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T X Gabriela Chiosis Lab
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What can we help you find today?

Bioinformatics postdoctoral scientist

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C Bioinformatics postdoctoral scientist available immediately in a multidisciplinary team studying maladaptive changes in proteome-wide protein-protein interaction networks in disease. These efforts will be conducted in collaboration with scientists and clinicians at Memorial Sloan Kettering Cancer Center, New York University Grossman School of Medicine, Weill Cornell Medical College, Nathan Kline Institute, and Columbia University, Taub Institute for Research on Alzheimer's Disease and the Aging Brain.

When people consider disease etiology, they often think about genetic or pathological causes of disease. To us, these are one of the many stressors that can affect the way cells behave. These changes, intrinsic to the cell or its milieu or the organism as a whole, accumulate over a lifetime, eventually leading to proteome changes, causing malfunction. This in turn has a negative effect on cell behavior and its network connections. In this context, we think of disease states as embodiments of exposure of cells to stressors. Understanding adaptive and maladaptive responses to stressors and how these differ between normal and diseased tissues remains unsatisfactorily addressed. A key to addressing this unresolved biological question is to study how stressors impact tissue-specific interactomes, the intricate proteome-wide cellular networks of proteins linked through interactions. In this context interactomes are maps of how stressors, including genetic lesions, proteotoxic and environmental insults, individually or combined, alter protein-protein interaction networks and perturb the system as a whole.

Our program takes advantage of properties of protein-protein interaction networks (i.e., interactome networks) to understand, diagnose and treat diseases, such as cancer and neurodegenerative diseases. We aim to investigate the identity and the architecture of interactome networks in cells exposed to chronic molecular and environmental stressors with the goal of understanding disease mechanisms and identifying vulnerabilities. Our multidisciplinary approach aims to take advantage of these vulnerabilities to discover and develop drug candidates, biomarkers, diagnostics, and treatment strategies. Compounds and diagnostics discovered by our team are currently in clinical evaluation in cancer and Alzheimer's disease. (<https://www.chiosislab.com/pipeline>).

This project we seek to fill this position for will combine tools from proteomics, chemical biology, network medicine, bioinformatics, computational biology, and experimental systems biology assays to address insights underlying molecular mechanisms and the influence of differential risk factors negatively impacting brain function at the cell, network, and connectome levels as they relate to the transition from healthy aging to pathologic neurodegeneration.

For publications relevant to this research please refer to :

- Nature Communications 2020 Jan 16;11(1):319. The epichaperome is a mediator of toxic hippocampal stress and leads to protein connectivity-based dysfunction. DOI: [10.1038/s41467-019-14082-5](https://doi.org/10.1038/s41467-019-14082-5)
- Nature Reviews Cancer 2018 Sep;18(9):562-575. Adapting to stress – chaperome networks in cancer. DOI: [10.1038/s41568-018-0020-9](https://doi.org/10.1038/s41568-018-0020-9)
- Nature 2016 Oct 20;538(7625):397-401. The epichaperome is an integrated chaperome network that facilitates tumour survival. DOI: [10.1038/nature19807](https://doi.org/10.1038/nature19807)
- Cell Reports 2020 Jun 30;31(13):107840. Molecular Stressors Engender Protein Connectivity Dysfunction through Aberrant N-Glycosylation of a Chaperone. DOI: [10.1016/j.celrep.2020.107840](https://doi.org/10.1016/j.celrep.2020.107840)
- Nature Communications 2018 Oct 19;9(1):4345. HSP90-incorporating chaperome networks as biosensor for disease-related pathways in patient-specific midbrain dopamine neurons.
- Molecular Neurobiology 2021. Profiling basal forebrain cholinergic neurons reveals a molecular basis for vulnerability within the Ts65Dn model of Down syndrome and Alzheimer's disease. DOI: [10.1007/s12035-021-02453-3](https://doi.org/10.1007/s12035-021-02453-3)
- FEBS Journal 2021. Disease-specific interactome alterations via epichaperomics: the case for Alzheimer's disease. DOI: [10.1111/febs.16031](https://doi.org/10.1111/febs.16031)

The successful candidate will:

- be a highly motivated researcher with a quantitative research background.
- be interested in contributing to cutting-edge research focusing on the dissection of the complex PPI network changes utilizing multi-omics data (mostly proteomics and transcriptomics)
- experience in multivariate analysis, differential expression analysis, pathway enrichment analysis and network analysis
- proficiency in data wrangling using (R:dplyr/tidyverse, Python:pandas/numpy)
- proficiency in R, Bioconductor and data visualization tools (ggplot2, plotly, Cytoscape)
- familiarity with proteomics data pipelines (DIA, DDN) and data types
- demonstrated experience in missing value imputations and data normalization
- have demonstrated ability to work independently and lead projects while also collaborating and assisting the group achieve its research goals
- some knowledge in machine learning and deep learning, experience working with cloud computing

infrastructure

Requirements:

- M.Sc or Ph.D in Bioinformatics, Computer Science, Life Sciences or related fields
- Creativity in problem solving and a team spirit
- Good communication/written skills
- Passion for science.
- Ability to work towards defined goals in an efficient, safe and scientifically sound manner.

Candidates with an ability to interact well with a large interdisciplinary team are encouraged to apply.

The fellow will receive professional and career mentorship along with opportunities to advance their own expertise to become an independent investigator.

Written applications, including a cover letter, CV and contact details of three professional referees should be forwarded to skichiosis@mskcc.org AND coratio2712@yahoo.com .

The applicant will be hired as part of the Chiosis lab at Memorial Sloan Kettering. For more information on Memorial Sloan Kettering Cancer Center and the Chiosis lab see www.mskcc.org and www.mskcc.org/chiosis

Memorial Sloan Kettering Cancer Center is located in New York City, in Manhattan's Upper East Side, adjacent to the Cornell University Weill Medical College and the Rockefeller University, and a cab drive away from New York University Grossman School of Medicine, Nathan Kline Institute, and Columbia University, Taub Institute for Research on Alzheimer's Disease and the Aging Brain. This rich scientific environment provides many unique and unparalleled research training opportunities (www.mskcc.org/education-training/postdoctoral)

To learn more about Postdoc compensation and benefits at MSK, [click here](#) .

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