

# 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](http://www.sidowlab.org)
- JIMB: [jimb.stanford.edu](http://jimb.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

---

#### COURSES

##### 2023-24

- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

#### GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)

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

## Publications

---

### PUBLICATIONS

- **SparseSignatures: An R package using LASSO-regularized non-negative matrix factorization to identify mutational signatures from human tumor samples.** *STAR protocols*  
Mella, L., Lal, A., Angaroni, F., Maspero, D., Piazza, R., Sidow, A., Antoniotti, M., Graudenzi, A., Ramazzotti, D.  
2022; 3 (3): 101513
- **Benchmarking challenging small variants with linked and long reads.** *Cell genomics*  
Wagner, J., Olson, N. D., Harris, L., Khan, Z., Farek, J., Mahmoud, M., Stankovic, A., Kovacevic, V., Yoo, B., Miller, N., Rosenfeld, J. A., Ni, B., Zarate, et al  
2022; 2 (5)
- **Aquila\_stLFR: diploid genome assembly based structural variant calling package for stLFR linked-reads.** *Bioinformatics advances*  
Liu, Y. H., Grubbs, G. L., Zhang, L., Fang, X., Dill, D. L., Sidow, A., Zhou, X.  
2021; 1 (1): vbab007
- **Aquila enables reference-assisted diploid personal genome assembly and comprehensive variant detection based on linked reads.** *Nature communications*  
Zhou, X., Zhang, L., Weng, Z., Dill, D. L., Sidow, A.  
2021; 12 (1): 1077
- **De novo mutational signature discovery in tumor genomes using SparseSignatures.** *PLoS computational biology*  
Lal, A., Liu, K., Tibshirani, R., Sidow, A., Ramazzotti, D.  
2021; 17 (6): e1009119
- **De novo diploid genome assembly for genome-wide structural variant detection.** *NAR genomics and bioinformatics*  
Zhang, L. n., Zhou, X. n., Weng, Z. n., Sidow, A. n.  
2020; 2 (1): lqz018
- **Assessment of human diploid genome assembly with 10x Linked-Reads data.** *GigaScience*  
Zhang, L., Zhou, X., Weng, Z., Sidow, A.  
2019; 8 (11)
- **Comprehensive genomic characterization of breast tumors with BRCA1 and BRCA2 mutations.** *BMC medical genomics*  
Lal, A. n., Ramazzotti, D. n., Weng, Z. n., Liu, K. n., Ford, J. M., Sidow, A. n.  
2019; 12 (1): 84
- **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. n., Lal, A. n., Wang, B. n., Batzoglou, S. n., Sidow, A. n.  
2018; 9 (1): 4453
- **Genome-wide reconstruction of complex structural variants using read clouds** *NATURE METHODS*  
Spies, N., Weng, Z., Bishara, A., McDaniel, J., Catoe, D., Zook, J. M., Salit, M., West, R. B., Batzoglou, S., Sidow, A.  
2017; 14 (9): 915-+
- **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., Asimenos, 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., Geirsdóttir, 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
- **Lineage-specific enhancers activate self-renewal genes in macrophages and embryonic stem cells.** *Science (New York, N.Y.)*  
Soucie, E. L., Weng, Z., Geirsdóttir, 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): aad5510
- **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.  
2013; 14
- **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  
2012; 489 (7414): 91-100
- **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  
2012; 489 (7414): 57-74
- **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  
2012; 22 (9): 1813-1831
- **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  
2011; 332 (6037): 1557-1561
- **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.  
2011; 474 (7352): 516-U148
- **A User's Guide to the Encyclopedia of DNA Elements (ENCODE)** *PLOS BIOLOGY*  
Myers, R. M., Stamatoiyannopoulos, 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)
- **Identifying a High Fraction of the Human Genome to be under Selective Constraint Using GERP plus** *PLOS COMPUTATIONAL BIOLOGY*  
Davydov, E. V., Goode, D. L., Sirota, M., Cooper, G. M., Sidow, A., Batzoglou, S.  
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*  
Zaghoul, 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.  
2010; 107 (23): 10602-10607
- **Evolutionary constraint facilitates interpretation of genetic variation in resequenced human genomes** *GENOME RESEARCH*  
Goode, D. L., Cooper, G. M., Schmutz, J., Dickson, M., Gonzales, E., Tsai, M., Karra, K., Davydov, E., Batzoglou, S., Myers, R. M., Sidow, A.  
2010; 20 (3): 301-310
- **ProPhylER: A curated online resource for protein function and structure based on evolutionary constraint analyses** *GENOME RESEARCH*  
Binkley, J., Karra, K., Kirby, A., Hosobuchi, M., Stone, E. A., Sidow, A.  
2010; 20 (1): 142-154
- **Jarid2/Jumonji Coordinates Control of PRC2 Enzymatic Activity and Target Gene Occupancy in Pluripotent Cells** *CELL*  
Peng, J. C., Valouev, A., Swigut, T., Zhang, J., Zhao, Y., Sidow, A., Wysocka, J.  
2009; 139 (7): 1290-1302

- **SHRiMP: Accurate Mapping of Short Color-space Reads** *PLOS COMPUTATIONAL BIOLOGY*  
Rumble, S. M., Lacroute, P., Dalca, A. V., Fiume, M., Sidow, A., Brudno, M.  
2009; 5 (5)
- **Genome-wide analysis of transcription factor binding sites based on ChIP-Seq data** *NATURE METHODS*  
Valouev, A., Johnson, D. S., Sundquist, A., Medina, C., Anton, E., Batzoglou, S., Myers, R. M., Sidow, A.  
2008; 5 (9): 829-834
- **The C-savignyi genetic map and its integration with the reference sequence facilitates insights into chordate genome evolution** *GENOME RESEARCH*  
Hill, M. M., Broman, K. W., Stupka, E., Smith, W. C., Jiang, D., Sidow, A.  
2008; 18 (8): 1369-1379
- **A high-resolution, nucleosome position map of C. elegans reveals a lack of universal sequence-dictated positioning** *GENOME RESEARCH*  
Valouev, A., Ichikawa, J., Tonthat, T., Stuart, J., Ranade, S., Peckham, H., Zeng, K., Malek, J. A., Costa, G., McKernan, K., Sidow, A., Fire, A., Johnson, et al  
2008; 18 (7): 1051-1063
- **Identification of the Otopetrin Domain, a conserved domain in vertebrate otopetrins and invertebrate otopetrin-like family members** *BMC EVOLUTIONARY BIOLOGY*  
Hughes, I., Binkley, J., Hurler, B., Green, E. D., Sidow, A., Ornitz, D. M.  
2008; 8
- **Fruit fly family fun** *CELL*  
Sidow, A., Lacroute, P.  
2007; 131 (7): 1222-1223
- **Functional architecture and evolution of transcriptional elements that drive gene coexpression** *SCIENCE*  
Brown, C. D., Johnson, D. S., Sidow, A.  
2007; 317 (5844): 1557-1560
- **Mammalian Comparative Sequence Analysis of the Agrp Locus** *PLOS ONE*  
Kaelin, C. B., Cooper, G. M., Sidow, A., Barsh, G. S.  
2007; 2 (8)
- **Constructing a meaningful evolutionary average at the phylogenetic center of mass** *BMC BIOINFORMATICS*  
Stone, E. A., Sidow, A.  
2007; 8
- **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
- **Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome** *GENOME RESEARCH*  
Margulies, E. H., Cooper, G. M., Asimenos, G., Thomas, D. J., Dewey, C. N., Siepel, A., Birney, E., Keefe, D., Schwartz, A. S., Hou, M., Taylor, J., Nikolaev, S., Montoya-Burgos, et al  
2007; 17 (6): 760-774
- **Extreme genomic variation in a natural population** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Small, K. S., Brudno, M., Hill, M. M., Sidow, A.  
2007; 104 (13): 5698-5703
- **A haplome alignment and reference sequence of the highly polymorphic Ciona savignyi genome** *GENOME BIOLOGY*  
Small, K. S., Brudno, M., Hill, M. M., Sidow, A.  
2007; 8 (3)
- **Structural and molecular evolutionary analysis of Agouti and Agouti-related proteins** *CHEMISTRY & BIOLOGY*  
Jackson, P. J., Douglas, N. R., Chai, B., Binkley, J., Sidow, A., Barsh, G. S., Millhauser, G. L.  
2006; 13 (12): 1297-1305

- **De novo discovery of a tissue-specific gene regulatory module in a chordate** *GENOME RESEARCH*  
Johnson, D. S., Zhou, Q., Yagi, K., Satoh, N., Wong, W., Sidow, A.  
2005; 15 (10): 1315-1324
- **Distribution and intensity of constraint in mammalian genomic sequence** *GENOME RESEARCH*  
Cooper, G. M., Stone, E. A., Asimenos, G., Green, E. D., Batzoglou, S., Sidow, A.  
2005; 15 (7): 901-913
- **Physicochemical constraint violation by missense substitutions mediates impairment of protein function and disease severity** *GENOME RESEARCH*  
Stone, E. A., Sidow, A.  
2005; 15 (7): 978-986
- **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*  
Kashuk, C. S., Stone, E. A., Grice, E. A., Portnoy, M. E., Green, E. D., Sidow, A., Chakravarti, A., McCallion, A. S.  
2005; 102 (25): 8949-8954
- **Trade-offs in detecting evolutionarily constrained sequence by comparative genomics** *ANNUAL REVIEW OF GENOMICS AND HUMAN GENETICS*  
Stone, E. A., Cooper, G. M., Sidow, A.  
2005; 6: 143-164
- **ABC: software for interactive browsing of genomic multiple sequence alignment data** *BMC BIOINFORMATICS*  
Cooper, G. M., Singaravelu, S. A., Sidow, A.  
2004; 5
- **Noncoding regulatory sequences of Gona exhibit strong correspondence between evolutionary constraint and functional importance** *GENOME RESEARCH*  
Johnson, D. S., Davidson, B., Brown, C. D., Smith, W. C., Sidow, A.  
2004; 14 (12): 2448-2456
- **Characterization of evolutionary rates and constraints in three mammalian genomes** *GENOME RESEARCH*  
Cooper, G. M., Brudno, M., Stone, E. A., Dubchak, I., Batzoglou, S., Sidow, A.  
2004; 14 (4): 539-548
- **Genome sequence of the Brown Norway rat yields insights into mammalian evolution** *NATURE*  
Gibbs, R. A., Weinstock, G. M., Metzker, M. L., Muzny, D. M., Sodergren, E. J., Scherer, S., Scott, G., Steffen, D., Worley, K. C., Burch, P. E., Okwuonu, G., Hines, S., Lewis, et al  
2004; 428 (6982): 493-521
- **Automated whole-genome multiple alignment of rat, mouse, and human** *GENOME RESEARCH*  
Brudno, M., Poliakov, A., Salamov, A., Cooper, G. M., Sidow, A., Rubin, E. M., Solovyev, V., Batzoglou, S., Dubchak, I.  
2004; 14 (4): 685-692
- **Genome sequence of the brown Norway rat yields insights into mammalian evolution** *Nature*  
Sidow A  
2004; 428
- **Chaining algorithms for alignment of draft sequence** *4th International Workshop on Algorithms in Bioinformatics (WABI 2004)*  
Sundararajan, M., Brudno, M., Small, K., Sidow, A., Batzoglou, S.  
SPRINGER-VERLAG BERLIN.2004: 326-337
- **Genomic regulatory regions: insights from comparative sequence analysis** *CURRENT OPINION IN GENETICS & DEVELOPMENT*  
Cooper, G. M., Sidow, A.  
2003; 13 (6): 604-610
- **Quantitative estimates of sequence divergence for comparative analyses of mammalian genomes** *GENOME RESEARCH*  
Cooper, G. M., Brudno, M., Green, E. D., Batzoglou, S., Sidow, A.  
2003; 13 (5): 813-820
- **LAGAN and Multi-LAGAN: Efficient tools for large-scale multiple alignment of genomic DNA** *GENOME RESEARCH*

- Brudno, M., Do, C. B., Cooper, G. M., Kim, M. F., Davydov, E., Green, E. D., Sidow, A., Batzoglou, S.  
2003; 13 (4): 721-731
- **The integrity of a cholesterol-binding pocket in Niemann-Pick C2 protein is necessary to control lysosome cholesterol levels** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Ko, D. C., Binkley, J., Sidow, A., Scott, M. P.  
2003; 100 (5): 2518-2525
  - **Functional evolution in the ancestral lineage of vertebrates or when genomic complexity was wagging its morphological tail.** *Journal of structural and functional genomics*  
Aburomia, R., Khaner, O., Sidow, A.  
2003; 3 (1-4): 45-52
  - **Sequence first. Ask questions later.** *CELL*  
Sidow, A.  
2002; 111 (1): 13-16
  - **Inference of functional regions in proteins by quantification of evolutionary constraints** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Simon, A. L., Stone, E. A., Sidow, A.  
2002; 99 (5): 2912-2917
  - **Partitioning of tissue expression accompanies multiple duplications of the Na plus /K+ ATPase alpha subunit gene** *GENOME RESEARCH*  
Serluca, F. C., Sidow, A., Mably, J. D., Fishman, M. C.  
2001; 11 (10): 1625-1631
  - **A double-deletion mutation in the Pitx3 gene causes arrested lens development in aphakia mice** *GENOMICS*  
Rieger, D. K., Reichenberger, E., McLean, W., Sidow, A., Olsen, B. R.  
2001; 72 (1): 61-72
  - **A novel member of the F-box/WD40 gene family, encoding dactylin, is disrupted in the mouse dactylaplasia mutant** *NATURE GENETICS*  
Sidow, A., Bulotsky, M. S., Kerrebrock, A. W., Birren, B. W., Altshuler, D., Jaenisch, R., Johnson, K. R., Lander, E. S.  
1999; 23 (1): 104-107