

General information

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Nationality: United States Citizen

Employment and education

2014–Present **Assistant Professor at Cold Spring Harbor Laboratory**

2010–2014 **Quantitative Biology Fellow at Cold Spring Harbor Laboratory**

2009–2010 **Postdoctoral Fellow at Cold Spring Harbor Laboratory**
Mentors: Bruce Stillman and Michael Zhang

2008–2009 **Postdoctoral Fellow at Princeton University**
Mentors: Curtis Callan and Edward Cox

2002–2008 **Graduate study in Physics at Princeton University**
PhD in Physics, September 2008
Experimental Biophysics under Edward Cox, 2007–2008
Theoretical Biophysics under Curtis Callan, 2004–2008
Theoretical High Energy Physics under Juan Maldacena, 2003–2004

1998–2002 **Undergraduate study at Cornell University**
BA in Physics, summa cum laude, May 2002
BA in Mathematics, magna cum laude, May 2002

Professional activities

July 2016 Organizer of the “Measuring and Modeling Quantitative Sequence-Function Relationships” conference at the CSHL Banbury Center.

2016–Present Visiting Scholar at the Initiative for the Theoretical Sciences,
Graduate Center, City University of New York

August 2015 Participant in the “Machine learning, Inference, and Statistical Physics” working group at the Aspen Center for Physics.

2015–Present Participant in the “Scialog: Molecules Come to Life” series of workshops.

2013–Present Affiliate member of the [bioRxiv](#)

2010–Present Instructor for the Watson School of Biological Sciences at CSHL

2008–Present Member, American Physical Society

Awards

2015 [Inaugural Info-Metrics Prize](#), Info-Metrics Institute at American University

2014 [Scialog Fellow](#), Moore Foundation / Research Corporation for Science Advancement

2005 [Outstanding Teaching Assistant](#), American Association of Physics Teachers

2005 Teaching Prize, Princeton University Physics Department

2002 Van Zandt Williams, Sr. *41 Fellowship, Princeton University

2002 [Yennie Prize in Physics](#), Cornell University

2002 [Merrill Presidential Scholar](#), Cornell University

2002 Phi Beta Kappa

2001 [Barry M. Goldwater Scholarship](#)

Preprints

1. Ireland WT, **Kinney JB**. MPAthic: quantitative modeling of sequence-function relationships for massively parallel assays. [bioRxiv doi:10.1101/054676](https://doi.org/10.1101/054676) (2016).
2. Morrison MJ, **Kinney JB**. Modeling multi-particle complexes in stochastic chemical systems. [bioRxiv doi:10.1101/045435](https://doi.org/10.1101/045435) (2016).

Research publications

See my [Google Scholar page](#) for citation statistics.

1. Ipsaro JJ, Shen C, Eri A, Xu Y, **Kinney JB**, Joshua-Tor L, Vakoc CR, Shi J. Rapid generation of drug-resistance alleles at endogenous loci using CRISPR-Cas9 indel mutagenesis. [PLoS ONE 12\(2\):e0172177](https://doi.org/10.1371/journal.pone.0172177) (2017).
2. Senturk S, Shirole NH, Nowak DD, Corbo V, Pal D, Vaughan A, Tuveson DA, Trotman LC, Kepecs A, **Kinney JB**, Sordella R. Rapid and tunable method to temporally control gene editing based on conditional Cas9 stabilization. [Nat Commun 8:14370](https://doi.org/10.1038/ncomms14370) (2017).
3. Adams RM, Mora T*, Walczak AM*, **Kinney JB***. Measuring the sequence-affinity landscape of antibodies with massively parallel titration curves. [eLife 2016;5:e23156](https://doi.org/10.1038/nature23156) (2016). *Equal contribution.
4. Atwal G, **Kinney JB**. Learning quantitative sequence-function relationships from high-throughput biological data. [J Stat Phys 162\(5\):1203-1243](https://doi.org/10.1038/nature21243) (2016).
5. Sheu Y-J, **Kinney JB**, Stillman B. Concerted activities of Mcm4, Sld3 and Dbf4 in control of origin activation and DNA replication fork progression. [Genome Res 26:315-330](https://doi.org/10.1038/nrg3330) (2016).
6. **Kinney JB**. Unification of field theory and maximum entropy methods for learning probability densities. [Phys Rev E 92:032107](https://doi.org/10.1103/PhysRevE.92.032107). (2015).
7. Shi J, Wang E, Milazzo JP, Wang A, **Kinney JB**, Vakoc CR. Discovery of cancer drug targets by CRISPR-Cas9 screening of protein domains. [Nat Biotechnol 33\(6\):661-667](https://doi.org/10.1038/nbt3667) (2015).
8. Wang E, Kawaoka S, Roe J-S, Shi J, Hohmann AF, Xu Y, Bhagwat AS, Suzuki Y, **Kinney JB**, Vakoc CR. The transcriptional cofactor TRIM33 prevents apoptosis in B lymphoblastic leukemia by deactivating a single enhancer. [eLife 4:e06377](https://doi.org/10.1038/nature16377) (2015).
9. **Kinney JB**. Estimation of probability densities using scale-free field theories. [Phys Rev E 90:011301\(R\)](https://doi.org/10.1103/PhysRevE.90.011301) (2014).
10. **Kinney JB**, Atwal GS. Parametric inference in the large data limit using maximally informative models. [Neural Comput 26\(4\):637-653](https://doi.org/10.1162/NEUR.2014.264.637) (2014).
11. **Kinney JB**, Atwal GS. Equitability, mutual information, and the maximal information coefficient. [Proc Natl Acad Sci USA 111\(9\):3354-3359](https://doi.org/10.1073/pnas.1313354111) (2014).
12. Sheu Y-J, **Kinney JB**, Lengronne A, Pasero P, Stillman B. Domain within the helicase subunit Mcm4 integrates multiple kinase signals to control DNA replication initiation and fork progression. [Proc Natl Acad Sci USA 111\(18\):E1899-908](https://doi.org/10.1073/pnas.1318999111) (2014).
13. Razo-Mejia M, Boedicker JQ, Jones D, Deluna A, **Kinney JB**, Phillips R. Comparison of the theoretical and real-world evolutionary potential of a genetic circuit. [Phys Biol 11\(2\):026005](https://doi.org/10.1098/rspb.2014.0260) (2014).
14. Weirauch MT, Cote A, Norel R, Annala M, Zhao Y, Riley TR, Saez-Rodriguez J, Cokelaer T, Vedenko A, Talukder S, **DREAM5 Consortium**, Bussemaker HJ, Morris QD, Bulyk ML, Stolovitzky G, Hughes TR. Evaluation of methods for modeling transcription factor sequence specificity. [Nat Biotechnol 31\(2\):126-34](https://doi.org/10.1038/nbt312) (2013).

15. Melnikov A, Murugan A, Zhang X, Tesileanu T, Wang L, Rogov P, Feizi S, Gnirke A, Callan CG, **Kinney JB**, Kellis M, Lander ES, Mikkelsen TS. Rapid dissection and model-based optimization of inducible enhancers in human cells using a massively parallel reporter assay. [Nat Biotechnol 30\(3\):271-277](#) (2012).
16. **Kinney JB**, Murugan A, Callan CG, Cox EC. Using deep sequencing to characterize the biophysical mechanism of a transcriptional regulatory sequence. [Proc Natl Acad Sci USA 107\(20\):9158-9163](#) (2010).
17. Mustonen V, **Kinney JB**, Callan CG, Lässig M. Energy-dependent fitness: a quantitative model for the evolution of yeast transcription factor binding sites. [Proc Natl Acad Sci USA 105\(34\):12376-12381](#) (2008).
18. **Kinney JB**, Tkačik G, Callan CG. Precise physical models of protein-DNA interaction from high-throughput data. [Proc Natl Acad Sci USA 104\(2\):501-506](#) (2007).
19. **Kinney JB**, Maldacena J, Minwalla S, Raju S. An index for 4 dimensional super conformal theories. [Commun Math Phys 275\(1\):209-254](#) (2007).
20. Hines C, Childress L, **Kinney JB**, Sulzer M. Modeling of gravity-wave tail spectra in the middle atmosphere via numerical and Doppler-spread methods. [J Atmos Sol-Terr Phys 66:933-948](#) (2004).
21. **Kinney JB**, Mendell G. r -modes in accreting neutron stars with magnetoviscous boundary layers. [Phys Rev D 67:024032](#) (2003).

Other publications

1. **Kinney JB**. Mutual information: a universal measure of statistical dependence. [Biomedical Computation Review 10\(2\):33](#) (2014).
2. **Kinney JB**, Atwal GS Reply to Reshef et al.: Falsifiability or bust. [Proc Natl Acad Sci USA 111\(33\):E3364-E3364](#) (2014).
3. **Kinney JB**, Atwal GS Reply to Murrell et al.: Noise matters. [Proc Natl Acad Sci USA 111\(21\):E2161-E2161](#) (2014).
4. **Kinney JB** Biophysical models of transcriptional regulation from sequence data. [PhD dissertation, Princeton University](#) (2008).