



CALL FOR PAPERS

ICAFG 2022
Dec 13-14, 2022
Rome, Italy

The International Research Conference is a federated organization dedicated to bringing together a significant number of diverse scholarly events for presentation within the conference program. Events will run over a span of time during the conference depending on the number and length of the presentations.

ICAFG 2022 : International Conference on Advances in Functional Genomics is the premier interdisciplinary forum for the presentation of new advances and research results in the fields of Advances in Functional Genomics. The conference will bring together leading academic scientists, researchers and scholars in the domain of interest from around the world. Topics of interest for submission include, but are not limited to:

Functional genomics

Advances in functional genomics

Comparative analysis of protein-encoding genes in an evolutionary context

Discovery of lineage-specific and/or tissue-specific noncoding rnas

Prediction and characterization of protein-protein interactions

Discovery of promoters driving temporal or tissue-specific gene expression

Comparative analysis of photosynthetic pathways (c3, c4, and crassulacean acid metabolism)

Evolutionary analysis of genes involved in secondary metabolism

Signal transduction in plant-microbe/insect interactions and plant response to abiotic stress and climate change

Functional elucidation of regulatory genes and key enzymes based on integrative genomics

Development of new computational tools (programs, servers, and databases) for comparative genomics

Big data analysis tools for genomics research

translational bioinformatics

Specific molecular and pathway analysis

Computational systems biology

Bioinformatics algorithm

Medical and health informatics

Integrative data analysis

Genome annotation and comparative genomics

Traditional bioinformatics

Sequence analysis, comparison and alignment methods

Motif, gene and signal recognition

Molecular evolution, phylogenetics and phylogenomics

Determination or prediction of the structure of rna and protein in two and three dimensions;

Inference/ reconstruction of metabolic/ regulatory networks or models

Analysis of high-throughput biological data

