GXP BioInfonomics

Whole Exome Sequencing Data Analysis

Our comprehensive DNA analysis pipeline delivers clinically relevant insights from exome sequencing data. It was successfully used in the pilot study of the German network for personalized medicine.

Menzel M. et al. and Stenzinger A. **Benchmarking whole exome sequencing in the German network for personalized medicine**, European Journal of Cancer, Volume 211,2024

The following information is provided based on FASTQ data from DNA panels and Whole Exome Sequencing (WES) and enables the analysis of critical features such as:

- Somatic variants
- Actionable Mutations (e.g. EGFR, ALK, ROS1, RET, MET, NTRK, BRAF, KRAS)
- CNAs / CNVs – Somatic Copy Number Alterations / Variations
- HRD Scores - Homologous Recombination Deficiency
- TMB Status - Tumor Mutational Burden
- MSI Values - Microsatellite Instability
- HLA Class | Status
- LOH – Loss of Heterozygosity
- LST – Large Scale Transitions
- TAI – Telomeric Allelic Imbalance
- Mutation Signatures
- Neoepitopes

Raw data (FASTQ) can be safely uploaded via secured FTP to our servers located in Frankfurt, Germany.

Visit https://genxpro.net/bioinformatics/ for further information.

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