

## Homework #1. Self-Assessment of Background.

The course is going to assume a certain level of knowledge about biochemistry and cell biology, and most of you have had a fair amount of it already. With this homework as an exercise, please review some of that basic material. If any of this material is new to you, then you should consider spending some time reading a textbook to get up to speed. Ditto for knowing how to access genome and literature databases, which are addressed in the last question.

You should be able to:

1) Draw the structures of the following important biochemicals, using any system an organic chemist would understand.

- a) The 20 amino acids. Know their full names, their 3-letter codes, and their 1-letter codes.
- b) The 4 bases that compose DNA, the 4 bases that compose RNA, and cyclic AMP.
- c) Glucose, urea, creatine.
- d) Phosphatidyl serine, phosphatidyl inositol, acetyl coA, myristic acid, palmitic acid and cholesterol.

You should be familiar with:

2) The glycolytic pathway and the Krebs cycle. This includes the names and structures of the substrates and products and the names of the enzymes.

3) The electron transport chain of the mitochondrion. Just the names - no structures.

4) Understand the properties of amino acids in proteins. For example, you want to synthesize functional proteins, such as enzymes or antibodies, in an artificial chemical system from amino acids.

a) What is the smallest subset of amino acids that you need? Which ones do you want and why? Which ones are least necessary / most dispensable?

b) A synthetic organic chemist will help you create two new amino acids, with essentially any kind of chemical structure as the R group. What do you want and why?

5) Genome database / BLAST exercise.

You make a whole-cell extract of budding yeast, add rabbit muscle actin under polymerizing conditions, and centrifuge the actin filaments. You take the pellet, do a proteolytic digest and analyze peptides by tandem MS.

One peptide has the following sequence: L E A T E D L T S L S Y L N E P A V L.

Go to the Budding Yeast (*Saccharomyces cerevisiae*) Web Page, [www.yeastgenome.org](http://www.yeastgenome.org).

a) Do BLAST with the peptide as query. You want the program BLASTP and a protein database. What did you get? Click on the gene name to go to the web page for that gene. In addition to all the information that they give you on that page, check out all the stuff on right side.

What is the function of the protein?

What is the phenotype of a null mutant?

What is the molecular weight of the protein? What is its pI?

Where is the protein localized in the cell?

b) The protein has a close relative in the yeast genome - what is it? What is its function? What is its null phenotype?

c) Does the protein exist in other organisms, including humans? Take the complete protein sequence and do BLAST against everything. Go to the NCBI's home page, [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov), and find the BLAST page. Do BLASTP against the nr (non-redundant) database of all protein sequences.

d) Besides BLASTP, what are the other BLAST programs available to you? What types of query and database sequences are they for?

e) Go to PubMed, [www.pubmed.gov](http://www.pubmed.gov), and find a recent paper on this protein. Make sure you know how to access the original article, which may require going to the journal's web site (which is usually linked from PubMed) and may require using a WashU IP address (our library's subscriptions for web access are often based on the computer having a wustl ip.) Sometimes, one needs to connect to the journal web site by "linking out" from the WashU library, and the Becker Medical Library is a good place from which to do that...

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