

Figure Captions & Titles

20.109 Communication Workshop 2

Dr. Chiara Ricci-Tam

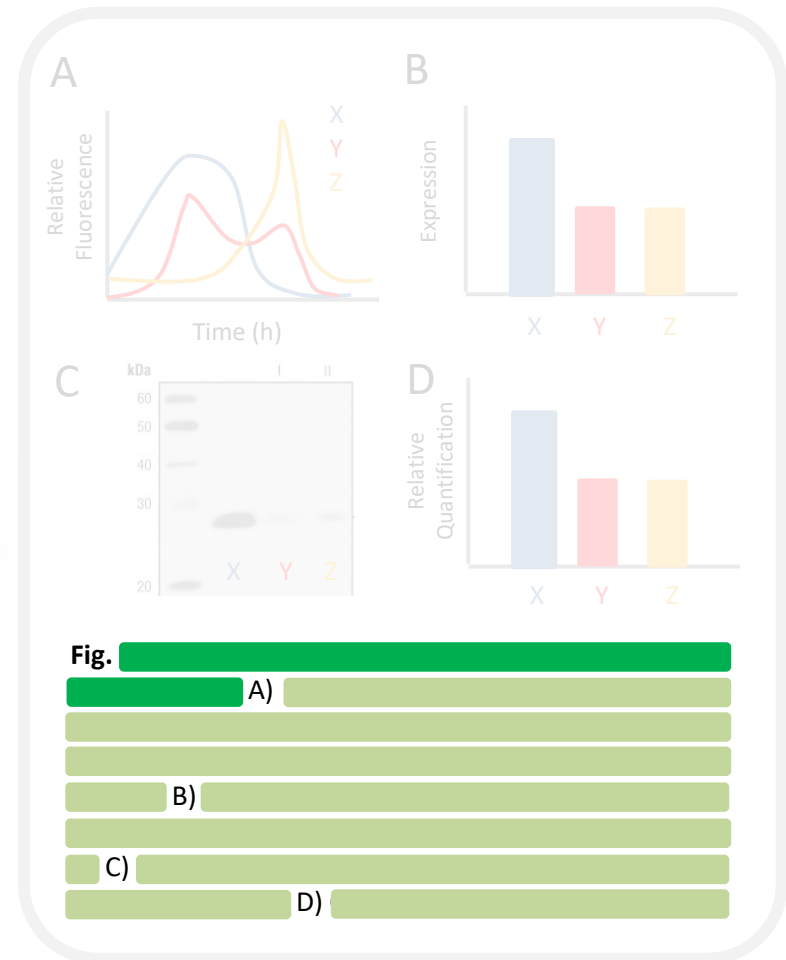
Dr. Sean Clarke



Communication Lab

Helping you communicate effectively.

mitcommlab.mit.edu/be/





Please sit in groups of 3-4,
without your lab partner

ACTIVITY – 5mins

Talk about your figure.

- What choices did you make? What would you do differently next time?
- How did you make your figures? What things were surprisingly hard?
- What tips are you adding to your figure making checklist?

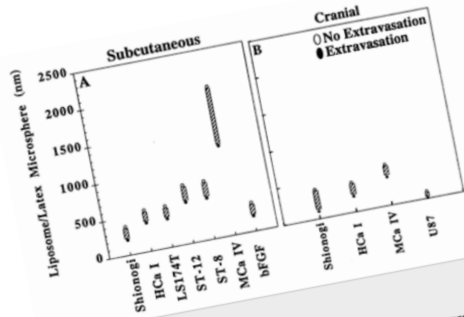
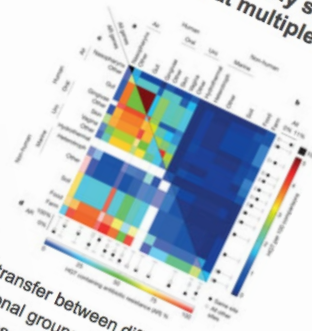


Figure 1

The vascular pore cutoff size for six different types of tumors grown in the dorsal of tumors grown in the cranial window (B) was evaluated. The solid circles represent extravasation at the indicated long-circulating liposome or latex bead size. The size range between the first particle that did not extravasate indicates the vascular pore cutoff size range (hatched bar). The majority of tumors have a vascular pore cutoff size range of 500-1000 nm when grown subcutaneously in the dorsal chamber. The interaction of the tumor with the subcutaneous microenvironment (A) leads to a smaller vascular pore cutoff size than the interaction with the subcutaneous microenvironment (A). Comparison of bFGF-induced vessels (bFGF-induced vascular pore sizes demonstrates that the presence of bFGF alone can lead to pores

Figure 3: HGT is ecologically structured by functional class and at multiple spatial scales



The frequency of transfer between different environments is shown for all functional groups (a, b) and for antibiotic resistance (AR) genes only (c, d). Box widths indicate the number of genes from each environment. a, When all

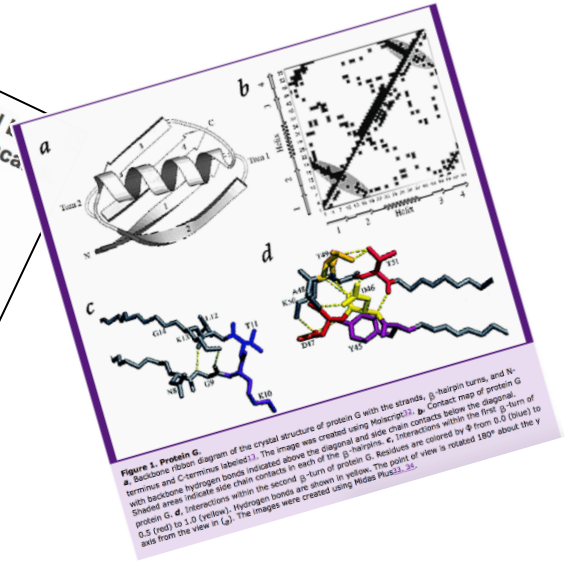


Figure 1. Protein G. a, Backbone ribbon diagram of the crystal structure of protein G with the strands, β -hairpin turns, and N-terminus and C-terminus labeled (1). The image was created using Molscript(2). b, Contact map of protein G with backbones and side chains indicated above the diagonal and side chain contacts below the diagonal. Shaded areas indicate side chain contacts in each of the β -hairpins. c, Interactions within the first β -turn of protein G. d, Interactions within the second β -turn of protein G. Residues are colored by ϕ from 0.0 (blue) to 0.5 (red) to 1.0 (yellow). Hydrogen bonds are shown in yellow. The point of view is rotated 180° about the y axis from the view in (a). The images were created using PyMol(3,25).

Captions and Titles

- Fig. [redacted]
 [redacted] A) [redacted]
 [redacted]
 [redacted] B) [redacted]
 [redacted]
 [redacted] C) [redacted]
 [redacted] D) [redacted]

Identify your process for making figures that highlight the message you are trying to communicate

1 MESSAGE What is the message of each figure?



2 DATA What data do you include in each figure to convey your message?

How can you present your data to support your message?



3 DESIGN What are some key design choices to think about?

All the data in a figure should support one clear message.

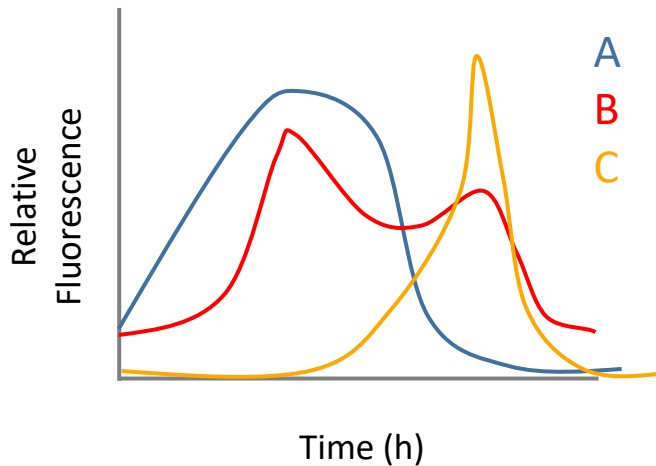


Fig. 1: A, B, and C have different dynamics under Condition X. A, B, and C were sampled using Method 1 and their fluorescence quantified with Method 2. Fluorescence data normalized to negative control.

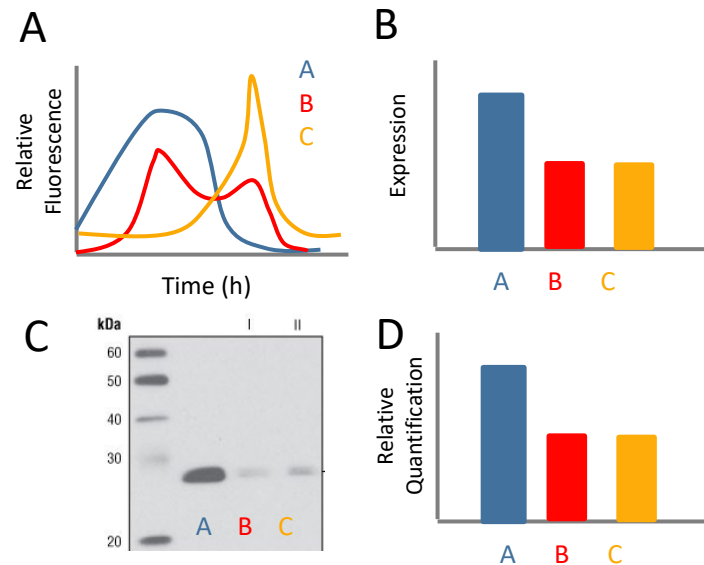


Fig. 1: A, B, and C have different dynamics under Condition X. A) A, B, and C were sampled using Method 1 and their fluorescence quantified with Method 2. Fluorescence data normalized to negative control. B) Gene expression data of samples A, B, and C, under condition X. Samples were collected at time T. C) Western blot analysis of samples A, B, and C, under condition X. D) Quantification of Western Blot.

How do you take a series of figures with messages and tell a story?

Organize your data to build one storyline

Rearrange until you've created a **logical series** of conclusions.

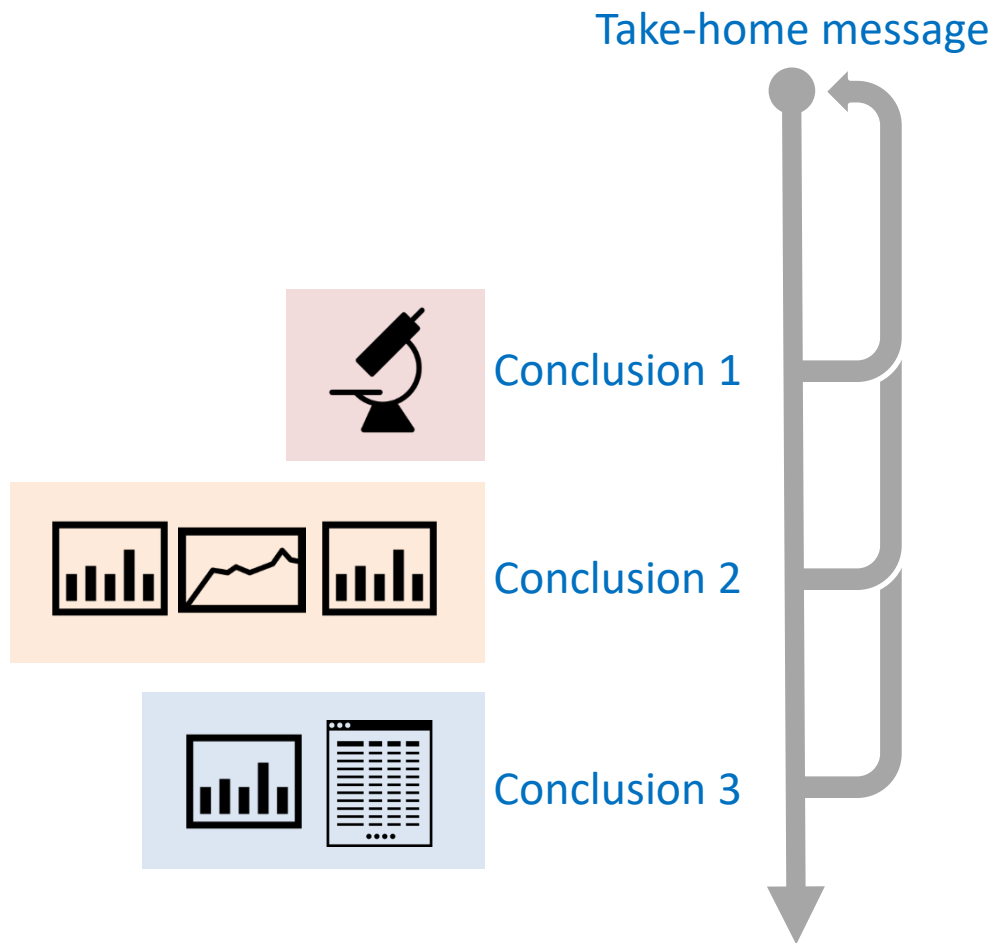


Identify **modules** that correspond to **conclusions**.



Organize figures to build a single storyline

Identify **modules** that correspond to **conclusions**.



Your title should highlight your figure's take-home message

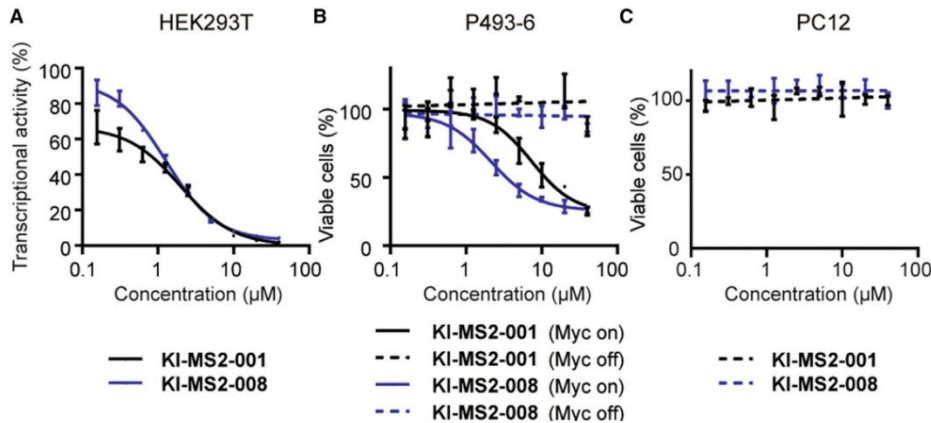


Figure 2. KI-MS2-001 and KI-MS2-008 Modulate Myc-Driven Transcription in Cells and Inhibit Viable Cell Levels in a Myc-Dependent Manner

(A) Dose-response curves for the Myc dual luciferase reporter assay in HEK293 cells in response to KI-MS2-001 or KI-MS2-008 treatment after 16 h ($n = 3$ technical replicates, error bars represent mean \pm SD). (B) Dose-response curves for P493-6 viable cell levels in response to KI-MS2-001 or KI-MS2-008 treatment with Myc expression left on or shut down with doxycycline after 3 days ($n = 3$ technical replicates, error bars represent mean \pm SD). (C) Dose-response curves for PC12 viable cell levels in response to KI-MS2-001 or KI-MS2-008 treatment after 5 days ($n = 3$ technical replicates, error bars represent mean \pm SD).

Title

- Take-home *message*
- What conclusion should the *reader evaluate* when looking at the figure?

You should be able to read your figure titles and understand the main message of your paper

Fig. 1. Discovery of a putative Max binder.

Fig. 2. KI-MS2-001 and KI-MS2-008 Modulate Myc-Driven transcription in cells and inhibit viable cell levels in a Myc-dependent manner.

Fig. 3. KI-MS2-008 and analogs engage Max *in vitro* and in live cells

Fig. 4. KI-MS2-008 induces Max/Max homodimerization

Fig. 5. KI-MS2-008 decreases Myc protein levels and affects the global Myc transcriptional program

Fig. 6. KI-MS2-008 treatment decreases c-Myc protein binding and increases Max protein binding at promoters of Myc-occupied genes

Fig. 7. KI-MS2-008 exhibits efficacy in cellular and murine cancer models

You should be able to read your figure titles and understand the main message of your paper

Fig. 1. **Discovery** of a putative Max binder.

Fig. 2. KI-MS2-001 and KI-MS2-008 **modulate** Myc-Driven transcription in cells and **inhibit** viable cell levels in a Myc-dependent manner.

Fig. 3. KI-MS2-008 and analogs **engage** Max *in vitro* and in live cells

Fig. 4. KI-MS2-008 **induces** Max/Max homodimerization

Fig. 5. KI-MS2-008 **decreases** Myc protein levels and **affects** the global Myc transcriptional program

Fig. 6. KI-MS2-008 treatment **decreases** c-Myc protein binding and **increases** Max protein binding at promoters of Myc-occupied genes

Fig. 7. KI-MS2-008 **exhibits** efficacy in cellular and murine cancer models

Figure titles are not the only kind of title...

- Title of a paper
- Figure captions
- Result section captions
- Slide titles

Article Titles

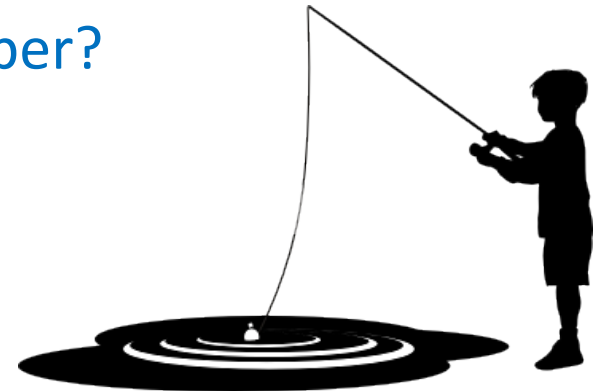
Why do they matter?



Attracting your audience: first judgment

Influencing whether someone will read or cite your paper

Indexing – Will readers even find your paper?



Titles

Effective titles are **messages**

What did you find? So what?

Let's take a look at this title

Stabilization of the Max Homodimer with a Small Molecule Attenuates Myc-Driven Transcription

Nicholas B. Struntz,^{1,2,3,13} Andrew Chen,^{1,2,3,13} Anja Deutzmann,⁴ Robert M. Wilson,^{1,2,3} Eric Stefan,^{1,2} Helen L. Evans,^{1,2,3} Maricela A. Ramirez,⁵ Tong Liang,⁵ Francisco Caballero,^{1,2} Mattheus H.E. Wildschut,^{1,2} Dylan V. Neel,^{1,2} David B. Freeman,^{1,2,6} Marius S. Pop,^{1,2,6} Marie McConkey,^{7,8,9} Sandrine Muller,⁹ Brice H. Curtin,^{1,2,3} Hanna Tseng,^{1,2} Kristen R. Frombach,^{1,2} Vincent L. Butty,^{1,10} Stuart S. Levine,^{1,10} Clementine Feau,⁹ Sarah Elmiligy,¹ Jiyoung A. Hong,^{1,2,11} Timothy A. Lewis,⁹ Amedeo Vetere,⁹ Paul A. Clemons,⁹ Scott E. Malstrom,¹ Benjamin L. Ebert,^{7,8,9} Charles Y. Lin,^{5,12} Dean W. Felsher,⁴ and Angela N. Koehler^{1,2,3,9,14,*}

What do you notice about this title?

What if the title was:

Attenuation of Myc-driven transcription

Okay I've made it better, right?

Screen to find small molecule that
attenuates Myc-driven transcription

What about this one:

Small molecule attenuation of Myc-driven transcription by Max homodimer stabilization

(for comparison, the published title)

Stabilization of the Max Homodimer with a Small Molecule Attenuates Myc-Driven Transcription

Effective titles are messages

What did you find? So what?

Avoid overly vague and short or excessively long and detailed titles

Focus on a message about what you found, not what you did

Put the thing you want to emphasize at the beginning

Titles are framed for your audience

Build and simplify your title by identifying nouns and verbs and focusing on key terms

KEY NOUNS

KEY VERBS

Novel methods for early prediction of undesirable interference by microbial inhabitants of the human gut with metabolism of the cardiac drug digoxin give rise to strategies for alleviating drug inactivation

NEW AND IMPROVED TITLE

Predicting and alleviating drug interference by human gut microbiome

TOO SIMPLIFIED = LESS INFORMATIVE

Novel methods for prediction of drug interference

Remember your audience to condense jargon for concision

Surveying somatic mutations in P53, EGFR, BRCA1, and HRAS for impact on MCF7 tumors with heterogeneous cell composition.

1 2 3

Replace jargon to attract a broader audience



Surveying the impact of breast cancer oncogenes on tumor heterogeneity

1 2 3

What if your story doesn't seem conclusive?

- Tell your story in a different way:
 - focus on the technology?
 - what did you learn?

Brief Communications Arising | 19 September 2018

Evidence that CD32a does not mark the HIV-1 latent reservoir

- Convey negative results

*A Raf-Competitive K-Ras Binder
Can Fail to Functionally
Antagonize Signaling.*

- Make a descriptive title that's clear and interesting

Captions

High-level **description** of what you did

The caption should give just enough info for the reader to understand **how the data was generated**

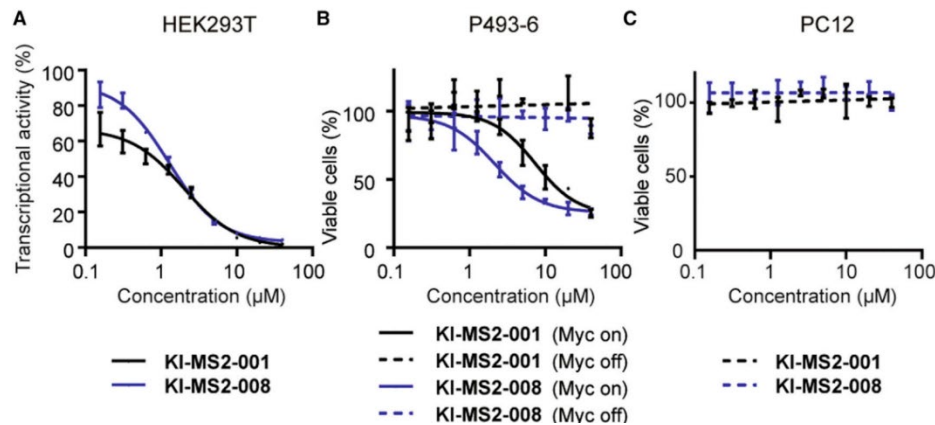


Figure 2. KI-MS2-001 and KI-MS2-008 Modulate Myc-Driven Transcription in Cells and Inhibit Viable Cell Levels in a Myc-Dependent Manner (A) Dose-response curves for the Myc dual luciferase reporter assay in HEK293 cells in response to KI-MS2-001 or KI-MS2-008 treatment after 16 h (n = 3 technical replicates, error bars represent mean ± SD). (B) Dose-response curves for P493-6 viable cell levels in response to KI-MS2-001 or KI-MS2-008 treatment with Myc expression left on or shut down with doxycycline after 3 days (n = 3 technical replicates, error bars represent mean ± SD). (C) Dose-response curves for PC12 viable cell levels in response to KI-MS2-001 or KI-MS2-008 treatment after 5 days (n = 3 technical replicates, error bars represent mean ± SD).

Caption

- **Descriptive**, not explanatory/interpretive
- Only enough method detail to make it clear how results were obtained.
- All types of figures should have captions

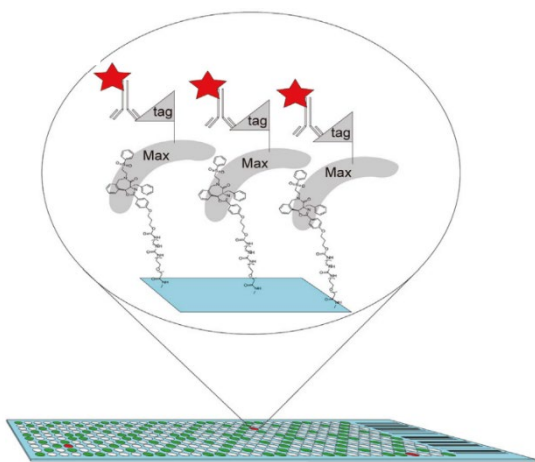


Figure 1. Discovery of a Putative Max Binder (A) Cartoon diagram of the Max (blue) dimerization network displaying transcriptional activation by the Myc (green)/Max heterodimer, transcriptional attenuation by the Max/Max homodimer, and transcriptional repression by Max/Mxd (purple) heterodimer. (B) Schematic of a small molecule microarray (SMM) showing SMM positives (red spots), which were detected by Alexa Fluor 647-labeled antibodies against the His-tag on the purified Max protein. (C) SMM screening results for DIV06 compound library, which is comprised mostly of products of diversity-oriented synthesis (n = 3 technical replicates). Histogram of composite Z scores and 3D scatterplot showing Z scores of feature to background ratios in triplicate for compounds on the SMMs. (D) Prioritization scheme for Max binders that modulate Myc-driven transcription leading to hit stock solution BRD-K19261677 (resynthesized as KI-MS2-001) and KI-MS2-008 as a more potent and synthetically accessible probe.

P493-6

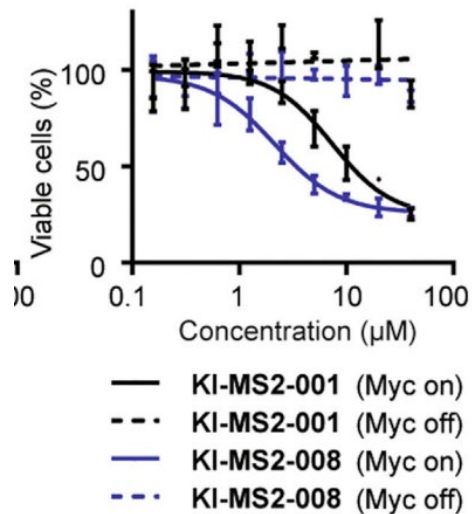


Figure 2. KI-MS2-001 and KI-MS2-008 Modulate Myc-Driven Transcription in Cells and Inhibit Viable Cell Levels in a Myc-Dependent Manner

(A) Dose-response curves for the Myc dual luciferase reporter assay in HEK293 cells in response to KI-MS2-001 or KI-MS2-008 treatment after 16 h (n = 3 technical replicates, error bars represent mean ± SD).

(B) Dose-response curves for P493-6 viable cell levels in response to KI-MS2-001 or KI-MS2-008 treatment with Myc expression left on or shut down with doxycycline after 3 days (n = 3 technical replicates, error bars represent mean ± SD).

(C) Dose-response curves for PC12 viable cell levels in response to KI-MS2-001 or KI-MS2-008 treatment after 5 days (n = 3 technical replicates, error bars represent mean ± SD).

(D) Immunoblots of c-Myc from P493-6 lysates, demonstrating doxycycline repressed expression of c-Myc and immunoblots of Max from P493-6 and PC12 lysates, showing the lack of functional Max in PC12 cells. (E) Summary of estimated IC50 values for the Myc reporter assay and viable cell levels.

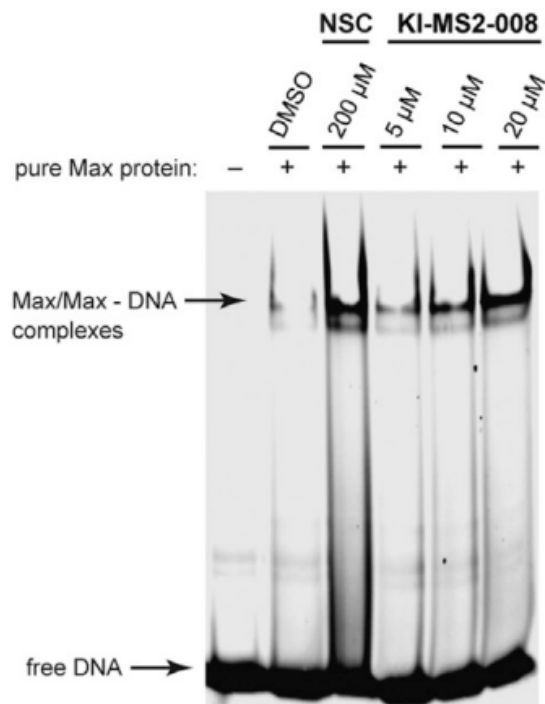


Figure 4. KI-MS2-008 Induces Max/Max

Homodimerization (A) Electrophoretic mobility shift assay (EMSA) utilizing Alexa Fluor 684-labeled E-box DNA incubated with P493-6 lysate treated with 10058-F4 (F4) or KI-MS2-008. (B) EMSA involving pure recombinant Max protein binding to Alexa Fluor 684-labeled E-box DNA incubated with NSC13728 or KI-MS2-008. (C) Plot of the distribution of sedimentation coefficients ($c(s)$) versus S , calculated from analytical ultracentrifugation sedimentation velocity experiments carried out with untreated Max protein or Max protein treated with 10 and 20 mM KI-MS2-008. (D) Size-exclusion chromatography of pure recombinant Max protein, Max protein with high KCl concentration, and Max protein with high KCl concentration treated with 10 mM KI-MS2-008.

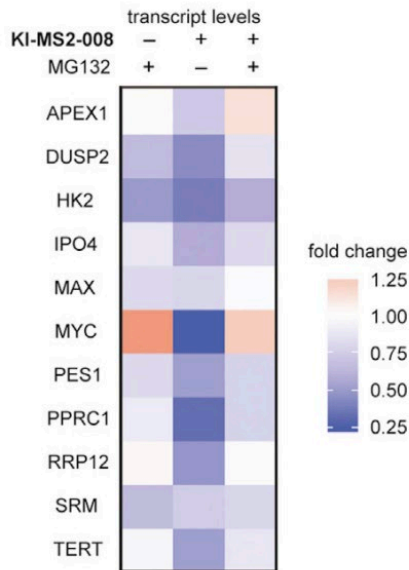


Figure 5. KI-MS2-008 Decreases Myc Protein Levels and Affects the Global Myc Transcriptional Program (A) Time course of c-Myc and Max protein levels in P493-6 treated with 10 mM KI-MS2-008 visualized by immunoblots. (B) c-Myc protein levels with 4 h of 10 mM KI-MS2-008 and/or proteasome inhibitor MG132 treatment in P493-6 visualized by immunoblots demonstrating partial rescue of c-Myc protein levels. (C) Scatterplot of RNA-seq data comparing Myc inactivation via doxycycline (8 h) and KI-MS2-008 treatment in P493-6 cells at 8 h of 10 mM KI-MS2-008. Green dots correspond to genes from the HALLMARK_MYC_TARGETS_V2 (HALLMARK MYC) gene set. (D) Gene set enrichment analysis (GSEA) plots of enrichment scores (ES) corresponding to RNA-seq datasets for P493-6 cells treated with 10 mM KI-MS2-008 for 8 h with normalized enrichment scores (NES) and nominal p values (n = 4 technical replicates). Four Myc target gene sets are shown. (E) GSEA plots of ES corresponding to RNA-seq datasets for P3HR1 cells and ST486 cells treated with 10 mM KI-MS2-008 for 8 h with NES and nominal p values (n = 4 technical replicates). HALLMARK_MYC_TARGETS_V2 (HALLMARK MYC) gene set is shown. (F) Heatmap showing fold changes in Myc-driven genes in response to 10 mM KI-MS2-008, 10 mM MG132, or the combination at 4 h as determined by qPCR (n = 3 technical replicates).

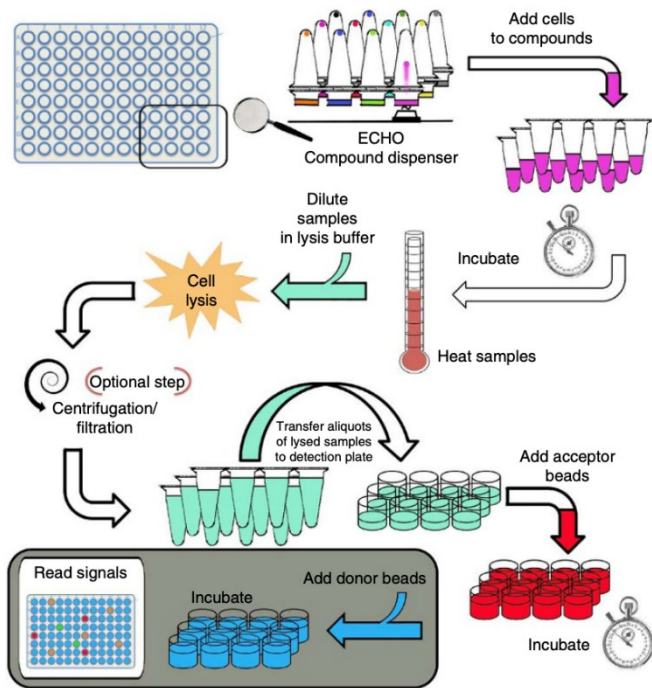


Figure 2 | The screen format assay procedure. Compound stock solutions are first dispensed into individual wells followed by the addition of a cell suspension to all wells. The samples are next preincubated for 30 min before placing the microplates in a PCR machine for heating to a predefined temperature for 3 min. The plate is then allowed to cool before samples are diluted with lysis buffer. At this point, it is optional to remove the cell debris and protein aggregates by means of centrifugation and/or filtration. The diluted samples must then be transferred to a suitable detection plate (unless detection can be made in the same plate). Finally, the detection is achieved by following a standard protocol for AlphaScreen bead additions, incubations and readings.

ACTIVITY

In the same groups of 3-4, not with your lab partner, talk about your title and caption.

- Was your title a message?
- Was your caption descriptive?
- What would you do differently?

Identify your process for making figures that highlight the message you are trying to communicate

1 MESSAGE What is the message of each figure?



2 DATA What data do you include in each figure to convey your message?

How can you present your data to support your message?



3 DESIGN What are some key design choices to think about?

Checklist for writing good titles

- Ensure that your title is a message
- Edit your title to highlight your key concepts
- Frame your titles for your audience
- Eliminate jargon

For every figure, ask yourself...

- Is the central message validated by the data shown?
- Which data are irrelevant?
- Are there any data/labels missing?
- What could be done to better highlight the most important data?
- Is there a better way to present the data?
- Do the statistics actually add anything here?

Optimize your figures with these reminders

High-level questions

- *Strategic purpose:*
 - What do you want to convey?
 - How will you and/or your audience use this figure?
- *Organizational structure:*
 - Where does this figure fit into the communication?
 - Why?

Checklist

- Choice of data
- Title/caption
 - Can figure stand alone?
- Consistent layout
 - Fonts, spacing, colors
- Text amount and placement
- Scale, axes, tick marks
- Error analysis
- Ink-to-whitespace ratio

These are our next steps

- Slides and tips will be on the wiki

Your next steps

- Bring an abstract to the next workshop.
 - Go to NCBI Pubmed or Google Scholar and search for a topic of interest.
 - Find the abstract and read it. If you like it, bring it.
- As you read, think about where you see abstracts, what goes into an abstract, and what makes a really good abstract!