Georgi K. Marinov

Curriculum Vitae

July 15, 2021

Department of Genetics
Stanford University School of Medicine
Stanford, CA 94305

E-mail: GKM359@gmail.com, marinovg@stanford.edu

Education

California Institute of Technology, Pasadena, CA, USA

2008 – 2014. PhD in Biology. Thesis committee: Barbara J. Wold (thesis supervisor), Alexei A. Aravin, Eric H. Davidson, Paul W. Sternberg.

Thesis: ***Functional genomic studies of the structure and regulation of eukaryotic transcriptomes***

Massachusetts Institute of Technology, Cambridge, MA, USA

2005 – 2008. B.S. in Biology

Sofia University "St. Kliment Ohridski", Sofia, Bulgaria

2004 – 2005. Completed one year in the B.S. in Molecular Biology program before transferring to the Massachusetts Institute of Technology.

High School of Mathematics "Geo Milev", Pleven, Bulgaria

1998 – 2004. Concentration in Biology.

Professional Experience

Skills and expertise

- **Experimental:** cell culture; basic molecular biology and biochemistry techniques; functional genomic assays and high-throughput sequencing short-read and single-molecule library generation (RNA-seq, small RNA-seq, ChIP-seq, ATAC-seq, MNAse-seq, Hi-C, WGBS, KAS-seq, nanopore sequencing, single-cell assays, and others).
- **Computational:** Python, R, MATLAB; extensive familiarity with multiple types of genomics data, including the statistical analysis of functional genomic assays; single-cell assays; de novo assembly and annotation of prokaryote and eukaryote genomes; de novo assembly and annotation of transcriptomes; genome resequencing and analysis of sequence variants; phylogenetic analysis, and many others.

Education and research

- **May 2017 – present.** Postdoctoral researcher in the laboratories of Dr. William Greenleaf and Dr. Anshul Kundaje, Department of Genetics, Stanford University.

  Working on a variety of projects, including: developing new methods for the characterization of chromatin structure in eukaryotic cells; developing and improving methods for carrying out massively parallel single-cell RNA-sequencing; high-throughput CRISPR screening techniques for the functional dissection of coding and noncoding regulatory elements in the genome.

- **January 2015 – July 2016.** Postdoctoral researcher in the laboratory of Dr. Michael Lynch, Department of Biology, IU Bloomington.

  Worked on studying the evolution of nuclear and mitochondrial genome organization and regulation in the ciliate genius *Paramecium* and on theoretical questions regarding the role of bioenergetics in the evolution of life.

- **July 2014 – December 2014.** Postdoctoral researcher in the laboratory of Dr. Barbara Wold, Division of Biology, California Institute of Technology.

- **September 2008 – June 2014.** PhD student in the laboratory of Dr. Barbara Wold, Division of Biology, California Institute of Technology.

  Worked on a wide variety of projects, including: as part of the ENCODE Consortium Project, development of methods for assessing, analyzing and integrating functional genomic datasets, in particular RNA-seq and ChIP-seq; studied the role of transcriptional regulators in the process of muscle differentiation using functional genomic tools; carried out early work in the field of single-cell transcriptomics, establishing frameworks for assessing and accounting for biological and technical cell-to-cell variability; studied the role of piRNA in regulating gene expression in *Drosophila*; studied the organization and regulation of gene expression in metazoan mitochondrial genomes using functional genomic techniques.

- **September 2005 – December 2007.** UROP (Undergraduate Research Opportunity Program) student in the lab of Dr. Leona Samson, Center for Environmental Health Sciences, Massachusetts Institute of Technology.

  Worked on understanding cellular response to DNA damage using biochemical techniques for measuring the activity of signal transduction network components.

Academic service

- **Reviewed manuscripts ($n = 45$) for:** *Genome Research*, *PLoS Computational Biology*, *Molecular Biology and Evolution*, *BMC Bionformatics*, *PLoS ONE*, *BMC Genetics*, *Nucleic Acids Research*, *Journal of Eukaryotic Microbiology*, *Scientific Reports*, *Journal of Phycology*, *Methods*, *Biotechniques*, *Epigenomics*, *Diversity*, *Zygon*.

- **Guest Editor for:** *Briefings in Functional Genomics*.

Academic Publications

(Google Scholar | ORCID)

Note: * and ‡ indicate equal contributions to a work, † indicates corresponding authors.

61. **Marinov GK**, Kim SH, Bagdatli ST, Trevino AE, Tycko J, Wu T, Bintu L, Bassik MC, He C, Kundaje A, Greenleaf WJ. 2021. Direct profiling of genome-wide dCas9 and Cas9 specificity using ssDNA mapping (CasKAS). (*bioRxiv* 2021.04.16.440202.)

60. Rangachev A, **Marinov G**, Mladenov M. 2021. The demographic and geographic impact of the COVID pandemic in Bulgaria and Eastern Europe in 2020. (*medRxiv* 2021.04.06.21254958.)

59. Kõivomägi M, Swaffer MP, Turner JJ, **Marinov G**, Skotheim JM. 2021. Localized phosphorylation of RNA Polymerase II by G1 cyclin-Cdk promotes cell cycle entry. (*bioRxiv* 2021.03.25.436872.)

58. Swaffer MP, Chandler-Brown D, Langhinrichs M, **Marinov G**, Greenleaf W, Kundaje A, Schmoller KM, Skotheim JM. 2021. Size-independent mRNA synthesis and chromatin-based partitioning mechanisms generate and maintain constant amounts of protein per cell. (*bioRxiv* 2020.08.28.272690).

57. Reggiardo RE, Maroli SV, Halasz H, Ozen M, Carrillo D, LaMontagne E, Whitehead L, Kim E, Malik S, Fernandes J, **Marinov G**, Collisson E, Demirci U, Kim DH. 2021. Epigenomic reprogramming of repetitive noncoding RNAs and IFN-stimulated genes by mutant KRAS. (*bioRxiv* 2020.11.04.367771)

56. Tan K-E, Ng WL, **Marinov GK**, Ken Hung-On Yu KHO, Tan LP, Liau ES, Goh SK, Yeo KS, Yip KY, Lo K-W, Khoo ASB, Yap LF, Ea CK Lim YY. 2021. Identification and characterization of a novel Epstein-Barr Virus-encoded circular RNA from *LMP-2* Gene. *Sci Rep* **11**:14392. (link)

55. **Marinov GK***, Trevino AE*, Xiang T*, Kundaje A, Grossman AR, Greenleaf WJ. 2020. Transcription-dependent domain-scale three-dimensional genome organization in the dinoflagellate *Breviolum minutum*. *Nat Genetics* **53**:613–617 (link) (*bioRxiv* 2020.07.01.181685) (link)

54. **Marinov GK***, Shipony Z*. 2020. Interrogating the accessible chromatin landscape of eukaryote genomes using ATAC-seq. *Methods Mol Biol* **2243**:183–226 (link).

53. Minnoye L, **Marinov GK**, Krausgruber T, Pan L, Marand AP, Secchia S, Greenleaf WJ, Furlong EEM, Zhao K, Schmitz RJ, Bock C, Aerts S. 2021. Chromatin accessibility profiling methods. *Nature Reviews Methods Primers* **1**:10. (link)

52. Tycko J, DelRosso N, Hess GT, Aradhana, Banerjee A, Mukund A, Van MV, Ego BK, Yao D, Spees K, Suzuki P, **Marinov GK**, Kundaje A, Bassik MC, Bintu L. 2020. High-Throughput Discovery and Characterization of Human Transcriptional Effectors. *Cell* **183**:2020–2035 (*bioRxiv* 2020.09.09.288324) (link)

51. He P, Williams BA, Trout D, **Marinov GK**, Amrhein H, Berghella L, Goh ST, Plajzer-Frick I, Afzal V, Pennacchio LA, Dickel DE, Visel A, Ren B, Hardison RC, Zhang Y, Wold BJ. 2020. The changing mouse embryo transcriptome at whole tissue and single-cell resolution. *Nature* **583**(7818):760–767 (*bioRxiv* 2020.06.14.150599). (link)

50. ENCODE Project Consortium. Moore JE, Purcaro MJ, Pratt HE, Epstein CB, Shoresh N, Adrian J, Kawli T, Davis CA, Dobin A, Kaul R, Halow J, Van Nostrand EL, Freese P, Gorkin DU, Shen Y, He Y, Mackiewicz M, Pauli-Behn F, Williams BA, Mortazavi A, Keller CA, Zhang XO, Elhajjajy SI, Huey J, Dickel DE, Snetkova V, Wei X, Wang X, Rivera-Mulia JC, Rozowsky J, Zhang J, Chhetri SB, Zhang J, Victorsen A, White KP, Visel A, Yeo GW, Burge CB, Lécuyer E, Gilbert DM, Dekker J, Rinn J, Mendenhall EM, Ecker JR, Kellis M, Klein RJ, Noble WS, Kundaje A, Guigó R, Farnham PJ, Cherry JM, Myers RM, Ren B, Graveley BR, Gerstein MB, Pennacchio LA, Snyder MP, Bernstein BE, Wold B, Hardison RC, Gingeras TR, Stamatoyannopoulos JA, Weng Z. 2020. Expanded encyclopaedias of DNA elements in the human and mouse genomes. *Nature* **583**(7818):699–710. (link)

49. ENCODE Project Consortium, Snyder MP, Gingeras TR, Moore JE, Weng Z, Gerstein MB, Ren B, Hardison RC, Stamatoyannopoulos JA, Graveley BR, Feingold EA, Pazin MJ, Pagan M, Gilchrist DA, Hitz BC, Cherry JM, Bernstein BE, Mendenhall EM, Zerbino DR, Frankish A, Flicek P, Myers RM. 2020. Perspectives on ENCODE. *Nature* **583**(7818):693–698. (link)

48. Shipony Z*, **Marinov GK***, Swaffer MP, Sinott–Armstrong NA, Skotheim JM, Kundaje A, Greenleaf WJ. 2020. Long-range single-molecule mapping of chromatin accessibility in eukaryotes. *Nat Methods* **17**:319–327. (*bioRxiv* 504662) (link)

47. Tycko J*, Wainberg M*, **Marinov GK***, Ursu O, Hess GT, Ego BK, Aradhana, Li A, Truong A, Trevino AE, Spees K, Yao D, Kaplow IM, Greenside PG, Morgens DW, Phanstiel DH, Snyder MP, Bintu L, Greenleaf WJ, Kundaje A, Bassik MC. 2019. Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. *Nat Commun* **10**:4063. (*bioRxiv* 520569) (link)

46. Movva R, Greenside P, **Marinov GK**, Nair S, Shrikumar A, Kundaje A. 2019. Deciphering regulatory DNA sequences and noncoding genetic variants using neural network models of massively parallel reporter assays. *PLoS ONE* **14**(6):e0218073 (*bioRxiv* 393926). (link)

45. Johri P*, **Marinov GK***, Doak TG, Lynch M. 2019. Population genetics of *Paramecium* mitochondrial genomes: recombination, mutation spectrum, and efficacy of selection. *Genome Biol Evol* **11**(5):1398–1416. (link)

44. **Marinov GK**. 2018. A decade of ChIP-seq. *Brief Funct Genomics* **17**(2):77–79. (link)

43. **Marinov GK**,†, Kundaje A. 2018. ChIP-ping the branches of the tree: functional genomics and the evolution of eukaryotic gene regulation. *Brief Funct Genomics* **17**(2):116–137. (link)

42. Mann M, Mehta A, Zhao JL, Lee K, **Marinov GK**, Garcia-Flores Y, Baltimore D. 2017. An NF-κB-microRNA regulatory network tunes macrophage inflammatory responses. *Nat Commun* **8**(1):851. (link)

41. Ng WL, **Marinov GK**, Chin YM, Lim YY Ea CK. 2017. Transcriptomic analysis of the role of RasGEF1B circular RNA in the TLR4/LPS pathway. *Sci Rep* **7**:12227. (link)

40. Polewski MD, Reveron-Thornton RF, Cherryholmes GA, **Marinov GK**, Aboody KS. 2017. *SLC7A11* over-expression in glioblastoma is associated with increased cancer stem-cell like properties. *Stem Cells Dev* **26**(17):1236–1246. (link)

39. **Marinov GK**. 2017. Identification of Candidate Functional Elements in the Genome from ChIP-seq Data. *Methods in Mol Biol* **1543**:19–45. (link)

38. **Marinov GK**. 2017. ChIP-seq for the Identification of Functional Elements in the Human Genome. *Methods in Mol Biol* **1543**:3–18. (link)

37. Lynch M, **Marinov GK**. 2017. Membranes, energetics, and evolution across the prokaryote-eukaryote divide. *eLife* **6**:e20437. (link)

36. **Marinov GK**. 2017. On the design and prospects of direct RNA sequencing. *Brief Funct Genomics* **16**(6):326–335. (link)

35. Johri P, Krenek S, **Marinov GK**. Doak TG, Berendonk TU, Lynch M. 2017. Population genomics of *Paramecium* species. *Mol Biol Evol* **34**(5):1194–1216. (link)

34. Polewski MD, Reveron-Thornton RF, Cherryholmes GA, **Marinov GK**, Cassady K, Aboody KS. 2016. Increased expression of system $\mathrm{x_C}^-$ in glioblastoma confers an altered metabolism and chemoresistance. *Mol Cancer Res* **14**(12):1229–1242. (link)

33. Ng WL, **Marinov GK**, Liau ES, Lam YL, Lim YY, Ea CK. 2016. Inducible RasGEF1B circular RNA is a positive regulator of ICAM-1 in the TLR4/LPS pathway. *RNA Biol* **13**(9):861–871. (link)

32. **Marinov GK**,†, Lynch M. 2016. Conservation and divergence of the histone code in nucleomorphs. *Biol Direct* **11**:18. (link)

31. Hur JK, Luo Y, Moon S, Ninova M, **Marinov GK**, Chung YD, Aravin AA. 2016. Splicing-independent loading of TREX on nascent RNA is required for efficient expression of dual-strand piRNA clusters in Drosophila. *Genes Dev* **30**:840–855. (link)

30. Gangaiaha D, **Marinov GK**, Roberts SA, Robson J, Spinola SM. 2015. Draft Whole-Genome Sequence of *Haemophilus ducreyi* Strain AUSPNG1, Isolated from a Cutaneous Ulcer of a Child from Papua New Guinea. *Genome Announc* **4**(1):e01661–15. (link)

29. **Marinov GK**,†, Lynch M. 2015. Diversity and Divergence of Dinofagellate Histone Proteins. *G3* **6**(2):397–422. (link)

28. Lynch M, **Marinov GK**. 2015. The bioenergetic costs of a gene. *Proc Natl Acad Sci U S A* **112**:15690–15695. (link)

27. Mehta A, Mann M, Zhao JL, **Marinov GK**, Majumdar D, Garcia-Flores Y, Du X, Erikci E, Chowdhury K, Baltimore D. 2015. The microRNA-212/132 cluster regulates B cell development by targeting Sox4. *J Exp Med* **212**:1679–1692. (link)

26. Manakov SA, Pezic D, **Marinov GK**, Pastor WA, Sachidanandam R, Aravin AA. 2015. MIWI2 and MILI Have Differential Effects on piRNA Biogenesis and DNA Methylation. *Cell Rep* **12**(8):1234–1243. (link)

25. Mehta A, Zhao JL, Sinha N, **Marinov GK**, Mann M, Kowalczyk MS, Galimidi RP, Du X, Erikci E, Regev A, Chowdhury K, Baltimore D. 2015. The MicroRNA-132 and MicroRNA-212 Cluster Regulates Hematopoietic Stem Cell Maintenance and Survival with Age by Buffering FOXO3 Expression. *Immunity* **42**(6):1021–1032. (link)

24. Smalley MD, **Marinov GK**, Bertani LE, DeSalvo G. 2015. Genome Sequence of *Magnetospirillum magnetotacticum* Strain MS-1. *Genome Announc* **3**(2):e00233–15. (link)

23. **Marinov GK***, Wang J*, Handler D, Wold BJ, Weng Z, Hannon GJ, Aravin AA, Zamore PD, Brennecke J, Toth KF. 2015. Pitfalls of mapping high throughput sequencing data to repetitive sequences: Piwi's genomic targets still not identified. *Dev Cell* **32**:765–771. (link)

22. Kim DH, **Marinov GK**, Pepke S, Singer ZS, He P, Williams BA, Schroth GP, Elowitz MB, Wold BJ. 2015. Single-Cell Transcriptome Analysis Reveals Dynamic Changes in lncRNA Expression during Reprogramming. *Cell Stem Cell* **16**(1):88–101. (link)

21. Abelin ACT, **Marinov GK**, Williams BA, McCue K, Wold BJ. 2014. A ratiometric-based measure of gene co-expression. *BMC Bioinformatics* **15**:331. (link)

20. Cheng Y, Ma Z, Kim BH, Wu W, Cayting P, Boyle AP, Sundaram V, Xing X, Dogan N, Li J, Euskirchen G, Lin S, Lin Y, Visel A, Kawli T, Yang X, Patacsil D, Keller CA, Giardine B; Mouse ENCODE Consortium, Kundaje A, Wang T, Pennacchio LA, Weng Z, Hardison RC, Snyder MP. 2014. Principles of regulatory information conservation between mouse and human. *Nature* **515**(7527):371–375. (link)

19. The Mouse ENCODE Consortium. 2014. A comparative encyclopedia of DNA elements in the mouse genome. *Nature* **515**(7527):355–364. (link)

18. Le Thomas A, **Marinov GK**, Aravin AA. 2014. A Transgenerational Process Defines piRNA Biogenesis in *Drosophila virilis*. *Cell Rep* **8**:1617–1623. (link)

17. Le Thomas A*, Stuwe E*, Li S, Du J, **Marinov GK**, Rozhkov N, Chen YC, Luo Y, Sachidanandam R, Toth KF, Patel D, Aravin AA. 2014. Transgenerationally inherited piRNAs trigger piRNA biogenesis by changing the chromatin of piRNA clusters and inducing precursor processing. *Genes Dev* **28**:1667–1680. (link)

16. Gasper WC, **Marinov GK**, Pauli-Behn F, Scott MT, Newberry K, DeSalvo G, Ou S, Myers RM, Vielmetter J, Wold BJ. 2014. Fully automated high-throughput chromatin immunoprecipitation for ChIP-seq: Identifying ChIP-quality p300 monoclonal antibodies. *Sci Rep* **4**:5152. (link)

15. Kellis M*, Wold BJ*, Snyder MP*, Bernstein BE*, Kundaje A‡, **Marinov GK**‡, Ward LD‡, Birney E, Crawford GE, Dekker J, Dunham I, Elnitski L, Farnham PJ, Feingold EA, Gerstein M, Giddings MC, Gilbert DM, Gingeras TR, Green ED, Guigo R, Hubbard T, Kent J, Lieb JD, Myers RM, Pazin MJ, Ren B, Stamatoyannopoulos JA, Weng Z, White KP, Hardison RC. 2014. Defining functional DNA elements in the human genome. *Proc Natl Acad Sci U S A* **111**(17):6131–6138. (link)

14. **Marinov GK***,†, Wang YE*, Chan DC, Wold BJ. 2014. Evidence for site-specific occupancy of the mitochondrial genome by nuclear transcription factors. *PLoS ONE* **9**(1):e84713. (link)

13. **Marinov GK**, Kundaje A, Park PJ, Wold BJ. 2014. Large-scale quality analysis of published ChIP-seq data. *G3* **4**(2):209–223. (link)

12. **Marinov GK***, Williams BA*, McCue K, Schroth GP, Gertz J, Myers RM, Wold BJ. 2014. From single-cell to cell-pool transcriptomes: stochasticity in gene expression and RNA splicing. *Genome Res* **24**:496–510. (link)

11. Mortazavi A, Pepke S, Jansen C, **Marinov GK**, Ernst J, Kellis M, Hardison R, Myers RM, Wold B. 2013. Integrating and mining the chromatin landscape of cell-type specificity using Self-Organizing Maps. *Genome Res* **23**:2136–2148. (link)

10. Wang YE, **Marinov GK**, Wold BJ, Chan DC. 2013. Genome-wide analysis reveals coating of the mitochondrial genome by TFAM. *PLoS ONE* **8**(8):e74513. (link)

9. Le Thomas A*, Rogers AK*, Webster A*, **Marinov GK***, Liao SE, Perkins EM, Hur JK, Aravin AA, Fejes-Tóth K. 2013. Piwi induces piRNA-guided transcriptional silencing and establishment of a repressive chromatin state. *Genes Dev* **27**:390–399. (link)

8. Yang F, Nichols NG, Li BC, **Marinov GK**, Said JW, Dervan PB. 2013. Antitumor activity of a pyrrole-imidazole polyamide *Proc Natl Acad Sci U S A* **110**(5):1863–1868. (link)

7. Raskatov JA, Nickols NG, Hargrove AE, **Marinov GK**, Wold B, Dervan PB. 2012. Gene expression changes in a tumor xenograft by a pyrrole-imidazole polyamide. *Proc Natl Acad Sci U S A* **109**(4):16041–16045. (link)

6. Djebali S, Davis CA, Merkel A, Dobin A, Lassmann T, Mortazavi A, Tanzer A, Lagarde J, Lin W, Schlesinger F, Xue C, **Marinov GK**, Khatun J, Williams BA, Zaleski C, Rozowsky J, Röder M, Kokocinski F, Abdelhamid RF, Alioto T, Antoshechkin I, Baer MT, Bar NS, Batut P, Bell K, Bell I, Chakrabortty S, Chen X, Chrast J, Curado J, Derrien T, Drenkow J, Dumais E, Dumais J, Duttagupta R, Falconnet E, Fastuca M, Fejes-Toth K, Ferreira P, Foissac S, Fullwood MJ, Gao H, Gonzalez D, Gordon A, Gunawardena H, Howald C, Jha S, Johnson R, Kapranov P, King B, Kingswood C, Luo OJ, Park E, Persaud K, Preall JB, Ribeca P, Risk B, Robyr D, Sammeth M, Schaffer L, See LH, Shahab A, Skancke J, Suzuki AM, Takahashi H, Tilgner H, Trout D, Walters N, Wang H, Wrobel J, Yu Y, Ruan X, Hayashizaki Y, Harrow J, Gerstein M, Hubbard T, Reymond A, Antonarakis SE, Hannon G, Giddings MC, Ruan Y, Wold B, Carninci P, Guigó R, Gingeras TR. 2012. Landscape of transcription in human cells. *Nature* **489**(7414):101–108. (link)

5. ENCODE Project Consortium, Bernstein BE, Birney E, Dunham I, Green ED, Gunter C, Snyder M. 2012. An integrated encyclopedia of DNA elements in the human genome. *Nature* **489**(7414):57–74. (link)

4. Landt SG*, **Marinov GK***, Kundaje A*, Kheradpour P, Pauli F, Batzoglou S, Bernstein BE, Bickel P, Brown JB, Cayting P, Chen Y, Desalvo G, Epstein C, Fisher-Aylor KI, Euskirchen G, Gerstein M, Gertz J, Hartemink AJ, Hoffman MM, Iyer VR, Jung YL, Karmakar S, Kellis M, Kharchenko PV, Li Q, Liu T, Liu XS, Ma L, Milosavljevic A, Myers RM, Park PJ, Pazin MJ, Perry MD, Raha D, Reddy TE, Rozowsky J, Shoresh N, Sidow A, Slattery M, Stamatoyannopoulos JA, Tolstorukov MY, White KP, Xi S, Farnham PJ, Lieb JD, Wold BJ, Snyder M. 2012. ChIP-seq guidelines and practices used by the ENCODE and modENCODE consortia. *Genome Res* **22**(9):1813–1831. (link)

3. Mouse ENCODE Consortium, Stamatoyannopoulos JA, Snyder M, Hardison R, Ren B, Gingeras T, Gilbert DM, Groudine M, Bender M, Kaul R, Canfield T, Giste E, Johnson A, Zhang M, Balasundaram G, Byron R, Roach V, Sabo PJ, Sandstrom R, Stehling AS, Thurman RE, Weissman SM, Cayting P, Hariharan M, Lian J, Cheng Y, Landt SG, Ma Z, Wold BJ, Dekker J, Crawford GE, Keller CA, Wu W, Morrissey C, Kumar SA, Mishra T, Jain D, Byrska-Bishop M, Blankenberg D, Lajoie BR, Jain G, Sanyal A, Chen KB, Denas O, Taylor J, Blobel GA, Weiss MJ, Pimkin M, Deng W, **Marinov GK**, Williams BA, Fisher-Aylor KI, Desalvo G, Kiralusha A, Trout D, Amrhein H, Mortazavi A, Edsall L, McCleary D, Kuan S, Shen Y, Yue F, Ye Z, Davis CA, Zaleski C, Jha S, Xue C, Dobin A, Lin W, Fastuca M, Wang H, Guigo R, Djebali S, Lagarde J, Ryba T, Sasaki T, Malladi VS, Cline MS, Kirkup VM, Learned K, Rosenbloom KR, Kent WJ, Feingold EA, Good PJ, Pazin M, Lowdon RF, Adams LB. 2012. An encyclopedia of mouse DNA elements (Mouse ENCODE). *Genome Biol* **13**(8):418. (link)

2. Reddy TE, Gertz J, Pauli F, Kucera KS, Varley KE, Newberry KM, **Marinov GK**, Mortazavi A, Williams BA, Song L, Crawford GE, Wold BJ, Willard HF, Myers RM. 2012. Effects of sequence variation on differential allelic transcription factor occupancy and gene expression. *Genome Res* **22**(5):860–869. (link)

1. ENCODE Project Consortium, Myers RM, Stamatoyannopoulos J, Snyder M, Dunham I, Hardison RC, Bernstein BE, Gingeras TR, Kent WJ, Birney E, Wold B, Crawford GE. 2011. A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS Biol* **9**(4):e1001046. (link)

Talks

Note: * indicates presenting author.

4. **Marinov GK**, Trevino AE, Xiang T, Grossman AR, Kundaje A, Greenleaf WJ. The evolution and diversity of three dimensional genome organization across the deep eukaryotic diversity. *Biology of Genomes. CSHL*. 2020 May 5-9; Cold Spring Harbor, NY/online). (**talk**)
3. **Marinov GK**, Shipony Z, Swaffer MP, Kundaje A, Greenleaf WJ. Long-range single-molecule mapping reveals the multikilobase-scale organization of accessible chromatin in eukaryotes. *Biology of Genomes. CSHL*. 2019 May 7-11; Cold Spring Harbor, NY. (**talk**)
2. Shipony Z, **Marinov GK***, Sinott–Armstrong N, Swaffer MP, Kundaje A, Greenleaf WJ. Long-range single-molecule mapping reveals the multikilobase-scale organization of accessible chromatin in eukaryotes. *ICEB18 — 2nd Epigenetics and Bioengineering Conference (EpiBio 2018)*. 2018 October 4–6; San Francisco, CA. (**talk**)
1. **Marinov GK**. Diversity and divergence of dinoflagellate histone proteins. *Midwest Protozoology Meeting*. 2015 May 01–02; Peoria, IL. (**talk**)

Poster presentations

Note: * indicates presenting author.

4. **Marinov GK**, Williams BA, Schroth GP, Myers RM, Wold B. *Biology of Genomes. CSHL*. Single-cell RNA-seq characterization of gene expression in lymphoblastoid cells. May 7–11 2013. Cold Spring Harbor, NY (**poster**)
3. **Marinov GK**, Williams BA, Mortazavi A, Trapnell C, Reddy T, Gertz G, Patcher L, Salzberg SL, Myers RM, Wold B. Genome-wide characterization of the transcriptome in ENCODE cell lines. *Systems Biology: Global Regulation of Gene Expression. CSHL*. March 23–27 2010. Cold Spring Harbor, NY (**poster**)
2. **Marinov GK**. 2006. Cellular Responses to 3-methyladenine DNA lesions. *The BioTECH*, **5**(1).
1. **Marinov GK**, Shah, D., and Samson, LD. Cellular Responses to 3-methyladenine DNA lesions. *BMES-Merck*, MIT, Cambridge, MA, USA, November 2006. (**poster**)

Honors and Awards

- First Prize at the National Biology Olympiad of Bulgaria in 2001, 2002, 2003, 2004.
- Bronze medal at the International Biology Olympiad in 2003.
- Silver medal at the International Biology Olympiad in 2004.
- Bulgarian National Fellowship for Excellence in Studies in 2004.
- Stanford School of Medicine Dean's Fellowship, 2018.

Funding and grants

Comprehensive genomic characterization of dinoflagellates and their nuclei. Xiang T, Zheng X, **Marinov GK**. Carnegie Institution for Science Seed Grant. 2019. $5,000.

Courses Taught

California Institute of Technology (teaching assistant)

- Bi 10. Cell Biology Laboratory – 2009, 2010
- Bi 188 Human Genetics and Genomics – 2011, 2013
- Bi 206. Biochemical and Genetic Methods in Biological Research – 2012

Stanford University

- Genetics/Developmental Biology Training Camp – 2017, 2018, 2019, *2020**.