

Capability

Bioinformatics

Applications

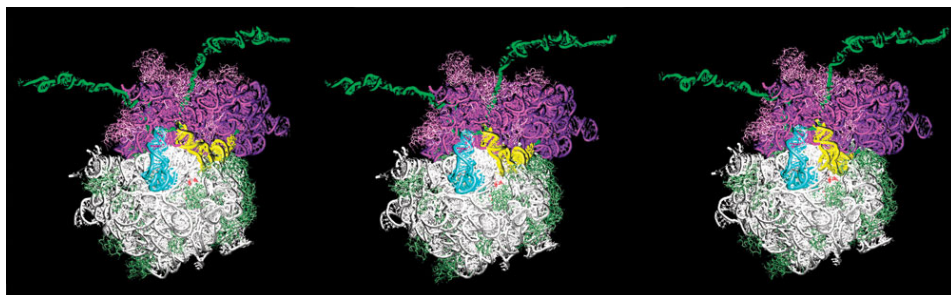
- Sequence analysis (DNA, and protein)
- Primer and probe design using unique approaches
- Protein structure elucidation
- Protein dynamics modeling
- *In silico* drug discovery
- Prediction of allosteric linkages in proteins
- Proprietary data storage, retrieval and security approaches

Benefits

- Bioinformatics capabilities without hiring in-house expertise
- U.S.-based entity with many years of experience
- Collaboration sponsors may acquire novel intellectual property
- Access to one of the largest genome sequence databases available

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Computational simulation of the function of the ribosome

Summary

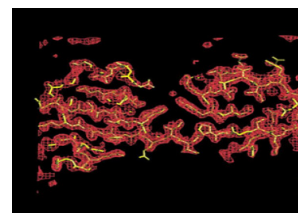
Bioinformatics is a crucial capability that allows for the testing of hypotheses quickly and easily without requiring costly and time consuming wet-lab experiments. Bioinformatics began during the 1960s at Los Alamos National Laboratory (LANL) with the kick-off of what later became the Human Genome Project. The Human Genome Project had already begun to grow out of work performed at Los Alamos before scientists met at the famous Alta Summit conference in Alta, Utah, in 1984. Given LANL's rich history in this area, many proprietary tools and approaches have been developed over the years that are accessible to companies in the pharmaceutical and biotechnology industries.

What can Los Alamos do?

The Laboratory's capabilities are wide ranging from DNA sequence analysis to protein structure and dynamics predictions. Because of LANL's ties to the Joint Genome Institute (JGI), the new organisms constantly being sequenced by JGI are being finished and annotated at Los Alamos. The suite of tools available for this pipeline is extensive and comparable to what is found in industry. Because of this, Los Alamos has the ability to compare many genomes at one time to identify novel sequences that encode new proteins and enzymes, as well as the ability to generate probes to specific regions. In fact, using our novel primer design capability, the Laboratory has developed assays to differentiate organisms within the same species with a high level of accuracy.

Proteins are another large area of focus at Los Alamos. As part of the Structure Prediction Initiative, LANL has developed strong capabilities in protein structure crystallization and structure prediction. Dr. Tom Terwilliger is leading the efforts in this area and is well-known for his contribution to the discipline by coding the application SOLVE.

To date, the largest protein dynamic simulation ever achieved was done by a LANL scientist who created a 3-D visualization of the bacterial ribosome. This work is continuing to unfold unique insights into how tRNAs move dynamically inside the ribosome to extend the protein sequence.



SOLVE/RESOLVE: electron-density map and auto-built atomic model for initiation factor 5a at a resolution of 2.1Å

Status:

Los Alamos is seeking partners interested in joint collaborations in bioinformatics to develop novel intellectual property in this area.

www.lanl.gov/partnerships/license/technologies/

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