genomics analyses as well as carrying out analyses over several levels of genomics and epigenomics information. This includes participation in the ENCODE and 1000 Genomes projects, for the latter as a member of both the analytical and structural variation groups.

I have experience with developing and applying state-of-the-art and emerging genomics and epigenomics technologies (array and next-generation-sequencing based) for the analysis of gene expression, genomic DNA sequence and structure, DNA methylation and chromatin modification, in human cells and human cell culture systems, including stem cell culture models. For example I was co-first author of the paper in Science (Korbel, Urban, Affourtit et al., 2007, PMID 17901297) on developing next-generation-sequencing based paired-end mapping of CNVs and SVs, an approach that is now a standard part of whole-human-genome sequencing projects such as the 1000 Genomes Project. Paired-end mapping is also a critical component of advanced RNA-Seq approaches, mapping of transposable elements and the study of long-range chromatin interactions using the HiC method.

Two main, and connected, directions of research in my laboratory are the investigation of the molecular effects of large genome variants during neuronal development using iPSC model systems and the study of the nature and effects of somatic genome variation in the brain using tissue culture models and primary tissue samples.

Teaching

COURSES

2018-19

- Frontiers in Biological Research: BIOC 215, DBIO 215, GENE 215 (Aut, Win, Spr)

2017-18

- Next Generation Sequencing and Applications: BIOS 201 (Win)

2016-17

- Next Generation Sequencing and Applications: BIOS 201 (Win)

2015-16

- Next Generation Sequencing and Applications: BIOS 201 (Win)

STANFORD ADVISEES

Doctoral Dissertation Advisor (AC)

Thomas Ward

Postdoctoral Research Mentor

Kasey Davis

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Genetics (Phd Program)

Publications

PUBLICATIONS

- **Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA.** *Nature communications*
  Yang, E., Bahn, J. H., Hsiao, E. Y., Tan, B. X., Sun, Y., Fu, T., Zhou, B., Van Nostrand, E. L., Pratt, G. A., Freese, P., Wei, X., Quinones-Valdez, G., Urban, et al
  2019; 10 (1): 1338

- **Haplotype-resolved and integrated genome analysis of the cancer cell line HepG2.** *Nucleic acids research*
  Zhou, B., Ho, S. S., Greer, S. U., Spies, N., Bell, J. M., Zhang, X., Zhu, X., Arthur, J. G., Byeon, S., Pattni, R., Saha, I., Huang, Y., Song, et al
  2019

- **Comprehensive, integrated, and phased whole-genome analysis of the primary ENCODE cell line K562.** *Genome research*
  Zhou, B., Ho, S. S., Greer, S. U., Zhu, X., Bell, J. M., Arthur, J. G., Spies, N., Zhang, X., Byeon, S., Pattni, R., Ben-Efraim, N., Haney, M. S., Haraksingh, et al
  2019

- **The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight.** *Science (New York, N.Y.)*
  Garrett-Bakelman, F. E., Darshi, M., Green, S. J., Gur, R. C., Lin, L., Macias, B. R., McKenna, M. J., Meydan, C., Mishra, T., Nasrini, J., Piening, B. D., Rizzardi, L. F., Sharma, et al
  2019; 364 (6436)

- **Extensive and deep sequencing of the Venter/HuRef genome for developing and benchmarking genome analysis tools.** *Scientific data*
  Zhou, B., Arthur, J. G., Ho, S. S., Pattni, R., Huang, Y., Wong, W. H., Urban, A. E.
  2018; 5: 180261

- **Genome amplification and cellular senescence are hallmarks of human placenta development.** *PLoS genetics*
  Velicky, P., Meinhardt, G., Plessl, K., Vondra, S., Weiss, T., Haslinger, P., Lendl, T., Aumayr, K., Mairhofer, M., Zhu, X., Schutz, B., Hannibal, R. L., Lindau, et al

2018; 14 (10): e1007698

- **1q21.1 microduplication: large verbal-nonverbal performance discrepancy and ddPCR assays of HYDIN/HYDIN2 copy number** *NPJ GENOMIC MEDICINE*
  Xavier, J., Zhou, B., Bilan, F., Zhang, X., Gilbert-Dussardier, B., Viaux-Savelon, S., Pattni, R., Ho, S. S., Cohen, D., Levinson, D. F., Urbana, A. E., Laurent-Levinson, C.
  2018; 3: 24

- **Whole-genome sequencing analysis of CNV using low-coverage and paired-end strategies is efficient and outperforms array-based CNV analysis.** *Journal of medical genetics*
  Zhou, B., Ho, S. S., Zhang, X., Pattni, R., Haraksingh, R. R., Urban, A. E.
  2018

- **ANALYZING THE MOLECULAR EFFECTS OF LARGE NEUROPSYCHIATRIC CNVS WITH IPSC BASED NEURONAL TISSUE CULTURE MODELS**
  Urban, A.
  OXFORD UNIV PRESS.2018: S33

- **Different mutational rates and mechanisms in human cells at pregastrulation and neurogenesis** *SCIENCE*
  Bae, T., Tomasini, L., Mariani, J., Zhou, B., Roychowdhury, T., Franjic, D., Pletikos, M., Pattni, R., Chen, B., Venturini, E., Riley-Gillis, B., Sestan, N., Urban, et al
  2018; 359 (6375): 550-+

- **Detection and Quantification of Mosaic Genomic DNA Variation in Primary Somatic Tissues Using ddPCR: Analysis of Mosaic Transposable-Element Insertions, Copy-Number Variants, and Single-Nucleotide Variants.** *Methods in molecular biology (Clifton, N.J.)*
  Zhou, B., Haney, M. S., Zhu, X., Pattni, R., Abyzov, A., Urban, A. E.
  2018; 1768: 173–90

- **Local and global chromatin interactions are altered by large genomic deletions associated with human brain development.** *Nature communications*
  Zhang, X., Zhang, Y., Zhu, X., Purmann, C., Haney, M. S., Ward, T., Khechaduri, A., Yao, J., Weissman, S. M., Urban, A. E.
  2018; 9 (1): 5356

- **Challenges and recommendations for epigenomics in precision health** *NATURE BIOTECHNOLOGY*
  Carter, A. C., Chang, H. Y., Church, G., Dombkowski, A., Ecker, J. R., Gil, E., Giresi, P. G., Greely, H., Greenleaf, W. J., Hacohen, N., He, C., Hill, D., Ko, et al
  2017; 35 (12): 1128–32

- **META-ANALYSIS OF WHOLE BLOOD GENE EXPRESSION IN MAJOR DEPRESSION: IDENTIFYING COHERENT GENE NETWORKS**
  Mostafavi, S., Jansen, R., Battle, A., Zhu, X., Shi, J., Montgomery, S., Urban, A., Weissman, M., Potash, J., van Grootheest, G., Smit, J., Sullivan, P., Levinson, et al
  ELSEVIER SCIENCE BV.2017: S288–S289

- **COMPREHENSIVE COMPARATIVE PERFORMANCE ANALYSIS OF HIGH-DENSITY OLIGOMER ARRAY PLATFORMS FOR THE DETECTION AND ANALYSIS OF HUMAN GENOMIC COPY NUMBER VARIATION**
  Haraksingh, R., Abyzov, A., Urban, A.
  ELSEVIER SCIENCE BV.2017: S301–S302

- **Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network** *SCIENCE*
  McConnell, M. J., Moran, J. V., Abyzov, A., Akbarian, S., Bae, T., Cortes-Ciriano, I., Erwin, J. A., Fasching, L., Flasch, D. A., Freed, D., Ganz, J., Jaffe, A. E., Kwan, et al
  2017; 356 (6336): 395-?

- **Characterizing regression in Phelan McDermid Syndrome (22q13 deletion syndrome).** *Journal of psychiatric research*
  Reierson, G., Bernstein, J., Froehlich-Santino, W., Urban, A., Purmann, C., Berquist, S., Jordan, J., O'Hara, R., Hallmayer, J.
  2017; 91: 139-144

- **One thousand somatic SNVs per skin fibroblast cell set baseline of mosaic mutational load with patterns that suggest proliferative origin.** *Genome research*
  Abyzov, A., Tomasini, L., Zhou, B., Vasmatzis, N., Coppola, G., Amenduni, M., Pattni, R., Wilson, M., Gerstein, M., Weissman, S., Urban, A. E., Vaccarino, F. M.
  2017

- **Comprehensive performance comparison of high-resolution array platforms for genome-wide Copy Number Variation (CNV) analysis in humans.** *BMC genomics*
  Haraksingh, R. R., Abyzov, A., Urban, A. E.

2017; 18 (1): 321

- **Principles and Approaches for Discovery and Validation of Somatic Mosaicism in the Human Brain** *GENOMIC MOSAICISM IN NEURONS AND OTHER CELL TYPES*
  Abyzov, A., Urban, A. E., Vaccarino, F. M., Frade, J. M., Gage, F. H.
  2017; 131: 3–24
- **Identification of Human Neuronal Protein Complexes Reveals Biochemical Activities and Convergent Mechanisms of Action in Autism Spectrum Disorders.** *Cell systems*
  Li, J., Ma, Z., Shi, M., Malty, R. H., Aoki, H., Minic, Z., Phanse, S., Jin, K., Wall, D. P., Zhang, Z., Urban, A. E., Hallmayer, J., Babu, et al
  2015; 1 (5): 361-374
- **Identification of Human Neuronal Protein Complexes Reveals Biochemical Activities and Convergent Mechanisms of Action in Autism Spectrum Disorders** *CELL SYSTEMS*
  Li, J., Ma, Z., Shi, M., Malty, R. H., Aoki, H., Minic, Z., Phanse, S., Jin, K., Wall, D. P., Zhang, Z., Urban, A. E., Hallmayer, J., Babu, et al
  2015; 1 (5): 361-374
- **46,XY disorders of sex development and congenital diaphragmatic hernia: A case with dysmorphic facies, truncus arteriosus, bifid thymus, gut malrotation, rhizomelia, and adactyly** *AMERICAN JOURNAL OF MEDICAL GENETICS PART A*
  Esplin, E. D., Chaib, H., Haney, M., Martin, B., Homeyer, M., Urban, A. E., Bernstein, J. A.
  2015; 167A (6): 1360-1364
- **Using iPSCs and genomics to catch CNVs in the act.** *Nature genetics*
  Urban, A. E., Purmann, C.
  2015; 47 (2): 100-101
- **Type I interferon signaling genes in recurrent major depression: increased expression detected by whole-blood RNA sequencing.** *Molecular psychiatry*
  Mostafavi, S., Battle, A., Zhu, X., Potash, J. B., Weissman, M. M., Shi, J., Beckman, K., Haudenschild, C., McCormick, C., Mei, R., Gameroff, M. J., Gindes, H., Adams, et al
  2014; 19 (12): 1267-1274
- **Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals** *GENOME RESEARCH*
  Battle, A., Mostafavi, S., Zhu, X., Potash, J. B., Weissman, M. M., McCormick, C., Haudenschild, C. D., Beckman, K. B., Shi, J., Mei, R., Urban, A. E., Montgomery, S. B., Levinson, et al
  2014; 24 (1): 14-24
- **Integrated systems analysis reveals a molecular network underlying autism spectrum disorders.** *Molecular systems biology*
  Li, J., Shi, M., Ma, Z., Zhao, S., Euskirchen, G., Ziskin, J., Urban, A., Hallmayer, J., Snyder, M.
  2014; 10 (12): 774-?
- **Integrated systems analysis reveals a molecular network underlying autism spectrum disorders.** *Molecular systems biology*
  Li, J., Shi, M., Ma, Z., Zhao, S., Euskirchen, G., Ziskin, J., Urban, A., Hallmayer, J., Snyder, M.
  2014; 10: 774-?
- **Child Development and Structural Variation in the Human Genome** *CHILD DEVELOPMENT*
  Zhang, Y., Haraksingh, R., Grubert, F., Abyzov, A., Gerstein, M., Weissman, S., Urban, A. E.
  2013; 84 (1): 34-48
- **Normalizing RNA-Sequencing Data by Modeling Hidden Covariates with Prior Knowledge.** *PloS one*
  Mostafavi, S., Battle, A., Zhu, X., Urban, A. E., Levinson, D., Montgomery, S. B., Koller, D.
  2013; 8 (7)
- **Normalizing RNA-sequencing data by modeling hidden covariates with prior knowledge.** *PloS one*
  Mostafavi, S., Battle, A., Zhu, X., Urban, A. E., Levinson, D., Montgomery, S. B., Koller, D.
  2013; 8 (7)
- **Somatic copy number mosaicism in human skin revealed by induced pluripotent stem cells** *NATURE*
  Abyzov, A., Mariani, J., Palejev, D., Zhang, Y., Haney, M. S., Tomasini, L., Ferrandino, A. F., Belmaker, L. A., Szekely, A., Wilson, M., Kocabas, A., Calixto, N. E., Grigorenko, et al
  2012; 492 (7429): 438-?

- **Copy Number Variation detection from 1000 Genomes project exon capture sequencing data** *BMC BIOINFORMATICS*
  Wu, J., Grzeda, K. R., Stewart, C., Grubert, F., Urban, A. E., Snyder, M. P., Marth, G. T.
  2012; 13

- **Extensive genetic variation in somatic human tissues** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  O'Huallachain, M., Karczewski, K. J., Weissman, S. M., Urban, A. E., Snyder, M. P.
  2012; 109 (44): 18018-18023

- **A Role of Genomic Copy Number Variation in the Complex Behavioral Phenotype of Alcohol Dependence: A Commentary** *ALCOHOLISM-CLINICAL AND EXPERIMENTAL RESEARCH*
  Urban, A. E.
  2012; 36 (9): 1483-1486

- **Mutations in DNMT1 cause autosomal dominant cerebellar ataxia, deafness and narcolepsy** *HUMAN MOLECULAR GENETICS*
  Winkelmann, J., Lin, L., Schormair, B., Kornum, B. R., Faraco, J., Plazzi, G., Melberg, A., Cornelio, F., Urban, A. E., Pizza, F., Poli, F., Grubert, F., Wieland, et al
  2012; 21 (10): 2205-2210

- **Genome-Wide Mapping of Copy Number Variation in Humans: Comparative Analysis of High Resolution Array Platforms** *PLOS ONE*
  Haraksingh, R. R., Abyzov, A., Gerstein, M., Urban, A. E., Snyder, M.
  2011; 6 (11)

- **A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans** *PLOS GENETICS*
  Stewart, C., Kural, D., Stroemberg, M. P., Walker, J. A., Konkel, M. K., Stuetz, A. M., Urban, A. E., Grubert, F., Lam, H. Y., Lee, W., Busby, M., Indap, A. R., Garrison, et al
  2011; 7 (8)

- **Identification of genomic indels and structural variations using split reads** *BMC GENOMICS*
  Zhang, Z. D., Du, J., Lam, H., Abyzov, A., Urban, A. E., Snyder, M., Gerstein, M.
  2011; 12

- **CNVnator: An approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing** *GENOME RESEARCH*
  Abyzov, A., Urban, A. E., Snyder, M., Gerstein, M.
  2011; 21 (6): 974-984

- **The promise of stem cell research for neuropsychiatric disorders** *JOURNAL OF CHILD PSYCHOLOGY AND PSYCHIATRY*
  Vaccarino, F. M., Urban, A. E., Stevens, H. E., Szekely, A., Abyzov, A., Grigorenko, E. L., Gerstein, M., Weissman, S.
  2011; 52 (4): 504-516

- **Mapping copy number variation by population-scale genome sequencing** *NATURE*
  Mills, R. E., Walter, K., Stewart, C., Handsaker, R. E., Chen, K., Alkan, C., Abyzov, A., Yoon, S. C., Ye, K., Cheetham, R. K., Chinwalla, A., Conrad, D. F., Fu, et al
  2011; 470 (7332): 59-65

- **A map of human genome variation from population-scale sequencing** *NATURE*
  Altshuler, D., Durbin, R. M., Abecasis, G. R., Bentley, D. R., Chakravarti, A., Clark, A. G., Collins, F. S., De La Vega, F. M., Donnelly, P., Egholm, M., Flicek, P., Gabriel, S. B., Gibbs, et al
  2010; 467 (7319): 1061-1073

- **Behavior, Brain, and Genome in Genomic Disorders: Finding the Correspondences** *JOURNAL OF DEVELOPMENTAL AND BEHAVIORAL PEDIATRICS*
  Grigorenko, E. L., Urban, A. E., Mencl, E.
  2010; 31 (7): 602-609

- **Variation in Transcription Factor Binding Among Humans** *SCIENCE*
  Kasowski, M., Grubert, F., Heffelfinger, C., Hariharan, M., Asabere, A., Waszak, S. M., Habegger, L., Rozowsky, J., Shi, M., Urban, A. E., Hong, M., Karczewski, K. J., Huber, et al
  2010; 328 (5975): 232-235

- **EBNA1 regulates cellular gene expression by binding cellular promoters** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

Canaan, A., Haviv, I., Urban, A. E., Schulz, V. P., Hartman, S., Zhang, Z., Palejev, D., Deisseroth, A. B., Lacy, J., Snyder, M., Gerstein, M., Weissman, S. M.
2009; 106 (52): 22421-22426

- **The genetic architecture of Down syndrome phenotypes revealed by high-resolution analysis of human segmental trisomies** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Korbel, J. O., Tirosh-Wagner, T., Urban, A. E., Chen, X., Kasowski, M., Dai, L., Grubert, F., Erdman, C., Gao, M. C., Lange, K., Sobel, E. M., Barlow, G. M., Aylsworth, et al
  2009; 106 (29): 12031-12036

- **Distinct Genomic Aberrations Associated with ERG Rearranged Prostate Cancer** *GENES CHROMOSOMES & CANCER*
  Demichelis, F., Setlur, S. R., Beroukhim, R., Perner, S., Korbel, J. O., LaFargue, C. J., Pflueger, D., Pina, C., Hofer, M. D., Sboner, A., Svensson, M. A., Rickman, D. S., Urban, et al
  2009; 48 (4): 366-380

- **Analysis of copy number variants and segmental duplications in the human genome: Evidence for a change in the process of formation in recent evolutionary history** *GENOME RESEARCH*
  Kim, P. M., Lam, H. Y., Urban, A. E., Korbel, J. O., Affourtit, J., Grubert, F., Chen, X., Weissman, S., Snyder, M., Gerstein, M. B.
  2008; 18 (12): 1865-1874

- **High-Resolution Copy-Number Variation Map Reflects Human Olfactory Receptor Diversity and Evolution** *PLOS GENETICS*
  Hasin, Y., Olender, T., Khen, M., Gonzaga-Jauregui, C., Kim, P. M., Urban, A. E., Snyder, M., Gerstein, M. B., Lancet, D., Korbel, J. O.
  2008; 4 (11)

- **A procedure for highly specific, sensitive, and unbiased whole-genome amplification** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Pan, X., Urban, A. E., Palejev, D., Schulz, V., Grubert, F., Hu, Y., Snyder, M., Weissman, S. M.
  2008; 105 (40): 15499-15504

- **MEDME: An experimental and analytical methodology for the estimation of DNA methylation levels based on microarray derived MeDIP-enrichment** *GENOME RESEARCH*
  Pelizzola, M., Koga, Y., Urban, A. E., Krauthammer, M., Weissman, S., Halaban, R., Molinaro, A. M.
  2008; 18 (10): 1652-1659

- **The current excitement about copy-number variation: how it relates to gene duplications and protein families** *CURRENT OPINION IN STRUCTURAL BIOLOGY*
  Korbel, J. O., Kim, P. M., Chen, X., Urban, A. E., Weissman, S., Snyder, M., Gerstein, M. B.
  2008; 18 (3): 366-374

- **Systematic analysis of transcribed loci in ENCODE regions using RACE sequencing reveals extensive transcription in the human genome** *GENOME BIOLOGY*
  QianWu, J., Du, J., Rozowsky, J., Zhang, Z., Urban, A. E., Euskirchen, G., Weissman, S., Gerstein, M., Snyder, M.
  2008; 9 (1)

- **Paired-end mapping reveals extensive structural variation in the human genome** *SCIENCE*
  Korbel, J. O., Urban, A. E., Affourtit, J. P., Godwin, B., Grubert, F., Simons, J. F., Kim, P. M., Palejev, D., Carriero, N. J., Du, L., Taillon, B. E., Chen, Z., Tanzer, et al
  2007; 318 (5849): 420-426

- **Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project** *NATURE*
  Birney, E., Stamatoyannopoulos, J. A., Dutta, A., Guigo, R., Gingeras, T. R., Margulies, E. H., Weng, Z., Snyder, M., Dermitzakis, E. T., Stamatoyannopoulos, J. A., Thurman, R. E., Kuehn, M. S., Taylor, et al
  2007; 447 (7146): 799-816

- **Systematic prediction and validation of breakpoints associated with copy-number variants in the human genome** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Korbel, J. O., Urban, A. E., Grubert, F., Du, J., Royce, T. E., Starr, P., Zhong, G., Emanuel, B. S., Weissman, S. M., Snyder, M., Gerstein, M. B.
  2007; 104 (24): 10110-10115

- **Assessing the performance of different high-density tiling microarray strategies for mapping transcribed regions of the human genome** *GENOME RESEARCH*
  Emanuelsson, O., Nagalakshmi, U., Zheng, D., Rozowsky, J. S., Urban, A. E., Du, J., Lian, Z., Stolc, V., Weissman, S., Snyder, M., Gerstein, M. B.

2007; 17 (6): 886-897

- **High-resolution mapping of DNA copy alterations in human chromosome 22 using high-density tiling oligonucleotide arrays** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

  Urban, A. E., Korbel, J. O., Selzer, R., Richmond, T., Hacker, A., Popescu, G. V., Clubells, J. F., Green, R., Emanuel, B. S., Gerstein, M. B., Weissman, S. M., Snyder, M.

  2006; 103 (12): 4534-4539

- **Global identification of human transcribed sequences with genome tiling arrays** *SCIENCE*

  Bertone, P., Stolc, V., Royce, T. E., Rozowsky, J. S., Urban, A. E., Zhu, X. W., Rinn, J. L., Tongprasit, W., Samanta, M., Weissman, S., Gerstein, M., Snyder, M.

  2004; 306 (5705): 2242-2246

- **The ENCODE (ENCyclopedia of DNA elements) Project** *SCIENCE*

  Feingold, E. A., Good, P. J., Guyer, M. S., Kamholz, S., Liefer, L., Wetterstrand, K., Collins, F. S., Gingeras, T. R., Kampa, D., Sekinger, E. A., Cheng, J., Hirsch, H., Ghosh, et al

  2004; 306 (5696): 636-640

- **Identification of novel functional elements in the human genome** *67th Cold Spring Harbor Symposium on Quantitative Biology*

  Lian, Z., Euskirchen, G., Rinn, J., Martone, R., Bertone, P., Hartman, S., Royce, T., Nelson, K., Sayward, F., Luscombe, N., Yang, J., Li, J. L., Miller, et al

  COLD SPRING HARBOR LAB PRESS, PUBLICATIONS DEPT.2003: 317–322