Sample 1:

PGC-1b in the Regulation of Hepatic Glucose and Energy Metabolism*

Jiandie Lin et al. J. Biol. Chem., Vol. 278, Issue 33, 30843-30848, August 15, 2003

Peroxisome proliferator-activated receptor gamma coactivator-1a (PGC-1a) is a transcriptional coactivator that regulates multiple aspects of **cellular energy metabolism**, including mitochondrial biogenesis, hepatic gluconeogenesis, and beta-oxidation of fatty acids. PGC-1a mRNA levels are increased in both type-1 and type-2 **diabetes** and may contribute to elevated hepatic glucose production in diabetic states. We have recently described PGC-1b, a novel transcriptional coactivator that is a homolog of PGC-1a. Although PGC-1b shares significant sequence similarity and tissue distribution with PGC-1a, the biological activities of PGC-1b in the regulation of cellular **metabolism** is unknown. In this study, we used an adenoviral-mediated expression system to study the function of PGC-1b both in cultured **hepatocytes** and in the **liver** of rats. PGC-1b, like PGC-1a, potently induces the expression of an array of mitochondrial genes involved in oxidative metabolism. However, in contrast to PGC-1a, PGC-1b poorly activates the expression of gluconeogenic genes in hepatocytes or liver in vivo, illustrating that these two coactivators play distinct roles in hepatic glucose metabolism. The reduced ability of PGC-1b to induce gluconeogenic genes is due, at least in part, to its inability to physically associate with and coactivate hepatic nuclear receptor 4a (HNF4 a) and forkhead transcription factor O1 (FOXO1), two critical transcription factors that mediate the activation of gluconeogenic gene expression by PGC-1a. These data illustrate that PGC-1b and PGC-1a have distinct arrays of activities in **hepatic** energy **metabolism**.

231 words

IS Unit 9/26/06 5:55 PM
Comment: Title could be made punchier. How about PGC-1b regulates hep gluc and energy metabolism? Why no mention of organism?

IS Unit 9/26/06 5:51 PM
Comment: End of "Background section". Answers questions a: Where does this study come from? Takes 3 sentences. Note the "big picture" items: "cellular energy metabolism" and "diabetes"

IS Unit 9/26/06 5:38 PM
Comment: Transition phrase, tying what is known (PGC1alpha) to what is less known: (PGC1beta)

IS Unit 9/26/06 5:32 PM
Comment: Answer to question b: What is the question this study answers? Takes 1 sentence. Note the use of a "signal" word: "unknown."

IS Unit 9/26/06 5:39 PM
Comment: Answer to question c: What did you do? Takes 1 sentence. Note the signal: "In this study" to indicate that now we're talking about our work.

IS Unit 9/26/06 5:39 PM
Comment: Note comparison that ties new results to old ones.

IS Unit 9/26/06 5:41 PM
Comment: "However" "in contrast" signal a difference.

IS Unit 9/26/06 5:42 PM
Comment: Answer to question d: What did you find? Takes 3 (long) sentences. Note that observations are summarized without mention of numerical data.

IS Unit 9/26/06 5:47 PM
Comment: Answer to question e: what does it mean? Note how this statement answers the question asked above by reusing the same keywords, i.e "metabolic" and "hepatic."

Sample 2:

Cellular and Molecular Bases of the Initiation of Fever

IS Unit 9/26/06 6:07 PM
Comment: Better title? Including mention of PGE2? Of organism?

Steiner AA, Ivanov AI, Serrats J, Hosokawa H, Phayre AN, et al. (2006) Cellular and Molecular Bases of the Initiation of Fever. PLoS Biol 4(9): e284

All phases of lipopolysaccharide (LPS)-induced **fever** are mediated by prostaglandin **(PG) E_2**. **It is known** that the second febrile phase (which starts at ~1.5 h post-LPS) and subsequent phases are mediated by **PGE_2** that originated in endotheliocytes and perivascular cells of the brain. However, the location and phenotypes of the cells that produce **PGE_2** triggering the first febrile phase (which starts at ~0.5 h) remain unknown. By studying PGE_2 synthesis at the enzymatic level, we found that it was activated in the lung and liver, but not in the brain, at the onset of the first phase of LPS fever in rats. This activation involved phosphorylation of cytosolic phospholipase A_2 ($cPLA_2$) and transcriptional up-regulation of cyclooxygenase (COX)-2. The number of cells displaying COX-2 immunoreactivity surged in the lung and liver (but not in the brain) at the onset of fever, and the majority of these cells were identified as macrophages. When **PGE_2** synthesis in the periphery was activated, the concentration of **PGE_2** increased both in the venous blood (which collects PGE_2 from tissues) and arterial blood (which delivers PGE_2 to the brain). Most importantly, neutralization of circulating **PGE_2** with an anti-PGE_2 antibody both delayed and attenuated LPS fever. It is concluded that **fever** is initiated by circulating **PGE_2** synthesized by macrophages of the LPS-processing organs (lung and liver) via phosphorylation of $cPLA_2$ and transcriptional up-regulation of COX-2. Whether PGE_2 produced at the level of the blood–brain barrier also contributes to the development of the first phase remains to be clarified.

IS Unit 9/26/06 6:02 PM
Comment: Note the repetition of "activate" that provides continuity with sentence before.

251 words