Scientist/Sr. Scientist, Bioinformatics

**Research | South San Francisco, CA, United States**

**Summary:**  
As part of our commitment to bring effective therapies to patients with cancer, we are seeking a motivated computational biologist to join a new team focused on the development of personalized medicine for patients with malignant disease. Employing data from state-of-the-art genomic analyses, the bioinformatics scientist will discover molecular signatures (e.g., combinations of somatic mutations and gene expression patterns) that predict clinical response to Onyx compounds, including carfilizomib and oprozomib, in patients with multiple myeloma and solid tumors. Signatures will be derived from the genomes and transcriptomes of tumors biopsied from patients on Onyx clinical trials and of cancer cell lines exposed to Onyx drugs; publicly and commercially available genomic databases (e.g., GEO, dbGaP and NextBio) will also be employed. A second goal will be to identify novel therapeutic targets, especially for non-responsive patients. The new hire will collaborate internally with both preclinical research and clinical science in order to validate pathways associated with drug response and translate findings into clinical practice, thereby gaining rare exposure to the entire drug development process. The scientist will also collaborate externally with international academic institutions, research consortiums and CROs.  
   
**Essential/Primary Duties, Functions and Responsibilities:**

* Contribute to analysis of proprietary genomics data derived from Onyx patient samples to define predictors of drug response and to propose novel drug targets.
* Lead cancer cell line analyses:

1. Identify molecular subtypes of cancer responsive to proteasome inhibition by integrating proprietary sensitivity data with public genetic and gene expression profiles,
2. Select representative cell lines for research studies,
3. Analyze data from siRNA screens, and
4. Compare molecular profiles of cell lines and patient samples.

* Help evaluate bioinformatics software and hardware solutions for NGS analysis.
* Analyze proteomics data from patient plasma samples to define predictors of drug response.
* Mine publicly and commercially available databases to identify:

1. Pathways/targets contributing to carfilzomib activity, and
2. New disease indications for proteasome inhibition.

* Contribute to analysis of data generated from collaborative multiple myeloma genomic profiling efforts with academic institutions and research consortiums.
* Present findings internally and at research meetings.
* Publish findings in peer-reviewed journals.
* Other Duties as assigned.

**Requirements**   
   
**Work Experience:**

* Ph.D. with 0-8 years of post-doctoral industry experience.

**Functional/Technical Knowledge & Skills:**

* Mastery of Linux and at least one programming language (e.g., Java, R, C/C++ or Python). Experience with cloud computing and/or distributed compute clusters is a plus.
* Analysis on next-generation sequencing data (e.g., RNA-Seq or Exome/Whole Genome sequencing) or other very large datasets. Experience building bioinformatics pipelines is a plus.
* Basic understanding of statistics (e.g., statistical tests, multiple test corrections, linear regression). Knowledge of statistical methods related to common genetic and gene expression studies is a plus.
* Evidence of above skills and of writing proficiency from peer-reviewed publications.
* Ability to prepare and present scientific results.

**Education/Training:**

* Ph.D. in Bioinformatics, Biology, Physics, Statistics, or Computer Science with at least 5 years of bioinformatics experience.