Figure A28.1 Illustrative Pitch Template Example on Molecular Biology (reverse-engineered)

This example is reversed engineered based on: Myburg A. A, Grattapaglia D, Tuskan G. A et al (2014). The genome of Eucalyptus grandis. Nature, 510(7505):356-62. doi: 10.1038/nature13308.

Pitcher's name	Marita Smith	FoR category		Molecular biology	Date completed	11/2/15
(A) Working Title	Genetic sequencing of Eucalypts					
(B) Basic Research Question	What are the key genes of *Eucalypt grandis*?					
(C) Key paper(s)	Tuskan, G. A *et al*. (2006). The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray). *Science*, 313, 1596-1604. Kullan, A. R. K, van Dyk, M. M, Jones, N, Kanzler, A, Bayley, A, Myburg, A. A. (2012). High-density genetic linkage maps with over 2,400 sequence-anchored DArT markers for genetic dissection in an F2 pseudo-backcross of *Eucalyptis grandis x E. urophylla*. *Tree Genet. Genomes*, 8, 163-175.					
(D) Motivation/Puzzle	*Eucalyptis grandis* (flooded gum) is an Australian native Eucalypt species that has become popular worldwide as a key species in timber plantations. It grows quickly, is hardy and provides key renewable resources such as paper and biomaterials. In order to improve the yield of resources from these plantations, an understanding of the genetic makeup of this species would be beneficial. Genetic sequencing would facilitate the selective breeding of trees better suited to dealing with climate change. In addition to accelerating the production of renewable timber, the Eucalypts produce a range of specialised metabolites, including terpenes, which display unique medical and pharmaceutical properties. Increased genetic understanding of this species would provide a more comprehensive screening of the production capacity of these metabolites.					
THREE	**Three core aspects of any empirical research project i.e. the "iDioTs" guide**					
(E) Idea?	Genetic sequencing is an important tool in understanding the makeup of plants and animals. It enables the identification of key genes involved in cellular processes and the resultant protein products. In plants, it thus provides a platform for selective breeding, biotechnology and comparative biology. The species *Eucalyptis grandis* is a strong target for genetic sequencing because of its cumulative net worth in plantations across the world, which would benefit from targeted breeding programs. In addition, its potential range of untapped metabolite resources would benefit from further study, potentially providing new medical, pharmaceutical or biofuel compounds.					
(F) Data?	-Whole genome shotgun sequencing and assembly will be performed using a suitable candidate of *Eucalyptis grandis* - The genome data will allow the determination of the phylogenetic position and evolutionary development of *Eucalyptis grandis,* using previously sequenced plant genomes -Gene maps of genes responsible for biomass production and water conservation to determine those crucial for future selective breeding -Analysis of terpene genes and expression profiles to identify spectrum of useful compounds capable of being produced by *Eucalyptis grandis.*					
(G) Tools?	-A suitable candidate tree must be bred and selected for genetic analysis. -Physical apparatus, including automated genomic sequencers, genetic libraries and extensive computer analysis.					

TWO	Two key questions
(H) What's New?	This species, a key global player, has not been genetically sequenced nor its potential tapped as a renewable resource. This project will provide the genome of *Eucalyptis grandis* and provide useful information for means to selectively breed resilient, faster growing stock; produce new metabolites; and further serves as a useful comparative study in its own right for plant genetics.
(I) So What?	Renewable resources are commodities in today's changing economic climate. A means of securing the world's lumber and pulp supplies is sorely needed. Furthermore, metabolites for medical, pharmaceutical and biofuel applications are in demand. The data derived from this project is likely to inform future better management and expansion of *Eucalyptis grandis* plantations internationally.
ONE	**One bottom line**
(J) Contribution	The primary source of the contribution will be a complete genome of *Eucalyptis grandis* and the identification of key genes useful in accelerated lumber and metabolite production.
(K) Other considerations	Is Collaboration needed/desirable? -Idea: no; -Data; yes –multi-institutional preferred -Tools; yes –representatives and funding from various institutions Target journals – *Nature, Phytochemistry* "Risk" assessment: -"no result" risk: low. Genetic sequencing will provide a detailed map of the capabilities of *Eucalyptis grandis*. It is possible that the range of genes identified may have fewer applications than hypothesized, but this is unlikely due to the spectrum of metabolites already documented in this species. -"competitor risk"(i.e. being beaten by a competitor): low. A study of this size will necessitate a coordinated, international effort involving a wide range of researchers. It is not something achievable by a small lab. -risk of "obsolescence": Low. The economic value of *Eucalyptis grandis* means new information regarding its capabilities will be in demand.