BIOGRAPHICAL SKETCH

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NAME: Zohar Shipony

eRA COMMONS USER NAME (credential, e.g., agency login): ZHENGZUO1

POSITION TITLE: Postdoctoral Researcher

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Tel-Aviv University, Tel-Aviv, Israel	B.S.	06/2008	Biology
Weizmann Institute of Science, Israel.	M.S.	07/2010	Biology
Weizmann Institute of Science, Israel.	PhD	08/2016	Genetics
Stanford University, CA, U.S.	Postdoc		Genetics

A. Personal Statement

My past research focused on DNA methylation and the rate of epigenetic mutation in cancer and normal cells. My current research and interests focus on the various parts that make transcription work, starting from the components of the enhancer that activates gene expression through PolII that creates the RNA molecules.

B. Positions and Honors

EMBO Fellowship award – 2016
HFSP Fellowship award – 2016

08/24/2018 – present Postdoctoral fellow in the laboratories of William J. Greenleaf, Department of Genetics, Stanford University School of Medicine, CA

C. Contributions to Science

Development of UMI-RRBS, a quantitative method bisulfite sequencing platform.

Disocvering the differences between somatic and embryonic stem cells in maintaining epigenetic memory and calculating the epigenetic mutation rate of somatic cells.

Development of SMAC-seq, a single molecule DNA accessibility method.

D. Additional Information: Research Support and/or Scholastic Performance

Shipony, Z., Marinov, G.K., Swaffer, M.P., et al. 2018. Long-range single-molecule mapping of chromatin accessibility in eukaryotes: Supplemental Tables and Figures. BioRxiv.

Klemm, S.L., Shipony, Z. and Greenleaf, W.J. 2019. Chromatin accessibility and the regulatory epigenome. Nature Reviews. Genetics 20(4), pp. 207–220.

Tovy, A., Spiro, A., McCarthy, R., et al. 2017. p53 is essential for DNA methylation homeostasis in naïve embryonic stem cells, and its loss promotes clonal heterogeneity. Genes & Development 31(10), pp. 959–972.

Shipony, Z., Mukamel, Z., Cohen, N.M., et al. 2014. Dynamic and static maintenance of epigenetic memory in pluripotent and somatic cells. Nature 513(7516), pp. 115–119.

Gafni, O., Weinberger, L., Mansour, A.A., et al. 2013. Derivation of novel human ground state naive pluripotent stem cells. Nature 504(7479), pp. 282–286.

Rais, Y., Zviran, A., Geula, S., et al. 2013. Deterministic direct reprogramming of somatic cells to pluripotency. Nature 502(7469), pp. 65–70.

Tal, O., Lim, H.Y., Gurevich, I., et al. 2011. DC mobilization from the skin requires docking to immobilized CCL21 on lymphatic endothelium and intralymphatic crawling. The Journal of Experimental Medicine 208(10), pp. 2141–2153.

Zeevi, D., Sharon, E., Lotan-Pompan, M., et al. 2011. Compensation for differences in gene copy number among yeast ribosomal proteins is encoded within their promoters. Genome Research 21(12), pp. 2114–2128.