Approved by the Regents
May 20, 2021

# PROMOTION RECOMMENDATION
# THE UNIVERSITY OF MICHIGAN
# MEDICAL SCHOOL
# DEPARTMENT OF BIOLOGICAL CHEMISTRY
# DEPARTMENT OF COMPUTATIONAL MEDICINE AND BIOINFORMATICS

Peter L. Freddolino, Ph.D., assistant professor of biological chemistry, Department of Biological Chemistry, and assistant professor of computational medicine and bioinformatics, Department of Computational Medicine and Bioinformatics, Medical School, is recommended for promotion to associate professor of biological chemistry, with tenure, Department of Biological Chemistry, and associate professor of computational medicine and bioinformatics, without tenure, Department of Computational Medicine and Bioinformatics, Medical School.

Academic Record:

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| Ph.D. | 2009 | University of Illinois at Urbana-Champaign |
| B.S. | 2004 | California Institute of Technology |

Professional Record:

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| 2015-present | Assistant Professor of Biological Chemistry, University of Michigan |
| 2015-present | Assistant Professor of Computational Medicine and Bioinformatics, University of Michigan |

Summary of Evaluation:

Teaching: Dr. Freddolino has mentored 13 graduate students, four undergraduate students, five post-doctoral fellows, two visiting scholars, and 18 rotating graduate students. With the exception of the undergraduates, all of these mentees have published peer-reviewed articles and have continued on to further educational training or faculty positions in their chosen field. Dr. Freddolino redesigned the curriculum for the Bioinformatics 524/525 class when he became course director in 2018. Under his leadership, the class has nearly doubled, from 40 students in winter of 2017 to approximately 80 students in winter 2020. In addition, Dr. Freddolino has provided the biochemistry lectures for the first year medical school gastrointestinal sequence and has redesigned these lectures.

Research: Dr. Freddolino advances the research capabilities of our institution by bringing a unique set of modern approaches to our community. He is expert at both experimental and computational methods for analyzing large data sets, often referred to as "big data." His research involves developing experimental and theoretical tools to understand and manipulate cellular decision making, generating quantitative and predictive models of cellular regulatory and metabolic networks. He has focused his efforts to date on defining the logic and evolution of bacterial regulatory networks, and the interplay between bacterial chromosomal structure and gene regulation. Importantly, he also uses the tools he develops to address key problems in multiple fields through a growing network of collaborators.

Already a prolific and well-cited author when he was first appointed, Dr. Freddolino has continued his strong productivity as an assistant professor, producing 22 peer-reviewed publications, all in front-line journals, with a few publications at the highest level in his field, including *Cell*, and *Cell Systems*. His work is very well supported by NIH and NSF grants, where he currently serves as the principal investigator or co-principal investigator on three awards. Dr. Freddolino has significant funded effort as a co-investigator on a computational structural biology project with his close collaborator in DCMB, Dr. Yang Zhang, and as a core faculty member on the new Bioinformatics T-32 Pre-doctoral training grant.

Recent and Significant Publications:
Zhang C, Freddolino PL, Zhang Y: COFACTOR: improved protein function prediction by combining structure, sequence and protein-protein interaction information. *Nucleic Acids Res* 45(W1): W291-W299, 01/2017. PM28472402/PMC5793808

Kroner GM, Wolfe MB, Freddolino PL: *Escherichia coli* Lrp regulates one-third of the genome via direct, cooperative, and indirect routes. *J Bacteriol* 201: e00411-418, 01/2018. PM30420454/ PMC6349092

Scholz SA, Diao R, Wolfe MB, Fivenson EM, Lin XN, Freddolino PL: High-Resolution Mapping of the *Escherichia coli* Chromosome Reveals Positions of High and Low Transcription. *Cell Systems* 8(3): 212-225. e9, 01/2019. PM30904377/PMC6508686

Walker DM, Freddolino PL*, Harshey RM: A Well-Mixed *E. coli* Genome: Widespread Contacts Revealed by Tracking Mu Transposition. *Cell* 180(4): 703-716.e18, 01/2020. PM32059782

Wolfe MB, Schagat TL, Paulsen MT, Magnuson B, Ljungman M, Park D, Zhang C, Campbell ZT,Goldstrohm AC, Freddolino PL: Principles of mRNA control by human PUM proteins elucidated from multi-modal experiments and integrative data analysis. *RNA*, (in press, 09/2020)

Service: Dr. Freddolino is a member of six departmental or institutional committees, including co-chair of the Biological Chemistry Admissions Committee, a member of the DCMB Diversity, Equity, and Inclusion (DEI) committee, and serves on the Medical School's Basic Science IT (BRIT) committee. Nationally, he has served on an NIH study section (ad hoc), is a member of the editorial board for *Scientific Reports*, is on the advisory board of a major scientific web site (*Ecocyc/Biocyc*), has served as invited session chair for two major scientific meetings in his field, and reviews manuscripts for a large number of journals.

External Reviewers:
Reviewer A: "Overall, Dr. Freddolino is a very accomplished researcher with excellent funding, publication and training records. He has already made important contributions to our understanding of regulatory principles of gene expression in a natural cellular context, asking difficult questions and developing tools to address them. Without doubt, Dr. Freddolino is on the right trajectory. His closest peer, at a similar career stage and research area, is Dr. Joseph Wade (Wadsworth Center) who uses genome-wide approaches to study transcription networks in enteric bacteria. While both investigators are strong candidates for tenure, Dr. Freddolino's research is more impactful, as it addresses fundamental questions applicable beyond the bacterial kingdom and utilizes an unusually diverse range of approaches, including advanced computation."

Reviewer B: “This is an easy and clear-cut example of a very productive and collaborative investigator who is having a large impact on our understanding of how microbial genomes are structured, particularly in relation to gene expression…Overall, Dr. Freddolino has demonstrated that he is an expert on genome-wide studies of bacterial chromosomal architecture and gene expression.”

Reviewer C: “Dr. Freddolino bridges several fields: he is a sophisticated bioinformatician and an experimentalist who can devise cutting edge approaches and evaluate next-generation sequencing data like few bench scientists. I have been extremely impressed with his ability to bring genome-wide approaches to the study of chromosome structure.”

Reviewer D: “Finally, I will add that Peter’s lab has also helped drive the development of an important new software tool called COFACTOR, that enables excellent protein function prediction. I spoke with Peter at length about this tool and its capabilities during a visit to Michigan more than a year ago now and came away with the sense that this tool is going to be very powerful in a number of applications. And again, it highlights Peter’s accomplishments and prowess as a computational biologist. I think he is every bit as good as his postdoc advisor, who is generally regarded as a leader in this area.”

Reviewer E: “The most notable aspect I would highlight is the depth and breadth of expertise Dr. Freddolino has in a variety of sub-fields within the umbrella of Biological Chemistry including structural biology, chemical biology, bioinformatics, systems biology, and cell biology. He routinely leverages a wide variety of disparate but complementary experimental methodologies to address novel questions in several important fields including chromosome structure as it relates to gene regulation and antibiotic resistance. Dr. Freddolino is not a ‘one-trick pony’….he’s more of a ‘ten-trick pony.’”

Reviewer F: “I expect that Peter’s research trajectory will only continue to be more insightful, innovative, and fruitful in the coming years, as well as perhaps to venture into new areas in system biology, genome organization, and structural biology.”

Reviewer G: “I am impressed with Dr. Freddolino’s scholarly activity. His long-term aim of understanding bacterial regulatory networks and their interactions well enough to create quantitative, predictive models of cellular behavior is a challenging undertaking, and Dr. Freddolino’s systems biology approach is proving to be a fruitful one…I would rank Dr. Freddolino at or near the top of his peer group who are working in the same field.”

Reviewer H: “In summary, Dr. Freddolino is a highly productive faculty member. His research accomplishments are comparable to leading researchers of his career stage in the field of bioinformatics. If he were considered for promotion in my department, he would definitely meet the research requirements here. Hence, I fully support the tenure and promotion of Dr. Freddolino to the rank of Associate Professor at your university. I also see he has great potential to achieve much more in his future career path.”

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### Summary of Recommendation:

Dr. Freddolino has already made important contributions to the fields of biological chemistry and computational medicine and bioinformatics. He is a pioneering researcher, and successful mentor and instructor. I am pleased to recommend Peter L. Freddolino, Ph.D. for promotion to associate professor of biological chemistry, with tenure, Department of Biological Chemistry, and associate professor of computational medicine and bioinformatics, without tenure, Department of Computational Medicine and Bioinformatics, Medical School.

Marschall S. Runge

Marschall S. Runge, M.D., Ph.D.
Executive Vice President of Medical Affairs
Dean, Medical School

May 2021