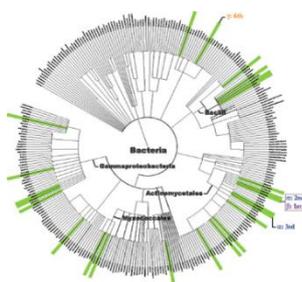
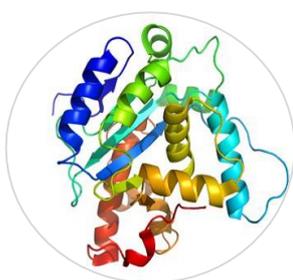




# NSilico

*Improved efficiencies for biotech research.*

**Biotech enterprises can benefit from an 80% time reduction on research project data analysis and management thanks to the Bio-Mapper software system, developed by CIT's NSilico team.**



The BioMapper system manages complex research processes in one integrated package. Information from large scale genomic sequencing projects can be easily annotated, reported on and analysed through this system.

### The Need

NSilico designed a system to address the need for integration and management of research and enterprise processes, with high levels of data throughput. Other biopharma systems exist as separate repositories of knowledge with which researchers have to interact manually to complete a programme of research. NSilico sought input from over 120 professional biotech researchers in order to develop a soft-ware framework that responds to industry/academic demands.

### The Solution

Biomapper has been developed as a cloud based Software as a Service (SaaS) solution. As user needs increase this structure accommodates quick and easy application of extended features. This is achieved through the managed

online, secure and scalable infrastructure provided.

This well proven business model extends itself to research labs of any size and it has the capacity for users to select a pricing model appropriate to usage. The design allows for comprehensive workflows without any need for data conversions or programming.

### Critical Success Factors

NSilico developed the system on the basis of feed-back from professional biotech researchers. As the system has been designed by biologists for biologists, it is intuitive to the research management needs of its users.

Research labs of any size can avail of NSilico's Biomapper.

### Benefits

The software has the potential to significantly speed up both routine *in silico* analysis and wet lab documentation. This helps to streamline the process from experimentation to publication and/or patent application, with all the necessary reporting and IP requirements in place.

“A full viral genome was sequenced and annotated in 24 hours with the Bio-mapper. The equivalent for a student would amount to three months of wet lab work.”

Dr. Roy Sleater  
Department of Biological Sciences, CIT

“Researchers consult many different databases and services, they have to manually copy and transform data between these services. This system frees researchers time to focus on biology as opposed to IT.”

Paul Walsh  
Department of Computing, CIT

