



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

