
Curriculum Vitae

Date Prepared: August 25, 2026
Name: Bo Li
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Education:

9/2004- 7/2008	BE	Computer Science and Engineering	Shanghai Jiao Tong University
9/2008- 5/2010	MS	Computer Science	University of Wisconsin- Madison
9/2008- 7/2013	PhD	Computer Science (Colin Dewey, PhD)	University of Wisconsin- Madison

Postdoctoral Training:

8/2013- 6/2017	Postdoctoral Researcher	Computational Biology (Lior Pachter, PhD)	University of California, Berkeley
7/2017- 4/2019	Postdoctoral Associate	Computational Biology (Aviv Regev, PhD)	Broad Institute of MIT and Harvard

Faculty Academic Appointments:

5/2019- 3/2020	Member of the Faculty	Medicine	Harvard Medical School
4/2020- 7/2021	Assistant Professor	Medicine	Harvard Medical School

Appointments at Hospitals/Affiliated Institutions:

5/2019- 7/2021	Research Staff (Assistant Investigator)	Center for Immunology and Inflammatory Diseases, Division of Rheumatology, Allergy and Immunology	Massachusetts General Hospital
5/2019- 3/2020	Associate Scientist	Klarman Cell Observatory	Broad Institute of MIT and Harvard

4/2020-7/2021	Associate Member	Klarman Cell Observatory	Broad Institute of MIT and Harvard
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Appointments at Genentech:

8/2021-7/2022	Senior Scientist	DSSC	Research
8/2022-9/2024	Principal Scientist	CTG / BRAID	gCS
10/2024-	Principal Scientist II	Biology Research AI Development	AIBT, CS CoE

Major Administrative Leadership Positions:

Local

5/2019-7/2021	Director, Bioinformatics and Computational Biology Program, Center for Immunology and Inflammatory Diseases	Massachusetts General Hospital
2021-2022	Co-lead, TGi technology workstream Lead, Spatial Pod team	Genentech
2022-	Co-lead, gRED Small Cell Lung Cancer Group	Genentech
2025-	Lead, FDFM Lung Cancer Perturbation team	Genentech
2026-	Co-lead, FDFM Lung Oncology BiT Team	Genentech

Committee Service:

Local

2014-2015	Postdoc Industry Exploration Program (PIEP)	University of California, Berkeley Committee Member
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International

2016	Program Committee Member, RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-SEQ)	International Conference on Research in Computational Molecular Biology (RECOMB)
2016	Program Committee Member	International Joint Conferences on Artificial Intelligence
2020	Program Committee Member	RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges

2021	Program Committee Member	International Conference on Research in Computational Molecular Biology (RECOMB)
2026	Program Committee Member	Intelligent Systems for Molecular Biology (ISMB)

Professional Societies:

2012	International Society for Computational Biology
2014	
2019-2024	
2026-	

Editorial Activities:

Ad hoc Reviewer

BMC Bioinformatics
 BMC Genomics
 Bioinformatics
 Cell Reports
 Genome Biology
 Genome Research
 GigaScience
 Nature Biotechnology
 Nature Communications
 Nature Machine Intelligence
 Nature Methods
 Nucleic Acids Research

Honors and Prizes:

2004	First Place, Association for Computing Machinery – International Collegiate Programming Contest (ACM-ICPC) Asia Programming Contest, Beijing Site	ACM-ICPC Committee	Programming Contest
2005 & 2006	Scholarship	Orient Overseas Container Line Corporation, China	
2005	Fifth Place, ACM-ICPC Asia Programming Contest, Taipei Site	ACM-ICPC Committee	Programming Contest
2005	Second Place, ACM-ICPC Asia	ACM-ICPC Committee	Programming Contest

	Programming Contest, Beijing Site		
2006	Thirteenth Place, Google Code Jam, China	Google, China	Programming Contest
2007	State Scholarship	Ministry of Education, China	
2008	Alumni Scholarship	Computer Sciences Department, University of Wisconsin-Madison	
2010-2012	Morgridge Institute for Research Support for Senior Graduate Students in Computation and Informatics in Biology and Medicine	Morgridge Institute for Research	Research
2013	Finalist, Lane Fellows in Computational Biology	Carnegie Mellon University	Postdoctoral Fellowship
2025	Nominee, Scientific & Technical Mentorship Award	Genentech	Mentorship
2025	CBT Innovation Grant	Genentech	Research
2026	AIBT/CBM Innovation Fund Award	Genentech	Research

Report of Scholarship

Peer-Reviewed Scholarship in print or other media:

Research Investigations

1. **Li B**, Ruotti V, Stewart RM, Thomson JA, Dewey CN. RNA-Seq gene expression estimation with read mapping uncertainty. *Bioinformatics* 2010; 26(4):493-500.
 - Citation (Google Scholar): **1,438**
2. Chung D, Kuan PF, **Li B**, Sanalkumar R, Liang K, Bresnick EH, Dewey C, Keleş S. Discovering transcription factor binding sites in highly repetitive regions of genomes with multi-read analysis of ChIP-Seq data. *PLoS Comput. Biol.* 2011; 7(7):e1002111.
 - In Brief. *Nature Reviews Genetics*. 2011; 12:588.
3. **Li B**, Dewey CN. RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. *BMC Bioinform.* 2011; 12:323.
 - Citation (Google Scholar): **24,477**
4. Haas BJ*, Papanicolaou A*, Yassour M, Grabherr M, Blood PD, Bowden J, Couger MB, Eccles D, **Li B**, Lieber M, MacManes MD, Ott M, Orvis J, Pochet N, Strozzi F, Weeks N, Westerman R,

William T, Dewey CN, Henschel R, LeDuc RD, Friedman N, Regev A. *De novo* transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. *Nat. Protoc.* 2013; 8(8):1494-512.

5. **Li B***, Fillmore N*, Bai Y, Collins M, Thomson JA, Stewart R, Dewey CN. Evaluation of *de novo* transcriptome assemblies from RNA-Seq data. *Genome Biol.* 2014; 15(12):553.
6. Zeng X, **Li B**, Welch R, Rojo C, Zheng Y, Dewey CN, Keleş S. Perm-seq: mapping protein-DNA interactions in segmental duplication and highly repetitive regions of genomes with prior-enhanced read mapping. *PLoS Comput. Biol.* 2015; 11(10):e1004491.
7. Choudhary K, Shih NP, Deng F, Ledda M, **Li B**, Aviran S. Metrics for rapid quality control in RNA structure probing experiments. *Bioinformatics* 2016; 32(23):3575-3583.
8. **Li B**, Tambe A, Aviran S, Pachter L. PROBER provides a general toolkit for analyzing sequencing-based toeprinting assays. *Cell Syst.* 2017; 4(5):568-574.
9. Haas BJ, Dobin A, Stransky N, **Li B**, Yang X, Tickle T, Bankapur A, Ganote C, Doak TG, Pochet N, Sun J, Wu CJ, Gingeras TR, Regev A. STAR-Fusion: Fast and Accurate Fusion Transcript Detection from RNA-Seq. *BioRxiv* 2017.
10. Gaublomme JT*†, **Li B***, McCabe C, Knecht A, Yang Y, Drokhlyansky E, Van Wittenberghe N, Waldman J, Dionne D, Nguyen L, De Jager PL, Yeung B, Zhao X, Habib N, Rozenblatt-Rosen O†, Regev A†. Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. *Nat. Commun.* 2019; 10: 2907.
11. Popescu DM*, Botting RA*, Stephenson E*, Green K, Webb S, Jardine L, Calderbank EF, Polanski K, Goh I, Efremova M, Acres M, Maunder D, Vegh P, Gitton Y, Park JE, Vento-Tormo R, Miao Z, Dixon D, Rowell R, McDonald D, Fletcher J, Poyner E, Reynolds G, Mather M, Moldovan C, Mamanova L, Greig F, Young MD, Meyer KB, Lisgo S, Bacardit J, Fuller A, Millar B, Innes B, Lindsay S, Stubbington MJT, Kowalczyk MS, **Li B**, Ashenberg O, Tabaka M, Dionne D, Tickle TL, Slyper M, Rozenblatt-Rosen O, Filby A, Carey P, Villani AC, Roy A, Regev A, Chédotal A, Roberts I, Göttgens B, Behjati S, Laurenti E†, Teichmann SA†, Haniffa M†. Decoding human fetal liver haematopoiesis. *Nature* 2019; 574(7778):365-371.
12. Haas BJ†, Dobin A, **Li B**, Stransky N, Pochet N, Regev A. Accuracy assessment of fusion transcript detection via read-mapping and *de novo* fusion transcript assembly-based methods. *Genome Biol.* 2019; 20(1):213.
13. Sen P, Wilkie AR, Ji F, Yang Y, Taylor IJ, Velazquez-Palafox M, Vanni EAH, Pesola JM, Fernandez R, Chen H, Morsett LM, Abels ER, Piper M, Lane RJ, Hickman SE, Means TK, Rosenberg ES, Sadreyev RI, **Li B**, Coen DM, Fishman JA, El Khoury J. Linking indirect effects of cytomegalovirus in transplantation to modulation of monocyte innate immune function. *Sci. Adv.* 2020; 6(17):eaax9856.
14. Slyper M*, Porter CBM*, Ashenberg O*, Waldman J, Drokhlyansky E, Wakiro I, Smillie C, Smith-Rosario G, Wu J, Dionne D, Vigneau S, Jané-Valbuena J, Tickle TL, Napolitano S, Su M, Patel AG, Karlstrom A, Gritsch S, Nomura M, Waghray A, Gohil SH, Tsankov AM, Jerby-Arnon L, Cohen O, Klughammer J, Rosen Y, Gould J, Nguyen L, Hofree M, Tramontozzi PJ, **Li B**, Wu CJ, Izar B, Haq R, Hodi FS, Yoon CH, Hata AN, Baker SJ, Suvà ML, Bueno R, Stover EH, Clay MR, Dyer MA, Collins NB, Matulonis UA, Wagle N, Johnson BE, Rotem A, Rozenblatt-Rosen O†, Regev A†. A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. *Nat. Med.* 2020; 26:792-802.

15. Lavaert M, Liang KL, Vandamme N, Park JE, Roels J, Kowalczyk MS, **Li B**, Ashenberg O, Tabaka M, Dionne D, Tickle TL, Slyper M, Rozenblatt-Rosen O, Vandekerckhove B, Leclercq G, Regev A, Van Vlierberghe P, Guillems M, Teichmann SA, Saey Y, Taghon T. Integrated scRNA-seq identifies human postnatal thymus seeding progenitors and regulatory dynamics of differentiating immature thymocytes. *Immunity* 2020; 52(6):1088-1104.e6.
16. **Li B**[†], Gould J, Yang Y, Sarkizova S, Tabaka M, Ashenberg O, Rosen Y, Slyper M, Kowalczyk MS, Villani AC, Tickle T, Hacohen N, Rozenblatt-Rosen O[†], Regev A[†]. Cumulus provides cloud-based data analysis for large-scale single-cell and single-nucleus RNA-seq. *Nat. Methods* 2020; 17:793-798.
17. Bao EL, Nandakumar SK, Liao X, Bick AG, Karjalainen J, Tabaka M, Gan OI, Havulinna AS, Kiiskinen TTJ, Lareau CA, de Lapuente Portilla AL, **Li B**, Emdin C, Codd V, Nelson CP, Walker CJ, Churchhouse C, de la Chapelle A, Klein DE, Nilsson B, Wilson PWF, Cho K, Pyarajan S, Gaziano JM, Samani, NJ, FinnGen, 23andMe Research Team, Regev A, Palotie A, Neale BM, Dick JE, Natarajan P, O'Donnell CJ, Daly MJ, Milyavsky M, Kathiresan S, Sankaran VG. Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. *Nature* 2020; 586(7831):769-775.
18. Ward RA, Thompson GR 3rd, Villani AC, **Li B**, Mansour MK, Wuethrich M, Tam JM, Klein BS, Vyas JM. The known unknowns of the immune response to *Coccidioides*. *J. Fungi (Basel)* 2021; 7(5):377.
19. Delorey TM*, Ziegler CGK*, Heimberg G*, Normand R*, Yang Y*, Segerstolpe A*, Abbondanza D*, Fleming SJ*, Subramanian A*, Montoro DT*, Jagadeesh KA*, Dey KK*, Sen P*, Slyper M*, Pita-Juárez YH*, Phillips D*, Biermann J*, Bloom-Ackermann Z, Barkas N, Ganna A, Gomez J, Melms JC, Katsyv I, Normandin E, Naderi P, Popov YV, Raju SS, Niezen S, Tsai LTY, Siddle KJ, Sud M, Tran VM, Vellarikkal SK, Wang Y, Amir-Zilberstein L, Atri DS, Beechem J, Brook OR, Chen J, Divakar P, Dorceus P, Engreitz JM, Essene A, Fitzgerald DM, Fropf R, Gazal S, Gould J, Grzyb J, Harvey T, Hecht J, Hether T, Jané-Valbuena J, Leney-Greene M, Ma H, McCabe C, McLoughlin DE, Miller EM, Muus C, Niemi M, Padera R, Pan L, Pant D, Pe'er C, Pfiffner-Borges J, Pinto CJ, Plaisted J, Reeves J, Ross M, Rudy M, Rueckert EH, Siciliano M, Sturm A, Todres E, Waghray A, Warren S, Zhang S, Zollinger DR, Cosimi L, Gupta RM, Hacohen N, Hibshoosh H, Hide W, Price AL, Rajagopal J, Tata PR, Riedel S, Szabo G, Tickle TL, Ellinor PT[^], Hung D[^], Sabeti PC[^], Novak R[^], Rogers R[^], Ingber DE[^], Jiang ZG[^], Juric D[^], Babadi M[^], Farhi SL[^], Izar B[^], Stone JR[^], Vlachos IS^{^†}, Solomon IH[^], Ashenberg O[^], Porter CBM[^], **Li B**[^], Shalek AK^{^†}, Villani AC^{^†}, Rozenblatt-Rosen O^{^†}, Regev A^{^†}. COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. *Nature* 2021; 595(7865):107-113.
20. Jardine L*, Webb S*, Goh I, Londoño MQ, Reynolds G, Mather M, Olabi B, Stephenson E, Botting RA, Horsfall D, Engelbert J, Maunder D, Mende N, Murnane C, Dann E, McGrath J, King H, Kucinski I, Queen R, Carey CD, Shrubsole C, Poyner E, Acres M, Jones C, Ness T, Coulthard R, Elliott N, O'Byrne S, Haltalli MLR, Lawrence JE, Lisgo S, Balogh P, Meyer KB, Prigmore E, Ambridge K, Jain MS, Efremova M, Pickard K, Creasey T, Bacardit J, Henderson D, Coxhead J, Filby A, Hussain R, Dixon D, McDonald D, Popescu D-M, Kowalczyk MS, **Li B**, Ashenberg Q, Tabaka M, Dionne D, Tickle TL, Slyper M, Rozenblatt-Rosen O, Regev A, Behjati S, Laurenti E, Wilson NK[^], Roy A[^], Göttgens B[^], Roberts I[^], Teichmann SA[^], Haniffa M^{^†}. Blood and immune development in human fetal bone marrow and Down syndrome. *Nature* 2021; 598(7880):327-331.
21. Ouspenskaia T*, Law T*, Clauser KR*, Klaeger S*, Sarkizova S, Aguet F, **Li B**, Christian E, Knisbacher BA, Le PM, Hartigan CR, Keshishian H, Apffel A, Oliveira G, Zhang W, Chen S, Chow YT, Ji Z, Jungreis I, Shukla SA, Justesen S, Bachireddy P, Kellis M, Getz G, Hacohen N, Keskin DB[^], Carr SA[^], Wu CJ^{^†}, Regev A^{^†}. Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. *Nat. Biotechnol.* 2022; 40(2):209-217.

22. Subramanian A*†, Alperovich M*, Yang Y, **Li B**. Biology-inspired data-driven quality control for scientific discovery in single-cell transcriptomics. *Genome Biol.* 2022; 23(1):267.
23. Kudo T, Meireles AM, Moncada R, Chen Y, Wu P, Gould J, Hu X, Kornfeld O, Jesudason R, Foo C, Höckendorf B, Corrada Bravo H, Town JP, Wei R, Rios A, Chandrasekar V, Heinlein M, Chuong AS, Cai S, Lu CS, Coelho P, Mis M, Celen C, Kljavin N, Jiang J, Richmond D, Thakore P, Benito-Gutiérrez E, Geiger-Schuller K, Hleap JS, Kayagaki N, de Sousa e Melo F, McGinnis L, **Li B**, Singh A, Garraway L, Rozenblatt-Rosen O, Regev A, Lubeck E. Multiplexed, image-based pooled screens in primary cells and tissues with PerturbView. *Nat. Biotechnol.* 2025; 43(7):1091-1100.
24. Roels J, Ghaedi H, Kancherla J, Yang Y, Ganesan R, Babu P, Williams K, Yao X, Pradhan R, Guan X, Yuen K, Maddalo D, Mariathasan S, Banchereau R, **Li B**, Krishnamurty AT, Bravo HC, Müller S†, Dey A†. The Hippo Pathway Is Dysregulated in Cancer-Associated Fibroblasts in Anti-PD-L1-Resistant Cancer. *Cancer Res.* 2026; 86(11):2592-2605.
25. Gould J, Hleap Lozano JS, Wu P, Kudo T, Guan J, Zhu A, Lubeck E, Ge XM, Waterman AA, Biancalani T, Rozenblatt-Rosen O, Metcalfe C, Singh A, Richmond D, Regev A, **Li B**. SCALLOPS: a scalable, integrated computational framework for Optical Pooled Screens. *BioRxiv* 2026.
26. Orcutt-Jahns B*, Hueros RAR*, Meireles AM*, Cox C, Ghita L, Kamm J, Celen C, Yang Y, Zargari-Pariset E, Rouzbeh N, Zhou Y, Wang J, Sabri S, Kudo T, Thakore PI, Richmond D, Biancalani T, Kim H, Gherardini PF, Schroth GP, Turley SJ, Rozenblatt-Rosen O, Bravo HC†, **Li B**†, Geiger-Schuller K†. Linking live-cell behavior to transcriptional responses across perturbations using dynamic caging. *BioRxiv* 2026.

* contributed equally

^ senior / co-senior authors

† corresponding / co-corresponding authors

Thesis:

Li B. Computational analysis of RNA-Seq data in the absence of a known genome [dissertation]. Madison, Wisconsin: University of Wisconsin-Madison; July 2013.