Note: There will now be ~5 assignments throughout the term. Each assignment is worth some proportional fraction of your final grade. Your lowest assignment grade will still be dropped providing a total for the "assignment component" of your final grade as 56%.

Note: Please adhere to the stated expectations: "I expect that you'll interact with your colleagues throughout the course, in discussing any readings, during class, or in considering any assignments. However, your submitted assignments should reflect and be of your own individual work."

Note: When searching online you shouldn't need to request custom pricing or quote information. That is, for questions requiring online work, only use information that is readily available online.

Note: These assignments are both due by 9a Monday March 2nd and will be graded and ready for pickup by office hours that day, so that you can review any materials before the March 5 midterm. Please submit your assignment by email to: endy@stanford.edu

Note: Please send any questions about this assignment by email to endy@stanford.edu. I'll try to respond in real time.

Assignment #2 DNA Engineering

Part 1. Using the standard single letter amino acid abbreviations, what message does the following sequence of DNA encode? (Hint: search online for a DNA translation tool).

CGTGAAGCTCTTCATGCTTGTAAAGAACGTTCTCCTCGTGGTCGTGCTATGGATAATGCT

Part 2. Choose any two English words or phrases that you like. Encode both words in a single DNA sequence using the fewest number of DNA bases possible. Each individual word or individual phrase must be at least 7 letters in length. A +5% assignment grade bonus (and bragging rights) will be given to most efficient encoding (i.e., greatest fractional reduction in number of DNA bases used, relative to the total length of the two words or phrases). (Hint: find online or make a good reverse translation tool).

Assignment #3 RNA Engineering

Part 1. You have been hired by Microbesoft, Inc. to develop a RNA-based control system for conditionally regulating the expression of a protein-encoded enzyme. The specific application requires that as little protein as possible be expressed in the absence of the controlling input signal, and that as few cellular resources are wasted as possible. You can choose between (i) a 5'-based RNA element that non-destructively (reversibly) interacts with and occludes ribosome loading on a ribosome binding site, or (ii) a ribozyme-based riboswitch that is integrated into the 3' untranslated region (UTR) and that irreversibly cleaves the transcript in the absence of an input signal, resulting in rapid mRNA degradation. Which control mechanism do you choose? Why (one paragraph or less)?

Part 2. BioBricks & Mortar, Inc. would like you to help them debug a metabolic pathway that they have been engineering by developing a new riboswitch that is responsive to the intracellular levels of berberine (http://en.wikipedia.org/wiki/Berberine). Their engineers tell you that they have a hunch that their current version of the pathway might be producing morphine instead (http://en.wikipedia.org/wiki/Morphine). Start by outlining the evolutionary selections that you could use to select an RNA aptamer that can serve as an input sensor for berberine but not morphine. Second, sketch out the component-level architecture for the resulting riboswitch and its integration into a DNA-encoded mRNA transcript that will result in berberine levels being converted to a green fluorescent protein signal.