

In-House Projects

| Sl No. | Project Title | Collaboration |
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| 1 | Stress tolerance in Rice: Substrate specificity of detoxifying protein and their induction by regulatory proteins | GKVK, UAS, Bangalore |
| 2 | Study on effects and role of regulatory proteins under oxidative stress in resistant and susceptible rice varieties | GKVK, UAS, Bangalore |
| 3 | Differential gene expression studies on abiotic stress in <i>Oryza sativa</i> . | GKVK, UAS, Bengaluru |
| 4 | Identification of spliceosomal variants from transcriptome data of resistant and susceptible rice varieties | GKVK, UAS, Bengaluru |
| 5 | In silico screening of small molecules to promote tuberization in <i>Solanum tuberosum</i> | GKVK, UAS, Bengaluru |
| 6 | Mitogen activated protein kinase-1 and cell division control protein-42 are putative drug targets for the binding of novel natural lead molecules: A therapeutic intervention against <i>Candida albicans</i> | DSCE, Bengaluru |
| 7 | Carbon fullerene act as potential lead molecule against prospective molecular targets of biofilm-producing multi-drug resistant <i>Acinetobacter baumannii</i> and <i>Pseudomonas aeruginosa</i> : Computational modeling and MD simulation studies | St. Pius X college, Kasaragod |
| 8 | "Transcriptome study of susceptible and resistant variety to identify expression levels of kinases, ribosomal factors and Transcription factors" | GKVK, UAS, Bengaluru |
| 9 | "Algorithm development to study preferential interaction pattern and biological significance of protein-protein interactions." | PDBe, EBI, UK |
| 10 | An efficient pipeline for structural analysis variant detection using common workflow language. | Pathogen Informatics lab, EBI, UK |
| 11 | Rice expression atlas: A database for BPT201 and TN4 varieties of <i>Oryza sativa</i> | GKVK, UAS, Bengaluru |
| 12 | Tool development for integrated analysis of omics data | In-house |
| 13 | Plant mineral-nutrient information system | GKVK, UAS, Bengaluru |
| 14 | Role of Abscisic acid in plant growth and regulation | GKVK, UAS, Bengaluru |
| 15 | "Re-profiling of natural inhibitor via combinatorial drug screening: Brefeldin A variant design as an effective antagonist leading to Epac2 structure modification and antibody design for identification " | In-house |
| 16 | "Preliminary Analysis of RNA-Seq Data in Females Reveals Novel Mutant Genes Significantly Expressed in Alzheimers disease" | In-house |

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| 17 | Analysis of Non-Mutating Regions and Clustering of tuberculosis sample | In-house |
| 18 | Socks metagenome analysis | BAMU, Aurangabad |
| 19 | Sanitary pads metagenome analysis | BAMU, Aurangabad |
| 20 | Solanum tuberosum RNA Seq data analysis | GKVK, UAS, Bengaluru |
| 21 | Metagenome Profiling of anterior uterine samples to improve In-vitro fertilization success ratio | BAMU, Aurangabad |
| 22 | Tracing the occurrence of API and resistant bacteria from effluents of bulk antibiotic industries from bangalore | In-house |
| 23 | 3D-QSAR analysis of plant derivatives with BrefeldinA and cAMP for effective interaction with Epac2 | In-house |
| 24 | RNA-seq analysis for understanding recurrence of glioma in brain tumour cases. | IISc, Bengaluru |
| 25 | Small molecule discovery for SLAC1 and ALMT12 | RCB, Faridabad |
| 26 | Watermelon QTL seq analysis | IAHR, Bengaluru |
| 27 | SASA integration to MD analysis tool | In-house |
| 28 | Mitochondrial metagenomic analysis | BAMU, Aurangabad |
| 29 | NF-kB work | BBC |
| 30 | Deciphering the relevance of repurposing of the potential drugs towards major molecular targets of SARS-CoV-2: Molecular mechanisms of therapeutic modeling by molecular docking and dynamic simulation studies | St. Pius X college, Kasaragod |
| 31 | Natural lead molecules probably act as potential inhibitors against prospective targets of SARS-CoV-2: Therapeutic insight for COVID-19 from computational modelling, molecular docking and dynamic simulation studies | St. Pius X college, Kasaragod |