The Celera Genomics Group, located in Rockville, MD, and South San Francisco, CA, is engaged principally in integrating advanced technologies to discover and develop new therapeutics. Celera intends to leverage its proteomic, bioinformatic, and genomic capabilities to identify and validate drug targets and diagnostic marker candidates, and to discover and develop new therapeutics. Its Celera Discovery System™ online platform, marketed exclusively through the Applied Biosystems Knowledge Business, is an integrated source of information based on the human genome and other biological and medical sources.

Major Responsibilities:
Provide computational analysis and algorithmic software development as part of an exceptional multi-disciplinary team of mass spectrometrists, computational chemists, medicinal chemists, biologists, computer scientists, software engineers, and mathematicians working within Celera Genomics' Informatics division. The candidate will develop algorithms that incorporate models based on probability theory, graph theory, data structures, numerical methods, simulations, mathematical modeling, SVMs, HMMs, optimization, multivariate analysis, classification, segmentation, decision trees, and neural networks. Also the candidate will provide scientific and computational support for the small molecule lead identification and optimization effort. The ideal candidate will combine a strong background in computational mathematics, an understanding of proteomics, computational chemistry, biology, and drug development, and solid interpersonal, organizational, and systems analysis skills.

Skills/Knowledge Requirements:
• PhD/MS in computational mathematics, applied mathematics, computer science, computational chemistry, or equivalent engineering or science discipline • Proficiency in mathematics, organic/computational chemistry, and software engineering domains, as well as intellectual agility and the ability to quickly assimilate new concepts • Experience in scientific domain is preferable, especially familiarity with protein informatics and structure based drug design is desirable • Familiarity with C/C++, Perl, Python, and/or Java is preferable • Experience with existing bioinformatics and computational chemistry tools and industry standards pertaining to image processing routines, large scale sequence databases, and software application development. Especially related to proteins, protein and gene expression, and peptide sequencing • Familiarity with mathematical and modeling software such as Matlab, Octave, NIHImage, and See5 is preferable • Familiarity with the following topics is a plus: QSAR, PSAR, various force field theories, 3D search, protein-ligand docking.