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To the faculty search committee:

I am very happy to support Dmitri Papatsenko's application for a faculty position in your department. My research interests lie in the molecular mechanisms that control patterns of transcription in the early *Drosophila* embryo. I met Dmitri three years ago when he moved to our department as a member of the Claude Desplan laboratory. I am very familiar with his work, and have in fact started a collaboration with him in the last year.

Dmitri's main interest is in understanding the cis-elements that control transcriptional decisions. In the last twenty years, many investigators have addressed this question by studying the DNA binding characteristics of single proteins, or the cis elements that control the expression patterns of single genes. Dmitri has been part of this effort, having analyzed the transcription of the rhodopsin gene family in *Drosophila*. This work has led to the discovery of a new rhodopsin (rh8), which was published in *Development*. In subsequent work, he has identified specific cis elements that are common to all rhodopsin genes, and others that control the expression of specific rhodopsins in specific cell types. This work goes a long way toward describing how individual members of gene families acquire different patterns of transcription, and was published in *Mechanisms of Development*.

Similar studies in many labs have resulted in the identification of DNA-binding sites for about one hundred transcription factors. These studies have greatly increased our knowledge of the nature of regulatory sequences, but it is clear that much is still unknown. To better understand transcriptional regulation Dmitri is applying statistical methods for analysis of existing expression and sequence data. He and his coworkers have assembled a database containing all reported binding sites and cis-regulatory modules for twenty developmental genes of *Drosophila*. They have further used this information to design specific computational tools dedicated to mapping binding sites, binding site clusters, and cis-regulatory modules in *Drosophila*.

The complete sequences of several genomes suggest that higher animals and plants contain upwards of one thousand transcription factors. This suggests further that in vivo transcription mechanisms are much more complicated than previously thought. Advanced computational methods will be required to understand these complexities. Dmitri is at the forefront of this effort. His strategy involves extraction of regulatory

information from eukaryotic promoters and experimental validation of the detected biological signals.

In my opinion, Dmitri will excel as an independent researcher in this field because he represents a bridge between the experimentalists and the mathematicians who are interested in the regulation of transcription. In the last few years, he has gained hands-on experience in the techniques used by both, which should enable him to make really important contributions in the very near future. Our collaboration with Dmitri has really crystallized the way we currently think about the mechanisms that turn our particular enhancers on and off.

On a personal level, Dmitri is a very likeable person who fits in well here at NYU. He is a good citizen who is willing to help other researchers and students. I have heard him present his data several times, and he really shows enthusiasm for his research. He is a native Russian, and speaks with some accent, but this does not hinder his ability to communicate at all.

In summary, I believe Dmitri is an excellent candidate for an independent faculty position, and I recommend him with no reservations. If you need more information, please feel free to contact me directly.

Sincerely,

A handwritten signature in black ink, appearing to read 'S Small', written in a cursive style.

Stephen Small
Associate Professor of Biology
New York University