

Stanford



Jin Billy Li

Associate Professor of Genetics

CONTACT INFORMATION

• Administrative Contact

Maria Manzanilla-Owen - Administrative Associate

Email mariamo@stanford.edu

Tel 650-736-0295

Bio

ACADEMIC APPOINTMENTS

- Associate Professor, Genetics
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute
- Faculty Fellow, Stanford ChEM-H
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Director, Graduate Studies of Genetics PhD Program, (2014- present)
- Member, Stanford Diabetes Research Center, (2020- present)

HONORS AND AWARDS

- New Scholar Award, Ellison Medical Foundation (2012-2016)

PROFESSIONAL EDUCATION

- Postdoctoral Fellow, Harvard Medical School , Genomics and Technology
- Ph.D., Washington University in St. Louis , Genetics and Computational Biology (2005)
- M.S., Tsinghua University , Molecular Biology (1999)
- B.S., Tsinghua University , Biology (1997)

LINKS

- Li Lab Website: <http://lilab.stanford.edu>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

The Li Lab is primarily interested in RNA editing mediated by ADAR enzymes. We co-discovered that the major function of RNA editing is to label endogenous dsRNAs as "self" to avoid being recognized as "non-self" by MDA5, a host innate immune dsRNA sensor, leading us to pursue therapeutic applications in cancer, autoimmune diseases, and viral infection. The other major direction of the lab is to develop technologies to harness endogenous ADAR enzymes for site-specific transcriptome engineering.

Teaching

COURSES

2019-20

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

2018-19

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

2017-18

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

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Timothy Abbott, Nimit Jain

Postdoctoral Faculty Sponsor

Amruta Bhate, Rohini Datta, Shibin Hu, Qin Li, Paul Vogel

Doctoral Dissertation Co-Advisor (AC)

Julia Adamska

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)
- Biophysics (Phd Program)
- Genetics (Phd Program)

Publications

PUBLICATIONS

- **Adar RNA editing-dependent and -independent effects are required for brain and innate immune functions in *Drosophila*.** *Nature communications* Deng, P., Khan, A., Jacobson, D., Sambrani, N., McGurk, L., Li, X., Jayasree, A., Hejatko, J., Shohat-Ophir, G., O'Connell, M. A., Li, J. B., Keegan, L. P. 2020; 11 (1): 1580
- **Zinc Finger RNA-Binding Protein Zn72D Regulates ADAR-Mediated RNA Editing in Neurons.** *Cell reports* Sapiro, A. L., Freund, E. C., Restrepo, L., Qiao, H. H., Bhate, A., Li, Q., Ni, J. Q., Mosca, T. J., Li, J. B. 2020; 31 (7): 107654
- **Unbiased Identification of trans Regulators of ADAR and A-to-I RNA Editing.** *Cell reports* Freund, E. C., Sapiro, A. L., Li, Q., Linder, S., Moresco, J. J., Yates, J. R., Li, J. B. 2020; 31 (7): 107656

- **ADAR1: A New Target for Immuno-oncology Therapy.** *Molecular cell*
Bhate, A., Sun, T., Li, J. B.
2019; 73 (5): 866–68
- **Illuminating spatial A-to-I RNA editing signatures within the Drosophila brain** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Sapiro, A. L., Shmueli, A., Henry, G., Li, Q., Shalit, T., Yaron, O., Paas, Y., Li, J., Shohat-Ophir, G.
2019; 116 (6): 2318–27
- **Precise RNA editing by recruiting endogenous ADARs with antisense oligonucleotides.** *Nature biotechnology*
Merkle, T., Merz, S., Reautschnig, P., Blaha, A., Li, Q., Vogel, P., Wettengel, J., Li, J. B., Stafforst, T.
2019
- **Efficient and precise editing of endogenous transcripts with SNAP-tagged ADARs** *NATURE METHODS*
Vogel, P., Moschref, M., Li, Q., Merkle, T., Selvasaravanan, K. D., Li, J., Stafforst, T.
2018; 15 (7): 535–+
- **Evolutionary analysis reveals regulatory and functional landscape of coding and non-coding RNA editing.** *PLoS genetics*
Zhang, R., Deng, P., Jacobson, D., Li, J. B.
2017; 13 (2)
- **Dynamic landscape and regulation of RNA editing in mammals.** *Nature*
Tan, M. H., Li, Q., Shanmugam, R., Piskol, R., Kohler, J., Young, A. N., Liu, K. I., Zhang, R., Ramaswami, G., Ariyoshi, K., Gupte, A., Keegan, L. P., George, et al
2017; 550 (7675): 249–54
- **Regulation of gene expression and RNA editing in Drosophila adapting to divergent microclimates.** *Nature communications*
Yablonovitch, A. L., Fu, J., Li, K., Mahato, S., Kang, L., Rashkovetsky, E., Korol, A. B., Tang, H., Michalak, P., Zelhof, A. C., Nevo, E., Li, J. B.
2017; 8 (1): 1570
- **RNA editing by ADAR1 prevents MDA5 sensing of endogenous dsRNA as nonself.** *Science*
Liddicoat, B. J., Piskol, R., Chalk, A. M., Ramaswami, G., Higuchi, M., Hartner, J. C., Li, J. B., Seeburg, P. H., Walkley, C. R.
2015; 349 (6252): 1115–1120
- **Cis Regulatory Effects on A-to-I RNA Editing in Related Drosophila Species** *CELL REPORTS*
Sapiro, A. L., Deng, P., Zhang, R., Li, J. B.
2015; 11 (5): 697–703
- **Genetic mapping uncovers cis-regulatory landscape of RNA editing.** *Nature communications*
Ramaswami, G., Deng, P., Zhang, R., Anna Carbone, M., Mackay, T. F., Billy Li, J.
2015; 6: 8194–?
- **Enhanced Specificity and Efficiency of the CRISPR/Cas9 System with Optimized sgRNA Parameters in Drosophila** *CELL REPORTS*
Ren, X., Yang, Z., Xu, J., Sun, J., Mao, D., Hu, Y., Yang, S., Qiao, H., Wang, X., Hu, Q., Deng, P., Liu, L., Ji, et al
2014; 9 (3): 1151–1162
- **Quantifying RNA allelic ratios by microfluidic multiplex PCR and sequencing.** *Nature methods*
Zhang, R., Li, X., Ramaswami, G., Smith, K. S., Turecki, G., Montgomery, S. B., Li, J. B.
2014; 11 (1): 51–54
- **Deciphering the functions and regulation of brain-enriched A-to-I RNA editing.** *Nature neuroscience*
Li, J. B., Church, G. M.
2013; 16 (11): 1518–1522
- **Reliable Identification of Genomic Variants from RNA-Seq Data.** *American journal of human genetics*
Piskol, R., Ramaswami, G., Li, J. B.
2013; 93 (4): 641–651
- **Identifying RNA editing sites using RNA sequencing data alone** *NATURE METHODS*
Ramaswami, G., Zhang, R., Piskol, R., Keegan, L. P., Deng, P., O'Connell, M. A., Li, J. B.

2013; 10 (2): 128-132

- **RNA sequencing reveals a diverse and dynamic repertoire of the *Xenopus tropicalis* transcriptome over development** *GENOME RESEARCH*
Tan, M. H., Au, K. F., Yablonovitch, A. L., Wills, A. E., Chuang, J., Baker, J. C., Wong, W. H., Li, J. B.
2013; 23 (1): 201-216
- **Accurate identification of human Alu and non-Alu RNA editing sites** *NATURE METHODS*
Ramaswami, G., Lin, W., Piskol, R., Tan, M. H., Davis, C., Li, J. B.
2012; 9 (6): 579-?
- **Comment on "Widespread RNA and DNA Sequence Differences in the Human Transcriptome"** *SCIENCE*
Lin, W., Piskol, R., Tan, M. H., Li, J. B.
2012; 335 (6074)
- **Genome-Wide Identification of Human RNA Editing Sites by Parallel DNA Capturing and Sequencing** *SCIENCE*
Li, J. B., Levanon, E. Y., Yoon, J., Aach, J., Xie, B., LeProust, E., Zhang, K., Gao, Y., Church, G. M.
2009; 324 (5931): 1210-1213
- **Comparative and basal genomics identifies a flagellar and basal body proteome that includes the BBS5 human disease gene** *CELL*
Li, J. B., Gerdes, J. M., Haycraft, C. J., Fan, Y. L., Teslovich, T. M., May-Simera, H., Li, H. T., Blacque, O. E., Li, L. Y., Leitch, C. C., Lewis, R. A., Green, J. S., Parfrey, et al
2004; 117 (4): 541-552
- **A Quantitative Proteome Map of the Human Body.** *Cell*
Jiang, L., Wang, M., Lin, S., Jian, R., Li, X., Chan, J., Dong, G., Fang, H., Robinson, A. E., Snyder, M. P.
2020
- **GLOBAL LANDSCAPE AND GENETIC REGULATION OF RNA EDITING IN CORTICAL SAMPLES FROM INDIVIDUALS WITH SCHIZOPHRENIA**
Breen, M., Dobbyn, A., Li, Q., Roussos, P., Hoffman, G., Stahl, E., Chess, A., Li, J., Devlin, B., Buxbaum, J., CommonMind Consortium
ELSEVIER.2019: S112–S113
- **Illuminating spatial A-to-I RNA editing signatures within the *Drosophila* brain.** *Proceedings of the National Academy of Sciences of the United States of America*
Sapiro, A. L., Shmueli, A., Henry, G. L., Li, Q., Shalit, T., Yaron, O., Paas, Y., Billy Li, J., Shohat-Ophir, G.
2019
- **Global landscape and genetic regulation of RNA editing in cortical samples from individuals with schizophrenia.** *Nature neuroscience*
Breen, M. S., Dobbyn, A., Li, Q., Roussos, P., Hoffman, G. E., Stahl, E., Chess, A., Sklar, P., Li, J. B., Devlin, B., Buxbaum, J. D.
2019; 22 (9): 1402–12
- **The THO Complex Coordinates Transcripts for Synapse Development and Dopamine Neuron Survival.** *Cell*
Maeder, C. I., Kim, J., Liang, X., Kaganovsky, K., Shen, A., Li, Q., Li, Z., Wang, S., Xu, X. Z., Li, J. B., Xiang, Y. K., Ding, J. B., Shen, et al
2018
- **Pre-reproductive stress and fluoxetine treatment in rats affect offspring A-to-I RNA editing, gene expression and social behavior** *ENVIRONMENTAL EPIGENETICS*
Zaidan, H., Ramaswami, G., Barak, M., Li, J. B., Gaisler-Salomon, I.
2018; 4 (2): dvy021
- **Updates to the RNA mapping database (RMDB), version 2** *NUCLEIC ACIDS RESEARCH*
Yesselman, J. D., Tian, S., Liu, X., Shi, L., Li, J., Das, R.
2018; 46 (D1): D375–D379
- **A-to-I RNA editing in the rat brain is age-dependent, region-specific and sensitive to environmental stress across generations.** *BMC genomics*
Zaidan, H., Ramaswami, G., Golumbic, Y. N., Sher, N., Malik, A., Barak, M., Galiani, D., Dekel, N., Li, J. B., Gaisler-Salomon, I.
2018; 19 (1): 28
- **Updates to the RNA mapping database (RMDB), version 2.** *Nucleic acids research*
Yesselman, J. D., Tian, S., Liu, X., Shi, L., Li, J. B., Das, R.
2018; 46 (D1): D375–D379

- **Abnormalities in A-to-I RNA editing patterns in CNS injuries correlate with dynamic changes in cell type composition** *SCIENTIFIC REPORTS*
Gal-Mark, N., Shallev, L., Sweetat, S., Barak, M., Li, J. B., Levanon, E. Y., Eisenberg, E., Behar, O.
2017; 7
- **Molecular definition of a metastatic lung cancer state reveals a targetable CD109-Janus kinase-Stat axis.** *Nature medicine*
Chuang, C., Greenside, P. G., Rogers, Z. N., Brady, J. J., Yang, D., Ma, R. K., Caswell, D. R., Chiou, S., Winters, A. F., Grüner, B. M., Ramaswami, G., Spencley, A. L., Kopecky, et al
2017; 23 (3): 291-300
- **Deficiency of microRNA miR-34a expands cell fate potential in pluripotent stem cells** *SCIENCE*
Choi, Y. J., Lin, C., Rizzo, D., Chen, S., Kim, T. A., Tan, M. H., Li, J. B., Wu, Y., Chen, C., Xuan, Z., Macfarlan, T., Peng, W., Lloyd, et al
2017; 355 (6325): 596-?
- **DDX6 Represses Aberrant Activation of Interferon-Stimulated Genes.** *Cell reports*
Lumb, J. H., Li, Q., Popov, L. M., Ding, S., Keith, M. T., Merrill, B. D., Greenberg, H. B., Li, J. B., Carette, J. E.
2017; 20 (4): 819-31
- **Landscape of X chromosome inactivation across human tissues.** *Nature*
Tukiainen, T., Villani, A. C., Yen, A., Rivas, M. A., Marshall, J. L., Satija, R., Aguirre, M., Gauthier, L., Fleharty, M., Kirby, A., Cummings, B. B., Castel, S. E., Karczewski, et al
2017; 550 (7675): 244-48
- **The evolution and adaptation of A-to-I RNA editing.** *PLoS genetics*
Yablonovitch, A. L., Deng, P., Jacobson, D., Li, J. B.
2017; 13 (11): e1007064
- **Rewriting the transcriptome: adenosine-to-inosine RNA editing by ADARs.** *Genome biology*
Walkley, C. R., Li, J. B.
2017; 18 (1): 205
- **Protein recoding by ADAR1-mediated RNA editing is not essential for normal development and homeostasis.** *Genome biology*
Heraud-Farlow, J. E., Chalk, A. M., Linder, S. E., Li, Q., Taylor, S., White, J. M., Pang, L., Liddicoat, B. J., Gupte, A., Li, J. B., Walkley, C. R.
2017; 18 (1): 166
- **Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease.** *Nature genetics*
2017; 49 (12): 1664-70
- **Co-expression networks reveal the tissue-specific regulation of transcription and splicing.** *Genome research*
Saha, A., Kim, Y., Gewirtz, A. D., Jo, B., Gao, C., McDowell, I. C., Engelhardt, B. E., Battle, A.
2017; 27 (11): 1843-58
- **Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis.** *Genome research*
Yang, F., Wang, J., Pierce, B. L., Chen, L. S.
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- **The impact of rare variation on gene expression across tissues.** *Nature*
Li, X., Kim, Y., Tsang, E. K., Davis, J. R., Damani, F. N., Chiang, C., Hess, G. T., Zappala, Z., Strober, B. J., Scott, A. J., Li, A., Ganna, A., Bassik, et al
2017; 550 (7675): 239-43
- **Genetic effects on gene expression across human tissues.** *Nature*
Battle, A., Brown, C. D., Engelhardt, B. E., Montgomery, S. B.
2017; 550 (7675): 204-13
- **Adenosine-to-inosine RNA editing by ADAR1 is essential for normal murine erythropoiesis** *EXPERIMENTAL HEMATOLOGY*
Liddicoat, B. J., Hartner, J. C., Piskol, R., Ramaswami, G., Chalk, A. M., Kingsley, P. D., Sankaran, V. G., Wall, M., Purton, L. E., Seeburg, P. H., Palis, J., Orkin, S. H., Lu, et al
2016; 44 (10): 947-963
- **Identification of human RNA editing sites: A historical perspective.** *Methods (San Diego, Calif.)*
Ramaswami, G., Li, J. B.

2016; 107: 42-47

- **XenMine: A genomic interaction tool for the Xenopus community.** *Developmental biology*
Reid, C. D., Karra, K., Chang, J., Piskol, R., Li, Q., Li, J. B., Cherry, J. M., Baker, J. C.
2016
- **Editing of Cellular Self-RNAs by Adenosine Deaminase ADAR1 Suppresses Innate Immune Stress Responses** *JOURNAL OF BIOLOGICAL CHEMISTRY*
George, C. X., Ramaswami, G., Li, J. B., Samuel, C. E.
2016; 291 (12): 6158-6168
- **The Genomic Landscape and Clinical Relevance of A-to-I RNA Editing in Human Cancers** *CANCER CELL*
Han, L., Diao, L., Yu, S., Xu, X., Li, J., Zhang, R., Yang, Y., Werner, H. M., Eterovic, A. K., Yuan, Y., Li, J., Nair, N., Minelli, et al
2015; 28 (4)
- **The landscape of genomic imprinting across diverse adult human tissues** *GENOME RESEARCH*
Baran, Y., Subramaniam, M., Biton, A., Tukiainen, T., Tsang, E. K., Rivas, M. A., Pirinen, M., Gutierrez-Arcelus, M., Smith, K. S., Kukurba, K. R., Zhang, R., Eng, C., Torgerson, et al
2015; 25 (7): 927-936
- **Effect of predicted protein-truncating genetic variants on the human transcriptome** *SCIENCE*
Rivas, M. A., Pirinen, M., Conrad, D. F., Lek, M., Tsang, E. K., Karczewski, K. J., Maller, J. B., Kukurba, K. R., DeLuca, D. S., Fromer, M., Ferreira, P. G., Smith, K. S., Zhang, et al
2015; 348 (6235): 666-669
- **Genetic conflict reflected in tissue-specific maps of genomic imprinting in human and mouse.** *Nature genetics*
Babak, T., Deveale, B., Tsang, E. K., Zhou, Y., Li, X., Smith, K. S., Kukurba, K. R., Zhang, R., Li, J. B., van der Kooy, D., Montgomery, S. B., Fraser, H. B.
2015; 47 (5): 544-549
- **The role of Abcb5 alleles in susceptibility to haloperidol-induced toxicity in mice and humans.** *PLoS medicine*
Zheng, M., Zhang, H., Dill, D. L., Clark, J. D., Tu, S., Yablonovitch, A. L., Tan, M. H., Zhang, R., Rujescu, D., Wu, M., Tessarollo, L., Vieira, W., Gottesman, et al
2015; 12 (2)
- **Novel RNA Modifications in the Nervous System: Form and Function** *JOURNAL OF NEUROSCIENCE*
Satterlee, J. S., Basanta-Sanchez, M., Blanco, S., Li, J. B., Meyer, K., Pollock, J., Sadri-Vakili, G., Rybak-Wolf, A.
2014; 34 (46): 15170-15177
- **Allelic Expression of Deleterious Protein-Coding Variants across Human Tissues** *PLOS GENETICS*
Kukurba, K. R., Zhang, R., Li, X., Smith, K. S., Knowles, D. A., Tan, M. H., Piskol, R., Lek, M., Snyder, M., MacArthur, D. G., Li, J. B., Montgomery, S. B.
2014; 10 (5)
- **A-to-I RNA editing occurs at over a hundred million genomic sites, located in a majority of human genes** *GENOME RESEARCH*
Bazak, L., Haviv, A., Barak, M., Jacob-Hirsch, J., Deng, P., Zhang, R., Isaacs, F. J., Rechavi, G., Li, J. B., Eisenberg, E., Levanon, E. Y.
2014; 24 (3): 365-376
- **RADAR: a rigorously annotated database of A-to-I RNA editing** *NUCLEIC ACIDS RESEARCH*
Ramaswami, G., Li, J. B.
2014; 42 (D1): D109-D113
- **Novel RNA modifications in the nervous system: form and function.** *The Journal of neuroscience : the official journal of the Society for Neuroscience*
Satterlee, J. S., Basanta-Sanchez, M., Blanco, S., Li, J. B., Meyer, K., Pollock, J., Sadri-Vakili, G., Rybak-Wolf, A.
2014; 34 (46): 15170-77
- **Comparative RNA editing in autistic and neurotypical cerebella** *MOLECULAR PSYCHIATRY*
Eran, A., Li, J. B., Vatalaro, K., McCarthy, J., Rahimov, F., Collins, C., Markianos, K., MARGULIES, D. M., Brown, E. N., Calvo, S. E., Kohane, I. S., Kunkel, L. M.
2013; 18 (9): 1041-1048
- **Lack of evidence for existence of noncanonical RNA editing** *NATURE BIOTECHNOLOGY*
Piskol, R., Peng, Z., Wang, J., Li, J. B.
2013; 31 (1): 19-20

- **Versatile design and synthesis platform for visualizing genomes with Oligopaint FISH probes** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Beliveau, B. J., Joyce, E. F., Apostolopoulos, N., Yilmaz, F., Fonseka, C. Y., Mccole, R. B., Chang, Y., Li, J. B., Senaratne, T. N., Williams, B. R., Rouillard, J., Wu, C.
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- **The difficult calls in RNA editing** *NATURE BIOTECHNOLOGY*
Bass, B., Hundley, H., Li, J. B., Peng, Z., Pickrell, J., Xiao, X. G., Yang, L.
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- **Activity-Dependent A-to-I RNA Editing in Rat Cortical Neurons** *GENETICS*
Sanjana, N. E., Levanon, E. Y., Hueske, E. A., Ambrose, J. M., Li, J. B.
2012; 192 (1): 281-U569
- **A public resource facilitating clinical use of genomes** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Ball, M. P., Thakuria, J. V., Zaranek, A. W., Clegg, T., Rosenbaum, A. M., Wu, X., Angrist, M., Bhak, J., Bobe, J., Callow, M. J., Cano, C., Chou, M. F., Chung, et al
2012; 109 (30): 11920-11927
- **Scalable gene synthesis by selective amplification of DNA pools from high-fidelity microchips** *NATURE BIOTECHNOLOGY*
Kosuri, S., Eroshenko, N., LeProust, E. M., Super, M., Way, J., Li, J. B., Church, G. M.
2010; 28 (12): 1295-U108
- **Sequence based identification of RNA editing sites** *RNA BIOLOGY*
Eisenberg, E., Li, J. B., Levanon, E. Y.
2010; 7 (2): 248-252
- **A Robust Approach to Identifying Tissue-Specific Gene Expression Regulatory Variants Using Personalized Human Induced Pluripotent Stem Cells** *PLOS GENETICS*
Lee, J., Park, I., Gao, Y., Li, J. B., Li, Z., Daley, G. Q., Zhang, K., Church, G. M.
2009; 5 (11)
- **Multiplex padlock targeted sequencing reveals human hypermutable CpG variations** *GENOME RESEARCH*
Li, J. B., Gao, Y., Aach, J., Zhang, K., Kryukov, G. V., Xie, B., Ahlford, A., Yoon, J., Rosenbaum, A. M., Zaranek, A. W., LeProust, E., Sunyaev, S. R., Church, et al
2009; 19 (9): 1606-1615
- **Digital RNA allelotyping reveals tissue-specific and allele-specific gene expression in human** *NATURE METHODS*
Zhang, K., Li, J. B., Gao, Y., Egli, D., Xie, B., Deng, J., Li, Z., Lee, J., Aach, J., LeProust, E. M., Eggan, K., Church, G. M.
2009; 6 (8): 613-U90
- **Targeted and genome-scale strategies reveal gene-body methylation signatures in human cells** *NATURE BIOTECHNOLOGY*
Ball, M. P., Li, J. B., Gao, Y., Lee, J., LeProust, E. M., Park, I., Xie, B., Daley, G. Q., Church, G. M.
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- **Multiplex amplification of large sets of human exons** *NATURE METHODS*
Porreca, G. J., Zhang, K., Li, J. B., Xie, B., Austin, D., Vassallo, S. L., LeProust, E. M., Peck, B. J., Emig, C. J., Dahl, F., Gao, Y., Church, G. M., Shendure, et al
2007; 4 (11): 931-936
- **Procom: a web-based tool to compare multiple eukaryotic proteomes** *BIOINFORMATICS*
Li, J. B., Zhang, M., Dutcher, S. K., Stormo, G. D.
2005; 21 (8): 1693-1694
- **Analysis of Chlamydomonas reinhardtii genome structure using large-scale Sequencing of regions on linkage groups I and III** *JOURNAL OF EUKARYOTIC MICROBIOLOGY*
Li, J. B., Lin, S. P., Jia, H. G., Wu, H. M., Roe, B. A., Kulp, D., Stormo, G. D., Dutcher, S. K.
2003; 50 (3): 145-155