Saccharomyces cerevisiae Acclimation to Cold Shock Revealed Change in Expression of Genes Involved With Ribosome Biogenesis, Mitosis, and Nitrogen Catabolism

Acclimation of *Saccharomyces cerevisiae* to Low Temperature: A Chemostat-based Transcriptome Analysis. Tai, S. L., Daran-Lapujade, P., Walsh, M. C., Pronk, J. T., & Daran, J. M. (2007) *Molecular Biology of the Cell*, *18*, 5100-5112.

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BIOL 368: Bioinfomatics Laboratory

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Outline

- **Limitations of previous studies led to development of experiment using chemostat culture and low temperature acclimation.**
- ***S. cerevisiae* was grown in four different experimental conditions.**
- **DNA microarray analysis was used to analyze growth limitations applied to *S. cerevisiae.***
- ***S. cerevisiae* stores carbohydrates during chemostat culture for unknown reasons.**
- **Promoter analysis reveals regulation trends in gene regulation.**
- **Temperature response genes overlap in expression.**
- **Environmental stimulation responses differed in batch vs. chemostat cultures.**
- **Experimental design differences distinguish Dahlquist Lab data from Tai et al.**
- **Analysis of Δgln3 revealed significant difference in gene expression over time.**
- **Model expression profiles show that many biological processes are affected by cold shock.**
- **Ribosome biogenesis, mitosis, and nitrogen catabolism genes were affected in Tai et al. and Dahlquist Lab data analysis**

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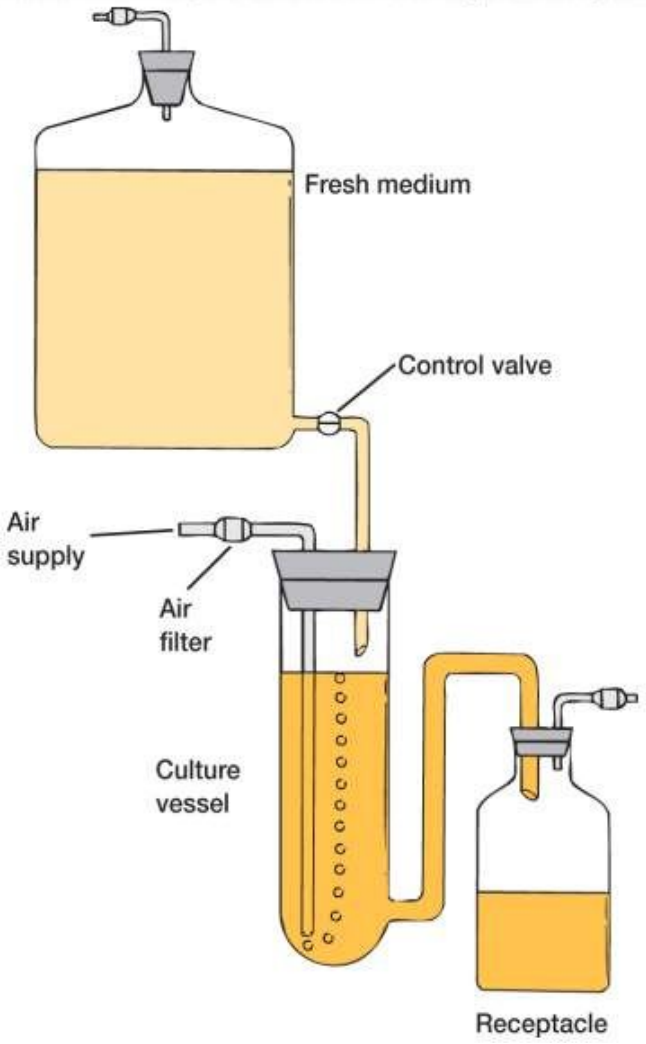
Chemostat Culture Allows For Fixed Experimental Conditions

- Chemostat culture involves the continuous addition of fresh medium.
- Allows for control of growth factors.
- Specific growth rate can be measured accurately.
- Batch culture is a closed system which does not allow for accurate measurement of specific growth rate.



http://classroom.sdmesa.edu/eschmid/f6-9_a_continuous_cultu.jpg

Low-temperature Acclimation and Cold Shock Have Differing Results

- **Cold shock entails a rapid decrease to near freezing temperatures.**
- **Low-temperature acclimation is the biological response of cells to steady decreases to near freezing temperatures.**
- **Trehalose is required for transcription in low temperature situations.**
  - **Not present in low temperature acclimation results.**

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S. Cerevisiae Grown In Varying Conditions of Temperature and Nutrient Content

Limiting nutrient	Growth temperature (°C)	$Y_{Glu/X}$ ($g_{DW} \cdot g_{glucose}^{-1}$)	q_{Glu}[a]	q_{EtOH}[a]	q_{CO2}[a]	Carbon recovery (%)	Residual glucose (mM)	Residual ammonia (mM)
Glucose	12	0.07 ± 0.01	−2.5 ± 0.2	3.8 ± 0.3	4.4 ± 0.3	100 ± 3	2.8 ± 1.1	65.2 ± 2.2
Glucose	30	0.07 ± 0.00	−2.3 ± 0.0	3.5 ± 0.0	3.8 ± 0.2	95 ± 1	0.3 ± 0.1	61.3 ± 4.5
Ammonium	12	0.05 ± 0.00	−3.6 ± 0.2	6.1 ± 0.3	6.0 ± 0.6	97 ± 4	90.0 ± 9.8	1.5 ± 0.2
Ammonium	30	0.04 ± 0.00	−4.0 ± 0.1	6.8 ± 0.2	7.4 ± 0.2	97 ± 2	85.1 ± 8.2	0.2 ± 0.1

Cultures were grown at 30 and 12°C ($D = 0.03\ h^{-1}$). Values represent the mean ± SD of data from three independent steady-state chemostat cultivations. $Y_{Glu/X}$, biomass yield on glucose; DW, dry weight.

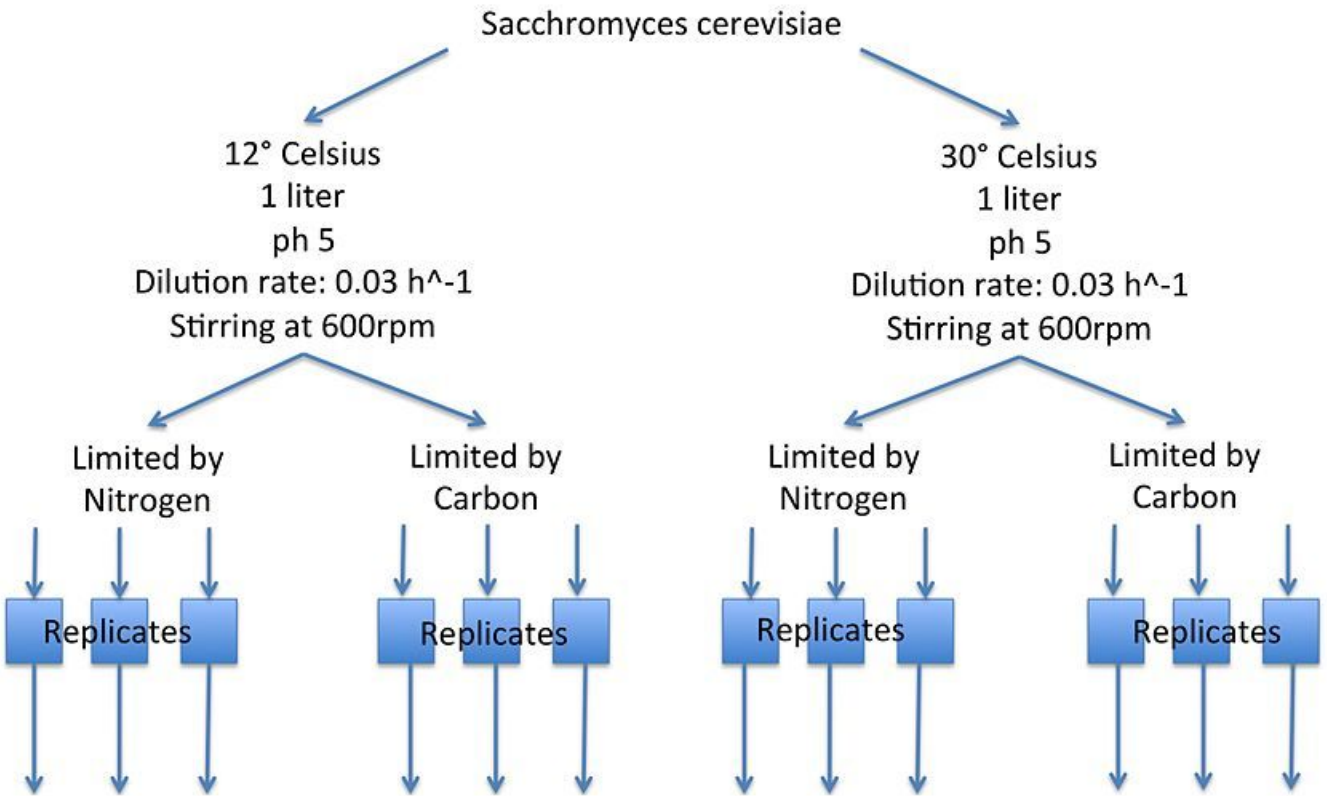
[a] Values expressed as mmol $\cdot\ g_{DW}^{-1} \cdot h^{-1}$.

Table 1

- ***S. Cerevisiae* is minimally affected by variation in temperature.**
- **Higher temperatures correlated with lesser amounts of a limiting nutrient corresponding residual residue.**
    - **Larger amounts of residual glucose at 12°C connected to possible contamination of gene sets.**

Tai et al., 2007

S. Cerevisiae Grown In Varying Conditions of Temperature and Nutrient Content



Microarrays

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Temperature and Nutrient Limitations Were Analyzed Using DNA Microarray Analysis

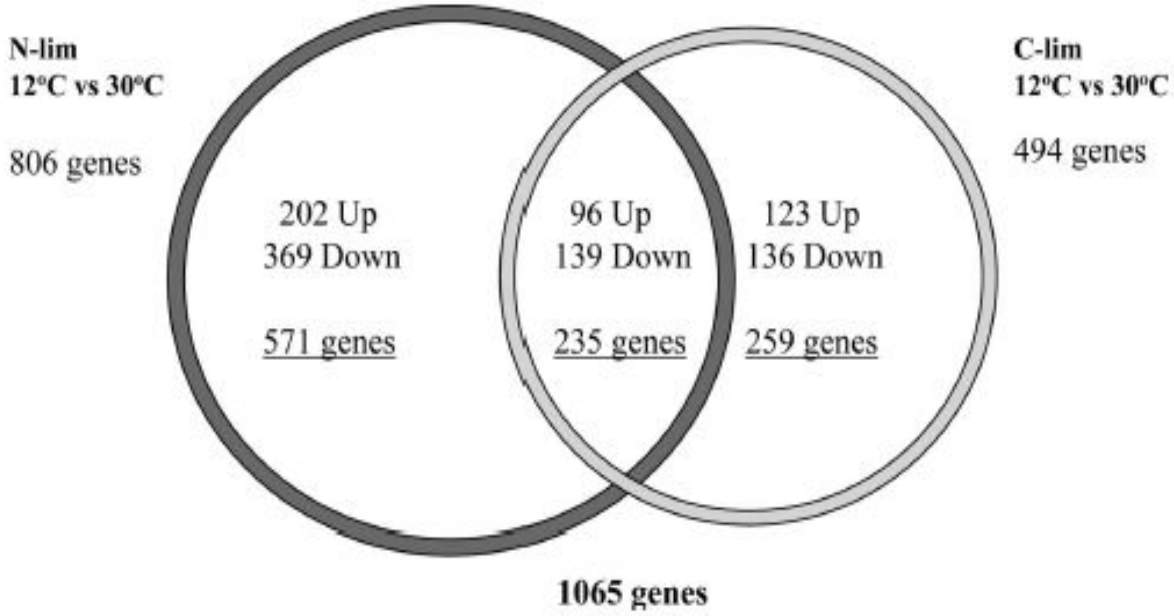
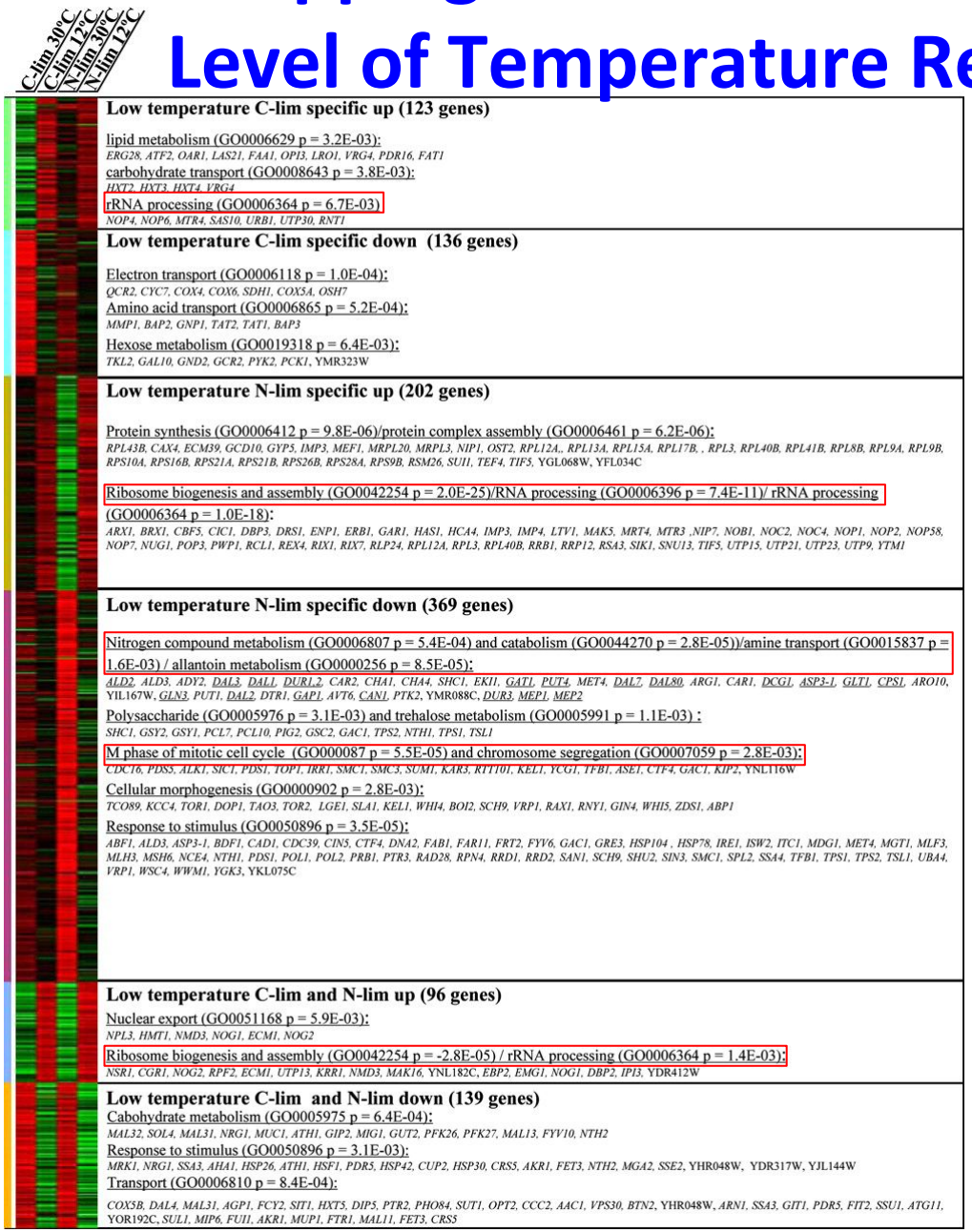


Figure 1

- **1065 represents the number of temperature responsive genes in *S. cerevisiae* genome.**

Tai et al., 2007

Heat Mapping Was Used To Identify Transcription Level of Temperature Responsive Genes



- Goal was to identify regulatory networks involved in acclimation of *S. cerevisiae* to low temperature.
- Observed changes in
  - Transporters of limiting nutrient
  - Translational machinery
- NCR genes and catabolite repression underlined

Figure 2

Tai et al., 2007

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S. cerevisiae Stores Protein and Carbohydrate In Chemostat Culture

Limiting nutrient	Growth temperature (°C)	Biomass dry weight ($g_{DW} \cdot l^{-1}$)	Whole cell protein ($g_{protein} \cdot g_{DW}^{-1}$)	Biomass nitrogen content ($mg_{nitrogen} \cdot g_{DW}^{-1}$)	Trehalose ($g_{equivalent\ glucose} \cdot g_{DW}^{-1}$)	Glycogen ($g_{equivalent\ glucose} \cdot g_{DW}^{-1}$)
Glucose	12	1.71 ± 0.09	0.40 ± 0.01	nd	<0.005	0.06 ± 0.01
Glucose	30	1.89 ± 0.06	0.43 ± 0.01	nd	0.02 ± 0.00	0.04 ± 0.00
Ammonium	12	2.27 ± 0.05	0.47 ± 0.03	63 ± 3	<0.005	0.02 ± 0.00
Ammonium	30	3.53 ± 0.01	0.34 ± 0.01	41 ± 2	0.04 ± 0.00	0.05 ± 0.01

Cultures were grown at 30 and 12°C ($D = 0.03\ h^{-1}$). Values represent the mean ± SD of data from three independent steady-state chemostat cultivations. DW, dry weight; nd, not determined.

Table 2

- **Trehalose and glycogen biosynthesis occurs under stress conditions.**
  - **Biosynthesis varies with temperature.**
- **Reason for storage of carbohydrates in nonfreezing temperature in unclear.**
  - **Trehalose was not produced in tps1 and tps2 strains, yet did not affect viability.**

Tai et al., 2007

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Promoter Analysis Reveals Regulation Trends in Gene Regulation

(A) 5′ upstream cis-regulatory motif

Regulatory cluster	Motif name	Putative-binding protein	Promoter element	occ[a]	Expected occ[b]	occ E[c]
Low Temperature C-lim Up			—			
Low Temperature C-lim Up			—			
Low Temperature N-lim Up	—	—	TGAAAAA	206	113.04	2.30E-11
	PAC	—	CGATGAG	57	17.49	6.1E-14
	—	—	TGAGATG	49	16.3	4.1E-07
Low Temperature N-lim Down	GATAA	Gln3/Gat1/Dal80/Gzf3	AGATAAG	203	102.57	3.1E-15
	STRE	Msn2/Msn4	ACCCCTT	29	8.73	1.6E-03
Low Temperature C- and N-lim Up	PAC	—	CGATGAG	30	8.39	5.0E-05
Low Temperature C- and N-lim Down	—	—	CGTCCAC	13	2.85	7.8E-03

(B) Overrepresentation of transcription factors (TF) binding targets

Regulatory cluster	Factor	p value	K[d]	P[e]
Low Temperature C-lim Up	Mbp1p	1.6E-03	10	65
Low Temperature C-lim Down	Hap2-Hap1	3.9E-05	3	4
	Hap3-Hap1	9.9E-06	3	3
Low Temperature N-lim Up	Fhl1p	3.4E-05	19	203
	Sfp1p	1.3E-03	7	51
Low Temperature N-lim Down	Gln3p	2.1E-07	20	92
	Gln3-Dal82	5.5E-07	8	15
	Hap2-Dal82	6.8E-05	5	9
Low Temperature C- and N-lim Up				
Low Temperature C- and N-lim Down	Aft2p	7.5E-04	10	34
	Hsf1p	3.0E-08	16	133
	Nrg1p	7.6E-07	14	128
	Phd1p	3.3E-04	9	99
	Rcs1p	1.1E-04	9	86
	Rox1p	6.0E-05	8	62
	Sok2p	5.7E-05	9	79
	Nrg1-Aft2	6.0E-05	5	20
	Phd1-Nrg1	1.4E-05	7	37
	Rox1-Phd1	7.8E-05	5	21
	Sok2-Nrg1	4.3E-07	8	33

(A) Significantly overrepresented *cis*-regulatory binding motifs in 5′ upstream regions. (B) Significantly overrepresented promoter elements that bind known transcription factors (TF) or TF pairs according to ChiP-on-chip analysis (Harbison *et al.*, 2004). C-Lim, glucose-limited; N-Lim, ammonium-limited.

[a] The number of occurrences of promoter element in the regulatory cluster.

[b] Expected number of occurrences of the promoter element in a randomly chosen cluster of genes of the same cluster size.

[c] The probability of finding the number of patterns with the same level of overrepresentation, which would be expected by chance alone.

[d] Number of genes in category in cluster.

[e] Number of genes in category in genome.

Table 3

- **STRE elements exist in promoters of downregulated genes in N-limited cultures**
- **Upregulation in both conditions show PAC regulatory motifs in promoters**
- **Common promoter sequences show possible regulation relationships**

Tai et al., 2007

Genes Common to All Researchers Were Categorized According to Regulation

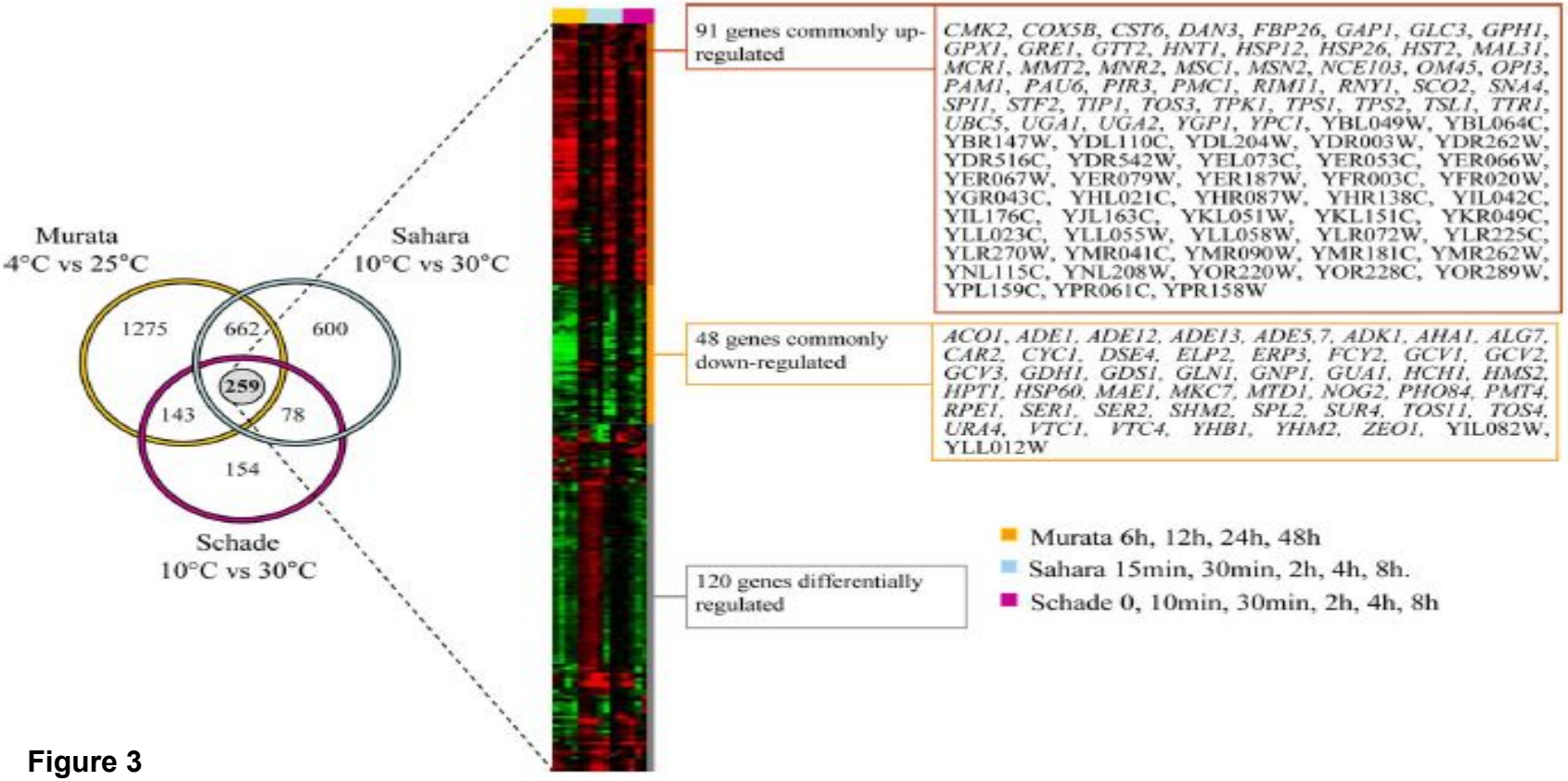

Figure 3

- **Sahara and Schade tested cold shock, dropping temperature to between 10 and 20 degrees Celsius**
- **Murata tested cold shock at temperatures below 10 degrees Celsius, which caused cell growth to cease.**

Tai et al., 2007

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Overlapping Genes Showing the Same Temperature Response

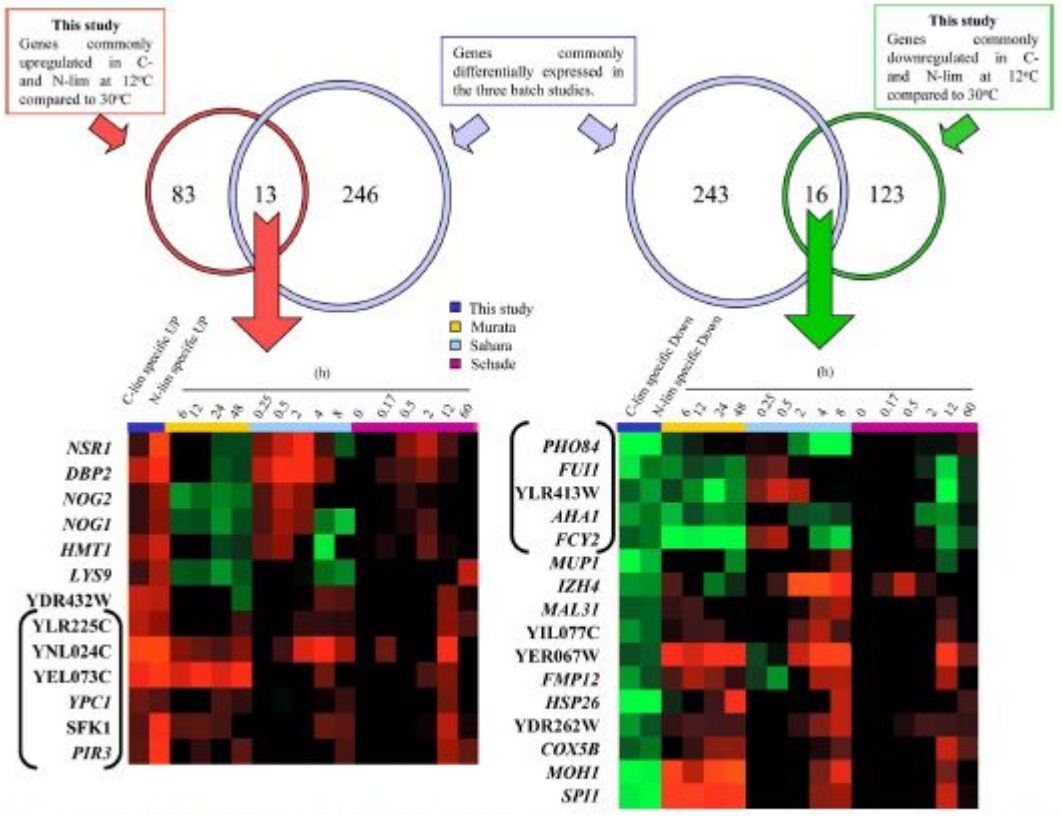

Figure 4

- Chemostat study compared with Sahara et al. 2002, Schade et al. 2004, and Murata et al. 2006
- 29 genes total were in common, only 11 showed consistency

Tai et al., 2007

Few Genes Simultaneously Respond to Temperature and Growth Rate

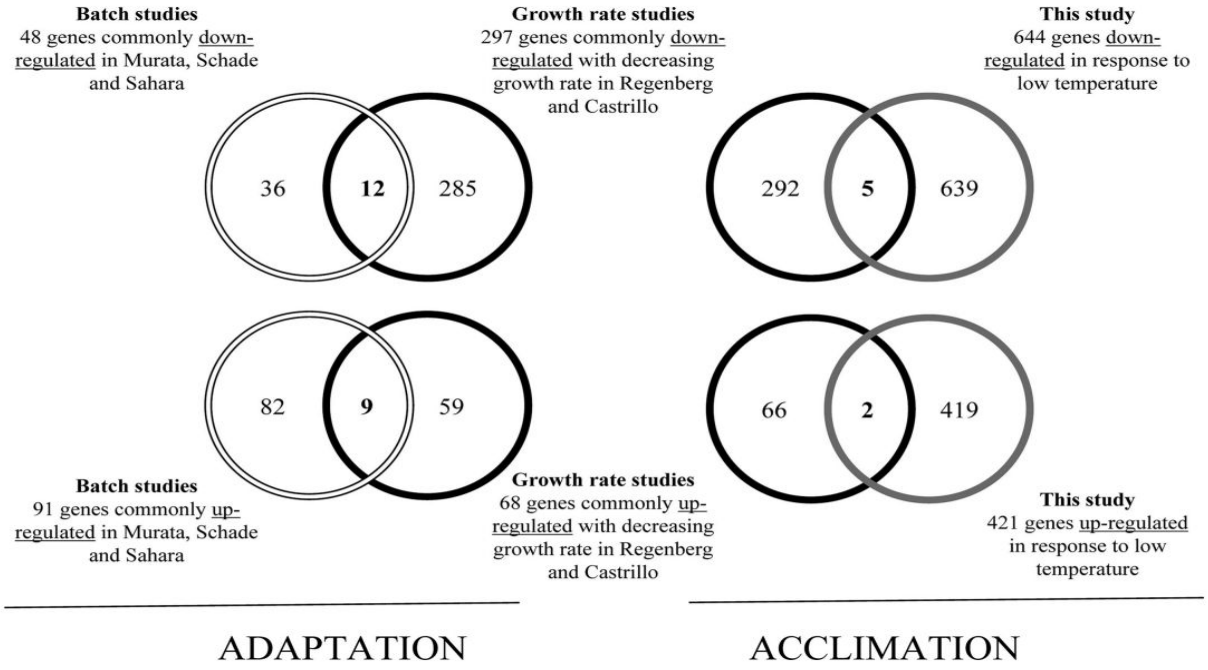

Figure 5

- **Studies examined changes in gene regulation in response to a decrease in growth rate compared to both the batch studies and study data for overlap in gene regulation.**
- **A very small number of genes overlap in response to both temperature decrease and growth rate decrease.**

Tai et al., 2007

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One Third of Low Temperature Response Genes in the Batch Studies are Attributed to ESR

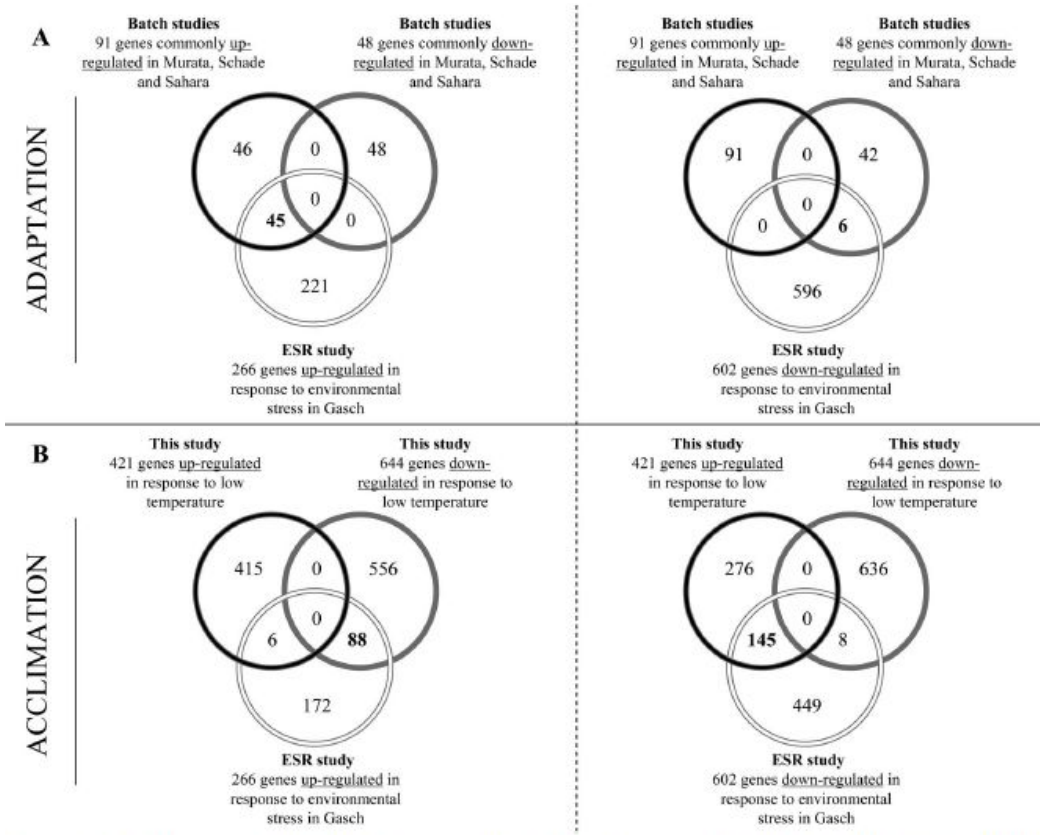

Figure 6

- **ESR: environmental stress response**
  - **General mechanism responds to multiple stimuli**
- **Batch and chemostat genes compared with Gasch et al. 2000**
- **Some genes showed opposite results in response to low temperatures**

Tai et al., 2007

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Experimental Design Differences Distinguish Dahlquist Lab Data from Tai et al. Data

	Dahlquist Lab	**Tai et al.**
Temperature	Cold Shock: 13℃ Recovery: 30℃	Cold Shock: 12℃ Recovery: 30℃
Time Points	15, 30, 60, 90, 120 min.	“Random Sampling”
Media	YPD rich media	Synthetic media limited by carbon or by nitrogen
Replicates	3-5 replicates	3 replicates
Strain	*S. cerevisiae,* Δgln3	*S. cerevisiae* strain CEN.PK113-7D

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25% of Δgln3 Genes Showed Significant Difference In Expression Over Time

ANOVA	*dGLN3*
p < 0.05	2393 (38.7%)
p < 0.01	1453 (23.5%)
p < 0.001	696 (11.2%)
p < 0.0001	320 (5.2%)
B & H p < 0.05	1549 (25.0%)
Bonferroni p < 0.05	155 (2.5%)

Genes Were Clustered According to Expression Pattern Using STEM Software

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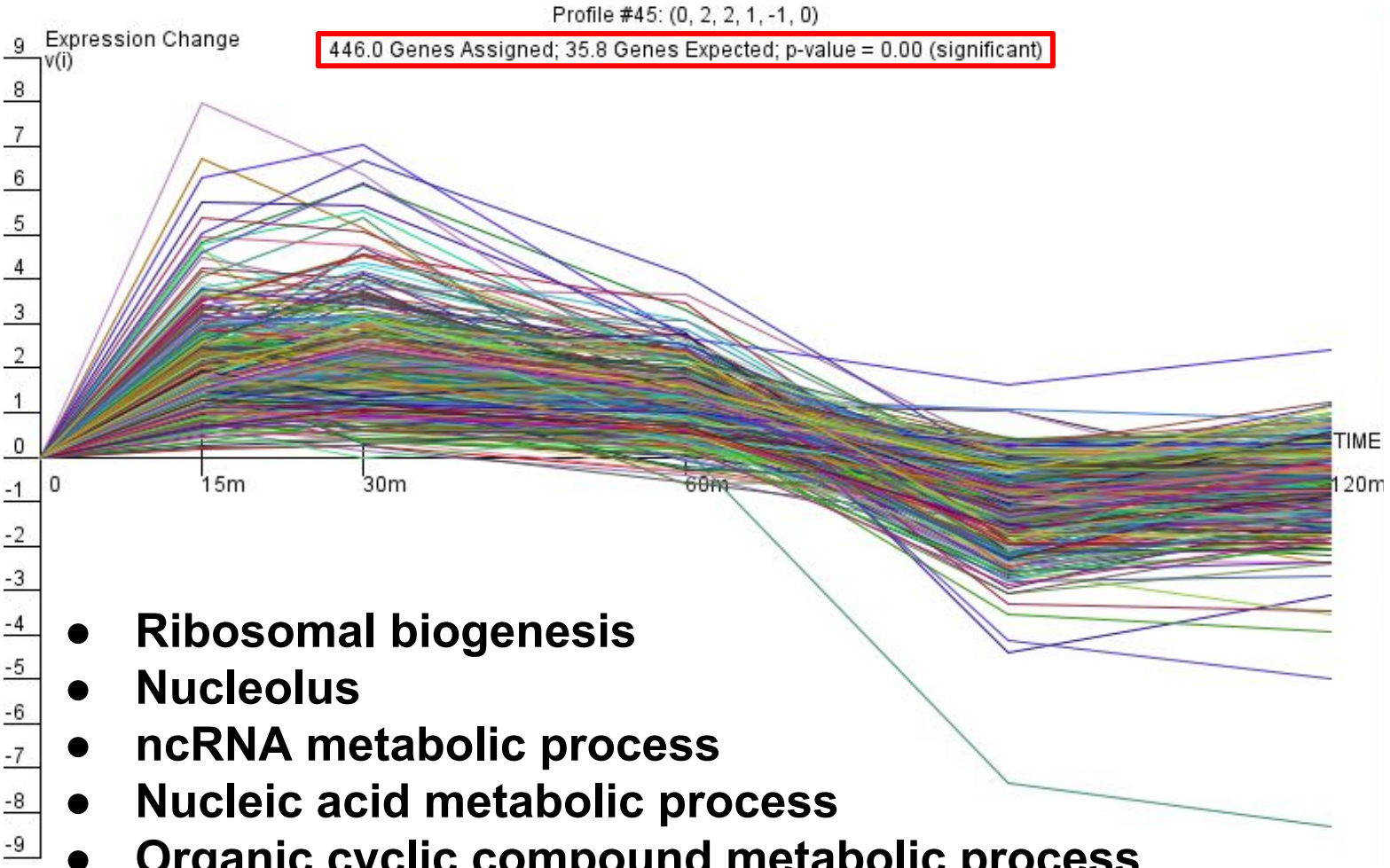
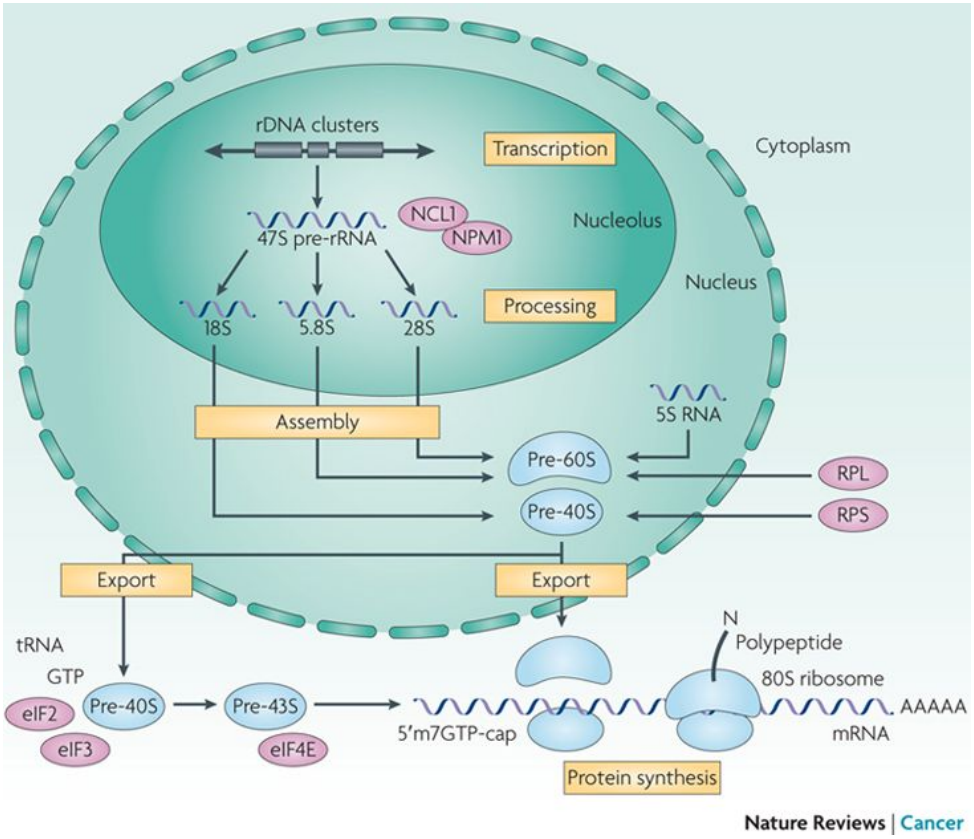
Profile 45 Indicated Upregulation During Cold Shock and Down Regulation During Recovery



- Ribosomal biogenesis
- Nucleolus
- ncRNA metabolic process
- Nucleic acid metabolic process
- Organic cyclic compound metabolic process
- Maturation of 5.8 rRNA from tricistronic rRNA transcript

Ribosomal Biogenesis is Upregulated During Cold Shock in dGLN3

- **Nucleolus: prime function is to transcribe nuclear DNA into 45S ribosomal precursor RNA and process RNA into 5.8S, 18S and 28S components**
- **ncRNA metabolic process: chemical reactions and pathways involving ncRNA transcripts**
- **Maturation of 5.8 rRNA from tricistronic rRNA transcript: processing of transcripts that contain small, large and 5.8S rRNA**

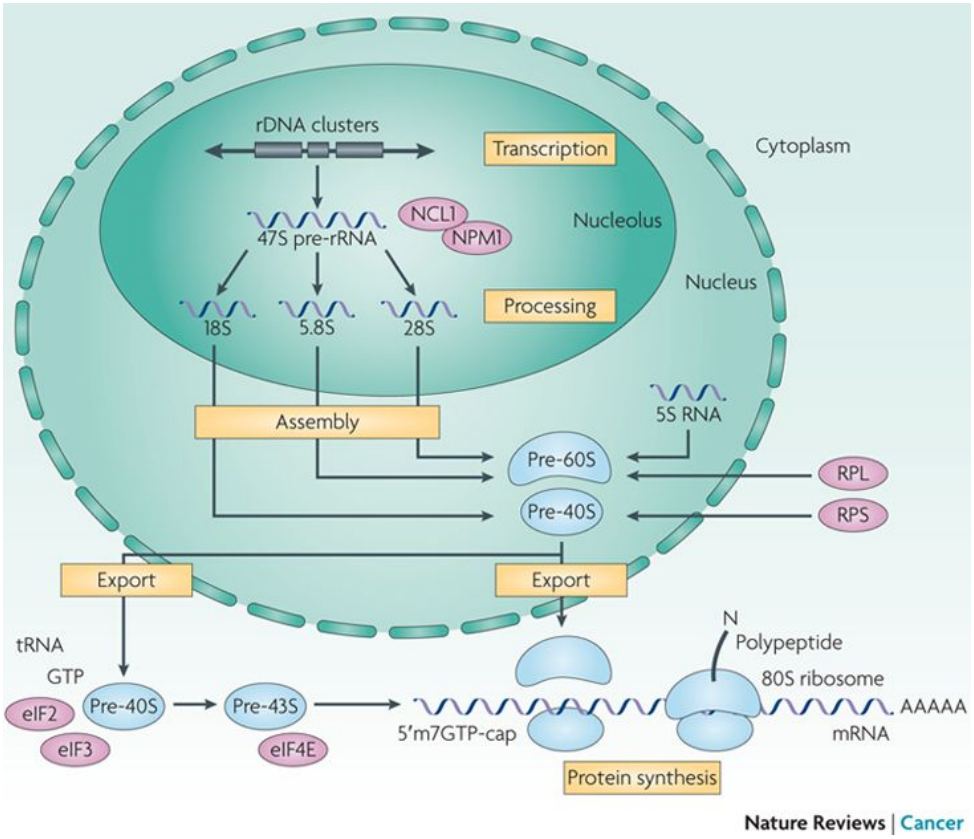


http://www.nature.com/nrc/journal/v10/n4/fig_tab/nrc2819_F3.html

Ribosomal Biogenesis is Upregulated During Cold Shock in dGLN3

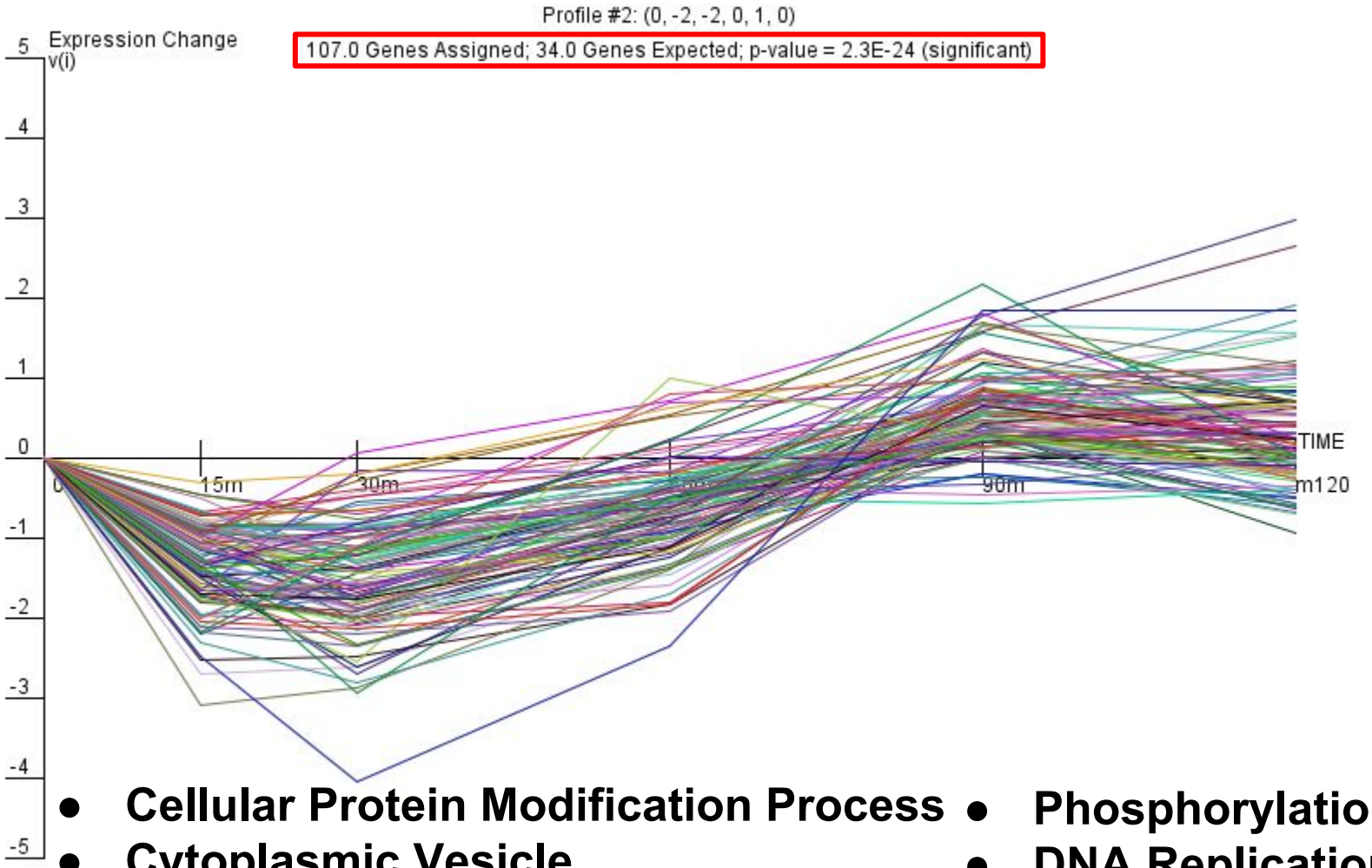
- Nucleic acid metabolic process
- Organic cyclic compound metabolic process
- Ribosomal biogenesis

- Increased ribosome genesis allows for increased protein expression
- Allows for cell to produce proteins that may protect it from cold shock
- Infanzon et al. (2010) found similar results



http://www.nature.com/nrc/journal/v10/n4/fig_tab/nrc2819_F3.html

Profile 2 Exhibits a Variance in DNA Replication During Onset of Cold Shock through Revcovery

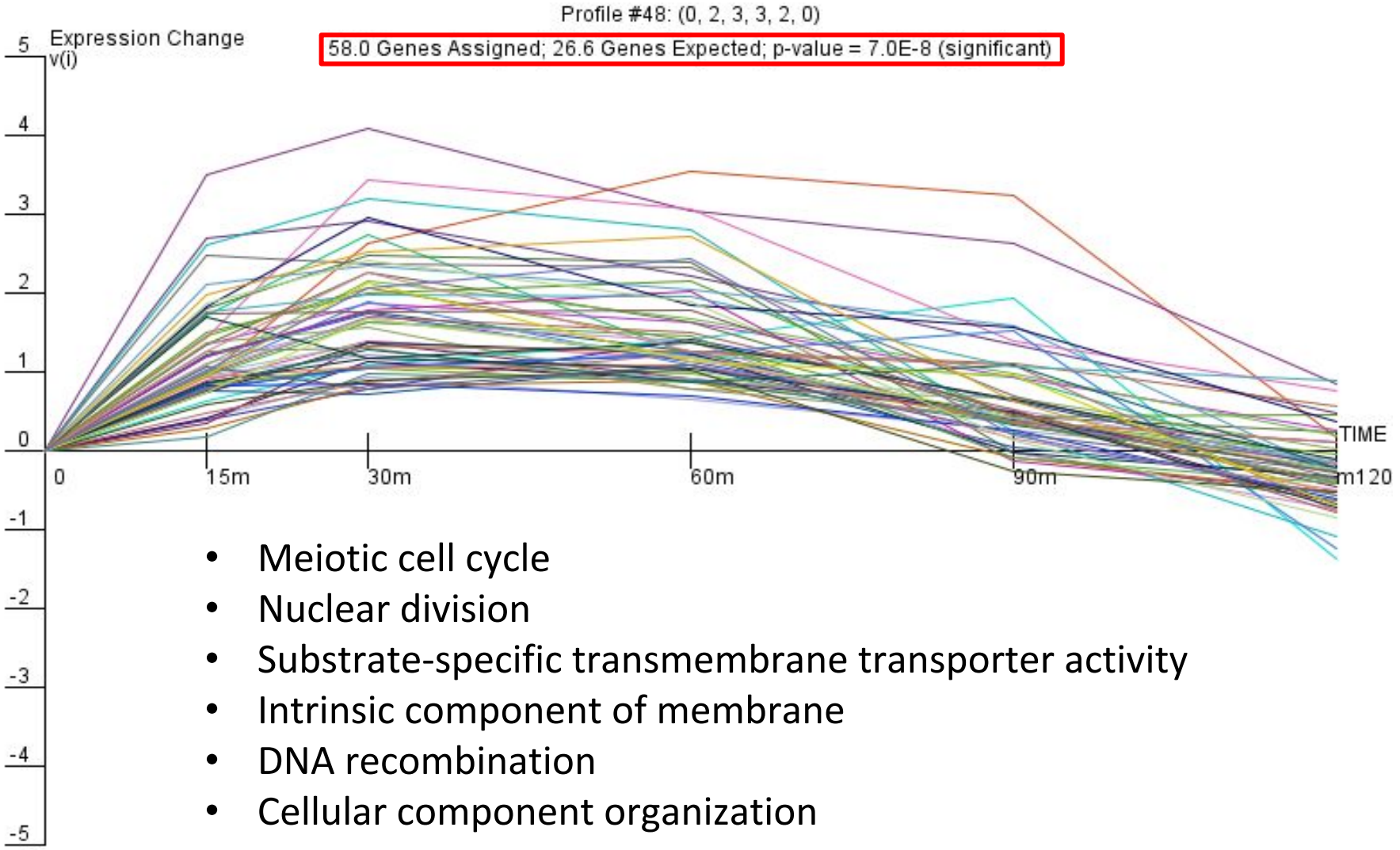


- Cellular Protein Modification Process
- Cytoplasmic Vesicle
- Mitotic Cell Cycle Phase Transition
- Phosphorylation
- DNA Replication
- Kinase Activity

DNA Synthesis is Initially Affected by Cold Shock then is Upregulated Through Recovery

- **Down regulation followed by an upregulation**
- **DNA synthesis and related processes are repressed during the period of cold shock.**
- **The other processes seem to inform the overall theme of *DNA replication*.**
    - **This suggests that once the cells cleared the cold shock the cells were able to reactivate pathways of DNA synthesis in the cell cycle, indicating that the cells do not allocate resources for growth amidst the environmental stress.**
    - **During cold stress proteins bind to single-stranded regions of the replication fork and blocks DNA replication (Ermolenko 2002).**

Profile 48 Shows Upregulation of Meiosis Related Processes

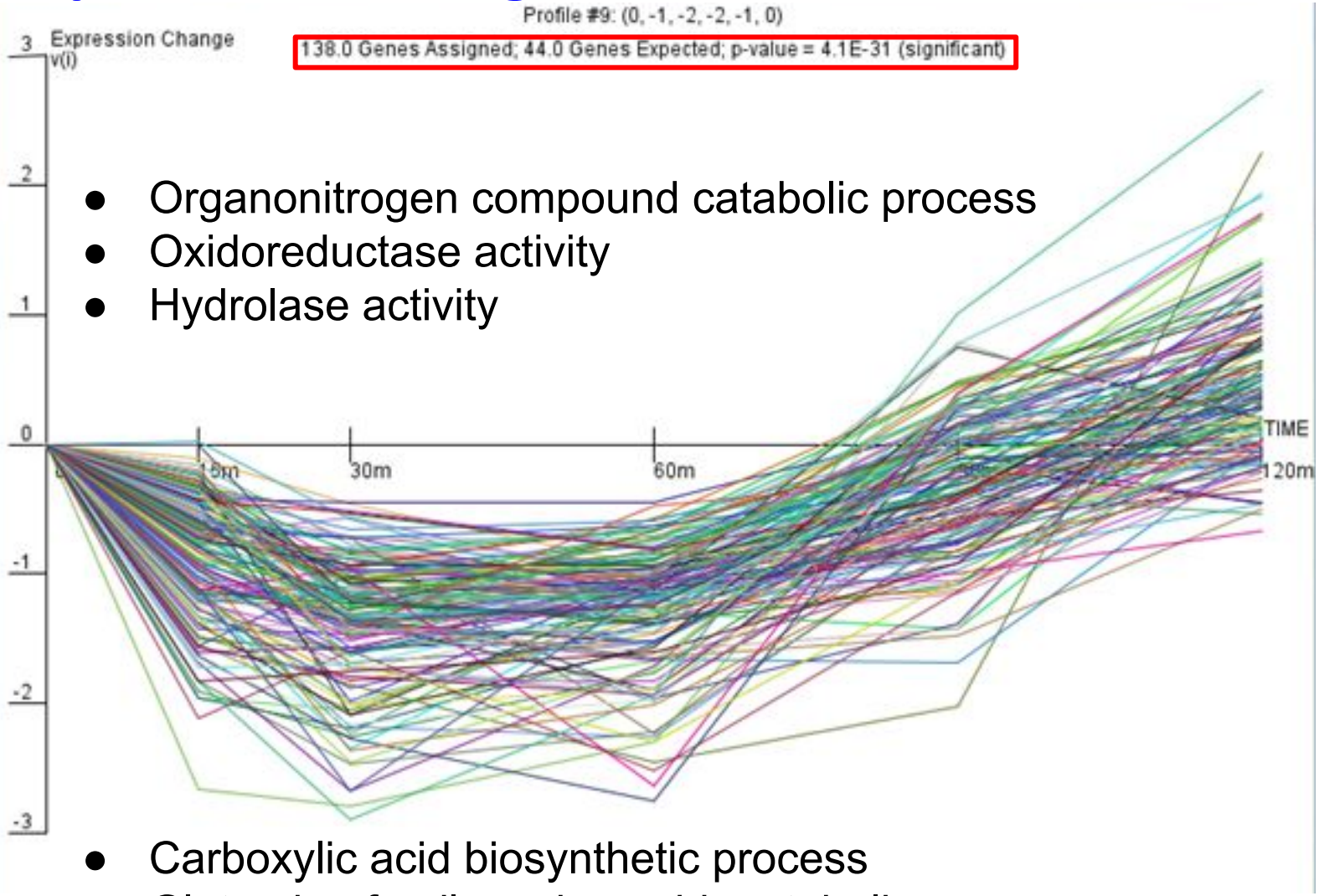


- Meiotic cell cycle
- Nuclear division
- Substrate-specific transmembrane transporter activity
- Intrinsic component of membrane
- DNA recombination
- Cellular component organization

Cold Stress Promoted Up-regulation of Meiosis Inhibiting Genes

- **Overall Theme: Meiosis**
- **This profile's graph contains slight upregulation followed by a slight douwnregulation of genes associated with meiosis.**
  - **Down regulation occurs after cold shock.**
- **Cold stress may positively regulate meiosis, while it is known that heat stress will denature proteins and prevent meiosis.**
  - **Process has greater tolerance for colder temperatures.**
- **It is likely that cold stress causes inhibition of meiosis and related functions.**
  - **Research by Xiang-Ping Zhu et. al. suggests inhibition of meiosis during cold shock and then a return to normal functioning after temperature is readjusted.**

Profile 9 Shows a Downregulation of Gene Expression During Cold Shock Time Points



- Organonitrogen compound catabolic process
- Oxidoreductase activity
- Hydrolase activity

- Carboxylic acid biosynthetic process
- Glutamine family amino acid metabolic process
- Transferase activity, transferring nitrogenous groups

Glutamine family amino acid biosynthesis was downregulated during cold shock

- **Organonitrogen compound catabolic process: The chemical reactions and pathways resulting in the breakdown of organonitrogen compound**
- **Glutamine family amino acid biosynthesis: The chemical reactions and pathways resulting in the formation of amino acids of the glutamine family, comprising arginine, glutamate, glutamine and proline**
- **Glutamine based amino acids contain nitrogen**
  - **Decreased nitrogenous organic compound catalysis results in less nitrogen available for biosynthesis (Cai 2012)**

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- Experimental design differences distinguish Dahlquist Lab data from Tai et al.
- Analysis of Δgln3 revealed significant difference in gene expression over time.
- Model expression profiles show that many biological processes are affected by cold shock.
- **Ribosome biogenesis, mitosis, and nitrogen catabolism genes were affected in Tai et al. and Dahlquist Lab data analysis**

Ribosome Biogenesis, Mitosis, and Nitrogen Catabolism Genes Were Affected in Tai et al. and Dahlquist Lab

Tai et al.	Similarities	Dahlquist Lab
Down regulation of target genes for glucose catabolite repression in cold shock conditions.	Genes involved with ribosome biogenesis and assembly upregulated in cold shock, but not in recovery. Down regulation of M-phase and chromosome segregation in cell cycle. Specific downregulation of genes responsible for nitrogen compound catabolism	Upregulation of genes related to meiosis inhibition.

Summary

- **Limitations of previous studies led to development of experiment using chemostat culture and low temperature acclimation.**
- ***S. cerevisiae* was grown in four different experimental conditions.**
- **DNA microarray analysis was used to analyze growth limitations applied to *S. cerevisiae.***
- ***S. cerevisiae* stores carbohydrates during chemostat culture for unknown reasons.**
- **Promoter analysis reveals regulation trends in gene regulation.**
- **Temperature response genes overlap in expression.**
- **Environmental stimulation responses differed in batch vs. chemostat cultures.**
- **Experimental design differences distinguish Dahlquist Lab data from Tai et al.**
- **Analysis of Δgln3 revealed significant difference in gene expression over time.**
- **Model expression profiles show that many biological processes are affected by cold shock.**
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References

Cai, L., & Tu, B. P. (2012). Driving the cell cycle through metabolism. Annual review of cell and developmental biology, 28, 59-87. doi: 10.1146/annurev-cellbio-092910-154010

Ermolenko, D. N., and G. I. Makhatadze. "Bacterial cold-shock proteins." Cellular and Molecular Life Sciences CMLS 59.11 (2002): 1902-1913. doi: 10.1128/jb.171.5.2337-2346.1989

Infanzon, B. A., Buckmelter, K. M., Liu, E. M., Sakhon, O. S., Citti, W. T., & Dahlquist, K. D. (2010). Saccharomyces cerevisiae responds to cold shock by inducing the transcription of ribosome biogenesis genes. *The FASEB Journal*, *24*(1 Supplement), 833-13.

Tai, S. L., Daran-Lapujade, P., Walsh, M. C., Pronk, J. T., & Daran, J. M. (2007). Acclimation of Saccharomyces cerevisiae to low temperature: a chemostat-based transcriptome analysis. Molecular Biology of the Cell, 18(12), 5100-5112. doi: 10.1091/mbc.E07-02-0131

Zhu, XP., You, F., Zhang, PJ. et al. Mar Biotechnol (2006) 8: 312. doi:10.1007/s10126-006-5128-3

Acknowledgments

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Good luck with finals!