Spring 2011 Genomics Exam #3
Proteomics, Synthetic and Systems Biology

There is no time limit on this test, though I don't want you to spend too much time on it. I have tried to design an exam that will take about the same amount of time as the first one. You are not allowed to read any papers to help with this exam. There are 4 pages, including this cover sheet, for this test. There are no Discovery Questions on this exam. You are not allowed discuss the test with anyone until all exams are turned in no later than noon on Monday May 9. **ELECTRONIC COPIES OF YOUR EXAM ANSWERS ARE DUE NO LATER THAN NOON ON MONDAY MAY 9**. You may use a calculator, a ruler, your notes, the book, and the internet except you cannot read any papers except those available from the reading schedule for this course. You may take this exam in as many blocks of time as you want. Submit your electronic version by noon (eastern time zone).

The **answers to the questions must be typed in a Word file and emailed to me as an attachment**. Be sure to backup your test answers just in case (I suggest a thumb drive or other removable medium). You will need to capture screen images as a part of your answers which you may do without seeking permission since your test answers will not be in the public domain. Remember to explain your thoughts in your own words and use screen shots to support your answers. Screen shots without ***your*** words are worth very few points.

DO NOT READ or DOWNLOAD ANY NEW PAPERS FOR THIS EXAM. RELY ON YOUR EXPERIENCE, AND YOUR SKILLS.

-3 pts if you do not follow this direction.
Please do not write or type your name on any page other than this cover page.
Staple all your pages (INCLUDING THE TEST PAGES) together when finished with the exam.

Name (please type):

Write out the full pledge and sign (electronic signature is ideal):

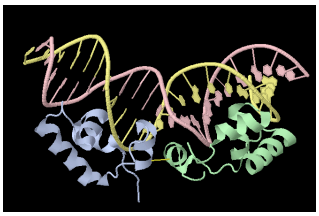
How long did this exam take you to complete?

12 points (3 pts each)

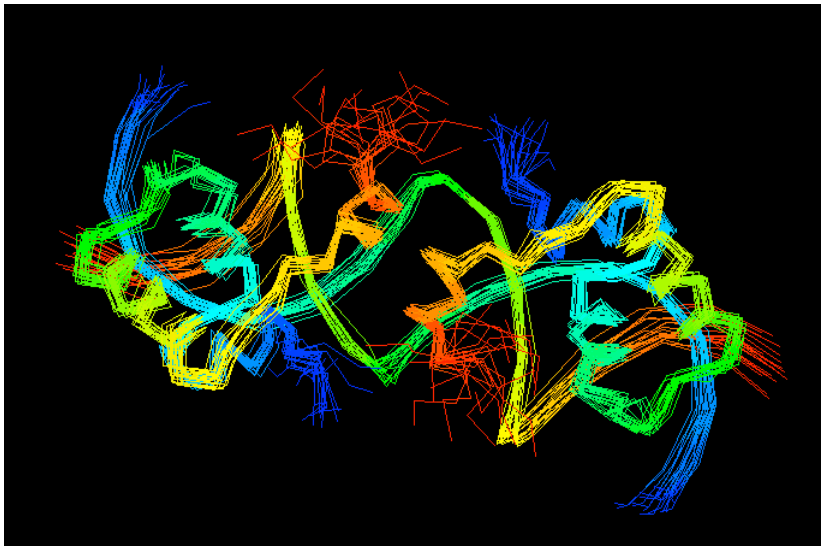
1) View this structure in FirstGlance (2KEI) and answer these questions.

a) What is holding these proteins together? (2 sentence maximum)

disulfide bond



b) View the molecule in "all models" and submit a screen shot in this exam.



c) What is happening at the ends of the protein? (2 sentence maximum)

They are wiggling in space because their position is not critical

d) In contrast to c, what is happening at the portions of the protein bound to its ligand, compared to the ends? Explain why this difference makes sense. (3 sentence maximum)

These portions of the proteins are more rigid in their position and structure because they are binding to the DNA and as such have less freedom of movement.

18 points

2) In addition to this Word file, I have sent you a PDF file. Look at that figure and answer these questions. Do NOT look up any papers or abstracts to answer this question

2 pts each (10 total)

a) Above the gray horizontal line is a green box. "Mat" refers to maternal source. Inside that green box are 5 colors of edges. Explain what happens for each colored line in one sentence per color. Do NOT look up any external resources to answer this question – it is self-contained.

Light blue: Wnt8 on, Krl on, SoxB1 off, Krox on, Eve on, Pmar1 on (optional)

Dark blue: Represses the GSK-3 repressor which makes the light blue keep going.

Thin black: Suppression of SoxB1 which normally represses cB. Light blue keeps going.
Thin beige: Krox induces self, and Wnt8, and Otx and Eve.
Rust red: Maternal Otx induces Otx, and Krox.

4 pts

b) Look below the gray line. Explain how *Endo16* is induced. For your answer trace Endo16's induction back as far as you can follow it.

Endo16 is induced by Otx and UI. UI is induced by GataE which was induced by Otx. Therefore Endo16 is regulated by a feed forward loop. GataE is also induced by the maternal cB.

4 pts

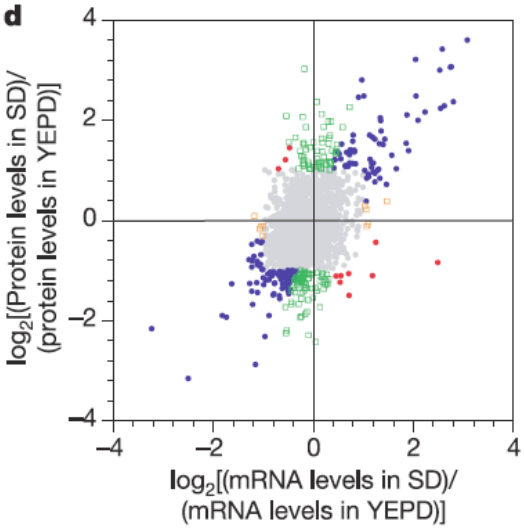
c) Use the circuit to identify the best candidate for what we called "Bmer" in the textbook. In two sentences or less, explain why you selected this protein to be the functional equivalent of "Bmer".

UI looks like it could be the Bmer because its induction comes after Otx which was responsible for the early inducation of Endo16. UI is responsible for the later induction of Endo16 and thus looks like Bmer.

18 points

3)

a) In the figure to the right, investigators measured yeast mRNA and protein levels for thousands of genes when cells were grown in either SD or YEPD media. Don't bother finding out the difference between the two media. Tell me what is happening for the expression patterns the genes grouped by the four colors (1 sentence for each color).



3 pts each

Green: altered protein but not mRNA
Red: negative correlation between protein and mRNA levels
Yellow/gold: altered mRNA but not protein
blue: positive correlation between protein and mRNA levels

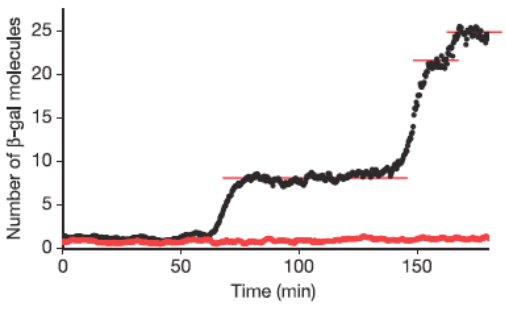
6 pts

b) What is the overall lesson from these data? (2 sentence maximum)

mRNA and proteins levels often correlate, but not always and not always positive correlation

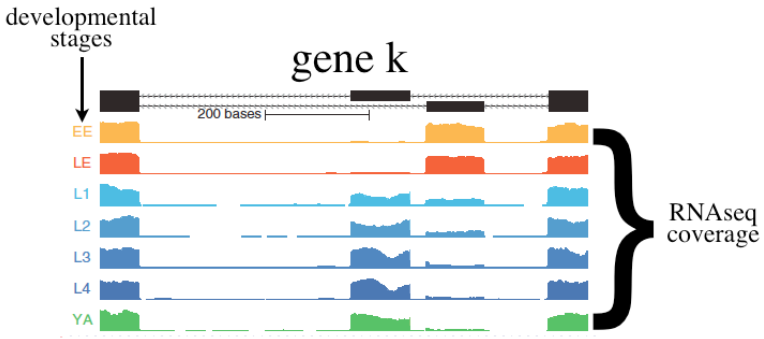
10 points

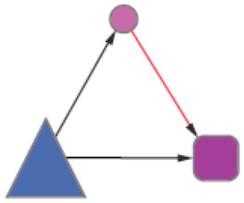
4) In the figure to the right, investigators engineered the β-galactose gene downstream of the pLac promoter. All cells contained LacI. The black line shows the number



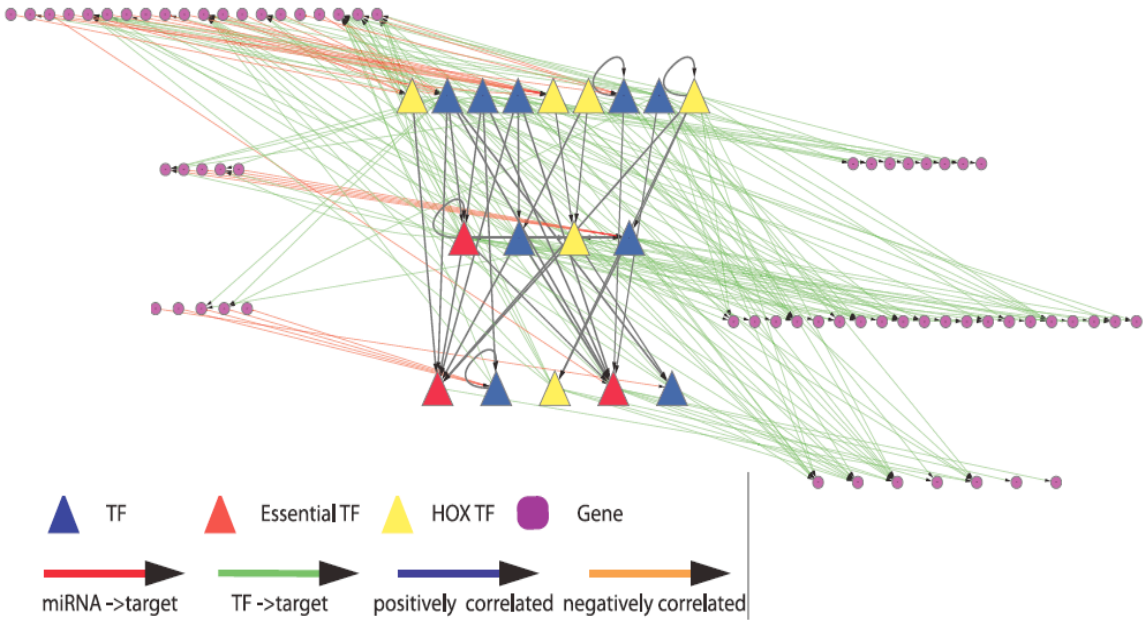
of β-galactosidase molecules produced over time inside one cell. The red line shows the number of
β-galactosidase molecules produced in a different cell during the same experiment.
a) Summarize the results you see in this figure. (3 sentences or less)
sporadic protein production (timing varies)
uneven bursts of quantity ranging from 4 – 13 molecules per burst.

11 points
5) For the figures below, answer these questions:
6 pts
a) Summarize the *gene k* figure below. (3 sentences or less)
early in development: exons 1,2, 4. later exons 1, 3, 4 (but less exclusive than early splicing).
5 pts
b) Name and describe the circuit motif in the three-point network. (2 sentences or less; the symbols for this figure are the same as in question 6 below)
Feed forward loop. Time delayed second wave of information to target.





16 points
6) The purple circles in rows are miRNAs. The other symbols are defined within the figure.
a) Explain why the three red triangles are called "essential"



based on the circuit diagram here. (3 sentences or less)

4 pts

The top triangle is required for the bottom 2. The bottom two have very large degree values and thus are tightly regulated which indicates their essential nature.

3 pts each

b) Describe 4 general patterns of relationships (you can choose any 4 that strike you) between miRNAs and the transcription factors in this figure. (1 sentence per pattern)

pattern 1: TF at the top regulate more than one TF below them.

pattern 2: multiple miRNAs can affect a single TF.

pattern 3: TF can affect multiple miRNAs

pattern 4: TF can have multiple targets but miRNAs seem to affect a single TF target.

15 points

7) **5 pts each**

a) Explain the overall purpose of the figure below. (2 sentences or less)

Showing the bifurcation of genes that used to be coregulated through fly development.

b) Draw a picture (similar to the other numbered boxes) for point 17 in the figure below. You do NOT have to provide any gene names. I recommend you do this by hand and scan it into your test. Use colors appropriately.

circles) are numbered 1 through 19. The colored insets show the expression level of each individual gene going through the split and ranked regulators from the physical (black) or functional (blue) regulatory network associated with the higher (H), lower (L), or middle (M) path. The uncolored inset shows

c) Read the highlighted figure legend for the figure and then describe the su(HW) data. We discussed this in class but did not reach clarity at that time. See if you can make sense of the data on your own now. (4 sentences or less)

The key is the H indication for Su(HW) which only means it is associated with the higher path, no that its induction is upregulated. Su(HW) is a repressor and when it goes down, its target genes are upregulated.