Writing Abstracts for Research Projects
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Organized by the Writing Across the Curriculum, Emerging Scholars, and Honors Scholars Programs

What is the structure of an abstract?

Based on the following abstract (which has been adapted from a past Emerging Scholar project), what can you tell about what goes into an abstract? Try to generate a list of what you feel are the *types* of information contained in the abstract.

Abstract 1

Title: Cranberry Juice And Grape Juice As Anti-Viral Agents and Cytotoxicity Studies

Defined phytochemicals in potable juices (grape juice and cranberry juice) have been shown to possess antiviral properties both in vitro and in vivo. However, cytotoxicity by chemical treatment of cells may mask any antiviral effects. Accordingly, testing is critical to validate the effect of the juices in question as antiviral agents.

Antiviral testing in cell culture has addressed the potential issue of cytotoxicity by monolayer pretreatment with cranberry and Concord grape juices. Such [cytotoxicity] testing employed trypan blue exclusion and cell subpassage. However, confirmatory testing to identify subtle effects by juices and other phytochemicals or nutraceuticals needs to be tested by a metabolic assay. This required a non-destructive bioluminescent cytotoxicity assay, which quantitatively measures the release of adenylate kinase (AK) from damaged cells. Release of AK from damaged cells, in complex with ADP, luciferein and luciferase additives from the ToxilightR BioAssay kit, yields an ATP spark – which can be detected by placement of the reaction mix in a luminometer. The luminometer was procured through a GRTI grant, which was used in this collaborative effort.

After the assay was perfected, the data collected from the luminometer showed that 50% Purple, Niagara, and pure cranberry juice reveal no cytotoxicity to monkey kidney cells grown in monolayer culture. This data confirms earlier results in that the antiviral effects were clearly due to the juices, and not artifact associated to host cell cytotoxicity.

What makes an abstract successful?

In small groups, read the following abstracts (which have also been adapted from past Emerging Scholar projects). Analyze in what ways they are successful and in what ways they can be improved.

Abstract 2

Title: Using the Mediation Methodology to Analyze the Northern Ireland communal conflict

Mediation is part of the conflict resolution family and falls in the Alternate Dispute Resolution category. Mediation is basically when two or more parties voluntarily come together with an impartial third party to resolve a conflict. The purpose of this paper is to explain the six steps to the mediation methodology presented in "Peacemakers Toolkit: Managing a Mediation Process" which is authored by Amy L. Smith and David R. Smock. I will be using the Northern Ireland Communal Conflict as a case study.

The six steps to the mediation process include: a) assessing the conflict, b) ensuring mediator readiness, c) ensuring conflict ripeness d) conducting track I mediation e) conducting track II- dialogue and f) constructing a peace agreement. The Northern Ireland Communal conflict deals with the tension between the Protestants who have held the majority of the population whereas the Catholics who have been the minority in Northern Ireland- a case of ethno-nationalism. The Protestants desired to be part of the UK as they identified themselves as British. On the other hand, the Catholics identified themselves as Irish and desired a separate governing structure from the United Kingdom. John W. Burton (1915- 2010) is considered by many to be one the founders of the conflict resolution scholarship.

Throughout this paper I will be mainly referencing to the works of John W. Burton. He derived the concept of "provention"- which involved eliminating the sources of conflict, removing the causes of conflict and promoting an atmosphere where conflict does not exist. "

Abstract 3

Title: Studying the Epigenomic Landscape of Lupus Patients

Since the completion of the Human Genome Project in 2003, a wealth of knowledge has been accumulated regarding diseases and the genes that code for them. To fully understand the complexities of the human genome, Next Generation Sequencing (NGS) technology has been employed. Here, we analyze NGS data from Reduced Representation Bisulfite Sequencing (RRBS-seq), a technology used to systematically capture the genome-wide methylation profiles on a single nucleotide level. The sequencing data comes from patients with Systemic Lupus Erythematosus (SLE), as well as from controls, and the goal of this analysis is to find differentially methylated regions in the genome and their corresponding genes.