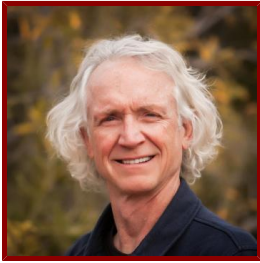


Stanford



Mike Cherry

Professor (Research) of Genetics

 NIH Biosketch available Online

Bio

ACADEMIC APPOINTMENTS

- Professor (Research), Genetics
- Member, Bio-X

ADMINISTRATIVE APPOINTMENTS

- Advisory Board, Laboratory of Neuro Imaging Resource, (2015- present)
- Advisory Board, FaceBase, (2015- present)
- Advisory Board, XenBase, Xenopus Knowledgebase, (2016- present)
- Advisory Board, GlyGen, Glycoscience Informatics Resource, (2020- present)
- Advisory Board, ZFIN, Zebrafish Genome Database, (2021- present)

HONORS AND AWARDS

- Ira Herskowitz Award, Genetics Society of America (August 2018)

PROFESSIONAL EDUCATION

- Ph.D., University of California , Molecular Biology (1985)
- B.S., Purdue University , Biochemistry (1979)
- B.S., Purdue University , Biological Sciences (1979)

COMMUNITY AND INTERNATIONAL WORK

- Stanford at The Tech, San Jose

LINKS

- Cherry Lab: <http://cherrylab.stanford.edu/>
- Saccharomyces Genome Database: <http://www.yeastgenome.org/>
- ENCODE Portal: <http://encodeproject.org/>
- Gene Ontology Consortium: <http://www.geneontology.org/>
- Alliance of Genomic Resources: <https://www.alliancegenome.org/>
- Human Cell Atlas: <https://data.humancellatlas.org>
- RegulomeDB: <http://www.regulomedb.org/>
- Lattice: <https://lattice-data.org/>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

The Cherry lab is involved in identifying, validating and integrating scientific information into encyclopedic databases essential for investigation as well as scientific education. Published results of scientific experimentation are a foundation of our understanding of the natural world and provide motivation for new experiments. The combination of in-depth understanding reported in the literature with computational analyses is an essential ingredient of modern biological research. Mastery of the volumes of published literature requires comprehensive databases that provide the facts and underlying experimental data in publically accessible ways. Curation, extraction and sorting of factual experimental data from peer-reviewed journal articles is necessary to acquire these data from its source. Large quantitative datasets using global studies extend our knowledge of genes, their products and their interactions. By integrating quantitative datasets with curated focused experimental results creates unique comprehensive databases. My group creates such essential databases and makes them available to scientists and educators seeking to understand experimental results and to teach scientific knowledge.

The exploration of the genes and other important elements of a genome involve the use of previous results to aid the design of experiments that explore, for example, gene regulation, protein function, and interaction of these processes. New technologies are being applied to the determination of many molecular interactions of the components of chromosomes and the specific controls for the generation of the many cell types that create an organism from a single set of chromosomes. These methods create very large datasets that cannot be appreciated without computational methods and access to databases of scientific results.

The Cherry lab specializes in designing and managing a public database of information for the budding yeast *Saccharomyces cerevisiae* and have recently begun applying my expertise to human genomic information. Our current projects address three areas of research: engineering for the design of databases and software for the effective integration of complex experimental results; defining standards for eukaryotic genomic data that measure reliability and quality; and developing vocabularies that enhance communication between researchers, and between computational resources. This research involves the collection and standardization of experimental results and the detailed descriptions of these data into complex biological models, application of flexible search and retrieval tools, distribution of the integrated information for the acceleration of discovery.

Three major bioinformatics resources funded by the National Institutes of Health are provided by the lab. The *Saccharomyces* Genome Database project is the foremost database on a single organism. It is the archetype of all such databases because of its high quality, rich design, completeness, easy of use, and facilitation of scientific discovery. The Gene Ontology Consortium invented a structured vocabulary for the specification and description of gene function, their involvement in biological processes and their location within subcellular complexes and components. This innovative knowledgebase has unified biological nomenclature and is crucial for the analysis of biological results. The ENCODE Data Coordination Center provides an essential component for the analysis and use of large-scale studies of the human genome. Our work specifies the accurate and complete submission of human genomic experimental results, verifies the data quality, specifies and compiles the dataset experimental details, integrates data with existing human genome databases, distributed these results with its analyses via a portal that serves the diverse biomedical research community of skilled bioinformaticists, biologists, and educators.

Teaching

COURSES

2021-22

- Computational Analysis of Biological Information: Introduction to Python for Biologists: GENE 218 (Spr)
- Introductory Python Programming for Genomics: BIOS 274 (Win)

2020-21

- Genomics: GENE 211 (Win)

2019-20

- Genomics: GENE 211 (Win)
- Introductory Python Programming for Genomics: BIOS 274 (Aut)

STANFORD ADVISEES

Postdoctoral Faculty Sponsor

Shengcheng Dong

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Genetics (Phd Program)

Publications

PUBLICATIONS

- **New Data and Collaborations at the Saccharomyces Genome Database: Updated reference genome, alleles, and the Alliance of Genome Resources.** *Genetics*
Engel, S. R., Wong, E. D., Nash, R. S., Aleksander, S., Alexander, M., Douglass, E., Karra, K., Miyasato, S. R., Simison, M., Skrzypek, M. S., Weng, S., Cherry, J. M.
1800
- **Dive into Epigenetics and Gene Regulation - Navigation using the ENCODE Portal**
Au, J. N., Gabdank, I., Luo, Y., Kagda, M., Lam, B., Youngworth, I., Adenekan, P., Baymuradov, U. K., Miyasato, S., Simison, M., Graham, K., Jolanki, O., Jou, et al
SPRINGERNATURE.2020: 744
- **Incorporation of a unified protein abundance dataset into the Saccharomyces genome database.** *Database : the journal of biological databases and curation*
Nash, R. S., Weng, S. n., Karra, K. n., Wong, E. D., Engel, S. R., Cherry, J. M.
2020; 2020
- **The Alliance of Genome Resources: Building a Modern Data Ecosystem for Model Organism Databases** *GENETICS*
Bult, C. J., Blake, J. A., Calvi, B. R., Cherry, J., DiFrancesco, V., Fullem, R., Howe, K. L., Kaufman, T., Mungall, C., Perrimon, N., Shimoyama, M., Sternberg, P. W., Thomas, et al
2019; 213 (4): 1189–96
- **The ENCODE Portal as an Epigenomics Resource.** *Current protocols in bioinformatics*
Jou, J., Gabdank, I., Luo, Y., Lin, K., Sud, P., Myers, Z., Hilton, J. A., Kagda, M. S., Lam, B., O'Neill, E., Adenekan, P., Graham, K., Baymuradov, et al
2019; 68 (1): e89
- **Transcriptome visualization and data availability at the Saccharomyces Genome Database.** *Nucleic acids research*
Ng, P. C., Wong, E. D., MacPherson, K. A., Aleksander, S., Argasinska, J., Dunn, B., Nash, R. S., Skrzypek, M. S., Gondwe, F., Jha, S., Karra, K., Weng, S., Miyasato, et al
2019
- **The Gene Ontology Resource: 20 years and still GOing strong** *NUCLEIC ACIDS RESEARCH*
Carbon, S., Douglass, E., Dunn, N., Good, B., Harris, N. L., Lewis, S. E., Mungall, C. J., Basu, S., Chisholm, R. L., Dodson, R. J., Hartline, E., Fey, P., Thomas, et al
2019; 47 (D1): D330–D338
- **Integration of macromolecular complex data into the Saccharomyces Genome Database.** *Database : the journal of biological databases and curation*
Wong, E. D., Skrzypek, M. S., Weng, S., Binkley, G., Meldal, B. H., Peretto, L., Orchard, S. E., Engel, S. R., Cherry, J. M., SGD Project
2019; 2019
- **New developments on the Encyclopedia of DNA Elements (ENCODE) data portal.** *Nucleic acids research*
Luo, Y. n., Hitz, B. C., Gabdank, I. n., Hilton, J. A., Kagda, M. S., Lam, B. n., Myers, Z. n., Sud, P. n., Jou, J. n., Lin, K. n., Baymuradov, U. K., Graham, K. n., Litton, et al
2019

- **Prevention of data duplication for high throughput sequencing repositories** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*
Gabdank, I., Chan, E. T., Davidson, J. M., Hilton, J. A., Davis, C. A., Baymuradov, U. K., Narayanan, A., Onate, K. C., Graham, K., Miyasato, S. R., Dreszer, T. R., Strattan, J., Jolanki, et al
2018
- **SnoVault and encodedD: A novel object-based storage system and applications to ENCODE metadata** *PLOS ONE*
Hitz, B. C., Rowe, L. D., Podduturi, N. R., Glick, D. I., Baymuradov, U. K., Malladi, V. S., Chan, E. T., Davidson, J. M., Gabdank, I., Narayana, A. K., Onate, K. C., Hilton, J., Ho, et al
2017; 12 (4)
- **Curated protein information in the Saccharomyces genome database** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*
Hellerstedt, S. T., Nash, R. S., Weng, S., Paskov, K. M., Wong, E. D., Karra, K., Engel, S. R., Cherry, J. M.
2017
- **The Encyclopedia of DNA elements (ENCODE): data portal update.** *Nucleic acids research*
Davis, C. A., Hitz, B. C., Sloan, C. A., Chan, E. T., Davidson, J. M., Gabdank, I. n., Hilton, J. A., Jain, K. n., Baymuradov, U. K., Narayanan, A. K., Onate, K. C., Graham, K. n., Miyasato, et al
2017
- **Saccharomyces genome database informs human biology.** *Nucleic acids research*
Skrzypek, M. S., Nash, R. S., Wong, E. D., MacPherson, K. A., Hellerstedt, S. T., Engel, S. R., Karra, K. n., Weng, S. n., Sheppard, T. K., Binkley, G. n., Simison, M. n., Miyasato, S. R., Cherry, et al
2017
- **ENCODE data at the ENCODE portal.** *Nucleic acids research*
Sloan, C. A., Chan, E. T., Davidson, J. M., Malladi, V. S., Strattan, J. S., Hitz, B. C., Gabdank, I., Narayanan, A. K., Ho, M., Lee, B. T., Rowe, L. D., Dreszer, T. R., Roe, et al
2016; 44 (D1): D726-32
- **Principles of metadata organization at the ENCODE data coordination center.** *Database : the journal of biological databases and curation*
Hong, E. L., Sloan, C. A., Chan, E. T., Davidson, J. M., Malladi, V. S., Strattan, J. S., Hitz, B. C., Gabdank, I., Narayanan, A. K., Ho, M., Lee, B. T., Rowe, L. D., Dreszer, et al
2016; 2016
- **Ontology application and use at the ENCODE DCC.** *Database : the journal of biological databases and curation*
Malladi, V. S., Erickson, D. T., Podduturi, N. R., Rowe, L. D., Chan, E. T., Davidson, J. M., Hitz, B. C., Ho, M., Lee, B. T., Miyasato, S., Roe, G. R., Simison, M., Sloan, et al
2015; 2015
- **Annotation of functional variation in personal genomes using RegulomeDB** *GENOME RESEARCH*
Boyle, A. P., Hong, E. L., Hariharan, M., Cheng, Y., Schaub, M. A., Kasowski, M., Karczewski, K. J., Park, J., Hitz, B. C., Weng, S., Cherry, J. M., Snyder, M.
2012; 22 (9): 1790-1797
- **Saccharomyces Genome Database Update: Server Architecture, Pan-Genome Nomenclature, and External Resources.** *Genetics*
Wong, E. D., Miyasato, S. R., Aleksander, S., Karra, K., Nash, R. S., Skrzypek, M. S., Weng, S., Engel, S. R., Cherry, J. M.
2023
- **Author Correction: Expanded encyclopaedias of DNA elements in the human and mouse genomes.** *Nature*
ENCODE Project Consortium, Moore, J. E., Purcaro, M. J., Pratt, H. E., Epstein, C. B., Shores, N., Adrian, J., Kawli, T., Davis, C. A., Dobin, A., Kaul, R., Halow, J., Van Nostrand, E. L., et al
2022
- **Author Correction: Perspectives on ENCODE.** *Nature*
ENCODE Project Consortium, Snyder, M. P., Gingeras, T. R., Moore, J. E., Weng, Z., Gerstein, M. B., Ren, B., Hardison, R. C., Stamatoyannopoulos, J. A., Graveley, B. R., Feingold, E. A., Pazin, M. J., Pagan, M., et al
2022
- **Describing the Impact of Genomic Variation on Function (IGVF) Consortium submitted on behalf of the IGVF Consortium members**
Fulton, L., Wang, T., Yue, F., Hitz, B., Cherry, J.
ELSEVIER SCIENCE INC.2022: S219

- **ClinGen Variant Curation Interface: a variant classification platform for the application of evidence criteria from ACMG/AMP guidelines.** *Genome medicine*
Preston, C. G., Wright, M. W., Madhavrao, R., Harrison, S. M., Goldstein, J. L., Luo, X., Wand, H., Wulf, B., Cheung, G., Mandell, M. E., Tong, H., Cheng, S., Iacocca, et al
1800; 14 (1): 6
- **The Gene Ontology resource: enriching a GOLD mine** *NUCLEIC ACIDS RESEARCH*
Carbon, S., Douglass, E., Good, B. M., Unni, D. R., Harris, N. L., Mungall, C. J., Basu, S., Chisholm, R. L., Dodson, R. J., Hartline, E., Fey, P., Thomas, P. D., Albou, et al
2021; 49 (D1): D325–D334
- **Data Sanitization to Reduce Private Information Leakage from Functional Genomics.** *Cell*
Gursoy, G., Emani, P., Brannon, C. M., Jolanki, O. A., Harmanci, A., Strattan, J. S., Cherry, J. M., Miranker, A. D., Gerstein, M.
2020; 183 (4): 905
- **Perspectives on ENCODE.** *Nature*
ENCODE Project Consortium, Snyder, M. P., Gingeras, T. R., Moore, J. E., Weng, Z., Gerstein, M. B., Ren, B., Hardison, R. C., Stamatoyannopoulos, J. A., Graveley, B. R., Feingold, E. A., Pazin, M. J., Pagan, M., et al
2020; 583 (7818): 693–98
- **An atlas of dynamic chromatin landscapes in mouse fetal development.** *Nature*
Gorkin, D. U., Barozzi, I., Zhao, Y., Zhang, Y., Huang, H., Lee, A. Y., Li, B., Chiou, J., Wildberg, A., Ding, B., Zhang, B., Wang, M., Strattan, et al
2020; 583 (7818): 744–51
- **CNN-Peaks: ChIP-Seq peak detection pipeline using convolutional neural networks that imitate human visual inspection.** *Scientific reports*
Oh, D., Strattan, J. S., Hur, J. K., Bento, J., Urban, A. E., Song, G., Cherry, J. M.
2020; 10 (1): 7933
- **Expanded encyclopaedias of DNA elements in the human and mouse genomes.** *Nature*
Moore, J. E., Purcaro, M. J., Pratt, H. E., Epstein, C. B., Shores, N. n., Adrian, J. n., Kawli, T. n., Davis, C. A., Dobin, A. n., Kaul, R. n., Halow, J. n., Van Nostrand, E. L., Freese, et al
2020; 583 (7818): 699–710
- **RNAcentral: a hub of information for non-coding RNA sequences (vol 47, pg D221, 2019)** *NUCLEIC ACIDS RESEARCH*
Sweeney, B. A., Petrov, A. I., Burkov, B., Finn, R. D., Bateman, A., Szymanski, M., Karlowski, W. M., Gorodkin, J., Seemann, S. E., Cannone, J. J., Gutell, R. R., Fey, P., Basu, et al
2019; 47 (D1): D1250–D1251
- **Integrative Meta-Assembly Pipeline (IMAP): Chromosome-level genome assembler combining multiple de novo assemblies.** *PloS one*
Song, G. n., Lee, J. n., Kim, J. n., Kang, S. n., Lee, H. n., Kwon, D. n., Lee, D. n., Lang, G. I., Cherry, J. M., Kim, J. n.
2019; 14 (8): e0221858
- **Updated regulation curation model at the Saccharomyces Genome Database** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*
Engel, S. R., Skrzypek, M. S., Hellerstedt, S. T., Wong, E. D., Nash, R. S., Weng, S., Binkley, G., Sheppard, T. K., Karra, K., Cherry, J.
2018
- **Evaluating the Clinical Validity of Gene-Disease Associations: An Evidence-Based Framework Developed by the Clinical Genome Resource.** *American journal of human genetics*
Strande, N. T., Riggs, E. R., Buchanan, A. H., Ceyhan-Birsoy, O., DiStefano, M., Dwight, S. S., Goldstein, J., Ghosh, R., Seifert, B. A., Sneddon, T. P., Wright, M. W., Milko, L. V., Cherry, et al
2017; 100 (6): 895-906
- **Outreach and online training services at the Saccharomyces Genome Database** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*
MacPherson, K. A., Starr, B., Wong, E. D., Dalusag, K. S., Hellerstedt, S. T., Lang, O., Nash, R. S., Skrzypek, M. S., Engel, S. R., Cherry, J. M.
2017
- **Active Interaction Mapping Reveals the Hierarchical Organization of Autophagy.** *Molecular cell*
Kramer, M. H., Farré, J., Mitra, K., Yu, M. K., Ono, K., Demchak, B., Licon, K., Flagg, M., Balakrishnan, R., Cherry, J. M., Subramani, S., Ideker, T.
2017; 65 (4): 761-774 e5

- **Expansion of the Gene Ontology knowledgebase and resources** *NUCLEIC ACIDS RESEARCH*
CARBON, S., Dietze, H., Lewis, S. E., Mungall, C. J., Munoz-Torres, M. C., Basu, S., Chisholm, R. L., Dodson, R. J., Fey, P., Thomas, P. D., Mi, H., Muruganujan, A., Huang, et al
2017; 45 (D1): D331-D338
- **RNAcentral: a comprehensive database of non-coding RNA sequences** *NUCLEIC ACIDS RESEARCH*
Petrov, A. I., Kay, S. J., Kalvari, I., Howe, K. L., Gray, K. A., Bruford, E. A., Kersey, P. J., Cochrane, G., Finn, R. D., Bateman, A., Kozomara, A., Griffiths-Jones, S., Frankish, et al
2017; 45 (D1): D128-D134
- **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
- **The Saccharomyces Genome Database Variant Viewer.** *Nucleic acids research*
Sheppard, T. K., Hitz, B. C., Engel, S. R., Song, G., Balakrishnan, R., Binkley, G., Costanzo, M. C., Dalusag, K. S., Demeter, J., Hellerstedt, S. T., Karra, K., Nash, R. S., Paskov, et al
2016; 44 (D1): D698-702
- **From one to many: expanding the Saccharomyces cerevisiae reference genome panel.** *Database : the journal of biological databases and curation*
Engel, S. R., Weng, S., Binkley, G., Paskov, K., Song, G., Cherry, J. M.
2016; 2016
- **Providing Access to Genomic Variant Knowledge in a Healthcare Setting: A Vision for the ClinGen Electronic Health Records Workgroup.** *Clinical pharmacology and therapeutics*
Overby, C. L., Heale, B. n., Aronson, S. n., Cherry, J. M., Dwight, S. n., Milosavljevic, A. n., Nelson, T. n., Niehaus, A. n., Weaver, M. A., Ramos, E. M., Williams, M. S.
2016; 99 (2): 157–60
- **Integration of new alternative reference strain genome sequences into the Saccharomyces genome database.** *Database : the journal of biological databases and curation*
Song, G., Balakrishnan, R., Binkley, G., Costanzo, M. C., Dalusag, K., Demeter, J., Engel, S., Hellerstedt, S. T., Karra, K., Hitz, B. C., Nash, R. S., Paskov, K., Sheppard, et al
2016; 2016
- **The Saccharomyces Genome Database: A Tool for Discovery.** *Cold Spring Harbor protocols*
Cherry, J. M.
2015; 2015 (12): pdb.top083840
- **The Saccharomyces Genome Database: Advanced Searching Methods and Data Mining.** *Cold Spring Harbor protocols*
Cherry, J. M.
2015; 2015 (12): pdb.prot088906
- **The Saccharomyces Genome Database: Exploring Biochemical Pathways and Mutant Phenotypes.** *Cold Spring Harbor protocols*
Cherry, J. M.
2015; 2015 (12): pdb.prot088898
- **The Saccharomyces Genome Database: Gene Product Annotation of Function, Process, and Component.** *Cold Spring Harbor protocols*
Cherry, J. M.
2015; 2015 (12): pdb.prot088914
- **The Saccharomyces Genome Database: Exploring Genome Features and Their Annotations.** *Cold Spring Harbor protocols*
Cherry, J. M.
2015; 2015 (12): pdb.prot088922
- **Gene Ontology Consortium: going forward** *NUCLEIC ACIDS RESEARCH*
Blake, J. A., Christie, K. R., Dolan, M. E., Drabkin, H. J., Hill, D. P., Ni, L., Sitnikov, D., Burgess, S., Buza, T., Gresham, C., McCarthy, F., Pillai, L., Wang, et al
2015; 43 (D1): D1049-D1056
- **RNAcentral: an international database of ncRNA sequences** *NUCLEIC ACIDS RESEARCH*

- Petrov, A. I., Kay, S. J., Gibson, R., Kulesha, E., Staines, D., Bruford, E. A., Wright, M. W., Burge, S., Finn, R. D., Kersey, P. J., Cochrane, G., Bateman, A., Griffiths-Jones, et al
2015; 43 (D1): D123-D129
- **AGAPE (Automated Genome Analysis Pipeline) for pan-genome analysis of *Saccharomyces cerevisiae*.** *PloS one*
Song, G., Dickins, B. J., Demeter, J., Engel, S., Gallagher, J., Choe, K., Dunn, B., Snyder, M., Cherry, J. M.
2015; 10 (3)
 - **Saccharomyces genome database provides new regulation data.** *Nucleic acids research*
Costanzo, M. C., Engel, S. R., Wong, E. D., Lloyd, P., Karra, K., Chan, E. T., Weng, S., Paskov, K. M., Roe, G. R., Binkley, G., Hitz, B. C., Cherry, J. M.
2014; 42 (Database issue): D717-25
 - **The Reference Genome Sequence of *Saccharomyces cerevisiae*: Then and Now.** *G3 (Bethesda, Md.)*
Engel, S. R., Dietrich, F. S., Fisk, D. G., Binkley, G., Balakrishnan, R., Costanzo, M. C., Dwight, S. S., Hitz, B. C., Karra, K., Nash, R. S., Weng, S., Wong, E. D., Lloyd, et al
2014; 4 (3): 389-398
 - **DATABASE, The Journal of Biological Databases and Curation, is now the official journal of the International Society for Biocuration.** *Database : the journal of biological databases and curation*
Gaudet, P., Munoz-Torres, M., Robinson-Rechavi, M., Attwood, T., Bateman, A., Cherry, J. M., Kania, R., O'Donovan, C., Yamasaki, C.
2013; 2013: bat077
 - **A guide to best practices for Gene Ontology (GO) manual annotation** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*
Balakrishnan, R., Harris, M. A., Huntley, R., Van Auken, K., Cherry, J. M.
2013
 - **InterMOD: integrated data and tools for the unification of model organism research.** *Scientific reports*
Sullivan, J., Karra, K., Moxon, S. A., Vallejos, A., Motenko, H., Wong, J. D., Aleksic, J., Balakrishnan, R., Binkley, G., Harris, T., Hitz, B., Jayaraman, P., Lyne, et al
2013; 3: 1802-?
 - **The new modern era of yeast genomics: community sequencing and the resulting annotation of multiple *Saccharomyces cerevisiae* strains at the Saccharomyces Genome Database** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*
Engel, S. R., Cherry, J. M.
2013
 - **The YeastGenome app: the Saccharomyces Genome Database at your fingertips** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*
Wong, E. D., Karra, K., Hitz, B. C., Hong, E. L., Cherry, J. M.
2013
 - **A gene ontology inferred from molecular networks** *NATURE BIOTECHNOLOGY*
Dutkowsky, J., Kramer, M., Surma, M. A., Balakrishnan, R., Cherry, J. M., Krogan, N. J., Ideker, T.
2013; 31 (1): 38-?
 - **Gene Ontology Annotations and Resources** *NUCLEIC ACIDS RESEARCH*
Blake, J. A., Dolan, M., Drabkin, H., Hill, D. P., Ni, L., Sitnikov, D., Bridges, S., Burgess, S., Buza, T., McCarthy, F., Peddinti, D., Pillai, L., CARBON, et al
2013; 41 (D1): D530-D535
 - **In the beginning there was babble ...** *AUTOPHAGY*
Klionsky, D. J., Bruford, E. A., Cherry, J. M., Hodgkin, J., Laulederkind, S. J., Singer, A. G.
2012; 8 (8): 1165-1167
 - **YeastMine-an integrated data warehouse for *Saccharomyces cerevisiae* data as a multipurpose tool-kit** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*
Balakrishnan, R., Park, J., Karra, K., Hitz, B. C., Binkley, G., Hong, E. L., Sullivan, J., Micklem, G., Cherry, J. M.
2012
 - **Considerations for creating and annotating the budding yeast Genome Map at SGD: a progress report** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*
Chan, E. T., Cherry, J. M.

2012

- **CvManGO, a method for leveraging computational predictions to improve literature-based Gene Ontology annotations** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*
Park, J., Costanzo, M. C., Balakrishnan, R., Cherry, J. M., Hong, E. L.
2012
- **Saccharomyces Genome Database: the genomics resource of budding yeast.** *Nucleic acids research*
Cherry, J. M., Hong, E. L., Amundsen, C., Balakrishnan, R., Binkley, G., Chan, E. T., Christie, K. R., Costanzo, M. C., Dwight, S. S., Engel, S. R., Fisk, D. G., Hirschman, J. E., Hitz, et al
2012; 40 (Database issue): D700-5
- **The Gene Ontology: enhancements for 2011** *NUCLEIC ACIDS RESEARCH*
Blake, J. A., Dolan, M., Drabkin, H., Hill, D. P., Ni, L., Sitnikov, D., Burgess, S., Buza, T., Gresham, C., McCarthy, F., Pillai, L., Wang, H., CARBON, et al
2012; 40 (D1): D559-D564
- **Toward an interactive article: integrating journals and biological databases** *BMC BIOINFORMATICS*
Rangarajan, A., Schedl, T., Yook, K., Chan, J., Haenel, S., Otis, L., Faelten, S., DePellegrin-Connelly, T., Isaacson, R., Skrzypek, M. S., Marygold, S. J., Stefancsik, R., Cherry, et al
2011; 12
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