

Bioinformatics Services

With our extensive scientific and regulatory expertise, we offer bioinformatic assessments to assist companies with characterizing and demonstrating the safety of microorganisms and microbial-derived products.

Background

Bioinformatics is crucial for addressing key scientific and regulatory questions, such as identifying genetic variations, predicting protein structures, confirming taxonomic identity, and understanding disease mechanisms.

Bioinformatics plays a vital role in research and development efforts, helping to accelerate product development, promote advancements in precision fermentation, and meet the societal shift towards a sustainable food supply.

Our solutions

Sequence Analysis (e.g., BLAST)

Comprehensive analysis of nucleotide or amino acid sequences to determine sequence homology with genes of potential concern, allergenic proteins, and other biological markers.

- Detects sequence similarity to infer homology
- Essential for bioinformatics applications
- Supports protein, DNA, and whole-genome analysis
- Genes of potential concern include toxins, virulence factors, and AMR genes
- Evaluate the potential allergenicity of a novel protein/organism

Genome Assembly

We can serve as collaborators to assist clients generate WGS data that is suitable for regulatory submission purposes.

- Essential for regulatory applications requiring product-specific WGS
- Using long and/or short-sequencing reads, genome assemblies represent the longest contiguous DNA sequences
- Genome annotation includes structural (coding vs. non-coding) and functional (homology-based) insights
- Straightforward for prokaryotes; complex for eukaryotes due to introns, exons, and splicing

Functional Annotation

By comparing protein sequences with databases of known proteins, bioinformatics can be used to predict the function of novel proteins, including the identification of active sites and binding sites.

Taxonomic identification (e.g., Phylogenetics)

Analyze specific sequences (e.g., 16s rRNA sequences, beta-tubulin) or whole genome sequences (e.g., Average Nucleotide Identity) to confirm the taxonomic identity of a microorganism.

- Prokaryotes: Requires WGS and may be supplemented with phenotypic testing
- Eukaryotes: Typically accomplished by combining phylogenetics, phenotypic testing, and WGS
- Ensures precise microbial classification for research and regulatory purposes

Secondary Metabolite Analysis

Identify Biosynthetic Gene Clusters involved in the production of secondary metabolites (e.g., mycotoxins, antibiotics, terpenes).

- Uses sequence analysis to detect nucleotide or protein sequences directly involved in metabolite production
- Analyzes complex biosynthetic pathways, including enzymes, cofactors, and regulators
- In-depth identification of BGCs for targeted secondary metabolites
- Literature-based gene identification for specific metabolite biosynthesis
- Focus areas include mycotoxins, biogenic amines, and antibiotics

Structural Modeling

Predict the 3D structure of proteins providing insights into their stability, folding, and potential interactions with other molecules.

- **Protein Modeling**
 - Visualize 3D structure of proteins based on amino acid sequence
 - Structural similarity on 3 dimensions

Stability and Degradation

Predict the stability of proteins under different conditions and their degradation products.

Customized Analysis

- Phenotype predictions
- Comparative genomics
- Transcriptomics
- Intrinsic AMR



The Intertek advantage

With over 30 years of scientific and regulatory expertise, Intertek provides customers with industry-leading risk assessments and scientific evaluation services.

Our record of success in regulatory approvals, and our strong relationships with regulatory authorities, provide the ideal foundation for companies applying for innovative compliance processes and techniques including bioinformatic assessments.

Total Quality. Assured.

For more information

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