How to Get Published in a *Science* Family Journal

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The *Science* family of journals

General science journals

Science

Science Advances

(open access, academic)

Specialty journals

Science Signaling

Science Translational Medicine

Science Immunology

Science Robotics (academic)

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A Word about Access

Science Robotics & *Science Immunology* too!

- **Immediate access**: Research authors receive a link to their article immediately after publication that can be put on a web page to allow free access to the article.
- **6 months after publication**: Accepted version of peer-reviewed content can be posted in authorized public repositories (such as PubMed Central).
- **12 months after publication**: Research content is freely available at the journal's website.

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Where to submit?

- Journal scope and audience
- Review process and criteria
- Article types and format
- Editorial board
- Access

- Sister journals
- Impact factor
- Acceptance (or rejection) rate
- Press and promotion

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Science

- Is your finding a big step forward with broad implications?
- Is your paper cross disciplinary?
- Did you apply a new technique to investigate difficult scientific questions?
- Is your research in the biological, physical, or social sciences?
- Is your study self-contained and suitable for the *Science* format?

Science Advances

- Does your funding agency require publication in an open access journal?
- Was your paper recommended from a *Science* journal?
- Did a member of the Academic Board encourage you to submit?

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Science family specialty journal

- Was your paper referred from another journal in the family?
- Is your research within the scope of one of the specialty journals?
- Were you approached by an editor of one of the journals at a conference?
- Did you receive an email from the journal encouraging you to submit?
- Have you reviewed for the journal?

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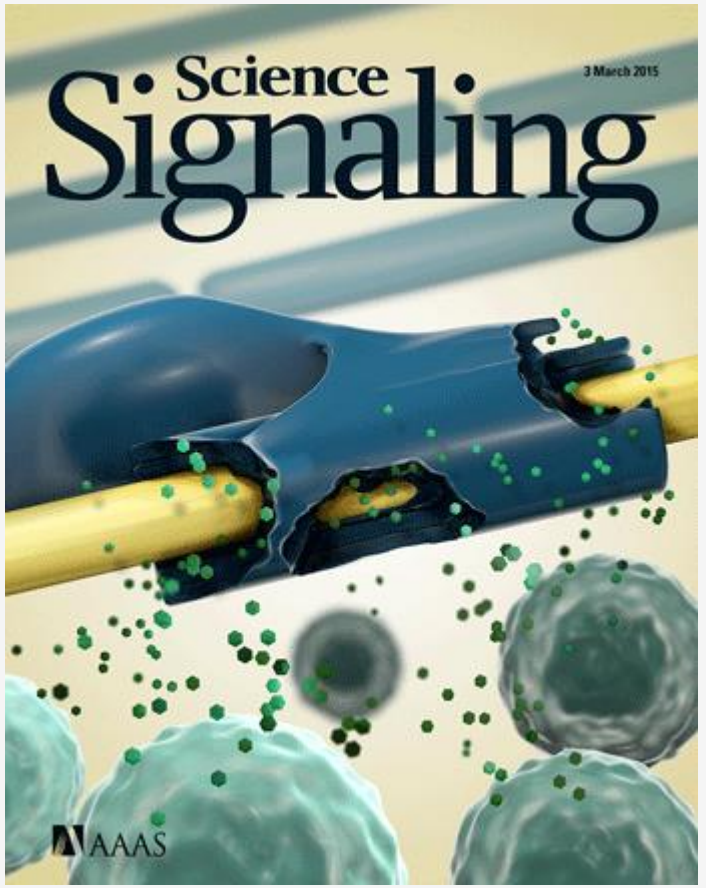
Science Signaling

- Do you study cellular or organismal regulation:
  - with implications for understanding physiology and pathophysiology?
  - with implications for treating disease?
  - with mechanistic insight? (for regulation of cellular processes)
  - with computational or modeling analysis leading to experimentally tested predictions?
- Was your paper recommended from *Science* or *Science Translational Medicine*?



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Research Resource

- Is the study not testing a specific hypothesis?
- Does the study present a novel technique or tool with validation, without investigating a biological question?
- Does the study provide a validated data set or describe applications of a validated database?
- Will the data, tool, approach, or database spur future studies in regulatory biology?

Research Article

- Is the study hypothesis-driven and are the hypotheses tested?
- Does the study provide a significant advance in understanding biological regulation?
- Does the study show in-vivo demonstration of regulatory events previously only analyzed in simpler systems?
- Does the study reveal previously unknown regulatory mechanisms?

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STRUCTURED REVIEW

Include the following information in your review:

1) **Rate the quality of the study, using the terms below, in your comments to the editor**
   - **Excellent**: exceptional research design, conclusions are fully supported by the data
   - **High**: strong research design, minimal additional experiments needed to support the conclusions
   - **Average**: strong experimental design, some additional experiments or controls needed to support the conclusions
   - **Fair**: uneven quality in experimental design, many additional experiments or controls needed
   - **Poor**: serious weaknesses in experimental design; conclusions are not adequately supported by the data
2) **Rate the impact of the study, using the terms below, in your comments to the editor**
   - **Very high**: Major advance with impact in several fields
   - **High**: Potential to advance one or more fields
   - **Average**: Important advance for a defined field
   - **Low**: Limited advance over previous studies or advance limited by flaws
3) **Indicate if any of the following deficiencies are present and provide details in the comments to the authors:**
   - Lacks mechanism
   - Conclusions not supported by the data
   - Missing or inappropriate quantification and statistical analysis
   - Too descriptive or phenomenological
   - Not within journal scope
   - Inappropriate or missing references
4) **Indicate if the manuscript requires any of the following and provide details in the comments to the authors:**
   - Additional controls
   - Additional experiments
   - Quantification and statistical analysis
   - Revision for language usage or clarity of presentation
   - Additional references

Practical tips for preparing your manuscript

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Five golden rules

- Know your audience
- Write clearly
- Write concisely
- Write accurately
- Follow instructions

≠

Know your audience

- Scientists in your field
- Scientists outside of your field
- Reviewers
- Editors

These people are drowning in information and very busy!

First stop - The editor

- May not be an expert in your field
- Has 40 active papers
- Fields multiple enquiries from authors a day
- Attends meetings (internal & external)
- Wants to find the best papers for the journal

Will ask

- Are there good reasons to proceed with this paper?
- Are there good reasons to reject this paper?
- Is the paper within the journal's scope?
- Will this be one of our best papers?
- Can I convince my fellow editors of the value of this paper?

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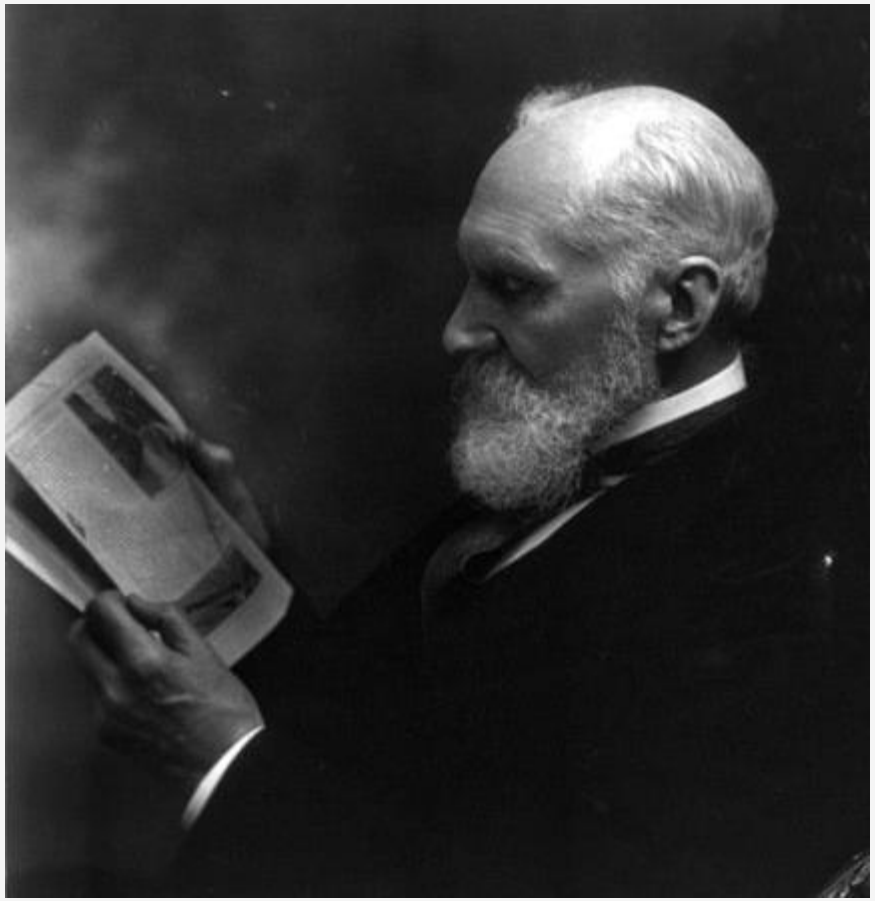
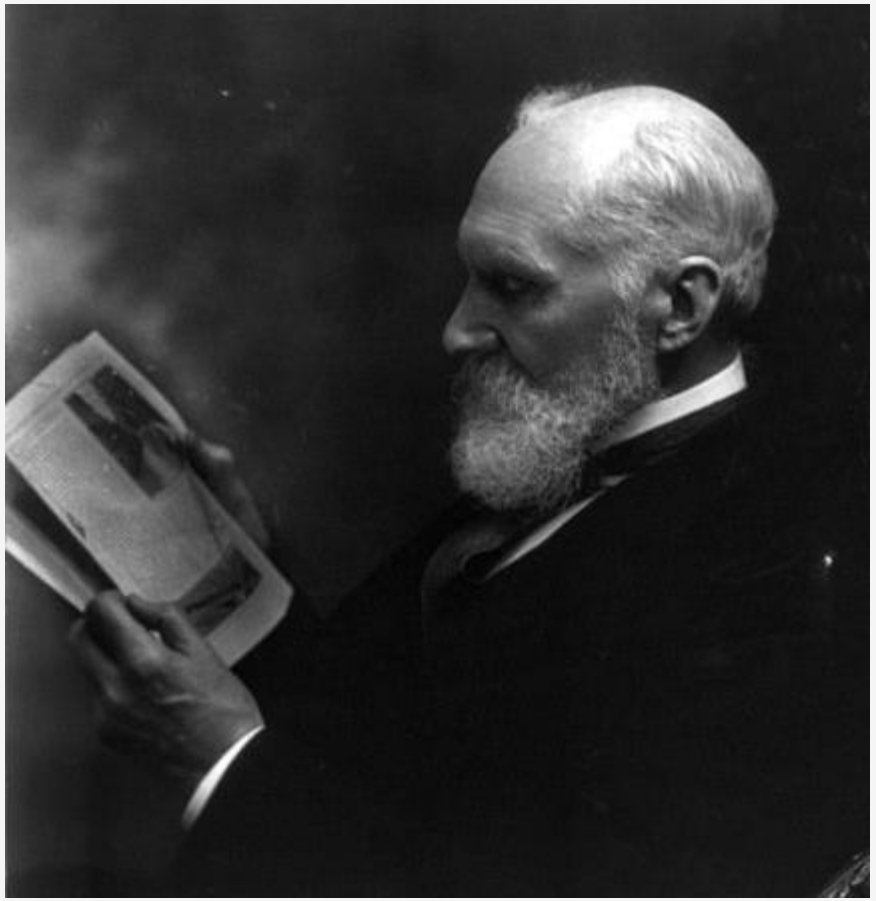
The reviewer

- Is a specialist in your field
- Is very busy running a lab and writing their own papers
- Wants the review process to be as efficient as possible



Will ask

- Is this correct?
- Is it interesting enough for a *Science* journal?
- If I saw this paper in *Science* or one of the sister journals would I say
  - **"Cool!"**
  - **"This changes my entire way of thinking!"**
  - **"I can't wait to share this with my lab!"**
  - **"What were those idiot editors thinking?"**



How can you maximize your paper's chance for success?

- Nothing substitutes for good content.
- To get into a top-tier journal, you will need an important result that advances the field.
- Your conclusions must be well supported by experiments.
- The statistics must be good.
- The experiments must be properly controlled.

How can you ensure that your paper meets these criteria?

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Before you start writing – start your own review process

- Is the result important?
- Do the conclusions advance new concepts?
- Is the approach original?
- Are the data reliable and reproducible (how many n)?
- Are the data properly quantified and statistically evaluated?
- Are experiments properly controlled?

Invite critique from your colleagues

- Assemble your figures into a presentation that matches the paper
- Organize the introduction the way you plan to present it in the paper
- Assemble your colleagues: Some within and some outside your lab
- Ask them to give you feedback
  - What controls are missing?
  - What data are being overinterpreted?
  - Where are there gaps in logic?
  - What data are presented out of order?
  - Why do they think the study is important?

You're almost ready to write

- Incorporate the feedback from your colleagues
- Go back to the lab and do more experiments, if necessary
- Make sure the controls are presented with the experiments
- Make sure the flow of the figures and data are logical
- Make sure you've set the stage for your study adequately

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Present your data effectively

DON'T

- Restate the data, which should be readily discerned from the figure or table
- State results without setting the experimental context, don't make the reader guess
- Present the study as a story in chronological order of experiments or refer to data shown later
- Use lab jargon or shorthand in the text or figures
- Use unnecessary or atypical abbreviations

DO

- Set the stage for the reader so that they can interpret the data
- Limit the results to a description of the data and their indication; use the Introduction to set the necessary background and the Conclusions to put the study into broader context
- Present the data in logical order, so that all results needed to make an interpretation are presented before the interpretation is drawn
- Be consistent in labeling and define any abbreviations used in the figures that differ from those used in the text
- Use only those abbreviations that are standard in your field and be sure to define them the first time they are used

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Common data presentation mistakes

- Lab jargon
  - Labeling Western blots with the name of the antibody, instead of the epitope or protein
- Inconsistent labels
  - Do not have 3 different ways of labeling the same stable cell line, use one set of abbreviations consistently throughout

Wordy, yet vague

A close-up of the MS0015203 binding mode showing the direct H-bond interactions between the ligand and GPR171 is shown in Fig. 1B.

- Option 1: Add method information and specifics of interaction to guide reader through the result
  - Molecular docking analysis predicted that the ligand MS0015203 formed H-bonds with residues XX, XX, and XX in XX extracellular loops and XX in the XX transmembrane domain of the receptor GPR171 (Fig. 1B).
- Option 2: If the figure is well labeled and very clear and method has already been described:
  - The ligand MS0015203 was predicted to form multiple H-bonds in residues in several regions of the receptor GPR171 (Fig. 1B).
  - The analysis predicted that the ligand MS0015203 formed H-bonds with residues in extracellular loops and a transmembrane domain of the receptor GPR171 (Fig. 1B).

Write clearly

- Avoid imprecise words
  - Regulates
  - Alters
  - Influence
- Avoid words with multiple meanings
  - Levels
  - Elevates
  - Significant
- Avoid lab jargon

- Precise
  - Stimulates the activity
  - Increases the abundance
  - Represses the gene's expression
- Unambiguous
  - Amount, abundance, or concentration
  - Increase
  - Substantial or important
- Genes, RNAs, and proteins
  - Use italics for genes and transcripts
  - Use plain text for proteins and active RNA molecules

Write concisely

- Avoid convoluted sentences with multiple clauses
- Avoid long complicated qualifying adjectives
- Avoid presenting published results as a historical review
- Use simple declarative sentences; divide into two sentences if necessary
- If published work is not in dispute, present it as a fact

Don't say in 4 words what can be said in 1!

Write accurately

- Avoid claims of novelty
- Avoid speculation
- Avoid superlatives
- Correlations ≠ cause and effect
- Written ≠ spoken language
- Don't anthropomorphize
  - Cells don't have feelings and proteins are not people!

Your paper is not a used car (grant or tweet).
Don't overinterpret, overstate, or oversell!

Play the role of reviewer again

- Are errors and typos eliminated?
- Do ideas follow logically and the text read smoothly?
- Are needlessly convoluted sentences avoided?
- Are the results described and not just a written statement of the data?
- Are the figures clear, well labeled, and selected to show the most critical information?
- Does the discussion appropriately account for other research?

Criticize yourself as you would criticize others

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Invite critique: Round 2

A scientist in your own specialty

A scientist in an unrelated specialty

A good editor for the English language

Ready, set, submit– But wait!

Think like the editor again for a minute:

What will he see first?

- The cover letter
- The title
- The abstract

First impressions

- Cover letter – outline the conclusions in plain and honest language, without exaggeration, but do say why you think the work is exciting.
- Is the title reflective of the main findings of the study?
- Does the abstract convey the main findings and importance.

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Practice while you read

As you read for Journal Club, consider these best practices and ‘pencil’-edit the papers.

As you read background materials for your research, find the errors and think about how the writing could be improved.

Help each other. Read each other’s manuscripts.

Don’t be afraid of the red pen!

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Before and after samples

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Title

Original: Targeting Poly (ADP-Ribose) Polymerase and the c-Myb-TopBP1-ATR-Chk1 Signaling Pathway in Castration-Resistant Prostate Cancer

Edited: Targeting Poly (ADP-Ribose) Polymerase and the c-Myb - Regulated DNA Damage Response Pathway in Castration-Resistant Prostate Cancer

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Results

Since we previously found that GPR171 is activated by a relatively long (16 amino acid) peptide (6), we sought to identify the minimal length required to activate the receptor. For this we used N-terminally truncated b-LEN-derived peptides and found that the C-terminal four amino acids (LLPP, present in both the mouse and rat b-LEN sequences) were necessary and sufficient to displace b-LEN from the receptor (fig. S1A).

- Problem 1: Stage is not set properly for understanding the experiment.
- Problem 2: Authors did not test for necessity because none of the tested peptides lack these residues. They only tested for sufficiency. Data are overinterpreted.
- Problem 3: Since should only be used when there is a temporal component. Most often it should be replaced with Because.
- Problem 4: Why was it important to see if a smaller peptide could affect receptor function?

Because we previously found that GPR171 is activated by a relatively long (16 amino acid) peptide (6), we sought to identify the minimal peptide required to activate the receptor. We used N-terminally truncated b-LEN-derived peptides to evaluate the minimal sequence that displaced radiolabeled b-LEN binding. The C-terminal four amino acids (LLPP, present in both the mouse and rat b-LEN sequences) were sufficient to displace b-LEN from the receptor (fig. S1A). Because this sequence is so small, small molecule ligands may exist that can affect receptor activity.

Abstract unedited

Androgen deprivation is the standard systemic treatment for advanced prostate cancer (PCa), but most patients ultimately develop castration-resistance. We show here that *MYB* is transcriptionally activated by androgen deprivation or impairment of androgen receptor (AR) signaling. *MYB* gene silencing significantly inhibited PCa growth in vitro and in vivo. Microarray data revealed that c-Myb shares a substantial subset of DNA damage response (DDR) target genes with AR, suggesting that c-Myb may replace AR for the dominant role in the regulation of their common DDR target genes in AR inhibition-resistant or AR-negative PCa. Gene signatures comprising *AR*, *MYB*, and their common DDR target genes are significantly correlated with metastasis, castration-resistance, recurrence, and shorter overall survival in PCa patients. We demonstrated in vitro that silencing of *MYB*, *BRCA1* or *TOPBP1* synergized with poly (ADP-ribose) polymerase (PARP) inhibitor olaparib (OLA) to increase cytotoxicity to PCa cells. We further demonstrated that targeting the c-Myb-TopBP1-ATR-Chk1 pathway by using the Chk1 inhibitor AZD7762 synergizes with OLA to increase PCa cytotoxicity. Our results reveal new mechanism-based therapeutic approaches for PCa by targeting PARP and the c-Myb-TopBP1-ATR-Chk1 pathway

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Abstract Edited

Androgen deprivation is the standard treatment for advanced prostate cancer (PCa), but most patients ultimately develop resistance and tumor recurrence. We found that *MYB* is transcriptionally activated by androgen deprivation therapy or genetic silencing of the androgen receptor (AR). *MYB* silencing inhibited PCa growth in culture and xenografts in mice. Microarray data revealed that c-Myb and AR shared a subset of target genes that encode DNA damage response (DDR) proteins, suggesting that c-Myb may supplant AR as the dominant regulator of their common DDR target genes in AR inhibition–resistant or AR-negative PCa. Gene signatures including *AR*, *MYB*, and their common DDR-associated target genes positively correlated with metastasis, castration resistance, tumor recurrence, and decreased survival in PCa patients. In culture and in xenograft-bearing mice, a combination strategy involving the knockdown of *MYB*, *BRCA1*, or *TOPBP1* or the abrogation of cell cycle checkpoint arrest with AZD7762, an inhibitor of the checkpoint kinase Chk1, increased the cytotoxicity of the poly[adenosine 5′-diphosphate (ADP)–ribose] polymerase (PARP) inhibitor olaparib in PCa cells. Our results reveal new mechanism-based therapeutic approaches for PCa by targeting PARP and the DDR pathway involving c-Myb, TopBP1, ataxia telangiectasia mutated– and Rad3-related (ATR), and Chk1.

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Research Article Abstract: Before (224 words)

Cells derived from ataxia telangiectasia (A-T) patients exhibit defective cell cycle checkpoints following ionizing radiation (IR), profound radiosensitivity and high levels of chromosome aberrations. We have shown that transient ATM kinase inhibition from +15 to +75 min following IR is sufficient to radiosensitize cells and accumulate persistent chromosome aberrations. We show here that DNA-PK kinase inhibition from +15 to + 75 min is also sufficient to radiosensitize cells and accumulate persistent chromosome aberrations. The ATM kinase-dependent mechanisms that ensure cell survival and suppress chromosome aberrations during this interval are independent of DNA-PK kinase activity. Neither the activation nor the recovery of the IR-induced G2/M cell cycle checkpoint are affected by ATM kinase inhibition from +15 to +75 min, indicating that 15 min of ATM kinase signaling is sufficient to induce this cell cycle checkpoint. Surprisingly, ATM kinase inhibition from +15 to +75 min abrogates IR-induced sister chromatid exchange (SCE), a phenotype attributed to the repair of damaged replication forks. Further, ATM kinase inhibition using either KU55933 or KU60019 is sufficient to disrupt camptothecin-induced SCE. Since DNA damage-induced SCE is maintained A-T cells that express no ATM protein, and the ATM kinase inhibitors have no effect on DNA damage-induced SCE in A-T cells, these data reveal that the consequences of acute ATM kinase inhibition and adaptation to ATM protein disruption are distinct in S-phase cells.

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Problems

Cells derived from ataxia telangiectasia (A-T) patients exhibit defective cell cycle checkpoints following ionizing radiation (IR), profound radiosensitivity and high levels of chromosome aberrations.

We have shown that transient ATM kinase inhibition from +15 to +75 min following IR is sufficient to radiosensitize cells and accumulate persistent chromosome aberrations.

We show here that DNA-PK kinase inhibition from +15 to + 75 min is also sufficient to radiosensitize cells and accumulate persistent chromosome aberrations.

The ATM kinase-dependent mechanisms that ensure cell survival and suppress chromosome aberrations during this interval are independent of DNA-PK kinase activity.

- What is radiosensitivity?
- What is the relationship of radiosensitivity to chromosome aberrations?

- ATM kinase = The kinase that phosphorylates ATM? NO

- What are ATM and DNA-PK?
- DNA-PK kinase = The kinase that phosphorylates DNA-PK? NO

- ATM kinase-dependent = Mechanisms that rely on phosphorylation of ATM? NO
- How does cell survival relate to radiosensitivity?

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More problems

Neither the activation nor the recovery of the IR-induced G2/M cell cycle checkpoint are affected by ATM kinase inhibition from +15 to +75 min, indicating that 15 min of ATM kinase signaling is sufficient to induce this cell cycle checkpoint.

Surprisingly, ATM kinase inhibition from +15 to +75 min abrogates IR-induced sister chromatid exchange (SCE), a phenotype attributed to the repair of damaged replication forks.

Further, ATM kinase inhibition using either KU55933 or KU60019 is sufficient to disrupt camptothecin-induced SCE.

- What is the IR-induced G2/M checkpoint?
- Why is this surprising? What do damaged replication forks have to do with IR-induced damage?
- Too much experimental detail.
- What is camptothecin?

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And more problems

Since DNA damage-induced SCE is maintained A-T cells that express no ATM protein, and the ATM kinase inhibitors have no effect on DNA damage-induced SCE in A-T cells, these data reveal that the consequences of acute ATM kinase inhibition and adaptation to ATM protein disruption are distinct in S-phase cells.

- Since should be because.
- Genes are expressed, not proteins.
- The information about S-phase is out of context.

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Did your eyes glaze over?

- Lack of context
- Too much methodological detail
- Imprecise language
- Too many undefined terms

Clean edited version with editorial queries (182 words)

ABSTRACT

Cells derived from ataxia telangiectasia (A-T) patients exhibit defective cell cycle checkpoints due to mutations in the gene encoding ATM (ataxia telangiectasia mutated). Following exposure to ionizing radiation (IR), A-T cells exhibit sensitivity to IR-induced cellular damage (radiosensitivity), resulting in abundant chromosome aberrations. ATM is a member of a family of kinases that become activated in response to DNA damage, and exposure of cells to IR triggers ATM activity and subsequent transient inhibition ATM causes radiosensitivity. We show that, despite activation and recovery from the G_2/M checkpoint following transient inhibition of ATM 15 minutes after cellular irradiation, the cells exhibited radiosensitivity and accumulation of persistent chromosome aberrations. With reversible inhibitors of DNA-PK (DNA-dependent protein kinase), another kinase involved in responding to DNA damage, and ATM, we show that these two kinases acted through distinct DNA repair mechanisms: ATM resolved DNA damage through a mechanism involving sister chromatid exchange (SCE), whereas DNA-PK acted through nonhomologous end joining. Furthermore, DNA damage-induced SCE occurred in A-T cells, suggesting that A-T cells have adapted to the loss of ATM and have alternative mechanisms to initiate SCE.

Comment [NG1]: Abstract cannot exceed 250 words. I have substantially revised this to make it more accessible and to put the new results into a broader context. I thought including the details of the methods and timing made the abstract difficult to follow.

Comment [NG2]: Are the last two the consequence of IR or are these present in the patients cells all the time? Correct as edited?

Comment [NG3]: We try to reserve "levels" for positions within a hierarchy. Please use abundant or concentration or amount as appropriate.

Comment [NG4]: Introduce the kinases in one sentence. Is this correct?

Abstract: Original 265 words!

Depolarization of resting membrane potential in select cells in *Xenopus* larvae induces normal melanocytes to undergo a conversion to a metastatic phenotype. Here, we show that this non-cell-autonomous process is mediated by cAMP, CREB, and the transcription factors Sox10 and Slug, which have been previously shown to be implicated in various cancers, including melanoma. Our microarray analysis reveals specific transcripts responsive to Vmem levels within a few hours of depolarization, and a set of 517 transcripts whose expression remains altered during the full hyperpigmented phenotype over a week later, linking instructor cell-depolarization to a range of developmental processes and disease states. We also show that voltage-dependent conversion of melanocytes involves the MSH-secreting melanotrope cells of the pituitary, and formulate a model for the molecular pathway linking the bioelectric properties of melanocyte cells' microenvironment in vivo to the genetic and cellular changes induced in this melanoma-like phenotype. Remarkably, the phenotype is all-or-none: each individual animal either undergoes melanocyte conversion or not, as a whole. This group decision is stochastic, resulting in varying percentages of hyperpigmented individuals for a given experimental treatment. To explain the observed stochasticity as an inherent dynamic property of this complex signaling system, we developed a novel computational method that reverse-engineered a dynamic regulatory network that quantitatively explained our complex dataset, and made correct predictions for new experiments. Taken together, these data (1) reveal new molecular details about a novel trigger of metastatic cell behavior in vivo, (2) suggest new targets for biomedical intervention, and (3) demonstrate proof-of-principle of a computational method for understanding stochastic decision-making by cells during development and cancer.

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Problems:

- Vague terminology: "select cells"
- Confusing connection between frogs and cancer: Hyperpigmented frogs have cancer?
- Undefined abbreviations: cAMP, MSH, CREB
- Using whose to refer to transcripts
- Too long (PubMed truncates at 250)
- Methodological context unclear
- Mixing background and results
- What did they do in this study versus what was already known?

Abstract: After 225 words

Experimentally induced depolarization of resting membrane potential in “instructor cells” in *Xenopus laevis* embryos causes hyperpigmentation in an all-or-none fashion in some tadpoles due to excess proliferation and migration of melanocytes. We showed that this stochastic process involved serotonin signaling, adenosine 3’,5’-monophosphate (cAMP), the transcription factors cAMP response element binding protein (CREB), Sox10, and Slug. Transcriptional microarray analysis of embryos taken at stage 15 (early neurula) and stage 45 (free-swimming tadpole) revealed changes in the abundance of 45 transcripts and 517 transcripts, respectively, between control embryos and embryos exposed to the instructor cell-depolarizing agent ivermectin. Bioinformatic analysis revealed that the human homologs of some of the differentially regulated genes were associated with cancer, consistent with the induced arborization and invasive behavior of converted melanocytes. We identified a physiological circuit that utilizes serotonergic signaling between instructor cells, melanotrope cells of the pituitary, and melanocytes to control the proliferation, cell shape, and migration properties of the pigment cell pool. To understand the stochasticity and properties of this multiscale signaling system, we applied a computational machine-learning method that iteratively explored network models to reverse engineer a stochastic dynamic model that recapitulated the frequency of the all-or-none hyperpigmentation phenotype produced in response to various pharmacological and molecular-genetic manipulations. This computational approach may provide insight into stochastic cellular decision-making that occurs during normal development and pathological conditions, such as cancer.

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Practice

- Although most PD cases are sporadic, at least seven genes have been reported to be implicated in the pathogenesis of familial PD (*1*).

(hint: too many words)

- *In vitro* studies indicated that several pathogenic mutations in LRRK2 caused an increase in the kinase activity, such as mutations R1441C in ROC GTPase domain and G2019S in kinase domain (*4-6*).

(hint: multiple problems, including a misplaced clause)

- While the physiological function of LRRK2 remains largely unknown, recent studies indicated a dispensable role of the intrinsic kinase activity of LRRK2 in neuron survival and its protective activity against neurotoxin (*10-12*).

(hint: multiple problems, especially temporal words)

- The current paper reports for the first time a sex reversal in transsexual people in the interstitial nucleus of the anterior hypothalamus (INAH) 3, a sexually dimorphic hypothalamic nucleus that was previously shown to be related to sexual orientation (citation 1, citation 2).

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