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Letter of Recommendation for Dr. Dmitri Papatsenko

Dear Sir/Madam,

I am writing this letter on behalf of Dr. Papatsenko who is currently being reviewed by your university for a possible faculty position. I have known Dr. Papatsenko for almost two years starting when he was an Associate Research Scientist in Claude Desplan's group. At the very outset, I'd like to state that even if I have known Dr. Papatsenko only for a relatively short time (after a chance meeting after his talk at Courant's Genomics seminar), I am very impressed by his depth of understanding of biological and mathematical ideas, ability to learn and integrate new material, to formulate research problems very clearly and to suggest innovative solutions that go beyond the state of the art in the field. Comparing him with other genomicists and biologists at the same level, I'd rate him among the very top few per cent.

His research in Molecular and Computational biology centers around various aspects of the following fundamental question: how can one understand the spatio temporal regulation of specific transcription in higher eukaryote by analyzing the sequence structure in the available genomic sequences? In particular, how far can one go in identifying promoter sequences from Drosophila genome sequences when the computational methods are coupled to molecular and developmental methods of genetics. Towards this end he has implemented (with some of his mathematical colleagues) an algorithm called Scanseq and by applying these algorithms (initially using PWM matrices to model sequence patterns), Dr. Papatsenko has gained many deep insights to both computational algorithms and biological mechanisms.

To explore the obvious consequences of these insights, he plans to integrate more powerful methods of describing patterns using Hidden Markov Models, understand the local recurring structures using Wavelets and provide a multi-scale analysis. In our discussions, following my suggestions he also plans to extend these methods to include "basis pursuit" algorithms. The results of these improved algorithms are expected to be very exciting.

He communicates his ideas very clearly and is an easy person to work with. He has a very wide background covering many areas of biology, statistics and computer science. I am very sure that he will prove to be an influential and successful researcher in his field.

I strongly recommend that Dr. Papatsenko be considered very favorably for the position he has applied for.

Yours sincerely,

B. Mishra

Professor of Computer Science & Mathematics (Courant, NYU) • Professor (Cold Spring Harbor Lab) • Professor of Human Genetics (Mt. Sinai School of

Medicine) • Co-director of

Center for Comparative Functional Genomics(NYU)