Ось переклад інформації про інструменти для біологів, молекулярних біологів, а також для аналізу даних секвенування і qPCR на англійську:

**Open Resources for Biologists and Molecular Biologists**

**Data Analysis and Statistical Processing**

1. [**Bioconductor**](https://www.bioconductor.org/): An open-source project that provides tools for the analysis and comprehension of high-throughput genomics data. Free and comprehensive suite of packages for R.
2. [**Galaxy**](https://usegalaxy.org/): A web-based platform for data analysis, providing a user-friendly interface to perform complex bioinformatics analyses. Free and open-source.
3. **DESeq2**: An R package for analyzing count data from RNA-seq experiments. It handles normalization, differential expression, and visualization. Free and open-source.
4. **EdgeR**: Another R package designed for differential expression analysis of RNA-seq data. Includes tools for normalization and visualization. Free and open-source.
5. [**BioPython**](https://biopython.org/): A collection of Python tools for computational molecular biology, including tools for sequence analysis, structural biology, and more. Free and open-source.

**Image Processing (Microscope Images)**

1. [**ImageJ**](https://imagej.nih.gov/ij/): A powerful open-source image processing program designed for scientific multidimensional images. It is particularly useful for microscopy. Free and open-source.
2. [**Fiji**](https://fiji.sc/): An image processing package based on ImageJ with additional features for complex image analysis, including plugins for microscopy data. Free and open-source.
3. [**CellProfiler**](https://cellprofiler.org/): A software for analyzing and quantifying cell images, including microscopy data. It helps in extracting features from images for biological analysis. Free and open-source.

**Sequencing Data Analysis**

1. **UCSC Genome Browser**: Provides a comprehensive set of tools and resources for visualizing and analyzing genome sequence data. Free and open-access.
2. **IGV (Integrative Genomics Viewer)**: A high-performance visualization tool for exploring large-scale genomic data sets. Free and open-source.
3. **GATK (Genome Analysis Toolkit)**: A toolkit for variant discovery in high-throughput sequencing data. Provides tools for variant calling and quality control. Free for academic use.
4. **HISAT2**: A fast and sensitive alignment program for mapping RNA-seq and DNA-seq data. Free and open-source.
5. [**STAR**](https://github.com/alexdobin/STAR): A fast RNA-seq aligner capable of handling large-scale RNA-seq data. Free and open-source.

**qPCR and Data Normalization**

1. **QuantStudio Real-Time PCR Software**: Software for analyzing qPCR data, including normalization and quantification of gene expression. Available with QuantStudio instruments.
2. **NormFinder**: A tool for determining the most stable reference genes for qPCR normalization. Free for academic use.
3. **GenEx**: Comprehensive software for qPCR data analysis, including normalization and statistical analysis. Paid software with a free trial.