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To whom it may concern

I am happy to write in support of the Stanford ChEM-H 2019 Seed Grant Competition proposal by Georgi Marinov, Zohar Shipony and Zheng Zuo titled "Single-molecule methods for direct base-pair mapping of *in vitro* and *in vivo* protein-DNA interactions".

My lab has deep interest and extensive history in developing new methods for mapping and studying chromatin structure, including chromatin accessibility, local chromatin folding, three-dimensional genome interactions, RNA-DNA interactions, and a number of other aspects of physical genomic organization.

Georgi and Zohar are postdoctoral scholars in my lab (Georgi is also co-advised by Prof. Anshul Kundaje). Both of them have extensive experience developing and applying high-throughput functional genomics technique, are highly skilled at both generating and analyzing the resulting datasets, and have been at the forefront of developing the long-read single-molecule chromatin accessibility mapping methods on which this proposal is based.

Our group currently collaborates extensively with both the Kundaje and the Fordyce labs on multiple other projects. This will be our first collaborative effort across all three groups bringing their combined genomics, biophysics and machine learning expertise together. The techniques for direct mapping of protein-DNA interactions outlined in the proposal will be a major further advance in the field and I am very excited for my lab to be part of their development.

I will be happy to provide the resources of my lab in support of this project, including cell culture facilities, lab space, molecular biology and biochemistry equipment, and Illumina and Oxford Nanopore sequencing instruments. I will also provide additional funding if necessary to bring some aspects of the project to completion, as well as in support of the future development of this line of research.

Sincerely,

William James Greenleaf, Ph.D.
Associate Professor
Department of Genetics and, by courtesy, Applied Physics
Stanford University