What is I M R D Anyway?

Susan Ruff
20.109
Spring 2007
Lab Reports (& Research Articles) tell a story.

**INTRODUCTION**
What you studied, and why it’s important.

**METHODS**
How you studied it.

**RESULTS**
What you saw.

**DISCUSSION**
Your interpretation of what you saw.

All examples are taken from or based on “The Deubiquitylation Activity of Ubp8 Is Dependent upon Sgf11 and Its Association with the SAGA Complex” by Kenneth K. Lee, et al., *Molecular and Cellular Biology*, Feb. 2005, p. 1173-1182.
INTRODUCTION What you studied, and why it’s important.

**Important large context**
- connects to
- **Smaller context**
  - connects to
  - **Even smaller context**
  - connects to
- **Specific area of research**

**Background funnel:**

**GAP:** What is not known about the specific area of research?

**Purpose:** What is the purpose of this research (and how does it help to fill the identified gap?)

**Approach:** What is done to achieve the stated purpose?
INTRODUCTION  What you studied, and why it’s important.

Role of chromatin in cell
conversion from active to inactive regulated by
Histone proteins
post-translational modifications include
Acetylation & Ubiquitylation (H2B)
both caused by
SAGA & SLIK
this activity depends on
Ubp8

Background funnel:

GAP: Little is known about UBPs.
Purpose: Understand how Ubp8 deubiquitylates H2B in context of SAGA.
Result: Identified Sgf11
Revised purpose: Understand relationship between Ubp8 & Sgf11 & how it relates to SAGA & SLIK.
Approach: [See article for two specified tests.]
MATERIALS & METHODS  How you studied it.

Professionally written:
*S. cerevisiae* strains. The genotypes of strains used for this study are listed in Table 1. Individual TAP-tagged strains and deletion strains were obtained from Open Biosystems. TAP-tagged strains with deletions were obtained by crossing and dissecting individual TAP-tagged strains and deletion strains.

Less professional:
We first obtained individual TAP-tagged strains and deletion strains from Open Biosystems. These strains are listed in Table 1. Then we crossed and dissected these strains to obtain TAP-tagged strains with deletions, which are also listed in Table 1.

Write methods topically, not chronologically. Past tense passive voice is acceptable.
RESULTS  What you saw.

Tell your story, but avoid interpreting results.

…The purification of Ubp8 looked similar to purifications of SAGA (Fig. 1A, compare lanes 2 and 3). In order to confirm this, we performed mass spectrometry analysis (MudPIT) of the purification product and confirmed that Ubp8 is only associated with proteins that were previously identified in the SAGA, SLIK, and ADA HAT complexes (Fig. 1C) (22)…

DISCUSSION  Your interpretation of what you saw.

…One possibility is that SPT20 may help to tether Ubp8 and Sgf11 to SAGA, since the loss of SPT20 increases H2B ubiquitylation levels, but not quite to the extent of a Ubp8 deletion (10).

If another reasonable researcher could dispute a claim, that claim belongs in the Discussion.
Design figures and tables carefully.

Readers skim by looking only at figures, tables, and captions. Tell your story.

Introduce each figure by number in the text.

The figure legend explains each part of the figure.
Design figures and tables carefully.

### TABLE 1. *S. cerevisiae* strains used for this study

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genotype</th>
<th>Reference or source</th>
</tr>
</thead>
<tbody>
<tr>
<td>By4741</td>
<td>his3Δ1 leu2Δ0 met15Δ0 ura3Δ0</td>
<td>Open Biosystems</td>
</tr>
<tr>
<td>YKL101</td>
<td>mata his3Δ1 leu2Δ0 met15Δ0 ura3Δ0:Ada2-TAP::HIS3 MX6</td>
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<td>YKL134</td>
<td>mata his3Δ1 leu2Δ0 met15Δ0 ura3Δ0:Ada2-TAP::HIS3 MX6 ubp8Δ::KANMX6</td>
<td>This study</td>
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</tr>
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<tr>
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<td>mata his3Δ1 leu2Δ0 met15Δ0 ura3Δ0:Ubp8-TAP::HIS3 MX6 sgf11Δ::KANMX6</td>
<td>This study</td>
</tr>
<tr>
<td>YKL138</td>
<td>mata his3Δ1 leu2Δ0 met15Δ0 ura3Δ0:sgf11-TAP::HIS3 MX6 ubp8Δ::KANMX6</td>
<td>This study</td>
</tr>
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<td>YKL60</td>
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<td>YKL120</td>
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<tr>
<td>YKH045</td>
<td>MATa ura3-1 leu2,3,-112 his3-11,-15 trp1-1 ade2-1 hkb1-1 hkb2-1 pRS314 (Flag-HTB1-CEN-TRP1) pRG145 (GAPDHprom-3HA-URA3 integrative)</td>
<td>10</td>
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<tr>
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<td>Mark Chandy</td>
</tr>
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</table>

Unlike for figures, the table number and title go on top of the table.
Lab Reports (& Research Articles) tell a story.

**INTRODUCTION** What you studied, and why it’s important.

**METHODS** How you studied it.

**RESULTS** What you saw.

**DISCUSSION** Your interpretation of what you saw.

The story should be cohesive.
The title and abstract must attract your audience.

**Title**  About 10 words long. Include important keywords.

**Abstract**  Less than 250 words.

**Introduction**
Covalent modifications of the histone tails and the cross talk between these modifications are hallmark features of gene regulation. The SAGA histone acetyltransferase complex is one of the most well-characterized complexes involved in these covalent modifications. The recent finding that the removal of the ubiquitin group from H2B is performed by a component of SAGA, Ubp8, is intriguing as it assigns two posttranslation modification processes to one complex. In this work, we characterize the association of Ubp8 with SAGA and the effect that acetylation and deubiquitylation have on one another in vitro and in vivo. We found not only that Ubp8 is a part of the SAGA complex, but also that its deubiquitylation activity requires Ubp8’s association with SAGA. Furthermore, we found that the Ubp8 association with SAGA requires Sgf11 and that this requirement is reciprocal. We also found that the acetylation and deubiquitylation activities of SAGA are independent of one another. However, we found that preacetylating histone H2B inhibited subsequent deubiquitylation. Additionally, we found that increasing the ubiquitylation state of H2B inhibited the expression of the ARG1 gene, whose repression was previously shown to require the RAD6 ubiquitin ligase. Taken together, these data indicate that the expression of some genes, including ARG1, is regulated by a balance of histone H2B ubiquitylation in the cell.

**Purpose**

**Results**

**Conclusion**
<table>
<thead>
<tr>
<th>Order of sections in paper</th>
<th>Possible order of writing</th>
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<tr>
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<td>Figures and Tables</td>
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<td>Authors</td>
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<tr>
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</table>
Plan time to set the paper aside.

Allow time over several days.
Write.

Sleep
Read
Revise
Print & proofread.
Writing Help

The Writing Center
web.mit.edu/writing

The Mayfield Handbook of Scientific and Technical Writing

Academic Integrity at the Massachusetts Institute of Technology: A Handbook for Students

“The Science of Scientific Writing” by Gopen & Swan
A Google search will generate many hits.

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20.109 writing Instructor
Harlan Breindel breindel@mit.edu