

Jesse D. Bloom

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<http://research.fhcrc.org/bloom/en.html>

Research Positions

- Associate Member, Fred Hutchinson Cancer Research Center, Division of Basic Sciences and Computational Biology Program (2011 – present)
- Affiliate Associate Professor, University of Washington, Department of Genome Sciences and Department of Microbiology (2011 – present)
- Investigator, Howard Hughes Medical Institute (2018 – present)

Education and Training

- Postdoctoral fellow in Biology, Caltech, 2007-2011, advisor Dr. David Baltimore.
- Ph.D. in Chemistry, Caltech, 2002-2007, advisor Dr. Frances Arnold.
- M. Phil. in Theoretical Chemistry, Cambridge, 2001-2002, advisor Dr. David Wales.
- B.S. in Biochemistry, University of Chicago, 1997-2001, advisor Dr. Susan Lindquist.

Awards and Honors

- Merck Irving S. Sigal Award from American Society for Microbiology 2017
- Top 10 on *bioRxiv* leaderboard (<http://blog.dhimmel.com/biorxiv-licenses/>) 2016
- HHMI-Simons Faculty Scholar 2016
- Anne Palmenberg award from American Society for Virology 2016
- Young Investigator in Virology Award from *Viruses* 2015
- Burroughs Wellcome Investigator in the Pathogenesis of Infectious Diseases 2015
- Pew Scholar in the Biomedical Sciences 2015
- Searle Scholar 2012
- Sloan Research Fellow 2012
- PopTech Science and Public Leadership Fellow 2010
- ASCIT Teaching Award for undergraduate research mentoring at Caltech 2007
- Demetriades-Tsafka Prize for best Caltech Ph.D. thesis in bioengineering 2007
- Churchill Scholarship 2001

Software

My lab currently maintains the following software packages:

- **dms_tools2** (http://jbloomlab.github.io/dms_tools2)
- **phydms** (<http://jbloomlab.github.io/phydms>)
- **dms_variants** (http://jbloomlab.github.io/dms_variants)

Publications

Below I list research papers on which I am first or corresponding author. A list that includes reviews and papers on which I am a secondary author is at

https://scholar.google.com/citations?user=S12x_eQAAAAJ

- 1) KS Xue and **JD Bloom**. "Linking influenza virus evolution within and between human hosts." *bioRxiv*. DOI 10.1101/812016 (2019).
- 2) M Sourisseau, DJP Lawrence, MC Schwarz, CH Storrs, EC Veit, **JD Bloom**[#], and MJ Evans[#]. "Deep mutational scanning comprehensively maps how Zika virus mutations affect viral growth and antibody escape." *Journal of Virology*. DOI 10.1128/JVI.01291-19 (2019).
- 3) JM Lee, R Eguia, SJ Zost, S Choudhary, PC Wilson, T Bedford, T Stevens-Ayers, M Boeckh, A Hurt, SS Lakdawala, SE Hensley, and **JD Bloom**. "Mapping person-to-person variation in viral mutations that escape polyclonal serum targeting influenza hemagglutinin." *eLife*. 8:e49324 (2019)
 - Computer code to reproduce paper: https://github.com/jbloombloomlab/map_flu_serum_Perth2009_H3_HA
- 4) YQ Soh, LH Moncla, R Eguia, T Bedford, and JD Bloom. "Comprehensive mapping of adaptation of the avian influenza polymerase protein PB2 to humans." *eLife*. 8:e45079 (2019)
- 5) AB Russell, E Elshina, J Kowalsky, AJ te Velthuis, and **JD Bloom**. "Single-cell virus sequencing of influenza infections that trigger innate immunity." *Journal of Virology*. 93:e00500-19 (2109)
 - Computer code to reproduce paper: https://github.com/jbloombloomlab/IFNsorted_flu_single_cell
- 6) AS Dingens, D Arenz, H Weight, J Overbaugh[#], and **JD Bloom**[#]. "An antigenic atlas of HIV-1 escape from broadly neutralizing antibodies distinguished functional and structural epitopes." *Immunity*. 50:520-532 (2019) (2019)
- 7) HM Machkovech, **JD Bloom**[#], AR Subramaniam[#]. "Comprehensive profiling of translation initiation in influenza-virus infected cells." *PLoS Pathogens*. 15:e1007518 (2019)
- 8) KS Xue and **JD Bloom**. "Reconciling disparate estimates of viral genetic diversity during human influenza infections." *Nature Genetics*. DOI: 10.10138/s41588-019-0349-3 (2019)
- 9) AS Dingens, P Acharya, HK Haddox, R Rawi, K Xu, GY Chuang, B Zhang, H Wei, JR Mascola, B Carragher, CS Potter, J Overbaugh, PD Kwong[#], and **JD Bloom**[#]. "Complete functional mapping of infection- and vaccine-elicited antibodies against the fusion peptide of HIV." *PLoS Pathogens*, 14:e1007159 (2018)
- 10) SK Hilton and **JD Bloom**. "Modeling site-specific amino-acid preferences deepens phylogenetic estimates of viral divergence." *Virus Evolution*, 4:vey033 (2018)
- 11) JM Lee^{*}, J Huddleston^{*}, MB Doud, KA Hooper, NC Wu, T Bedford[#], and **JD Bloom**[#]. "Deep mutational scanning of hemagglutinin helps predict evolutionary fates of H3N2 influenza variants." *PNAS*, 115:E8276-E8285 (2018)
 - Computer code to reproduce paper: <https://github.com/jbloombloomlab/Perth2009-DMS-Manuscript>
- 12) HK Haddox^{*}, AS Dingens^{*}, SK Hilton, J Overbaugh, and **JD Bloom**. "Mapping mutational effects along the evolutionary landscape of HIV envelope." *eLife*. 7:e34420 (2018)
 - Computer code to reproduce paper: <https://github.com/jbloombloomlab/EnvMutationalShiftsPaper>

- 13) MB Doud, JM Lee, and **JD Bloom**. "How single mutation affect viral escape from broad and narrow antibodies to H1 influenza hemagglutinin." *Nature Communications*. 9:1386 (2018)
 - Computer code to reproduce paper: https://github.com/jbloombloom/HA_antibody_ease_of_escape
- 14) AB Russell, C Trapnell, and **JD Bloom**. "Extreme heterogeneity of influenza virus infection in single cells." *eLife*. 7:e32303 (2018)
 - Computer code to reproduce paper: https://github.com/jbloombloom/flu_single_cell
- 15) KS Xue, AL Greninger, A Perez-Osorio, and **JD Bloom**. "Cooperating H3N2 influenza virus variants are not detectable in primary clinical samples." *mSphere*. 3:e00552-17 (2018)
- 16) SK Hilton, MB Doud, and **JD Bloom**. "phydms: Software for phylogenetic analyses informed by deep mutational scanning." *PeerJ*. 5:e3657 (2017)
 - The software described in this paper is at <http://jbloomlab.github.io/phydms/>
- 17) KS Xue, T Stevens-Ayers, AP Campbell, JA Englund, SA Pergam, M Boeckh, and **JD Bloom**. "Parallel evolution of influenza across multiple spatiotemporal scales." *eLife*. 6:e26875 (2017)
 - Town Hall by first-author Katherine Xue: <https://youtu.be/SxW7SUGsZKA?t=1m6s>
 - Coverage in *The Atlantic*: <https://www.theatlantic.com/health/archive/2017/06/evolution-of-the-flu/531693/>
- 18) AS Dingens, HK Haddock, J Overbaugh[#], and **JD Bloom**[#]. "Comprehensive mapping of HIV-1 escape from a broadly neutralizing antibody." *Cell Host & Microbe*, 21:777-787 (2017)
 - Preview: "Unconventional interrogation yields HIV's escape plan," *Cell Host & Microbe*, 21:777-787.
- 19) MB Doud, SE Hensley, and **JD Bloom**. "Complete mapping of viral escape from neutralizing antibodies." *PLoS Pathogens*. 13:e1006271 (2017)
 - Spotlight: "Influenza evolution: new insights into an old foe," *Trends in Microbiology*, 25:432-434.
- 20) **JD Bloom**. "Identification of positive selection in genes is greatly improved by using experimentally informed site-specific models." *Biology Direct*. 12:1 (2017)
- 21) Ashenberg, J Padmakumar, MB Doud, and **JD Bloom**. "Deep mutational scanning identifies sites in influenza nucleoprotein that affect viral inhibition by MxA." *PLoS Pathogens*, 13:e1006288 (2017)
- 22) HK Haddock, AS Dingens, and **JD Bloom**. "Experimental estimation of the effects of all amino-acid mutations to HIV Env." *PLoS Pathogens*. 12:e1006114 (2016)
- 23) MB Doud and **JD Bloom**. "Accurate measurement of the effects of all amino-acid mutations to influenza hemagglutinin." *Viruses*. 8:155 (2016)
- 24) KS Xue, KA Hooper, AR Ollodart, AS Dingens, and **JD Bloom**. "Cooperation between distinct viral variants promotes growth of H3N2 influenza in cell culture." *eLife*. 5:e13974 (2016)
 - Blog post: <http://www.molecularecologist.com/2016/03/when-times-are-good-or-bad-happy-or-sad-viral-quasispecies-like-to-stay-together/>

- 25) HM Machkovech, T Bedford, M Suchard, and **JD Bloom**. "Positive selection in CD8+ T-cell epitopes of influenza nucleoprotein revealed by a comparative analysis of human and swine viral lineages." *J. Virology*. 89:11275-11283 (2015)
- 26) MB Doud, O Ashenberg, and **JD Bloom**. "Site-specific amino-acid preferences are mostly conserved in two closely related protein homologs." *Mol. Biol. Evol.* 32:2944-2960 (2015)
- 27) KA Hooper, JE Crowe, and **JD Bloom**. "Influenza viruses with receptor-binding neuraminidases occur sporadically in several viral lineages and show no attenuation in cell culture or mice." *J. Virology*. 89:3737-3745 (2015)
- 28) **JD Bloom**. "Software for the analysis and visualization of deep mutational scanning data." *BMC Bioinformatics*. 16:168 (2015)
 - The software described in this paper is at http://jbloomlab.github.io/dms_tools2/
- 29) **JD Bloom**. "An experimentally informed evolutionary model improves phylogenetic fit to divergent lactamase homologs." *Mol. Biol. Evol.* 31:2753-2769 (2014).
- 30) B Thyagarajan and **JD Bloom**. "The inherent mutational tolerance and antigenic evolvability of influenza hemagglutinin." *eLife*. 3:e03300 (2014)
- 31) **JD Bloom**. "An experimentally determined evolutionary model dramatically improves phylogenetic fit." *Mol. Biol. Evol.* 31:1956-1978 (2014)
- 32) LI Gong and **JD Bloom**. "Epistatically interacting mutations are enriched during adaptive protein evolution." *PLoS Genetics*. 10:e1004328 (2014)
- 33) Ashenberg, LI Gong, and **JD Bloom**. "Mutational effects on stability are largely conserved during protein evolution." *Proc. Natl. Acad. Sci. USA*. 110:21071-21076 (2013)
- 34) KA Hooper and **JD Bloom**. "A mutant influenza virus that uses an N1 neuraminidase as the receptor-binding protein." *J. Virology*. 87:12531-12540 (2013)
- 35) LI Gong, MA Suchard, and **JD Bloom**. "Stability-mediated epistasis constrains the evolution of an influenza protein." *eLife*. 2:e00631 (2013)
 - Selected as an *eLife* early-career investigator outstanding paper
 - Insight article: "Influenza evolution navigates stability valleys," *eLife*, 2:e088842.
 - 203 Google Scholar citations
- 36) **JD Bloom**, JS Nayak, and D Baltimore. "A computational-experimental approach identifies mutations that enhance surface expression of an oseltamivir-resistant influenza neuraminidase." *PLoS One*. 6:e22201 (2011)
- 37) **JD Bloom**, LI Gong, and D Baltimore. "Permissive secondary mutations enable the evolution of influenza oseltamivir resistance." *Science*. 5983:1272-1275 (2010)
 - Perspectives: "Helping the resistance," *Science*, 328:1243-1244
 - 514 Google Scholar citations
- 38) **JD Bloom** and MJ Glassman. "Inferring stabilizing mutations from protein phylogenies: application to influenza hemagglutinin." *PLoS Comput. Biol.* 5:e1000349 (2009)
- 39) **JD Bloom**, Z Lu, D Chen, A Raval, OS Venturelli, and FH Arnold. "Evolution favors protein mutational robustness in sufficiently large populations." *BMC Biology*. 5:29 (2007)
- 40) **JD Bloom**, PA Romero, Z Lu, and FH Arnold. "Neutral genetic drift can alter promiscuous protein functions, potentially aiding functional evolution." *Biology Direct*. 2:17 (2007)

- 41) **JD Bloom**, A Raval, and CO Wilke. "Thermodynamics of neutral protein evolution." *Genetics*. 175:255-266 (2007)
- 42) **JD Bloom**, ST Labthavikul, CR Otey, and FH Arnold. "Protein stability promotes evolvability." *Proc. Natl. Acad. Sci. USA*. 103:5869-5874 (2006)
 - 875 Google Scholar citations
- 43) **JD Bloom**, DA Drummond, FH Arnold, and CO Wilke. "Structural determinants of the rate of protein evolution in yeast." *Mol. Biol. Evol.* 23:1751-1761 (2006)
- 44) **JD Bloom**, JJ Silberg, CO Wilke, DA Drummond, C Adami, and FH Arnold. "Thermodynamic prediction of protein neutrality." *Proc. Natl. Acad. Sci. USA*. 102:606-611 (2005)
 - 316 Google Scholar citations
- 45) **JD Bloom**, CO Wilke, FH Arnold, and C Adami. "Stability and the evolvability of function in a model protein." *Biophysical J.* 86:2758-2764 (2004)
- 46) **JD Bloom** and C Adami. "Evolutionary rate depends on number of protein-protein interactions independently of gene expression level: response." *BMC Evol. Biology*. 4:14 (2004)
- 47) **JD Bloom** and C Adami. "Apparent dependence of protein evolutionary rate on number of protein-protein interactions is linked to biases in protein-protein interaction data sets." *BMC Evol. Biology*. 3:21 (2003)

Current funding

Below I list funding for which I am the lead PI.

- Howard Hughes Medical Institute Investigator annual research budget (2018-2025)
- NIH/NIAID R01 AI127893 (2016-2021)
- NIH/NIAID R01 AI141707 (2018-2023)
- NIH/NIAID R01 AI140891 (2018-2023)
- Burroughs-Wellcome Young Investigator in the Pathogenesis of Infectious Diseases (2015-2020)

Service & Teaching

- Instructor for *Introduction to Computational Molecular Biology* (GENOME 541): lead course instructor in 2017, instructor in most other years
- Instructor for *Tools for Computational Biology*
- Faculty Area Director in *Computational Biology* for the Molecular and Cellular Biology graduate program
- I serve on thesis committees for 20 graduate students at the Fred Hutch and University of Washington
- Chair of faculty search committee for Basic Sciences Division at the Fred Hutch, 2016-2017
- Co-chair of faculty search committee for Computational Biology Program at the Fred Hutch, 2014-2015
- Guest editor for *eLife*, *PLoS Pathogens*, *mBio*, and *PLoS Genetics*

Trainees (graduate students and postdocs)

The start dates listed for graduate student students are when they joined my lab full time.

- **Current graduate students**
 - *Sarah Hilton* (2016 – present): PhD student in the Genome Sciences program. Sarah was awarded a position on the Viral Pathogenesis training grant.
 - *Katharine Dusenbury* (2017 – present): MD/PhD student in the Genome Sciences Program. Katharine was awarded a spot on the Genome Training Grant.
 - *David Bacsik* (2017 – present): MD/PhD student in the Genome Sciences program.
 - *Lauren Gentles* (2017 – present): PhD student in the Microbiology program. Lauren has received a NSF Graduate Fellowship.
 - *Allie Greaney* (2018 – present): MD/PhD student in the Genome Sciences program.
 - *Caelan Radford* (2018 – present): PhD student in the MCB program.
- **Current postdocs**
 - *Tyler Starr* (2018 – present): Tyler is joint-advised by Erick Matsen. He has received a WRF Fellowship.
 - *Tal Einav* (2019 – present): Tal has received the Mahan postdoctoral fellowship on computational biology.
- **Former graduate students:**
 - *Katherine Xue* (2014 – 2019) is now a James S. McDonnell postdoctoral fellow with Dmitri Petrov and David Relman at Stanford University.
 - *Juhye Lee* (2015 – 2019) is now completing the MD portion of her dual MD/PhD degree.
 - *Adam Dingens* (2015 – 2019) is now a research scientist in the Bloom and Overbaugh labs at the Hutch.
 - *Heather Machkovech* (2014 – 2018) is now completing the MD portion of her dual MD/PhD degree.
 - *Hugh Haddock* (2013 – 2017) is now a WRF Postdoctoral Fellow with David Baker at the University of Washington.
 - *Michael Doud* (2013 – present) is now completing his medical residency and fellowship at UC San Diego.
 - *Kathryn Hooper* (2012 – 2015) is now a research scientist at bluebird bio.
- **Former postdocs**
 - *Alistair Russell* (2015 – 2019) is now a faculty member at UC San Diego.
 - *Shirleen Soh* (2016 – 2019) is now a senior scientist at Merck in Singapore.
 - *Jeremy Roop* (2016 – 2018) is now a research scientist at Berkeley Brewing.
 - *Orr Ashenberg* (2013 – 2017) is now a computational biologist at the Klarman Cell Observatory at the Broad Institute of Harvard and MIT.
 - *Bargavi Thyagarajan* (2011 – 2014) is now a Scientific Officer at the HIV Vaccine Enterprise.