

Position: Bioinformatics Scientist (Proteomics analysis)

(Job Code: Proteo-HG)

Description:

We are seeking highly motivated individuals interested in applying computational and bioinformatic approaches to drug discovery. The research interest is focused on developing/applying innovative data analysis capabilities to gain insights into gene networks involved in proteome homeostasis and protein mis-folding and investigate their disease relevance. The open position is for a bioinformatics scientist with extensive experience in analyzing mass-spec proteomics datasets. Other high-throughput biological datasets such as microarray data, protein-protein interaction data, RNAi data, will also be explored and integrated. This scientist will be part of a bioinformatics team working closely with cross-discipline teams including biology, pharmacology, and medicinal chemistry.

Degree level required

Recent Ph.D. of bioinformatics, computational biology, or computer science/electrical engineering with exposure of life science. A strong publication record is essential. Postdoctoral experience and biotech/pharmaceutical industry experience is a plus.

Competencies (Knowledge and Skills)

- Proficiency in mass-spec proteomics analysis is a must. Broad experience in large-scale biological -omics data analysis (e.g. microarray expression datasets, protein interaction datasets) is preferred.
- Working knowledge of pathway and network analysis.
- Knowledge and experience in machine learning and data mining is preferred.
- Proficiency in R, matlab, or equivalent statistical software.
- Good programming skills. Can independently manipulate large datasets.
- Good understanding of data analysis methods and experimental design.
- Highly analytical with good technical and problem solving skills.
- Excellent written and verbal communication skills.
- Project management experience is a plus.