CeNT-18-2021

Director of Centre of New Technologies of the University of Warsaw, with the Project Leader, announce opening of the competition for the position of PhD Student in the Laboratory of Functional and Structural Genomics – Centre of New Technologies of the University of Warsaw.

JOB OFFER

Position in the project:	PhD Student
Laboratory:	Laboratory of Functional and Structural Genomics
Scientific discipline:	Life Sciences, Exact and Natural Sciences
Keywords:	Computational Genomics, Bioinformatics, Molecular Biology, next generation sequencing, replication stress, genetic instability, DNA double-strand breaks, genomics, chromatin loops, mammalian 3D genome, Topologically Associating Domains, cell differentiation, chromatin higher order organization, human genome. Bioinformatics, computational genomics, molecular biology, genomics, the next generation sequencing, experimental work, data analysis
Job type (employment contract/stipend):	PhD stipend
Part-time/full-time:	Full time
Number of job offers:	1
Remuneration/stipend amount/month:	4000 PLN gross gross
Position starts on:	Oct 1st 2021 or as soon as possible and formally allowed
Maximum period of contract/stipend agreement:	36 months with the possibility of extension up to 1 additional year
Institution:	Centre of New Technologies, University of Warsaw
Project leader:	Prof. dr hab. Dariusz Plewczyński
Project title:	Multiscale spatial reorganization of chromatin in response to replication stress and its role in cellular protection against genomic instability
Competition type:	OPUS
Financing institution:	NCN
Project description:	One of the greatest breakthroughs in biology was the discovery of the structure of our genetic material - DNA. It consists of very long threads built by small blocks, called nucleotides, which form genes and various elements regulating genes' activity. Physical characteristics and the proper functioning of our organism depend on their linear sequence. Strikingly, in every human cell, DNA, which is around two meters long, is packed in a tiny nucleus with a diameter of only ten micrometers. In addition to the order of nucleotides in the genome, it has been recently discovered that the way in which DNA is folded in the cell nucleus also

	influences numerous cellular processes, as it determines the spatial interactions between the given elements of DNA. This means that cells performing distinct functions in the organism will differ in their three-dimensional DNA organization. Importantly, recent scientific findings indicate that disruption of the 3D interactions between specific DNA fragments can cause many human diseases, including cancer. The three-dimensional DNA structure is, among other things, closely related to replication - a fundamental process through which a faithful copy of the whole genetic material of a cell (termed genome) is generated before each cell division. However, various internal and external factors can interfere with the replication process, eventually causing it to slow down. This situation is called replication stress, and it can lead to serious DNA damage, including chromosome breakage. Replication stress is one of the main causes of the phenomenon known as genetic instability, associated with increased frequency of mutations and other changes in the DNA. It is a characteristic feature of most cancers and has been found to contribute to the development of a number of other diseases such as neurodevelopmental disorders and neurodegenerative diseases. The main aim of this project is to determine how the spatial organization of the genome changes upon replication stress and how these changes help to protect the cell from the harmful consequences of this stress. By using the most modern methods relying on next-generation sequencing, we will compare the three-dimensional structure of the genome in correctly replicating cells and those exposed to replication stress. DNA regions that are particularly susceptible to stress-related damage will also be identified allowing to generate a comprehensive, genome-wide map of fragile sites in human cells. It will enable us to determine the characteristic features of those sites and subsequently to get novel insights into the causes of their breakage. In addition, we will investigate the consequences of permanent 3D changes emerging in cells due to replication stress in terms of their potential contribution to the development of cancer. Based on the obtained results, a computational model, determining genomic sites, where the damage may initiate or stimulate the development of cancer, will be created. Additionally, we will develop new tools enabling modeling of structural elements of DNA such as single DNA loops and dynamics of their formation. The execution of the project will significantly broaden our understanding of the mutual relations between replication stress, the spatial structure of the genome, and genetic instability. In addition, the obtained results can potentially be used in the diagnosis and therapy of diseases associated with chromosome fragility, such as cancer, autism, or mental developmental disorders.
Key responsibilities include:	1. Computational genomics data analysis for iBLESS, ChIA-PET, ChIA-Drop, Hi-C and HiChIP experimental data; 2. Three-dimensional computational modeling using ChIA-PET, ChIA-Drop, Hi-C and HiChIP experimental data; 3. Statistical analysis of epigenomic data, ATAC-seq, ChIP-seq, RNA-seq experimental data; 4. Analyzing the simulations results, formulating biological hyphothesis; 5. Commitment and full-time effort to the project; 6. Initiative in identifying and resolving problems relating to the research; 7. Management of His or Her work efficiently and increase the visibility through the publications; 8. Active participation in weekly lab meetings, scientific seminars and international conferences; 9. Publications and individual Young Researchers grants preparation

Profile of candidates/requirements:	Essential qualifications: The competition is open for persons who meet the conditions specified in the regulations on the allocation of resources for the implementation of tasks financed by the National Science Centre for OPUS 19 grant. - MSc degree in computer science, biophysics, genomics, bionformatics or related discipline. The MSc degree should be obtained before the date of employment in the project. We can wait till MSc thesis defense, if needed; - Confirmed status of a PhD student in bioinformatics / molecular biology / genomics. We can wait till PhD student status is acquired, if needed; - Excellent knowledge of English; - Team work skills and experience; - Documented experience with the whole genome sequencing and preferably epigenomics or 3D genomics datasets; - Bioinformatics and basic knowledge of chromatin-related genomics tools used in DNA sequencing, epigenomics, RNAseq, ATAC-seq data analysis, HiC, HiChIP, ChIA-PET, iBLESS; - Essential requirements cover the ability to work in collaboration with others, within a large research team, performing several parallel scientific tasks, independent thinking and finally the ability to deliver publishable results; - Needed the highly motivated individuals willing to work in an interdisciplinary environment under stress and with strict deadlines. Additional qualifications: - Priority will be given to candidates with expertise relevant to the OPUS project and in agreement with the general profile of the laboratory. Preliminary work done by applicant in the context of 3DGenomics will be treated as the strong asset. - Additionally, some wet lab experience will be welcomed, such as performing RNA-seq, ChIP-seq, ATAC-seq, iBLESS experiments or 3d genomics ChIA-PET, Hi-C and Hi-ChIP experiments.
Required documents:	1. Cover letter describing Candidate motivation; 2. Current curriculum vitae; 3. Copy of MSc certificate (or, if the MSc certificate has not been obtained yet, a certificate/document about the date of MSc defense); 4. Signed information on the personal data processing: 5. Motivation letter (why I would like to join 3DGenomics field?); 6. Letters of support from two or more scientists who are familiar with the Candidate (submitted directly to e-mail address below);

	7. Short written review-type document about recent advances in 3D genomics; 8. List of publications and conference presentations. 9. Document confirming the status of PhD Student (to be provided on the date of employment in the project, at the latest)
We offer:	• an opportunity to participate in an interdisciplinary project spanned across biology, physics and bioinformatics in the novel discipline of 3D genomics; • a unique multidisciplinary workplace in one of the best scientific institutions in Poland; • stimulating, young and friendly work environment; • access to the state-of-art NGS and computational equipment; • comprehensive training in molecular biology, bioinformatics, computational genomics, chromatin and 3D genomics; • opportunities for interdisciplinary and international collaborations; • possibility of further personal and scientific development. ***3D replication OPUS*** project provides unique opportunities for interdisciplinary work between molecular biology, biophysics, and bioinformatics, as well as well-established and long-lasting international collaborations with recognized academic institutes and universities in US, China and EU. Close collaboration with industry will be present as well. We provide also the access to modern 1D and 3D genomics equipments and support from other experienced researchers. International partners will be co-supervising your work at the laboratory.
Please submit the following documents to:	Prof. dr hab. Dariusz Plewczynski e-mail: d.plewczynski@cent.uw.edu.pl (entitle your email "PhD POSITION") www: https://4dnucleome.cent.uw.edu.pl
Application deadline:	15 September 2021
Date of announcing the results:	Not later than 30 September 2021
Method of notification about the results:	e-mail