

Stanford



Arend Sidow

Professor of Pathology and of Genetics

 NIH Biosketch available Online

Bio

BIO

Please refer to my NIH biosketch:

<http://mendel.stanford.edu/sidowlab/SidowCurrentBiosketch.pdf>

ACADEMIC APPOINTMENTS

- Professor, Pathology
- Professor, Genetics
- Member, Bio-X
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute

LINKS

- Sidow Lab Site: www.sidowlab.org
- JIMB: jimble.stanford.edu

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

We have a highly collaborative research program in the evolutionary genomics of cancer. We apply well-established principles of phylogenetics to cancer evolution on the basis of whole genome sequencing and functional genomics data of multiple tumor samples from the same patient. Introductions to our work and the concepts we apply are best found in the Newburger et al paper in *Genome Research* (2013) and the Sidow and Spies review in *TIGS* (2015).

More information can be found here: <http://www.sidowlab.org>

Teaching

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Chris Probert, Akshay Sanghi, Ben Siranosian

Orals Chair

Benjamin Braun

Doctoral Dissertation Advisor (AC)

Xin Zhou

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)
- Cancer Biology (Phd Program)
- Genetics (Phd Program)

Publications

PUBLICATIONS

- **High-quality genome sequences of uncultured microbes by assembly of read clouds.** *Nature biotechnology*
Bishara, A., Moss, E. L., Kolmogorov, M., Parada, A. E., Weng, Z., Sidow, A., Dekas, A. E., Batzoglou, S., Bhatt, A. S.
2018
- **HAPDeNovo: a haplotype-based approach for filtering and phasing de novo mutations in linked read sequencing data.** *BMC genomics*
Zhou, X., Batzoglou, S., Sidow, A., Zhang, L.
2018; 19 (1): 467
- **Multi-omic tumor data reveal diversity of molecular mechanisms that correlate with survival.** *Nature communications*
Ramazzotti, D., Lal, A., Wang, B., Batzoglou, S., Sidow, A.
2018; 9 (1): 4453
- **A research roadmap for next-generation sequencing informatics** *SCIENCE TRANSLATIONAL MEDICINE*
Altman, R. B., Prabhu, S., Sidow, A., Zook, J. M., Goldfeder, R., Litwack, D., Ashley, E., Asiminos, G., Bustamante, C. D., Donigan, K., Giacomini, K. M., Johansen, E., Khuri, et al
2016; 8 (335)
- **Lineage-specific enhancers activate self-renewal genes in macrophages and embryonic stem cells** *SCIENCE*
Soucie, E. L., Weng, Z., Geirsdottir, L., Molawi, K., Maurizio, J., Fenouil, R., Mossadegh-Keller, N., Gimenez, G., Vanhille, L., Beniazza, M., Favret, J., Berruyer, C., Perrin, et al
2016; 351 (6274): 680-U123
- **Extensive sequencing of seven human genomes to characterize benchmark reference materials.** *Scientific data*
Zook, J. M., Catoe, D., McDaniel, J., Vang, L., Spies, N., Sidow, A., Weng, Z., Liu, Y., Mason, C. E., Alexander, N., Henaff, E., McIntyre, A. B., Chandramohan, et al
2016; 3: 160025-?
- **svviz: a read viewer for validating structural variants** *BIOINFORMATICS*
Spies, N., Zook, J. M., Salit, M., Sidow, A.
2015; 31 (24): 3994-3996
- **Read clouds uncover variation in complex regions of the human genome.** *Genome research*
Bishara, A., Liu, Y., Weng, Z., Kashef-Haghighi, D., Newburger, D. E., West, R., Sidow, A., Batzoglou, S.
2015; 25 (10): 1570-1580
- **Constraint and divergence of global gene expression in the mammalian embryo** *ELIFE*
Spies, N., Smith, C. L., Rodriguez, J. M., Baker, J. C., Batzoglou, S., Sidow, A.
2015; 4
- **Concepts in solid tumor evolution** *TRENDS IN GENETICS*
Sidow, A., Spies, N.
2015; 31 (4): 208-214
- **Cell-lineage heterogeneity and driver mutation recurrence in pre-invasive breast neoplasia.** *Genome medicine*
Weng, Z., Spies, N., Zhu, S. X., Newburger, D. E., Kashef-Haghighi, D., Batzoglou, S., Sidow, A., West, R. B.

2015; 7 (1): 28-?

- **Maternal bias and escape from X chromosome imprinting in the midgestation mouse placenta.** *Developmental biology*
Finn, E. H., Smith, C. L., Rodriguez, J., Sidow, A., Baker, J. C.
2014; 390 (1): 80-92
- **Discovery of recurrent structural variants in nasopharyngeal carcinoma.** *Genome research*
Valouev, A., Weng, Z., Sweeney, R. T., Varma, S., Le, Q., Kong, C., Sidow, A., West, R. B.
2014; 24 (2): 300-309
- **Discovery of recurrent structural variants in nasopharyngeal carcinoma** *GENOME RESEARCH*
Valouev, A., Weng, Z., Sweeney, R. T., Varma, S., Quynh-Thu Le, Q. T., Kong, C., Sidow, A., West, R. B.
2014; 24 (2): 300-309
- **Inference of tumor phylogenies with improved somatic mutation discovery.** *Journal of computational biology*
Salari, R., Saleh, S. S., Kashef-Haghighi, D., Khavari, D., Newburger, D. E., West, R. B., Sidow, A., Batzoglou, S.
2013; 20 (11): 933-944
- **Transcription-factor occupancy at HOT regions quantitatively predicts RNA polymerase recruitment in five human cell lines** *BMC GENOMICS*
Foley, J. W., Sidow, A.
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- **Genome evolution during progression to breast cancer** *GENOME RESEARCH*
Newburger, D. E., Kashef-Haghighi, D., Weng, Z., Salari, R., Sweeney, R. T., Brunner, A. L., Zhu, S. X., Guo, X., Varma, S., Troxell, M. L., West, R. B., Batzoglou, S., Sidow, et al
2013; 23 (7): 1097-1108
- **The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes.** *Genome research*
Montgomery, S. B., Goode, D. L., Kvikstad, E., Albers, C. A., Zhang, Z. D., Mu, X. J., Ananda, G., Howie, B., Karczewski, K. J., Smith, K. S., Anaya, V., Richardson, R., Davis, et al
2013; 23 (5): 749-761
- **Global genomic profiling reveals an extensive p53-regulated autophagy program contributing to key p53 responses.** *Genes & development*
Kenzelmann Broz, D., Spano Mello, S., Biegging, K. T., Jiang, D., Dusek, R. L., Brady, C. A., Sidow, A., Attardi, L. D.
2013; 27 (9): 1016-1031
- **Architecture of the human regulatory network derived from ENCODE data** *NATURE*
Gerstein, M. B., Kundaje, A., Hariharan, M., Landt, S. G., Yan, K., Cheng, C., Mu, X. J., Khurana, E., Rozowsky, J., Alexander, R., Min, R., Alves, P., Abyzov, et al
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- **An integrated encyclopedia of DNA elements in the human genome** *NATURE*
Dunham, I., Kundaje, A., Aldred, S. F., Collins, P. J., Davis, C., Doyle, F., Epstein, C. B., Frietze, S., Harrow, J., Kaul, R., Khatun, J., Lajoie, B. R., Landt, et al
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- **ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia** *GENOME RESEARCH*
Landt, S. G., Marinov, G. K., Kundaje, A., Kheradpour, P., Pauli, F., Batzoglou, S., Bernstein, B. E., Bickel, P., Brown, J. B., Cayting, P., Chen, Y., DeSalvo, G., Epstein, et al
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- **Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements** *GENOME RESEARCH*
Kundaje, A., Kyriazopoulou-Panagiotopoulou, S., Libbrecht, M., Smith, C. L., Raha, D., Winters, E. E., Johnson, S. M., Snyder, M., Batzoglou, S., Sidow, A.
2012; 22 (9): 1735-1747
- **A Cell Cycle Phosphoproteome of the Yeast Centrosome** *SCIENCE*
Keck, J. M., Jones, M. H., Wong, C. C., Binkley, J., Chen, D., Jaspersen, S. L., Holinger, E. P., Xu, T., Niepel, M., Rout, M. P., Vogel, J., Sidow, A., Yates, et al
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- **Determinants of nucleosome organization in primary human cells** *NATURE*
Valouev, A., Johnson, S. M., Boyd, S. D., Smith, C. L., Fire, A. Z., Sidow, A.
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- **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
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- **Identifying a High Fraction of the Human Genome to be under Selective Constraint Using GERP plus** *PLOS COMPUTATIONAL BIOLOGY*
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2010; 6 (12)
- **Functional analyses of variants reveal a significant role for dominant negative and common alleles in oligogenic Bardet-Biedl syndrome** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Zaghloul, N. A., Liu, Y., Gerdes, J. M., Gascue, C., Oh, E. C., Leitch, C. C., Bromberg, Y., Binkley, J., Leibel, R. L., Sidow, A., Badano, J. L., Katsanis, N.
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Peng, J. C., Valouev, A., Swigut, T., Zhang, J., Zhao, Y., Sidow, A., Wysocka, J.
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- **A high-resolution, nucleosome position map of C. elegans reveals a lack of universal sequence-dictated positioning** *GENOME RESEARCH*
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- **Identification of the Otopetrin Domain, a conserved domain in vertebrate otopetrins and invertebrate otopetrin-like family members** *BMC EVOLUTIONARY BIOLOGY*
Hughes, I., Binkley, J., Hurle, B., Green, E. D., Sidow, A., Ornitz, D. M.
2008; 8
- **Fruit fly family fun** *CELL*
Sidow, A., Lacroute, P.
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- **Functional architecture and evolution of transcriptional elements that drive gene coexpression** *SCIENCE*
Brown, C. D., Johnson, D. S., Sidow, A.
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- **Mammalian Comparative Sequence Analysis of the Agrp Locus** *PLOS ONE*
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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
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 - **Phenotype-genotype correlation in Hirschsprung disease is illuminated by comparative analysis of the RET protein sequence** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
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 - **Trade-offs in detecting evolutionarily constrained sequence by comparative genomics** *ANNUAL REVIEW OF GENOMICS AND HUMAN GENETICS*
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 - **ABC: software for interactive browsing of genomic multiple sequence alignment data** *BMC BIOINFORMATICS*
Cooper, G. M., Singaravelu, S. A., Sidow, A.
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Sundararajan, M., Brudno, M., Small, K., Sidow, A., Batzoglou, S.
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 - **Inference of functional regions in proteins by quantification of evolutionary constraints** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
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 - **A double-deletion mutation in the Pitx3 gene causes arrested lens development in aphakia mice** *GENOMICS*
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 - **A novel member of the F-box/WD40 gene family, encoding dactylin, is disrupted in the mouse dactylaplasia mutant** *NATURE GENETICS*
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