



# Genomics and Proteomics Core Laboratories

[www.genetics.pitt.edu](http://www.genetics.pitt.edu)

## Roche (454) GS-FLX



### Next Generation Sequencing now available at the GPCL

Based on pyrosequencing technology, the FLX provides ultra deep sequencing of 250 bp (average length) segments of DNA, returning approximately 100 Mbases of data per run. Early this fall we will upgrade the capabilities as Roche releases their long read chemistry and software to allow for up to 500bp reads and up to 500 Mbases of data per run.



Software aligns the thousands of fragment reads into consensus sequence.

There are 3 distinct approaches to sample prep for genetic analysis, each optimal for different project aims:

- 1. Genomic Library preparation** for *de novo* or resequencing of genomic DNA or long PCR product. This includes analysis of small genomes from microorganisms and resequencing of specific regions for variant detection.
- 2. Paired End Library preparation** provides regions of sequence a known distance apart, allowing for assembly of contigs into scaffolds and analysis of genetic rearrangement.
- 3. Amplicon Library preparation** for analysis of somatic variants in complex cancer samples or genetic variability in human, animal, plant or microbial populations.

GS-FLX sequencing runs can be partitioned, either physically or through the use of sample ID tags, so that multiple samples requiring less than 100 Mbases of data can be run simultaneously.

The GPCL provides full support for this technology from project design to data analysis. Please contact us to discuss your ultra deep sequencing project and how the GS-FLX at Pitt can help you achieve your goals.

For further info on the Roche FLX contact Deborah Hollingshead: 412-648-1284 or [hollings@pitt.edu](mailto:hollings@pitt.edu)  
For general inquiries contact our main office: 412-648-9440