How to submit a manuscript for publishing?

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Adapted from a presentation by Dr. Sandra L. Schmid
Editor in Molecular Biology of the Cell

When to write a paper

- When you have an important discovery to report.
- When you have a complete story to tell.
- When you've made a significant advance.
- When your results are worth communicating to your field.
- When you've developed a new technique.

How to start:

- Gather the data
- Put together your figures
- Decide if you have a story and a bottom line
- Start by outlining your Results section

Molecular Cell
Article

Structural and Functional Roles of Daxx SIM Phosphorylation in SUMO Paralog-Selective Binding and Apoptosis Modulation

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SUMMARY

Small ubiquitin-like modifier (SUMO) conjugation and interaction are increasingly associated with various cellular processes. However, little is known about the cellular signaling mechanisms that regulate proteins for distinct SUMO paralog conjugation and interactions. Using the transcriptional coregulator Daxx as a model, we show that SUMO paralog-selective binding and conjugation are regulated by phosphorylation of the Daxx SUMO-interacting motif (SIM). NMR structural studies show that Daxx ^{732}E-I-I-V-L-S-D-S-D^{740} is a bona fide SIM that binds to SUMO-1 in a parallel orientation. Daxx-SIM is phosphorylated by CK2 kinase at residues S737 and S739. Phosphorylation promotes Daxx-SIM binding affinity toward SUMO-1 over SUMO-2/3, causing Daxx preference for SUMO-1 conjugation and interaction with SUMO-1-modified factors. Furthermore, Daxx-SIM phosphorylation enhances Daxx to sensitize stress-induced cell apoptosis via antiapoptotic gene repression. Our findings provide structural insights into the Daxx-SIM:SUMO-1 complex, a model of SIM phosphorylation-enhanced SUMO paralog-selective modification and interaction, and phosphorylation-regulated Daxx function in apoptosis.

INTRODUCTION

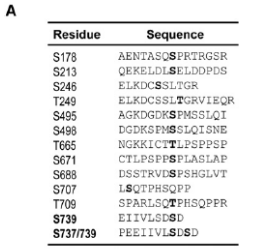
Covalent modification of proteins by a small ubiquitin-like modifier (SUMO) peptide on the lysine residue is an important post-translational event in the modulation of protein function (Gareau and Lima, 2010; Geiss-Friedlander and Melchior, 2007). The conjugation of mammalian SUMO isoforms (SUMO-1,-2, and -3) to protein substrates requires the E1-activating enzyme (SAE1/SAE2), the E2 conjugase (Ubc9), and, in some cases, E3 ligases (Gareau and Lima, 2010; Geiss-Friedlander and Melchior, 2007). In general, Ubc9 catalyzes the formation of an isopeptide bond between the C terminus of SUMO and the amino group of the target lysine via a direct interaction with a consensus motif ψ-K-X-E/D (where ψ is a large hydrophobic residue and X is any residue) present in protein substrates (Rodriguez et al., 2001; Sampson et al., 2001). We and others have shown that sumoylation can be facilitated by a SUMO-interacting motif (SIM) (Lin et al., 2006; Meulmeester et al., 2008; Zhu et al., 2008). SIM-dependent sumoylation was thought to be mediated by the noncovalent binding of SIM to the SUMO moiety of the Ubc9-SUMO thioester complex, allowing Ubc9 to more efficiently conjugate substrate lysine residue(s) not necessary localized in the consensus sumoylation motif. Currently, it is unclear whether protein conjugation with SUMO paralogs can be regulated by cellular signaling mechanisms that alter the affinity of SIM toward a selective SUMO paralog.

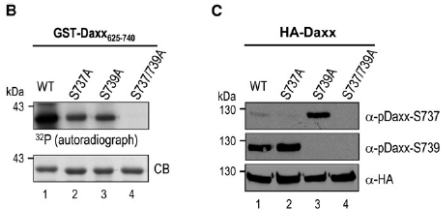
Daxx is a transcriptional coregulator involved in multiple cellular functions, including cell apoptosis (Salomoni and Khelifi, 2006; Shih et al., 2007). Daxx suppressed the expression of several antiapoptotic genes, correlating with its proapoptotic role in sensitizing stress-induced apoptosis (Croxton et al., 2006). The ability of Daxx to accumulate in PML nuclear bodies (PML NBs) also correlated with an increase in its pro-apoptotic function (Torii et al., 1999). We previously reported Daxx residues ^{733}I-I-V-L-S-D-S-D^{740} as a SIM important for Daxx sumoylation, Daxx interaction and repression of SUMO modified transcription factors and CBP, and Daxx targeting to PML NBs (Lin et al., 2006). Daxx SIM is evolutionally conserved among mammals (Figure 1A), while a similar sequence found in *Drosophila* can

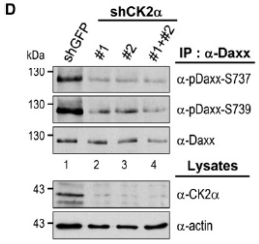
One example….

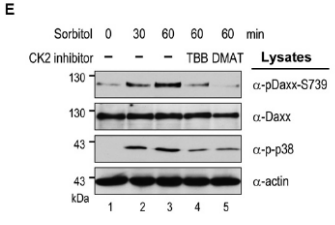
Gather your data, make your figures

True Chronological Order:

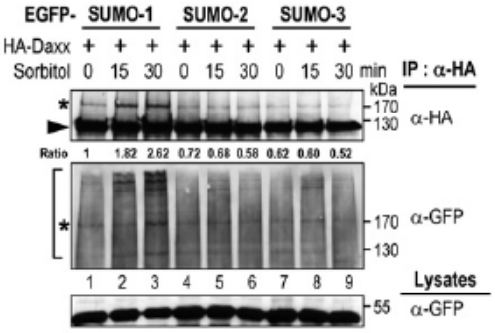


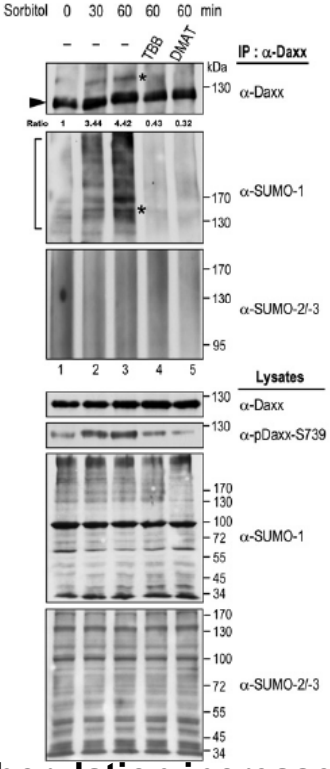


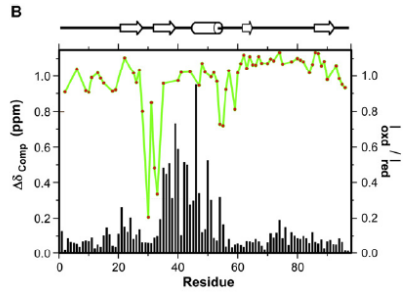


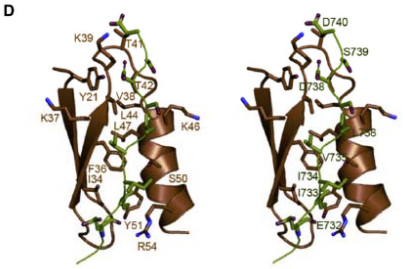


Daxx SIM phosphorylation in vitro & in vivo

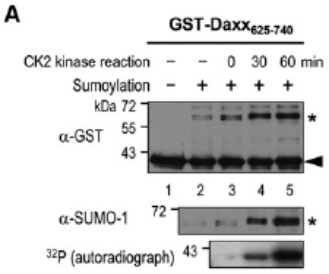


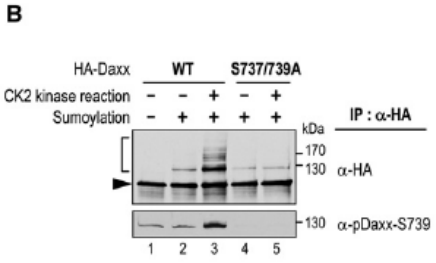






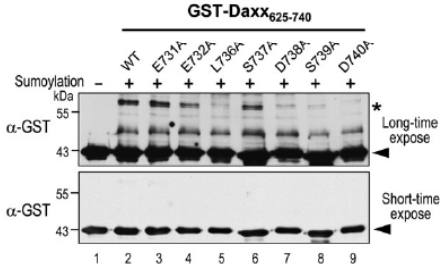
Daxx SIM/SUMO-1 NMR structure





SIM phosphorylation enhances Daxx sumoylation in vitro

Phosphorylation increases Daxx-SIM SUMO binding and paralog selection



SIM mutation affects Daxx sumoylation

Decide on the bottom line

Daxx SIM phosphorylation enhances SUMO paralog-selective binding

A strong paper/ complete story needs:

- **a discovery**
- **some mechanism**
- **broader implications**

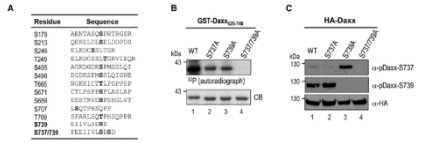
Arrange your figures like a storyboard

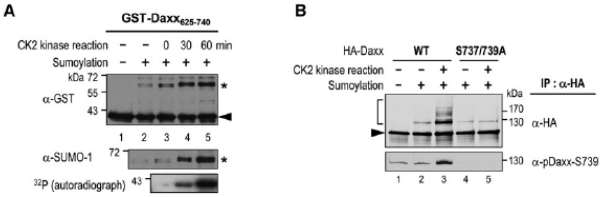
Logical Order: Telling a story

Initial Discovery: Discrepancy between in vitro and in vitro sumoylation of Daxx led to the finding of Daxx SIM phosphorylation

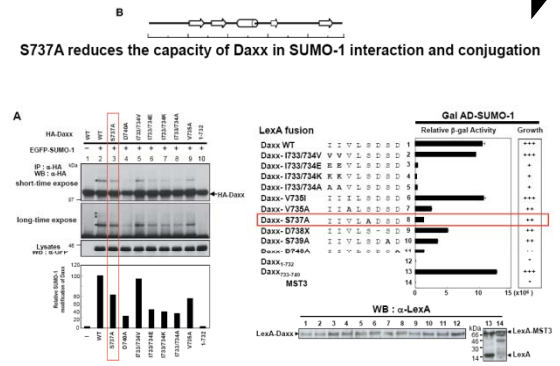
Mass spectrometry analysis revealed Daxx SIM phosphorylation

What is the consequence of Daxx-SIM phosphorylation?

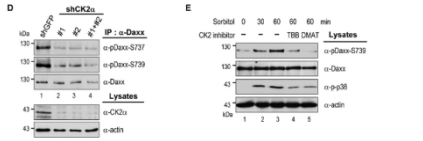




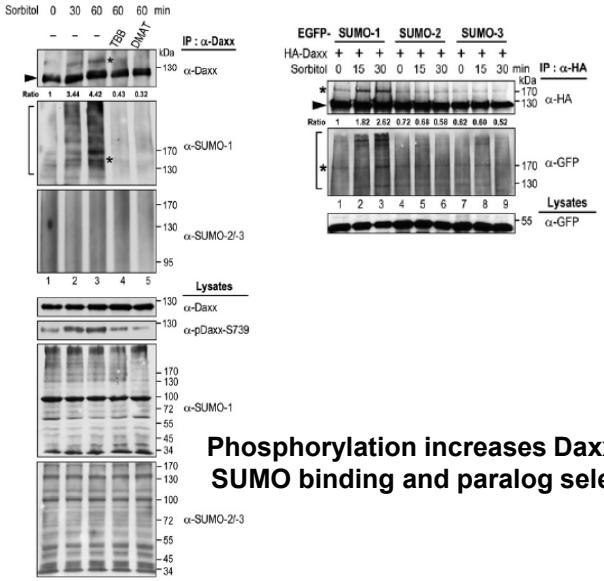
SIM phosphorylation enhances Daxx sumoylation in vitro



S737A reduces the capacity of Daxx in SUMO-1 interaction and conjugation



Daxx SIM phosphorylation by CK2 kinase in vitro & in vivo

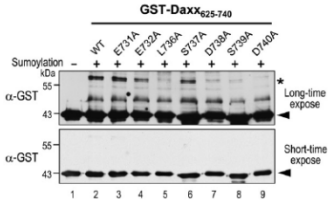


Phosphorylation increases Daxx-SIM SUMO binding and paralog selection

Lin, et al. Mol, Cell 2006, 24; 341-354

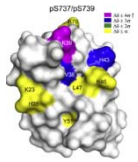
Daxx SIM/SUMO-1 NMR structure

Does phosphorylation preferentially enhance Daxx-SIM/SUMO-1 binding? What is a direct proof?



SIM mutation affects Daxx sumoylation

	Peptide	Kd (μM)	ITC △H (Kcal/mol)	ITC △S (cal/mol/deg)
SUMO-1	Daxx20	55.3 ± 14.2	0.83 ± 0.66	22.3 ± 2.6
	Daxx20-pS737/pS739	1.6 ± 0.4	-3.22 ± 0.98	15.9 ± 3.5
	Daxx20-pS737	4.6 ± 1.2	-1.91 ± 0.42	18.2 ± 2.0
	Daxx20-pS739	2.8 ± 0.3	-2.68 ± 0.74	16.5 ± 2.3
SUMO-3	Daxx20	102.5 ± 13.9	0.52 ± 0.09	20.1 ± 0.6
	Daxx20-pS737/pS739	11.9 ± 2.7	-1.46 ± 0.33	17.7 ± 0.7



and functional data

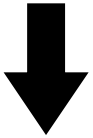
What is the cause?

Build an Outline Around Your Data/Results

A simple 2-step dance…….

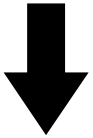
Introduce the experiment.

Why are you doing this? What do you expect to learn? Make and test a prediction.



Describe the result/finding.

What is the significance of the finding? What might it mean? What next important/interesting question is raised by these findings?



Introduce the experiment

Describe the result/finding

When you know what the story is, start writing

- Write a provisional title and abstract to express the bottom line.
- Keep focused on the bottom line. Exclude everything that does not contribute to that bottom line.
- Keep the logic flowing. Leave no gaps.

Decide where to submit your paper

Think about:

- Your audience: broad or specialized?
- Your presentation:

  - simple or more complex take-home message?

  - How many figures?

  - Should Results/Discussion be combined? How much do you have to say about your findings?
- The journal's scope and goals.

  Where were similar papers published?

  Who will manage the review?
- Ask others to help assess the degree of novelty in your work. Ask them to be critical.

Information for Authors

Molecular Cell publishes research articles and review material that focus on analyses at the molecular level, with an emphasis on new mechanistic insights. Launched in 1997, *Molecular Cell* publishes 24 issues a year. Its team of PhD-trained scientific editors works closely with authors, reviewers, and the scientific editorial board to ensure that the high standards of the journal are maintained while publishing breaking discoveries and the best in molecular mechanisms. All the content published in *Molecular Cell* (back to and including the first issue) is freely available starting 12 months after publication.

Aims and Scope

Molecular Cell publishes reports of novel results that are of unusual significance and of interest to researchers in the field. The journal focuses on analyses at the molecular level, with an emphasis on new mechanistic insights. The scope of the journal encompasses all of "traditional" molecular biology (including DNA replication, recombination and repair, gene expression, RNA processing, translation, and protein folding, modification, and degradation) as well as studies of the molecular interactions and mechanisms that underlie basic cellular processes. Some examples of such processes are signal transduction pathways, the cell cycle and checkpoints, and apoptosis.

We are also interested in the analyses that are beginning to emerge following the availability of the entire genome sequences of several organisms. The basic criterion for considering such papers is whether the results provide significant novel insights into, or raise provocative questions and hypotheses regarding, an interesting biological question. In addition to primary papers, *Molecular Cell* features review articles tailored to its broad readership.

Editorial Process

Editorial Timeline

All submissions are initially evaluated in depth by the scientific editors. Papers that do not conform to the general criteria for publication will be returned to the authors without detailed review as soon as possible. Otherwise, manuscripts will be sent to reviewers who have agreed in advance to assess the paper rapidly. The Editors will make every effort to reach decisions on these papers within a month of the submission date. If revisions are a condition of publication, we generally allow 2 months for revisions and consider only one revised version of the paper. Evaluations of conceptual advance and significance are made based on the literature available on the day of the final decision, not the day of submission. Accepted papers will be published within 3 months of acceptance. Any major changes after acceptance are subject to review and may delay publication.

READ THE INSTRUCTIONS TO AUTHORS!!

LOOK AT OTHER PAPERS PUBLISHED IN THE JOURNAL AND MATCH THE STYLE

NOW START WRITING

Introduction

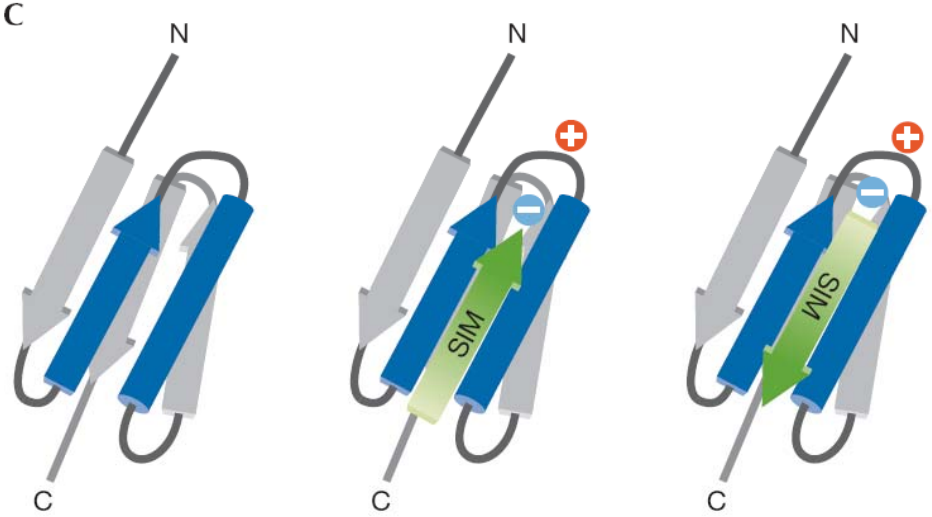
- Funnel from the broad background, to specific gaps, to questions answered by bottom line.
- This is not a literature review. You are setting up the question.
- Think of the terms in which you would justify your work to your parents. Get some sense of that into the introduction.
- Finish with a very brief (one-sentence) summary of the results and why they are important.

A

SRS2	: IIVI	
TDG	: VQEV	Baba *et al* 2005
DAXX	: IIVL	Lin *et al* 2006
PML	: IVII	Shen *et al* 2006

B

C



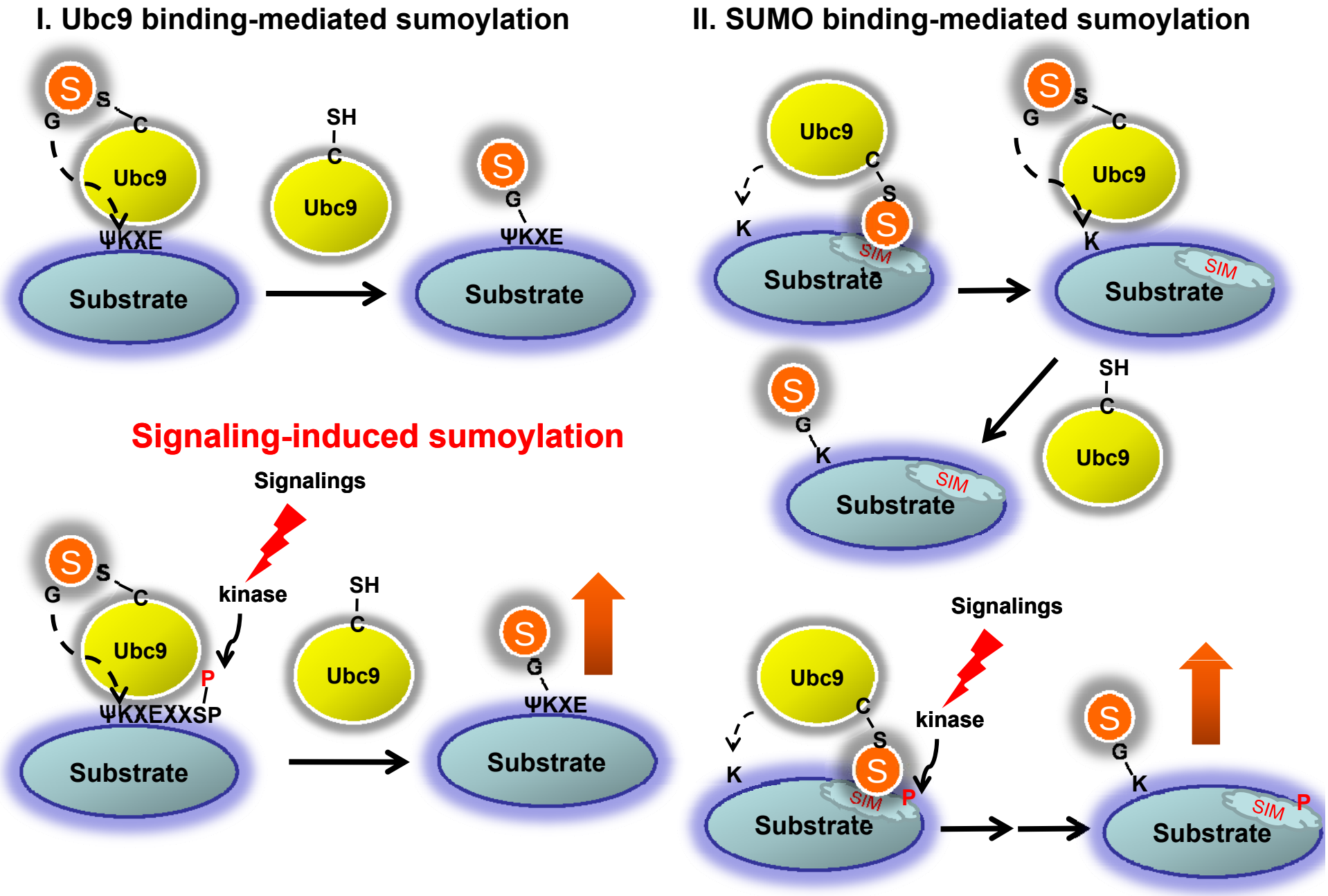
EMBO report 2007

Daxx SIM

KTSVATQCDPEEIIVLSDSD

Are the flanking acidic residues of Daxx SIM hydrophobic core involved in SUMO interaction and binding orientation?

Current modes in controlling protein sumoylation



The Results

- Tell a story. Follow your story line.
- Lead each paragraph with the experimental aim and primary result. Then elaborate.
- Describe why you are moving from one experiment to another.

One paragraph = one thought

- Numbers/data mostly in the figures. Don’t bury the reader in numbers.
- Lead with important result, follow with controls and secondary findings.

Sentence structure

- Make the topic the subject.
- Put the action in the verb. (An increase in heart rate occurred. Becomes: Heart rate increased.)
- Avoid long noun clusters.
- Talk about one thing at a time.
- Use parallel constructions. (It was both a long talk and very tedious. Becomes: The talk was both long and tedious.)
- Keep related words (e.g., subject and verb) together.
- Use the active voice. (There were a great number of dead leaves lying on the ground. Becomes: Dead leaves covered the ground.)

Less is always more. Don't use more words than needed. Be precise.

Paragraph structure

- One paragraph = one thought.
- A summary of this thought is the first (topic) sentence.
- Elaborate from this in a logical order (pro then con; most to least important evidence; chronological).
- Be direct and specific - tell us what will/did actually happen.
- Continuity requires reasoning.

Fraud: Don’t do it!

- Photoshop makes fraud easier to commit but also easier to detect.
- Fraudulent results can’t be repeated. Even if not “caught,” suspicion will hang over you.
- Any benefit from “cleaning up” your results is not worth the damage to your reputation.

Factors affecting frequency of image manipulation:

- Culture of image manipulation: perceived acceptability?
- Ease of image manipulation
- Understanding the line between acceptable and unacceptable manipulation.

Inappropriate Manipulation Examples

- Adjustment of specific feature
- Moving specific elements
- Cleaning up background
- Unreasonable adjustment of contrast

Adjustments of brightness, contrast, or color balance are acceptable if they are applied to the whole image and as long as they do not obscure or eliminate any information present in the original.

- Splicing

The grouping of images from different parts of the same gel, or from different gels, fields, or exposures must be made explicit by the arrangement of the figure.

JCB Feature

What's in a picture? The temptation of image manipulation

Mike Rossner[1] and Kenneth M. Yamada[2]
[1]Managing Editor, The Journal of Cell Biology
[2]Editor, The Journal of Cell Biology, and the National Institute of Dental and Craniofacial Research, National Institutes of Health

It's all so easy with Photoshop[1]. In the days before imaging software became so widely available, making adjustments to image data in the darkroom required considerable effort and/or expertise. It is now very simple, and thus tempting, to adjust or modify digital image files. Many such manipulations, however, constitute inappropriate changes to your original data, and making such changes can be classified as scientific misconduct. Skilled editorial staff can spot such manipulations using features in the imaging software, so manipulation is also a risky proposition.

Good science requires reliable data. Consequently, to protect the integrity of research, the scientific community takes strong action against perceived scientific misconduct. In the current definition provided by the U.S. government: "Research misconduct is defined as fabrication, falsification, or plagiarism in proposing, performing, or reviewing research, or in reporting research results." For example, showing a figure in which part of the image was either selectively altered or reconstructed to show something that did not exist originally (for example, adding or modifying a band in a polyacrylamide gel image) can represent falsification or fabrication.

Being accused of misconduct initiates a painful process that can disrupt one's research and career. To avoid such a situation, it is important to understand where the ethical lines are drawn between acceptable and unacceptable image adjustment.

Here we present some general guidelines for the proper handling of digital image data and provide some specific examples to illustrate pitfalls and inappropriate practices. There are different degrees of severity of a manipulation, depending on whether the alteration deliberately changes the interpretation of the data. That is, creating a result is worse than making weak data look better. Nevertheless, any manipulation that violates these guidelines is a misrepresentation of the original data and is a form of misconduct. All of the examples we will show here have been created by us using Photoshop; although they may appear bizarre, it is remarkable that they are actually based on real cases of digital manipulation discovered by a careful examination of digital images in a sample of papers submitted (or even accepted) for publication in a journal.

Why is it wrong to "touch up" images?

If you misrepresent your data, you are deceiving your colleagues, who expect and assume basic scientific honesty—that is, that each image you present is an accurate representation of what you actually observed. In addition, an image usually carries information beyond the specific point being made. The quality of an image has implications about the care with which it was obtained, and a frequent assumption (though not necessarily true) is that in order to obtain a presentation-quality image, you had to carefully repeat an experiment multiple times.

Manipulating images to make figures more simple and more convincing may also deprive you and your colleagues of seeing other information that is often hidden in a picture or other primary data. Well-known examples include evidence of low quantities of other molecules, variations in the pattern of localization, and interactions or cooperativity.

Journal guidelines

It is surprising that many journals say little or nothing in their "Instructions to Authors" about which types of digital manipulations are acceptable and which are not. The following journals provide some guidelines, but they vary widely in comprehensiveness.

Molecular and Cellular Biology. "Since the contents of computer-generated images can be manipulated for better clarity, the Publications Board at its May 1992 meeting decreed that a description of the software/hardware used should be put in the figure legend(s)."

Journal of Cell Science. "Image enhancement with computer software is acceptable practice, but there is a danger that it can result in the presentation of quite unrepresentative data as well as in the loss of real and meaningful signals. During manipulation of images, a

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Address correspondence to Mike Rossner, Journal of Cell Biology, Rockefeller University Press, 1114 1st Ave., 3rd fl., New York, NY 10021. Tel.: (212) 327-8881. Fax: (212) 327-8576. email: rossner@rockefeller.edu

[1]The general principles presented here apply to the manipulation of images using any powerful image-processing software; however, because of the popularity of Photoshop, we refer to several specific functions in this application.

J Cell Biol 2004
166:11-15

Discussion

- Start with bottom line with a very brief (1-3 sentence) summation.

  Do not repeat/rehash your results!

- Subsequent points go from most important / most related to bottom line to least important / least related.

One paragraph = one thought

- Distinguish between confirmatory and new, and established and speculated.
- Discuss different levels of significance.

Be Specific and Precise

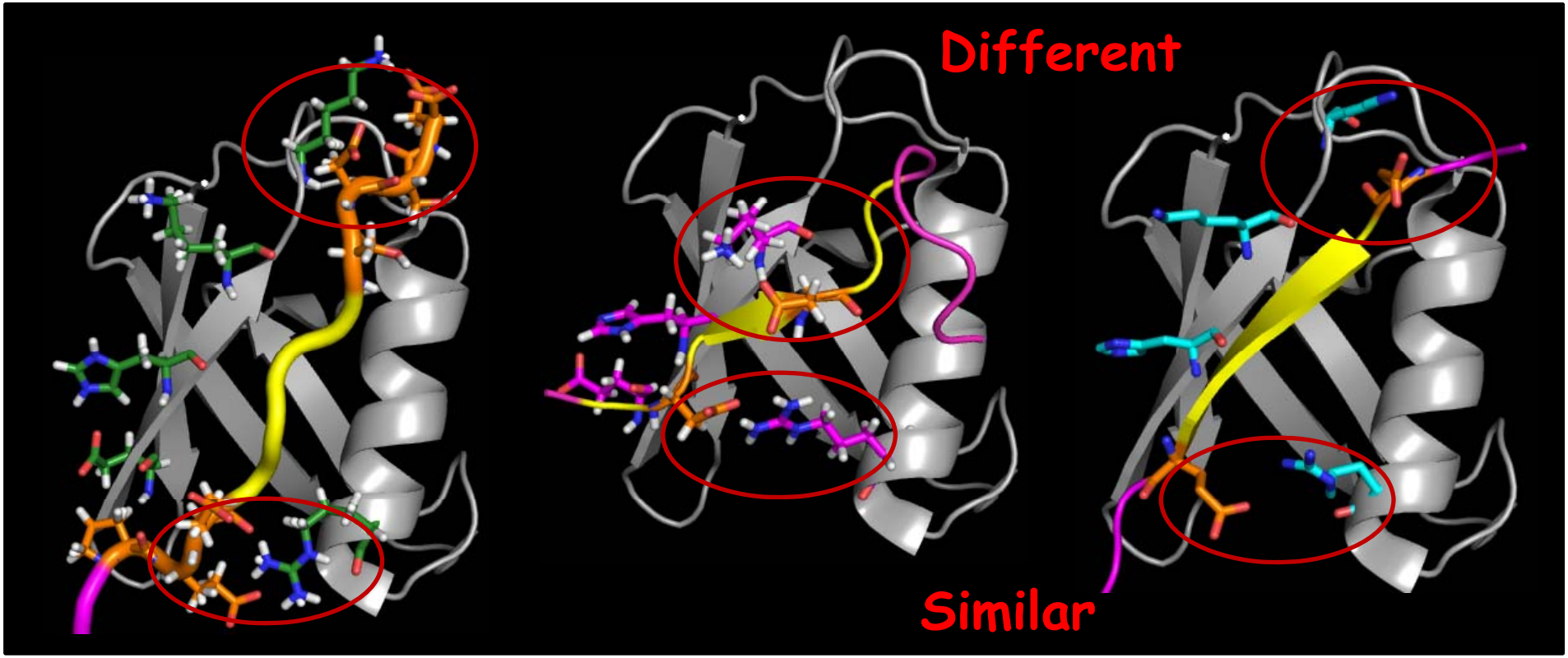
- Don’t just cite references, but describe.
- Watch out for lazy thoughts and stock phrases.
- Not “gives insight into…” but “shows that process X uses mechanism Y.”
- Not “opens up new ways of tackling disease X” but “suggests that approach Y will work against disease X.”

Don’t Be Afraid to Speculate

- Speculation can provide context. Novice readers need context. Again, why should we care?
- If you think your discovery might (in the future) prove to be the explanation for mystery X, don’t make the reader figure out the identity of mystery X. State it explicitly.
- Make all links. A link that is glaringly obvious to you will not occur to many of your readers.

Summary-(I)

Daxx	PIASx	RanBP2
729-DPE**EIIVL**SDSD-740	467-V**DVIDL**TIDSSSDEEEDP-485	2641-TPTL**E**Y**VILV**DLS-2629



Gene	Sequence	SIM	Phosphorylation	Structure
Daxx	^{729}DPE**E** **IIVL** **S**D**S**D^{740}	**1**	This study	This study
PIASxα	^{432}SKKKV**D** **VIDL** TIE**SSS**DEEEDPP^{454}	2	3	2
PML	^{550}GEA**EE**R **VVVI** **SSS**ED**S**DAENS^{570}	4	5	ND
PMSCL1	^{399}FLTS**D**A **PIIL** **S**D**S**EEEEMIILEP^{421}	6	6	ND
PIAS1	^{452}KNKKV**E** **VIDL** TID**SSS**DEEEEEPSA^{476}	3	6	ND
PIAS3	^{441}NKKKV**E** **VIDL** TIE**SSS**DEEDLPP^{465}	3	ND	ND
SP100	^{316}THHNQAS**D** **IIVI** **SS**EDSEGSTDVDEP^{340}	3	ND	ND
SAE2	^{580}TAQEQD**D** **VLIV** D**S**DEEDSSNNAD^{602}	ND	ND	ND
HDAC4	^{916}MPIASEFAP**D** **VVLV** S**S**GFDAVE^{937}	ND	ND	ND
PIAS4	^{461}PGA**D** **VVDL** TLDSS**SSS**EDEE^{480}	ND	ND	ND
MCAF-1	^{981}EQSAGS**EEDD**MT **LDIV** VG**SS**DSG^{960}	7	ND	7
BLM	^{243}IPGD**D** **LCIV** D**SS**LEES^{227}	8	ND	ND

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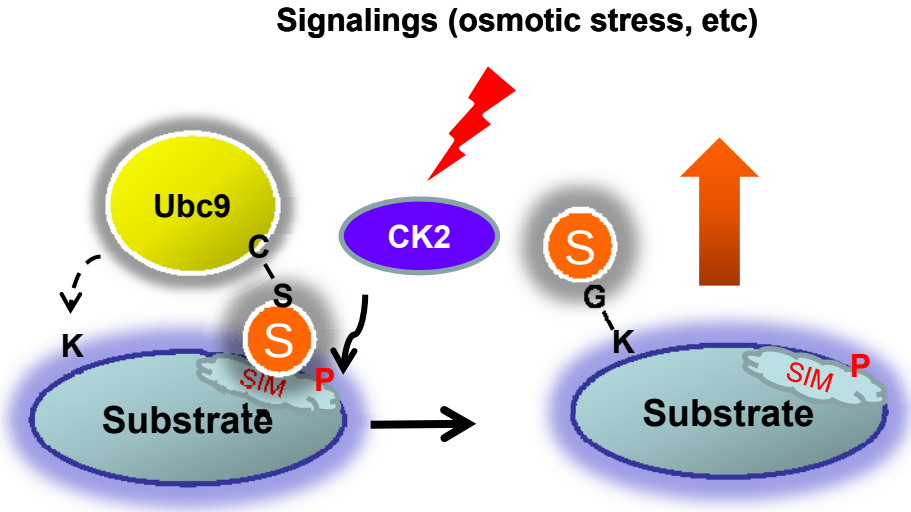
Summary-(II)

1. Daxx SIM phosphorylation enhances SUMO paralogue-selective binding.



2. The K39 of SUMO-1 is critical for phospho-Daxx SIM in SUMO binding affinity.

3. Daxx SIM phosphorylation is important for anti-apoptotic gene repression and apoptosis modulation.

SIMPLE capture of SUMO paralog

Potential SIM phosphorylation-enhanced (SIMPLE) SUMO-2/3 binding and conjugation

Pc2: 455- AALPQPE **VILL** DSDLDEPI - 473

BLM : 228- SEELSSD **VICL** ---DDGPI - 243

K-bZIP : 63- PPAIVCET **VIDL** TAPSQSG - 84

Materials and Methods

- Only describe methods used.
- Keep it extremely brief unless discussing an unusual technique.
- Include rationale for why an experiment was done a particular way.

Figures and Tables

- Every figure and table should have a clear point. Use that as the first sentence of the figure legend.
- Make intuitive figures. Provide simple labels so that the reader doesn’t have to battle with legends.
- Design a table so that the figures you want to compare are close to each other.

Now write your abstract:

1-2 sentences:

Give essential background

2-3 sentences:

state results

1-2 sentences:

state conclusion, and significance /implications of findings

Check character/word limits on Abstracts:

Often <150-200 characters

Editors assign papers and derive their first impressions from the abstract.

An abstract can have it all.

SUMMARY

Small ubiquitin-like modifier (SUMO) conjugation and interaction are increasingly associated with various cellular processes. However, little is known about the cellular signaling mechanisms that regulate proteins for distinct SUMO paralog conjugation and interactions. Using the transcriptional coregulator Daxx as a model, we show that SUMO paralog-selective binding and conjugation are regulated by phosphorylation of the Daxx SUMO-interacting motif (SIM). NMR structural studies show that Daxx ^{732}E-I-I-V-L-S-D-S-D^{740} is a bona fide SIM that binds to SUMO-1 in a parallel orientation. Daxx-SIM is phosphorylated by CK2 kinase at residues S737 and S739. Phosphorylation promotes Daxx-SIM binding affinity toward SUMO-1 over SUMO-2/3, causing Daxx preference for SUMO-1 conjugation and interaction with SUMO-1-modified factors. Furthermore, Daxx-SIM phosphorylation enhances Daxx to sensitize stress-induced cell apoptosis via antiapoptotic gene repression. Our findings provide structural insights into the Daxx-SIM:SUMO-1 complex, a model of SIM phosphorylation-enhanced SUMO paralog-selective modification and interaction, and phosphorylation-regulated Daxx function in apoptosis.

Background

Results

Conclusion & significance

Revising

- Set aside the paper for several days.
- Look for logical gaps and inconsistencies.
- Cut ruthlessly. Use simple, direct constructions.
- Have others read the paper and give written comments.

Style: Yes to simplicity; no to verbosity

- If you wouldn’t say it, don’t write it. Use, don’t utilize.
- Chop everything from single words to entire paragraphs.
- Repeat only the bottom line.

Cut, Cut, Cut

- Shorter sentences are clearer.
- Shorter paragraphs are clearer.
- Shorter papers are clearer.
- Is it worth creating a 20-page masterpiece if no-one will read it?

Sending the paper

- Write a cover letter that is short, gives context, says what is new, and is addressed to the right journal.
- Remember your audience and be concise.
- An editor is a generalist. Make your work accessible. Clearly state the significance and implications of your findings. Put them in a bigger context.

Responding to Reviews

- Don’t take it personally.
- Assume the referees are experts. If they didn’t understand, you didn’t communicate effectively.
- Fix or modify, even if you don’t fix in the suggested manner.

Write a cover letter with resubmission that acknowledges and responds to the referees.

Admit it if you chose the wrong journal.

Molecular Cell
Article

Structural and Functional Roles of Daxx SIM Phosphorylation in SUMO Paralog-Selective Binding and Apoptosis Modulation

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DOI 10.1016/j.molcel.2011.02.022

Success!!

SUMMARY

Small ubiquitin-like modifier (SUMO) conjugation and interaction are increasingly associated with various cellular processes. However, little is known about the cellular signaling mechanisms that regulate proteins for distinct SUMO paralog conjugation and interactions. Using the transcriptional coregulator Daxx as a model, we show that SUMO paralog-selective binding and conjugation are regulated by phosphorylation of the Daxx SUMO-interacting motif (SIM). NMR structural studies show that Daxx ^{732}E-I-I-V-L-S-D-S-D^{740} is a bona fide SIM that binds to SUMO-1 in a parallel orientation. Daxx-SIM is phosphorylated by CK2 kinase at residues S737 and S739. Phosphorylation promotes Daxx-SIM binding affinity toward SUMO-1 over SUMO-2/3, causing Daxx preference for SUMO-1 conjugation and interaction with SUMO-1-modified factors. Furthermore, Daxx-SIM phosphorylation enhances Daxx to sensitize stress-induced cell apoptosis via antiapoptotic gene repression. Our findings provide structural insights into the Daxx-SIM:SUMO-1 complex, a model of SIM phosphorylation-enhanced SUMO paralog-selective modification and interaction, and phosphorylation-regulated Daxx function in apoptosis.

INTRODUCTION

Covalent modification of proteins by a small ubiquitin-like modifier (SUMO) peptide on the lysine residue is an important post-translational event in the modulation of protein function (Gareau and Lima, 2010; Geiss-Friedlander and Melchior, 2007). The conjugation of mammalian SUMO isoforms (SUMO-1,-2, and -3) to protein substrates requires the E1-activating enzyme (SAE1/SAE2), the E2 conjugase (Ubc9), and, in some cases, E3 ligases (Gareau and Lima, 2010; Geiss-Friedlander and Melchior, 2007). In general, Ubc9 catalyzes the formation of an isopeptide bond between the C terminus of SUMO and the amino group of the target lysine via a direct interaction with a consensus motif ψ-K-X-E/D (where ψ is a large hydrophobic residue and X is any residue) present in protein substrates (Rodriguez et al., 2001; Sampson et al., 2001). We and others have shown that sumoylation can be facilitated by a SUMO-interacting motif (SIM) (Lin et al., 2006; Meulmeester et al., 2008; Zhu et al., 2008). SIM-dependent sumoylation was thought to be mediated by the noncovalent binding of SIM to the SUMO moiety of the Ubc9-SUMO thioester complex, allowing Ubc9 to more efficiently conjugate substrate lysine residue(s) not necessary localized in the consensus sumoylation motif. Currently, it is unclear whether protein conjugation with SUMO paralogs can be regulated by cellular signaling mechanisms that alter the affinity of SIM toward a selective SUMO paralog.

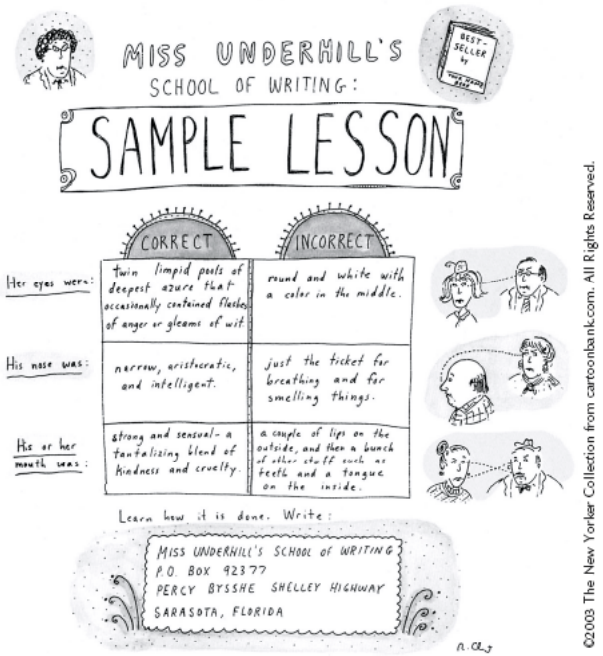
Daxx is a transcriptional coregulator involved in multiple cellular functions, including cell apoptosis (Salomoni and Khelifi, 2006; Shih et al., 2007). Daxx suppressed the expression of several antiapoptotic genes, correlating with its proapoptotic role in sensitizing stress-induced apoptosis (Croxton et al., 2006). The ability of Daxx to accumulate in PML nuclear bodies (PML NBs) also correlated with an increase in its pro-apoptotic function (Torii et al., 1999). We previously reported Daxx residues ^{733}I-I-V-L-S-D-S-D^{740} as a SIM important for Daxx sumoylation, Daxx interaction and repression of SUMO modified transcription factors and CBP, and Daxx targeting to PML NBs (Lin et al., 2006). Daxx SIM is evolutionally conserved among mammals (Figure 1A), while a similar sequence found in *Drosophila* can

The Journal of Cell Biology

JCB Feature

Me write pretty one day: how to write a good scientific paper

The scientific literature is exploding in quantity even as it stands still in literary quality. In this brief guide, I suggest a few small steps that the individual can take to make his or her writing clear, straightforward, and digestible.



So…what was your point?

The first step with any manuscript is to define your bottom line. Be realistic about how much the average reader will take away from an article. Non-experts will retain at most a single message. Make sure you have one, and then repeat it over and over again—at the end of the Abstract, in the Introduction, in the Results, and in the Discussion. In contrast, everything but this single sentence belongs in one section (Introduction, Results, or Discussion) only.

To uncover your bottom line, ask some questions: What was the mystery that you wanted to answer at the start? Have you answered it? What first got you excited about this area of research? With any luck, it was more than the idea that proteins X and Y might bind to each other—there was probably a bigger idea that motivated and intrigued you. Make sure you convey that reason and that excitement.

What is new? Break up the story into "It was previously shown that…" and "Now it is shown that…". Is there a significant difference between the two statements? Justify the interest of your work verbally to someone outside of which your volunteer has no familiarity or interest.

Does the reader need help understanding the significance? If you think your discovery might (in the future) prove to be the explanation for mystery X, don't make the reader figure out the identity of mystery X. State it explicitly, make clear that the link is only specula-

the number of known penguin species…". If your readers don't think that is exciting, they won't be convinced by you stating that it is.

Finally, include different levels at which your results are significant: e.g., (a) we have found a stem cell repressor, and (b) this may be one of many repressors for maintaining a generally

JCB, 2004

Communication is an Important Part of Science

- Master it
- Science does not exist until it is published
- Learn how to make your findings interesting and understandable to others

GOOD LUCK!

Editorial Process

1. Journal editor assistant will check whether the uploaded files (format and quality) are OK for review process and then pass to the Scientific Editor who will select a handling Editor (depends on the journals).

2. The handling editor will report to a team to discuss whether the manuscript is good for sending out for external review. **Criteria**: *conceptual advance*, *who will read the paper*, *avoid speculation*, *logic of the paper*, *and data sufficient to draw the conclusions.*

3. Handling editor selects reviewers: technical expertise, constructive suggestion and hold the standard for the journal. Avoid reviewers with conflict of interest.

Editorial Process

Decision process:

1. Manuscript is accepted
2. Minor revision: the editor invites an revised manuscript.
3. Major revision: need substantial amounts of revision. If the authors can provide new data to address the questions raised by reviewers, the editor will re-consider the manuscript.
4. Reject: submit to some other journals

How Editor write his/her decision letter:
access the reviewer's comments very carefully, including general level of interests, the conceptual advance, and the technical competency of the manuscript.

Editorial Process

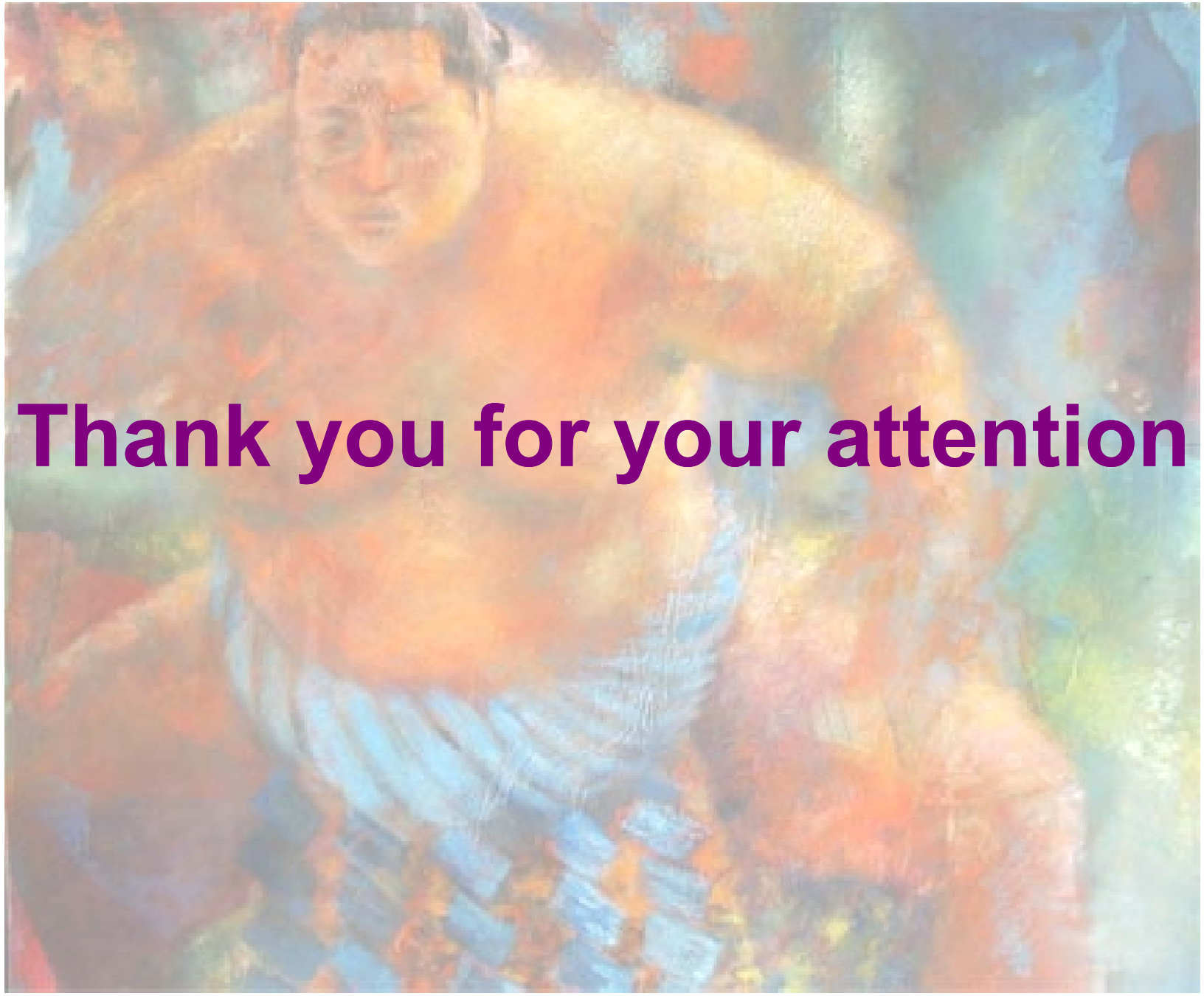
Rebuttal letter:

Authors should offer well-reason, scientifically based response to reviewers' comments and editorial concern.

After manuscript acceptance:

Format and quality of files, supplemental information, highlights and cover image. Final run of editing (galley proof). Follow journal instruction.

Preview, author interview, press conference


Thank you for your attention