


# Stanford


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## Idan Gabdank

Senior Biocuration Scientist, Biomedical Data Science

 NIH Biosketch available Online

 Resume available Online

### Bio

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#### BIO

Dr. Gabdank is a Senior Biocuration Scientist with the Lattice team, where his research interests focus on advancing computational genomics through data-driven portfolio management and strategic decision-making frameworks. His work involves developing data standards and assessment methodologies that optimize research impact and guide investment strategies in genomics initiatives. This includes facilitating cross-functional collaborations between researchers and federal agencies, overseeing computational genomics programs, and leading the development of data pipelines and curation standards. Before joining Lattice, Idan served as Program Director at the National Human Genome Research Institute and Director of Data Science at Stanford University School of Medicine, where he provided strategic oversight for multi-institutional genomics consortia, including the ENCODE and IGVF consortia. Idan received his PhD in Bioinformatics from Ben Gurion University of the Negev, specializing in computational approaches to genomic data analysis and standardization.

#### CURRENT ROLE AT STANFORD

Manage data wrangling and curation for innovative cutting-edge single cell and CRISPR screen experiments within the Billion Cell Project funded by CZI, serving as a key member of the Lattice team at Stanford working in close collaboration with CZI and academy labs to ensure standardized data processing and quality control across high-throughput experimental datasets. Integrate AI tools and automate cloud-based pipelines for data validation and curation, streamlining quality assurance processes and reducing manual oversight requirements while maintaining data integrity standards.

#### HONORS AND AWARDS

- Research Excellence Prize, Ben Gurion University of the Negev (2010)
- Human Frontier Science Program Long-Term Cross-Disciplinary Fellowship, Human Frontier Science Program (2011 - 2014)

### Professional

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#### WORK EXPERIENCE

- Program Director - National Human Genome Research Institute (August 11, 2024 - March 24, 2025)
- Principal Data Wrangler - Stanford (October 1, 2018 - August 11, 2024)

### Publications

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#### PUBLICATIONS

- **Deciphering the impact of genomic variation on function.** *Nature* 2024; 633 (8028): 47-57

- **Multicenter integrated analysis of noncoding CRISPRi screens.** *Nature methods*  
Yao, D., Tycko, J., Oh, J. W., Bounds, L. R., Gosai, S. J., Lataniotis, L., Mackay-Smith, A., Doughty, B. R., Gabdank, I., Schmidt, H., Guerrero-Altamirano, T., Siklenka, K., Guo, et al  
2024
- **The ENCODE Uniform Analysis Pipelines.** *Research square*  
Hitz, B. C., Lee, J. W., Jolanki, O., Kagda, M. S., Graham, K., Sud, P., Gabdank, I., Strattan, J. S., Sloan, C. A., Dreszer, T., Rowe, L. D., Podduturi, N. R., Malladi, et al  
2023
- **The ENCODE4 long-read RNA-seq collection reveals distinct classes of transcript structure diversity.** *bioRxiv : the preprint server for biology*  
Reese, F., Williams, B., Balderrama-Gutierrez, G., Wyman, D., Çelik, M. H., Rebboah, E., Rezaie, N., Trout, D., Razavi-Mohseni, M., Jiang, Y., Borsari, B., Morabito, S., Liang, et al  
2023
- **The ENCODE Uniform Analysis Pipelines.** *bioRxiv : the preprint server for biology*  
Hitz, B. C., Jin-Wook, L., Jolanki, O., Kagda, M. S., Graham, K., Sud, P., Gabdank, I., Strattan, J. S., Sloan, C. A., Dreszer, T., Rowe, L. D., Podduturi, N. R., Malladi, et al  
2023
- **The EN-TEEx resource of multi-tissue personal epigenomes & variant-impact models.** *Cell*  
Rozowsky, J., Gao, J., Borsari, B., Yang, Y. T., Galeev, T., Gürsoy, G., Epstein, C. B., Xiong, K., Xu, J., Li, T., Liu, J., Yu, K., Berthel, et al  
2023; 186 (7): 1493-1511.e40
- **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
- **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
- **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
- **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
- **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
- **Recompleting the *Caenorhabditis elegans* genome.** *Genome research*  
Yoshimura, J. n., Ichikawa, K. n., Shoura, M. J., Artiles, K. L., Gabdank, I. n., Wahba, L. n., Smith, C. L., Edgley, M. L., Rougvie, A. E., Fire, A. Z., Morishita, S. n., Schwarz, E. M.  
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
- **Intricate and Cell Type-Specific Populations of Endogenous Circular DNA (eccDNA) in *Caenorhabditis elegans* and *Homo sapiens*.** *G3 (Bethesda, Md.)*  
Shoura, M. J., Gabdank, I., Hansen, L., Merker, J., Gotlib, J., Levene, S. D., Fire, A. Z.  
2017; 7 (10): 3295-3303
  - **SnoVault and encodeD: 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)
  - **Intricate and Cell Type-Specific Populations of Endogenous Circular DNA (eccDNA) in *Caenorhabditis elegans* and *Homo sapiens*** *G3: GENES, GENOMES, GENETICS*  
Shoura, M., Gabdank, I., Merker, J., Gotlib, J., Levene, S., Fire, A.  
2017; 7: 3295-3303
  - **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
  - **A streamlined tethered chromosome conformation capture protocol** *BMC GENOMICS*  
Gabdank, I., Ramakrishnan, S., Villeneuve, A. M., Fire, A. Z.  
2016; 17
  - **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
  - **Gamete-Type Dependent Crossover Interference Levels in a Defined Region of *Caenorhabditis elegans* Chromosome V.** *G3 (Bethesda, Md.)*  
Gabdank, I., Fire, A. Z.  
2014; 4 (1): 117-120
  - **On topological indices for small RNA graphs** *COMPUTATIONAL BIOLOGY AND CHEMISTRY*  
Churkin, A., Gabdank, I., Barash, D.  
2012; 41: 35-40
  - **The RNAmute web server for the mutational analysis of RNA secondary structures** *NUCLEIC ACIDS RESEARCH*  
Churkin, A., Gabdank, I., Barash, D.  
2011; 39: W92-W99
  - **Single-base Resolution Nucleosome Mapping on DNA Sequences** *JOURNAL OF BIOMOLECULAR STRUCTURE & DYNAMICS*  
Gabdank, I., Barash, D., Trifonov, E. N.  
2010; 28 (1): 107-121
  - **FineStr: a web server for single-base-resolution nucleosome positioning** *BIOINFORMATICS*  
Gabdank, I., Barash, D., Trifonov, E. N.  
2010; 26 (6): 845-846
  - **Preferential translation of Hsp83 in *Leishmania* requires a thermosensitive polypyrimidine-rich element in the 3' UTR and involves scanning of the 5' UTR** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
David, M., Gabdank, I., Ben-David, M., Zilka, A., Orr, I., Barash, D., Shapira, M.

2010; 16 (2): 364-374

- **Nucleosome DNA Bendability Matrix (C-elegans)** *JOURNAL OF BIOMOLECULAR STRUCTURE & DYNAMICS*  
Gabdank, I., Barash, D., Trifonov, E. N.  
2009; 26 (4): 403-411
- **Computational identification of three-way junctions in folded RNAs: a case study in Arabidopsis.** *In silico biology*  
Cohen, A., Bocobza, S., Veksler, I., Gabdank, I., Barash, D., Aharoni, A., Shapira, M., Kedem, K.  
2008; 8 (2): 105-120
- **In silico design of small RNA switches** *IEEE TRANSACTIONS ON NANOBIOSCIENCE*  
Avihoo, A., Gabdank, I., Shapira, M., Barash, D.  
2007; 6 (1): 4-11
- **Primordia vita. Deconvolution from modern sequences.** *Annual Meeting of the Deutsche-Gesellschaft-fur-Zuchtungskunde e V*  
Trifonov, E. N., Gabdank, I., Barash, D., Sobolevsky, Y.  
SPRINGER.2006: 559-65
- **Tracing ancient mRNA hairpins** *JOURNAL OF BIOMOLECULAR STRUCTURE & DYNAMICS*  
Gabdank, I., Barash, D., Trifonov, E. N.  
2006; 24 (2): 163-169