



# Pioneers in Genomics Education Program - Terms and Conditions

## 1. Introduction

This document sets out the conditions under which the Pioneers in Genomics Education Program is offered.

Inquiries about the Grant should be addressed to:

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## 2. Outline of the Pioneers in Genomics Education Program

The Pioneers in Genomics Education Program (henceforth referred to as The Program) is an effort to bring cutting edge industry genomics applications and tools into leading educational curriculum with an aim to reduce gaps between industrial discovery and basic research. Moreover, the Program helps to foster linkages with select leaders in education and assist in their training endeavor. The Program also creates a network and facilitate collaboration between participants of this Program. This Program also aims to give affordable access to cutting edge bioinformatics tools to current and future researchers and scientists in industry and academia.

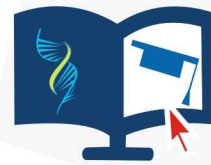
## 3. Application and Selection Process

Applicants may self-nominate, providing all required details themselves. The Partner Organization/ Genomics Pioneer is the Nominee (henceforth referred to as Partner Organization/ Genomics Pioneer). Applications should consist of a completed nomination form ([Online Form](#)), unless already pre-nominated. Applications will be confirmed by email.

## 4. Terms of Reference and Assessment Criteria

### 4.1 About the Program

- Perpetual network licenses for our proprietary bioinformatics software (total licenses will be decided after evaluating the needs at the Partner Organization/ Genomics Pioneer)
- Catalog OciChip™ arrays, spotted with 50 mer oligonucleotide probes, on open platform
- Guaranteed 30 prospective students\* every 6 months for the Partner Organization/ Genomics Pioneer through marketing programs and campaigns run to promote the initiatives of the Partner Organization/ Genomics Pioneer.
- Online forum/ ticketing based support on software issues or technical questions (guaranteed response within 36 hours)



- One online meeting spread over a week for each of Genchek™, Genowiz™ and OptGene™ software (at a convenient time of the Partner Organization/ GenomicsPioneer) where an expert will present ongoing real world case study on the applications of these tools and solutions – Applicable for the first year only. One day on-site visit by a Bioinformatics expert
- 15% discount on list prices for custom genomics projects in the following areas, on which the Partner Organization/ Genomics Pioneer is working, for the calendar year starting from the date of selection.
  - Gene Expression services with commercial arrays/ OciChip™ arrays
  - SNP Genotyping / Copy Number Variation services with commercial arrays
  - Sequencing services for plasmid DNA/ PCR product

## 4.2 Eligibility of the Applicant

Closed network of leaders playing a key role in shaping up graduate and post-graduate level education at colleges, universities, select educational institutes and companies having a dedicated in-house educational programs in bioinformatics.

## 4.3 Total Participation Cost

### Industry

Rupees 8 lakhs, payable in installments for the Partner Organization/ Genomics Pioneer

- 5 lakhs upfront
- 1.5 lakhs within 6 months of the Program induction
- 1.5 lakhs within 12 months of the Program induction

### Academia

Rupees 2 lakhs payable in installments

- 1 lakh upfront
- 50,000 within 6 months of the induction
- 50,000 within 12 months of the induction

\* Only based on the interest of the Partner Organization

## Proprietary Bioinformatics Software from Ocimum - Applications

The following is just one of the applications of our proprietary bioinformatics software. We have developed a systematic workflow for design, optimization and validation of the gene of interest. The five-step procedure outlined in the figure below, starts from a preselected genomic regions of interest, which may have been identified by genome-wide screening experiments or through a candidate gene approach. A typical example would be the promoter region of a tumor suppressor gene (TP53 gene).



### BEGIN: Genomic Regions of Interest

- Identified by genome-wide mapping experiments or a candidate gene approach
- e.g. Promoter region of tumor suppressing gene



### Data Import and Graphical Visualization (Genchek™ - a sequence analysis software)

- Loading of the Genomic region of interest (multiple file formats supported such as GenBank, FASTA, EMBL)
- Modify or create a sequence of your interest on Sequence Editor
- Perform ORF Analysis, RE Analysis, Oligo Analysis, search similar sequences using BLAST, MSA etc. using Graphical Viewer



### Optimize the Gene of interest (OptGene™ - a gene optimization software)

- Optimize gene of interest for expression in any organism of choice
- Alter the gene sequence without affecting the corresponding AA of the protein



### Computational Validation (Genowiz™ - a gene expression analysis software)

- Assessment of Differential Expression patterns of the gene of interest
- Robust statistical analysis of the gene of interest



### Pathway interaction study and Gene Ontology of the gene of interest (Genowiz™)

- Study Upregulation and Downregulation of the genes of interest.



### RESULT: Gene ready for use in clinical trials after experimental validation

- Export in standardized XML format

In the first step, the region of interest is imported in to a sequence analysis tool, Genchek™ software. One can modify and create a sequence of interest using the Sequence Editor feature and also perform advanced sequence analysis using Genchek™. Second, using OptGene™, a gene optimization tool, the gene of interest can be optimized for expression in any organism of choice without altering the corresponding aminoacids of the protein. Third, the accuracy of all designed assays is computationally assessed, using Genowiz™, a gene expression analysis tool. Genowiz™ allows import of data from any Affymetrix data formats which is then used for studying the differential expression patterns.



Fourth, the candidate genes are checked to see the alternate pathways they may be affecting by their upregulation or downregulation. Fifth, the most promising assay is selected, experimentally tested and further optimized based on the outcome of the experimental validation. After completion of these five steps, the candidate biomarker is ready for application and further validation in clinical studies.

You may also go through the following links for exclusive videos on Genowiz™ and Genchek™ functionalities:

<http://www3.ocimumbio.com/data-analysis-insights/analytical-tools/genowiz/genowiz-tour>

<http://www3.ocimumbio.com/data-analysis-insights/analytical-tools/genchek/genchek-tour>

## Customer Testimonials for our Bioinformatics Software:

### Genchek™

"Although Java programs can be "buggy" and lack-luster in appearance, this program does an excellent job departing from the norm. It looks very attractive and has many useful features. Easy to browse, with a clean and somewhat intuitive interface. The tools that performed best for nucleotide analysis include: The contig assembly module, restriction enzyme analysis, the ORF finding module, the BLAST suite, multiple sequence alignment (for DNA), and the primer design module. Especially surprising was the above average performing primer design module. Primer analysis was quick and efficient, with an easy read-out and informative "expert" data options."

- Dr. Peter Azmi, University of Toronto

"It is interesting. I had been using DNASTar for analysis. Genchek has many things integrated into one platform which is the nice thing and the pricing is also very attractive."

- Dr. M. Padmavati, former Senior Scientist, Monsanto Research Center

### Genowiz™

"Data analysis (storage, integration, annotation, statistical analysis and clustering) is a challenging task in this uncharted area of translational genomics. Ocimum Biosolutions has the tools to tackle the complexity."

- Dr. Ashok Amin, Director Rheumatology Research Laboratory, Hospital for Joint Diseases, New York

"This works perfectly. I have imported and defined annotation file this morning (Australia time) and I cannot get enough of it! I have done GO analysis with complete stats, pathways are online and NCBI links to any gene I select from the heat map are fully functional etc..."

What can I say? I have 2 postgrad students jumping for joy in my office when they saw what it can do..."

- Dragana Stanley, CSIRO, Australia

### OptGene™

"OptGene™ combines a whole suite of gene design and analysis packages into one user-friendly and user-customizable program that replaces three programs that I used previously."

- Dr. Don Merlo, Dow AgroSciences

