



Gavin Sherlock

Professor of Genetics

Bio

ACADEMIC APPOINTMENTS

- Professor, Genetics
- Member, Bio-X
- Member, Stanford Cancer Institute

ADMINISTRATIVE APPOINTMENTS

- Faculty Co-Director, Medicine Teaching and Mentoring Academy, (2016- present)

HONORS AND AWARDS

- John Buckley Entrance Scholarship for Science, Manchester University (1988-1991)
- Prize Studentship, The Wellcome Trust (1991-1994)
- Cold Spring Harbor Fellowship, Cold Spring Harbor Laboratory (1996-1997)
- Army Breast Cancer Research Fellowship, Department of Defence (1997-1998)

PROFESSIONAL EDUCATION

- B.Sc., Manchester University , Genetics (1991)
- Ph.D., Manchester University , Molecular Biology (1994)

LINKS

- Sherlock Lab Home Page: <https://web.stanford.edu/group/sherlocklab/>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Adaptive Evolution and the Fitness Landscape

When yeast are evolved under various selective pressures in a chemostat, mutations that arise and provide an adaptive advantage will expand within the population. We have pioneered the use of high throughput sequencing to determine the identity of such mutations, as well as to understand the dynamics of the mutations within the populations, and the interactions between the mutations (such as epistasis). Further, we have developed a DNA barcode based lineage tracking system to determine the distribution of fitness effects (DFE) for newly arising beneficial mutations. We have also characterized what we call the genotype-fitness map for beneficial mutations, and have investigated why beneficial mutations provide a positive fitness effect. We are also interested in how beneficial mutations trade-off for different traits, and how those trade-offs constrain adaptive evolution.

Teaching

COURSES

2023-24

- Genetics, Molecular Biology and Evolution: HUMBIO 2A (Aut)
- Genomics: GENE 211 (Win)

2022-23

- Genetics, Evolution, and Ecology: HUMBIO 2A (Aut)
- Genomics: GENE 211 (Win)

2021-22

- Genetics, Evolution, and Ecology: HUMBIO 2A (Aut)
- Genomics: GENE 211 (Win)

2020-21

- Genetics, Evolution, and Ecology: HUMBIO 2A (Aut)
- Genomics: GENE 211 (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Veronica Behrens, James Ferrare, Kelsey Fryer, Alyssa Yoxsimer

Postdoctoral Faculty Sponsor

Michelle Hays, Po-Hsiang Hung, Jason Tarkington, Elisa Visher

Doctoral Dissertation Advisor (AC)

Darren Lam

Doctoral Dissertation Co-Advisor (AC)

Danica Schmidtke

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **Changes in the distribution of fitness effects and adaptive mutational spectra following a single first step towards adaptation.** *Nature communications*
Aggeli, D., Li, Y., Sherlock, G.
2021; 12 (1): 5193
- **Single nucleotide mapping of trait space reveals Pareto fronts that constrain adaptation.** *Nature ecology & evolution*
Li, Y., Petrov, D. A., Sherlock, G.
2019
- **The dynamics of adaptive genetic diversity during the early stages of clonal evolution.** *Nature ecology & evolution*
Blundell, J. R., Schwartz, K., Francois, D., Fisher, D. S., Sherlock, G., Levy, S. F.

2018

- **Hidden Complexity of Yeast Adaptation under Simple Evolutionary Conditions** *CURRENT BIOLOGY*
Li, Y., Venkataram, S., Agarwala, A., Dunn, B., Petrov, D. A., Sherlock, G., Fisher, D. S.
2018; 28 (4): 515-+
- **Development of a Comprehensive Genotype-to-Fitness Map of Adaptation-Driving Mutations in Yeast.** *Cell*
Venkataram, S., Dunn, B., Li, Y., Agarwala, A., Chang, J., Ebel, E. R., Geiler-Samerotte, K., Hérisant, L., Blundell, J. R., Levy, S. F., Fisher, D. S., Sherlock, G., Petrov, et al
2016; 166 (6): 1585-1596 e22
- **Quantitative evolutionary dynamics using high-resolution lineage tracking.** *Nature*
Levy, S. F., Blundell, J. R., Venkataram, S., Petrov, D. A., Fisher, D. S., Sherlock, G.
2015; 519 (7542): 181-186
- **Spindle architecture constrains karyotype in budding yeast.** *bioRxiv : the preprint server for biology*
Helsen, J., Reza, M. H., Sherlock, G., Dey, G.
2023
- **Evolution of haploid and diploid populations reveals common, strong, and variable pleiotropic effects in non-home environments.** *eLife*
Chen, V., Johnson, M. S., Hérisant, L., Humphrey, P. T., Yuan, D. C., Li, Y., Agarwala, A., Hoelscher, S. B., Petrov, D. A., Desai, M. M., Sherlock, G.
2023; 12
- **Arrayed in vivo barcoding for multiplexed sequence verification of plasmid DNA and demultiplexing of pooled libraries.** *bioRxiv : the preprint server for biology*
Li, W., Miller, D., Liu, X., Tosi, L., Chkaiban, L., Mei, H., Hung, P., Parekkadan, B., Sherlock, G., Levy, S. F.
2023
- **Improved Sugarcane-Based Fermentation Processes by an Industrial Fuel-Ethanol Yeast Strain.** *Journal of fungi (Basel, Switzerland)*
Muller, G., de Godoy, V. R., Dário, M. G., Duval, E. H., Alves-Jr, S. L., Bücken, A., Rosa, C. A., Dunn, B., Sherlock, G., Stambuk, B. U.
2023; 9 (8)
- **Paths to adaptation under fluctuating nitrogen starvation: The spectrum of adaptive mutations in *Saccharomyces cerevisiae* is shaped by retrotransposons and microhomology-mediated recombination.** *PLoS genetics*
Hays, M., Schwartz, K., Schmidtke, D. T., Aggeli, D., Sherlock, G.
2023; 19 (5): e1010747
- **Experimental evolution for cell biology.** *Trends in cell biology*
Helsen, J., Sherlock, G., Dey, G.
2023
- **An improved algorithm for inferring mutational parameters from bar-seq evolution experiments.** *BMC genomics*
Li, F., Mahadevan, A., Sherlock, G.
2023; 24 (1): 246
- **Insufficient evidence for non-neutrality of synonymous mutations.** *Nature*
Kruglyak, L., Beyer, A., Bloom, J. S., Grossbach, J., Lieberman, T. D., Mancuso, C. P., Rich, M. S., Sherlock, G., Kaplan, C. D.
2023; 616 (7957): E8-E9
- **Yca1 metacaspase: Diverse functions determine how yeast live and let die.** *FEMS yeast research*
Lam, D. K., Sherlock, G.
2023
- **Fit-Seq2.0: An Improved Software for High-Throughput Fitness Measurements Using Pooled Competition Assays.** *Journal of molecular evolution*
Li, F., Tarkington, J., Sherlock, G.
2023
- ***S. cerevisiae* Cells Can Grow without the Pds5 Cohesin Subunit.** *mBio*
Choudhary, K., Itzkovich, Z., Alonso-Perez, E., Bishara, H., Dunn, B., Sherlock, G., Kupiec, M.
2022: e0142022

- **Neural networks enable efficient and accurate simulation-based inference of evolutionary parameters from adaptation dynamics.** *PLoS biology*
Avecilla, G., Chuong, J. N., Li, F., Sherlock, G., Gresham, D., Ram, Y.
2022; 20 (5): e3001633
- **How to Use the Candida Genome Database.** *Methods in molecular biology (Clifton, N.J.)*
Skrzypek, M. S., Binkley, J., Sherlock, G.
2022; 2542: 55-69
- **Quantifying rapid bacterial evolution and transmission within the mouse intestine.** *Cell host & microbe*
Vasquez, K. S., Willis, L., Cira, N. J., Ng, K. M., Pedro, M. F., Aranda-Diaz, A., Rajendram, M., Yu, F. B., Higginbottom, S. K., Neff, N., Sherlock, G., Xavier, K. B., Quake, et al
2021
- **Evolutionary dynamics and structural consequences of de novo beneficial mutations and mutant lineages arising in a constant environment.** *BMC biology*
Kinnersley, M., Schwartz, K., Yang, D., Sherlock, G., Rosenzweig, F.
2021; 19 (1): 20
- **Adaptation is influenced by the complexity of environmental change during evolution in a dynamic environment.** *PLoS genetics*
Boyer, S., Herissant, L., Sherlock, G.
2021; 17 (1): e1009314
- **Acquisition, transmission and strain diversity of human gut-colonizing crAss-like phages.** *Nature communications*
Siranosian, B. A., Tamburini, F. B., Sherlock, G. n., Bhatt, A. S.
2020; 11 (1): 280
- **Improved discovery of genetic interactions using CRISPRiSeq across multiple environments** *GENOME RESEARCH*
Jaffe, M., Dziulko, A., Smith, J. D., St Onge, R. P., Levy, S. F., Sherlock, G.
2019; 29 (4): 668–81
- **Gene flow contributes to diversification of the major fungal pathogen *Candida albicans*** *NATURE COMMUNICATIONS*
Ropars, J., Mauffrais, C., Diogo, D., Marcet-Houben, M., Perin, A., Sertour, N., Mosca, K., Permal, E., Laval, G., Bouchier, C., Ma, L., Schwartz, K., Voelz, et al
2018; 9: 2253
- **Diff-seq: A high throughput sequencing-based mismatch detection assay for DNA variant enrichment and discovery** *NUCLEIC ACIDS RESEARCH*
Aggeli, D., Karas, V. O., Sinnott-Armstrong, N. A., Varghese, V., Shafer, R. W., Greenleaf, W. J., Sherlock, G.
2018; 46 (7)
- **Using the Candida Genome Database.** *Methods in molecular biology (Clifton, N.J.)*
Skrzypek, M. S., Binkley, J., Sherlock, G.
2018; 1757: 31–47
- **Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus *Aspergillus*.** *Genome biology*
de Vries, R. P., Riley, R., Wiebenga, A., Aguilar-Osorio, G., Amillis, S., Uchima, C. A., Anderluh, G., Asadollahi, M., Askin, M., Barry, K., Battaglia, E., Bayram, Ö., Benocci, et al
2017; 18 (1): 28-?
- **Seeking Goldilocks During Evolution of Drug Resistance.** *PLoS biology*
Sherlock, G., Petrov, D. A.
2017; 15 (2)
- **The Candida Genome Database (CGD): incorporation of Assembly 22, systematic identifiers and visualization of high throughput sequencing data** *NUCLEIC ACIDS RESEARCH*
Skrzypek, M. S., Binkley, J., Binkley, G., Miyasato, S. R., Simison, M., Sherlock, G.
2017; 45 (D1): D592-D596
- **iSeq: A New Double-Barcode Method for Detecting Dynamic Genetic Interactions in Yeast** *G3-GENES GENOMES GENETICS*
Jaffe, M., Sherlock, G., Levy, S. F.
2017; 7 (1): 143-153

- **Extremely Rare Polymorphisms in *Saccharomyces cerevisiae* Allow Inference of the Mutational Spectrum.** *PLoS genetics*
Zhu, Y. O., Sherlock, G., Petrov, D. A.
2017; 13 (1)
- **Preparation of Yeast DNA Sequencing Libraries.** *Cold Spring Harbor protocols*
Schwartz, K., Sherlock, G.
2016; 2016 (10): pdb prot088930-?
- **High-Throughput Yeast Strain Sequencing.** *Cold Spring Harbor protocols*
Schwartz, K., Sherlock, G.
2016; 2016 (10): pdb top077651-?
- **Analysis of Repair Mechanisms following an Induced Double-Strand Break Uncovers Recessive Deleterious Alleles in the *Candida albicans* Diploid Genome** *MBIO*
Feri, A., Loll-Kripplbeier, R., Commere, P., Maufrais, C., Sertour, N., Schwartz, K., Sherlock, G., Bougnoux, M., d'Enfert, C., Legrand, M.
2016; 7 (5)
- **Whole Genome Analysis of 132 Clinical *Saccharomyces cerevisiae* Strains Reveals Extensive Ploidy Variation** *G3-GENES GENOMES GENETICS*
Zhu, Y. O., Sherlock, G., Petrov, D. A.
2016; 6 (8): 2421-2434
- **Heterozygote Advantage Is a Common Outcome of Adaptation in *Saccharomyces cerevisiae*** *GENETICS*
Sellis, D., Kvitek, D. J., Dunn, B., Sherlock, G., Petrov, D. A.
2016; 203 (3): 1401-?
- **How to Use the *Candida* Genome Database.** *Methods in molecular biology (Clifton, N.J.)*
Skrzypek, M. S., Binkley, J., Sherlock, G.
2016; 1356: 3-15
- **Structured nucleosome fingerprints enable high-resolution mapping of chromatin architecture within regulatory regions** *GENOME RESEARCH*
Schep, A. N., Buenrostro, J. D., Denny, S. K., Schwartz, K., Sherlock, G., Greenleaf, W. J.
2015; 25 (11): 1757-1770
- **A single nucleotide polymorphism uncovers a novel function for the transcription factor *Ace2* during *Candida albicans* hyphal development.** *PLoS genetics*
Calderón-Noreña, D. M., González-Novo, A., Orellana-Muñoz, S., Gutiérrez-Escribano, P., Arnáiz-Pita, Y., Dueñas-Santero, E., Suárez, M. B., Bougnoux, M., del Rey, F., Sherlock, G., d'Enfert, C., Correa-Bordes, J., de Aldana, et al
2015; 11 (4)
- **The Valley-of-Death: Reciprocal sign epistasis constrains adaptive trajectories in a constant, nutrient limiting environment** *GENOMICS*
Chiotti, K. E., Kvitek, D. J., Schmidt, K. H., Koniges, G., Schwartz, K., Donckels, E. A., Rosenzweig, F., Sherlock, G.
2014; 104 (6): 431-437
- **Experimental evolution: prospects and challenges.** *Genomics*
Rosenzweig, F., Sherlock, G.
2014; 104 (6 Pt A): v-vi
- **Literature-based gene curation and proposed genetic nomenclature for cryptococcus.** *Eukaryotic cell*
Inglis, D. O., Skrzypek, M. S., Liaw, E., Moktali, V., Sherlock, G., Stajich, J. E.
2014; 13 (7): 878-883
- **Ex Uno Plures: Clonal Reinforcement Drives Evolution of a Simple Microbial Community** *PLOS GENETICS*
Kinnersley, M., Wenger, J., Kroll, E., Adams, J., Sherlock, G., Rosenzweig, F.
2014; 10 (6)
- **Extensive and coordinated control of allele-specific expression by both transcription and translation in *Candida albicans*** *GENOME RESEARCH*
Muzzey, D., Sherlock, G., Weissman, J. S.
2014; 24 (6): 963-973
- **PHENOTYPIC AND GENOTYPIC CONVERGENCES ARE INFLUENCED BY HISTORICAL CONTINGENCY AND ENVIRONMENT IN YEAST** *EVOLUTION*

- Spor, A., Kvittek, D. J., Nidelet, T., Martin, J., Legrand, J., Dillmann, C., Bourgeois, A., de Vienne, D., Sherlock, G., Sicard, D.
2014; 68 (3): 772-790
- **PortEco: a resource for exploring bacterial biology through high-throughput data and analysis tools.** *Nucleic acids research*
Hu, J. C., Sherlock, G., Siegele, D. A., Aleksander, S. A., Ball, C. A., Demeter, J., Gouni, S., Holland, T. A., Karp, P. D., Lewis, J. E., Liles, N. M., McIntosh, B. K., Mi, et al
2014; 42 (1): D677-84
 - **Curation accuracy of model organism databases.** *Database : the journal of biological databases and curation*
Keseler, I. M., Skrzypek, M., Weerasinghe, D., Chen, A. Y., Fulcher, C., Li, G., Lemmer, K. C., Mladinich, K. M., Chow, E. D., Sherlock, G., Karp, P. D.
2014; 2014
 - **The Candida Genome Database: The new homology information page highlights protein similarity and phylogeny.** *Nucleic acids research*
Binkley, J., Arnaud, M. B., Inglis, D. O., Skrzypek, M. S., Shah, P., Wymore, F., Binkley, G., Miyasato, S. R., Simison, M., Sherlock, G.
2014; 42 (1): D711-6
 - **The Aspergillus Genome Database: multispecies curation and incorporation of RNA-Seq data to improve structural gene annotations.** *Nucleic acids research*
Cerqueira, G. C., Arnaud, M. B., Inglis, D. O., Skrzypek, M. S., Binkley, G., Simison, M., Miyasato, S. R., Binkley, J., Orvis, J., Shah, P., Wymore, F., Sherlock, G., Wortman, et al
2014; 42 (1): D705-10
 - **Identification of cell cycle-regulated genes periodically expressed in U2OS cells and their regulation by FOXM1 and E2F transcription factors** *MOLECULAR BIOLOGY OF THE CELL*
Grant, G. D., Brooks, L., Zhang, X., Mahoney, J. M., Martyanov, V., Wood, T. A., Sherlock, G., Cheng, C., Whitfield, M. L.
2013; 24 (23): 3634-3650
 - **Whole genome, whole population sequencing reveals that loss of signaling networks is the major adaptive strategy in a constant environment.** *PLoS genetics*
Kvittek, D. J., Sherlock, G.
2013; 9 (11)
 - **Ras Signaling Gets Fine-Tuned: Regulation of Multiple Pathogenic Traits of Candida albicans** *EUKARYOTIC CELL*
Inglis, D. O., Sherlock, G.
2013; 12 (10): 1316-1325
 - **Comparative metabolic footprinting of a large number of commercial wine yeast strains in Chardonnay fermentations.** *FEMS yeast research*
Richter, C. L., Dunn, B., Sherlock, G., Pugh, T.
2013; 13 (4): 394-410
 - **Recurrent Rearrangement during Adaptive Evolution in an Interspecific Yeast Hybrid Suggests a Model for Rapid Introgression** *PLOS GENETICS*
Dunn, B., Paulish, T., Stanbery, A., Piotrowski, J., Koniges, G., Kroll, E., Louis, E. J., Liti, G., Sherlock, G., Rosenzweig, F.
2013; 9 (3)
 - **Improved Gene Ontology Annotation for Biofilm Formation, Filamentous Growth, and Phenotypic Switching in Candida albicans** *EUKARYOTIC CELL*
Inglis, D. O., Skrzypek, M. S., Arnaud, M. B., Binkley, J., Shah, P., Wymore, F., Sherlock, G.
2013; 12 (1): 101-108
 - **Assembly of a phased diploid Candida albicans genome facilitates allele-specific measurements and provides a simple model for repeat and indel structure** *GENOME BIOLOGY*
Muzzey, D., Schwartz, K., Weissman, J. S., Sherlock, G.
2013; 14 (9)
 - **Comprehensive annotation of secondary metabolite biosynthetic genes and gene clusters of Aspergillus nidulans, A. fumigatus, A. niger and A. oryzae.** *BMC microbiology*
Inglis, D. O., Binkley, J., Skrzypek, M. S., Arnaud, M. B., Cerqueira, G. C., Shah, P., Wymore, F., Wortman, J. R., Sherlock, G.
2013; 13: 91-?
 - **Turbidostat culture of Saccharomyces cerevisiae W303-1A under selective pressure elicited by ethanol selects for mutations in SSD1 and UTH1** *FEMS YEAST RESEARCH*
Avrahami-Moyal, L., Engelberg, D., Wenger, J. W., Sherlock, G., Braun, S.

2012; 12 (5): 521-533

- **APJ1 and GRE3 Homologs Work in Concert to Allow Growth in Xylose in a Natural *Saccharomyces sensu stricto* Hybrid Yeast** *GENETICS*
Schwartz, K., Wenger, J. W., Dunn, B., Sherlock, G.
2012; 191 (2): 621-U504
- **Analysis of the *Saccharomyces cerevisiae* pan-genome reveals a pool of copy number variants distributed in diverse yeast strains from differing industrial environments** *GENOME RESEARCH*
Dunn, B., Richter, C., Kvitek, D. J., Pugh, T., Sherlock, G.
2012; 22 (5): 908-924
- **Different selective pressures lead to different genomic outcomes as newly-formed hybrid yeasts evolve** *BMC EVOLUTIONARY BIOLOGY*
Piotrowski, J. S., Nagarajan, S., Kroll, E., Stanbery, A., Chiotti, K. E., Kruckeberg, A. L., Dunn, B., Sherlock, G., Rosenzweig, F.
2012; 12
- **The *Candida* genome database incorporates multiple *Candida* species: multispecies search and analysis tools with curated gene and protein information for *Candida albicans* and *Candida glabrata*** *NUCLEIC ACIDS RESEARCH*
Inglis, D. O., Arnaud, M. B., Binkley, J., Shah, P., Skrzypek, M. S., Wymore, F., Binkley, G., Miyasato, S. R., Simison, M., Sherlock, G.
2012; 40 (D1): D667-D674
- **The *Candida* genome database incorporates multiple *Candida* species: multispecies search and analysis tools with curated gene and protein information for *Candida albicans* and *Candida glabrata*.** *Nucleic acids research*
Inglis, D. O., Arnaud, M. B., Binkley, J., Shah, P., Skrzypek, M. S., Wymore, F., Binkley, G., Miyasato, S. R., Simison, M., Sherlock, G.
2012; 40 (Database issue): D667-74
- **The *Aspergillus* Genome Database (AspGD): recent developments in comprehensive multispecies curation, comparative genomics and community resources.** *Nucleic acids research*
Arnaud, M. B., Cerqueira, G. C., Inglis, D. O., Skrzypek, M. S., Binkley, J., Chibucos, M. C., Crabtree, J., Howarth, C., Orvis, J., Shah, P., Wymore, F., Binkley, G., Miyasato, et al
2012; 40 (Database issue): D653-9
- **GC-Content Normalization for RNA-Seq Data** *BMC BIOINFORMATICS*
Risso, D., Schwartz, K., Sherlock, G., Dudoit, S.
2011; 12
- **Hunger Artists: Yeast Adapted to Carbon Limitation Show Trade-Offs under Carbon Sufficiency** *PLOS GENETICS*
Wenger, J. W., Piotrowski, J., Nagarajan, S., Chiotti, K., Sherlock, G., Rosenzweig, F.
2011; 7 (8)
- **DNA methylation profiling reveals novel biomarkers and important roles for DNA methyltransferases in prostate cancer** *GENOME RESEARCH*
Kobayashi, Y., Absher, D. M., Gulzar, Z. G., Young, S. R., McKenney, J. K., Peehl, D. M., Brooks, J. D., Myers, R. M., Sherlock, G.
2011; 21 (7): 1017-1027
- **Integrated genomic analyses of ovarian carcinoma** *NATURE*
Bell, D., Berchuck, A., Birrer, M., Chien, J., Cramer, D. W., Dao, F., Dhir, R., Disaia, P., Gabra, H., Glenn, P., Godwin, A. K., GROSS, J., Hartmann, et al
2011; 474 (7353): 609-615
- **Reciprocal Sign Epistasis between Frequently Experimentally Evolved Adaptive Mutations Causes a Rugged Fitness Landscape** *PLOS GENETICS*
Kvitek, D. J., Sherlock, G.
2011; 7 (4)
- **A User's Guide to the Encyclopedia of DNA Elements (ENCODE)** *PLOS BIOLOGY*
Myers, R. M., Stamatoyannopoulos, J., Snyder, M., Dunham, I., Hardison, R. C., Bernstein, B. E., Gingeras, T. R., Kent, W. J., Birney, E., Wold, B., Crawford, G. E., Bernstein, B. E., Epstein, et al
2011; 9 (4)
- **Rapid Evolution of Simple Microbial Communities in the Laboratory** *14th Evolutionary Biology Meeting*
Kinnersley, M., Wenger, J. W., Sherlock, G., Rosenzweig, F. R.
SPRINGER-VERLAG BERLIN.2011: 107-120
- **Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads** *BMC GENOMICS*

- Martin, J., Bruno, V. M., Fang, Z., Meng, X., Blow, M., Zhang, T., Sherlock, G., Snyder, M., Wang, Z.
2010; 11
- **Annotare-a tool for annotating high-throughput biomedical investigations and resulting data** *BIOINFORMATICS*
Shankar, R., Parkinson, H., Burdett, T., Hastings, E., Liu, J., Miller, M., Srinivasa, R., White, J., Brazma, A., Sherlock, G., Stoeckert, C. J., Ball, C. A.
2010; 26 (19): 2470-2471
 - **Comprehensive annotation of the transcriptome of the human fungal pathogen *Candida albicans* using RNA-seq** *GENOME RESEARCH*
Bruno, V. M., Wang, Z., Marjani, S. L., Euskirchen, G. M., Martin, J., Sherlock, G., Snyder, M.
2010; 20 (10): 1451-1458
 - **Microarray karyotyping of maltose-fermenting *Saccharomyces* yeasts with differing maltotriose utilization profiles reveals copy number variation in genes involved in maltose and maltotriose utilization** *JOURNAL OF APPLIED MICROBIOLOGY*
Duval, E. H., Alves, S. L., Dunn, B., Sherlock, G., Stambuk, B. U.
2010; 109 (1): 248-259
 - **A Genome-Wide Analysis Reveals No Nuclear Dobzhansky-Muller Pairs of Determinants of Speciation between *S. cerevisiae* and *S. paradoxus*, but Suggests More Complex Incompatibilities** *PLOS GENETICS*
Kao, K. C., Schwartz, K., Sherlock, G.
2010; 6 (7)
 - **TB database 2010: Overview and update** *TUBERCULOSIS*
Galagan, J. E., Sisk, P., Stolte, C., Weiner, B., Koehrsen, M., Wymore, F., Reddy, T. B., Zucker, J. D., Engels, R., Gellesch, M., Hubble, J., Jin, H., Larson, et al
2010; 90 (4): 225-235
 - **Bulk Segregant Analysis by High-Throughput Sequencing Reveals a Novel Xylose Utilization Gene from *Saccharomyces cerevisiae*** *PLOS GENETICS*
Wenger, J. W., Schwartz, K., Sherlock, G.
2010; 6 (5)
 - **The Aspergillus Genome Database, a curated comparative genomics resource for gene, protein and sequence information for the Aspergillus research community** *NUCLEIC ACIDS RESEARCH*
Arnaud, M. B., Chibucos, M. C., Costanzo, M. C., Crabtree, J., Inglis, D. O., Lotia, A., Orvis, J., Shah, P., Skrzypek, M. S., Binkley, G., Miyasato, S. R., Wortman, J. R., Sherlock, et al
2010; 38: D420-D427
 - **New tools at the *Candida* Genome Database: biochemical pathways and full-text literature search** *NUCLEIC ACIDS RESEARCH*
Skrzypek, M. S., Arnaud, M. B., Costanzo, M. C., Inglis, D. O., Shah, P., Binkley, G., Miyasato, S. R., Sherlock, G.
2010; 38: D428-D432
 - **Industrial fuel ethanol yeasts contain adaptive copy number changes in genes involved in vitamin B1 and B6 biosynthesis** *GENOME RESEARCH*
Stambuk, B. U., Dunn, B., Alves, S. L., Duval, E. H., Sherlock, G.
2009; 19 (12): 2271-2278
 - **Gene Ontology and the annotation of pathogen genomes: the case of *Candida albicans*** *TRENDS IN MICROBIOLOGY*
Arnaud, M. B., Costanzo, M. C., Shah, P., Skrzypek, M. S., Sherlock, G.
2009; 17 (7): 295-303
 - **Evolution of pathogenicity and sexual reproduction in eight *Candida* genomes** *NATURE*
Butler, G., Rasmussen, M. D., Lin, M. F., Santos, M. A., Sakthikumar, S., Munro, C. A., Rheinbay, E., Grabherr, M., Forche, A., Reedy, J. L., Agrafioti, I., Arnaud, M. B., Bates, et al
2009; 459 (7247): 657-662
 - **Implementation of GenePattern within the Stanford Microarray Database** *NUCLEIC ACIDS RESEARCH*
Hubble, J., Demeter, J., Jin, H., Mao, M., Nitzberg, M., Reddy, T. B., Wymore, F., Zachariah, K., Sherlock, G., Ball, C. A.
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