Preparing Effective *poster* PRESENTATIONS

A Resource for **Poster Presentations**

Created by the Vanderbilt University English Language Center (ELC)

Table of Contents

Poster Presentations

This resource[1] was developed by the Vanderbilt University English Language Center (ELC) to support international and multilingual students prepare effective poster presentations. Use the following reference sheet to prepare your poster presentation[2], then find information on some common questions. For individualized support, you can schedule a virtual coaching session at **https://www.vanderbilt.edu/elc/coaching/**

Acknowledgement:
We would like to thank the graduate students at Vanderbilt University who voluntarily provided valuable language data for the development of this resource. Refer to the Appendix for more on how we extracted the sample language from the poster presentations.

[1] Motivation for creating this resource: our research showed that there is a huge gap between textbook language and the actual poster presentation language. For example, instead of saying "The Table shows…", presenters commonly use simple language along with posture like "Here [point at the table], [results]" (More examples can be found in the **ELC Poster Presentation Resource 1**). Hence, we want to further research and analysis on real language example used by presenters at Vanderbilt in order to extract and provide you the most ESSENTIAL language for effective poster communication in this resource.

[2] See similar recommendation for structure of poster presentations in an existing Vanderbilt University resource at: **https://my.vanderbilt.edu/researchfair/preparation/#contents**

Reference Sheet

Poster Presentations

1. Poster presentation structure:

	Selected Sample Language Drawn on real examples of presenters at Vanderbilt	**Your presentation**
Research question / Background *What field is your work in? What is your specific research question?*	– "Our main question is whether [research question]." – "I'm investigating [X] to understand [key research focus]."	
Significance *What new knowledge can your work contribute to the field?*	– "[X] is an important [problem/condition] because [reason]." – "This study provides an opportunity to better understand [phenomenon] and its effects on [population/field]."	
Methods *What experiments/tasks have been done?*	– "To explore this question, we conducted [type of analysis or experiment]." – "In our study, we used [model/system/participants] and [experimental procedure]."	
Results *What has been found so far?*	– "Here we can see that [main finding]." – "These results suggest that [interpretation of findings]."	
Conclusions / Future Directions *(You can remind your audience of your research question first) What do the findings mean? What comes next?*	– "With these results in mind, it seems that [summary of findings]." – "Our preliminary data suggest that [factor/treatment] may cause [effect] in [population/subjects]." – "Further research will test [hypothesis] in [population/system] or explore [next step]."	

2. What if my research does not fit in with the structure recommended above?
While it is possible, most research has categories like Research Question and Results.

3. How long should my poster presentation be?
Although 2-5 minutes are typical, we recommend preparing several versions of different lengths. You should prepare at least a 1-minute pitch that highlights your key message.

4. How formal should my presentation be?
Poster presentations usually sound conversational as the audience often comes and goes randomly. It is recommended to always assume your audience does not have background knowledge of your topic. Or, before you start your presentation, you can confirm:

- How much do you know about [your topic]?
- Have you studied or worked on [your topic] before?
- Do you want a short background explanation or just the main findings?

5. **I prepared my presentation using the reference sheet above. Should I memorize my presentation?**
   Absolutely NOT. Use the content you prepared as guides and adapt to your research.

6. **What do I need to know if I am giving a poster presentation asynchronously?**
   Common formats:
   - **Live virtual session:** wait in your assigned designated virtual [?]room and present your poster when attendees join (they may enter at different times similar to an in-person session); or
   - **Pre-recorded session:** record and upload your poster and presentation in advance, and during the scheduled time, either
     - Join the meeting to answer audience questions live, or
     - Respond to questions in writing (e.g., via chat or comments).
   - Either way, you can use the reference sheet above to help prepare your presentation.

7. **I have more questions, or I want to practice my presentation. How can I get more help from the ELC?**
   You can book an appointment for Individual Language Coaching at **https://www.vanderbilt.edu/elc/coaching/**. Let our coaches know what you wish to work on. Some possible activities include:
   - Prepare your presentation using the reference sheet above during one of our Individual Language Coaching sessions.
   - 1-minute pitch – use plain language to introduce your work to our coaches in 1 minute.
   - Rehearse your presentation section by section – practice speaking through one section (e.g., The background) at a time for feedback.
   - Audience adaptation and time management practice – rehearse different versions of your presentation (e.g., 3-minute, 1-minute, 1-sentence versions etc.) and receive feedback.
   - Q & A Simulation - invite our consultants to raise questions after you give your presentation.
   - Transitions and cohesion – ask our coaches to focus on / provide language you can use for transitions between/within sections.
   - Simplify and clarify scientific terminology[3] – explain jargon or terminology in your field to our coaches and check whether they can understand your speech without having background knowledge in your field.

[3] Tips and Strategies for explaining complex scientific jargon (see some real examples used by Vanderbilt presenters)

a. Use language that signals a common section in research work
   - Example: "*We tested this by doing* **a primary pull down the GFP IP"**.
   - "*We tested this by doing"* clearly indicates that "**a primary pull down the GFP IP" refers to a research method even if this is your first time hearing it.**

b. Use analogies
   - original "cancer phenotype" in biology
   - modified: "cancer phenotype refers to observable characteristics and behaviors of cancer cells *like the behaviors you observe of a worker in a factory who breaks all rules*"

c. Pair jargon with definitions
   - original: "melanoma antigen gene"
   - modified: "melanoma antigen gene, *the genes that are normally silent in adult cells but are active in cancer cells*"

Appendix

How We Extracted Sample Language from Real Vanderbilt Poster Presentations
We developed this guide by analyzing language in two recorded poster presentations from Vanderbilt graduate students. After transcribing the recordings, we identified language that signals each section of a research project such as the **Research Question, Methods, Results,** and **Conclusions.**

These sample expressions illustrate how effective presenters help their audience follow the structure of a poster presentation step by step. We believe these expressions are useful for any field and can help both presenters and listeners stay oriented throughout a presentation.

The Poster Presentation from Student A

Student A's presentation contains a significant amount of technical jargon, which can make it difficult for a general audience to follow. However, the student also used rhetorical questions and clear section-signaling language, that helps listeners recognize the overall structure even without understanding every detail. This shows how important it is to use language that guides the audience through each part of a poster presentation. From this transcript, we identified sample language that can make any poster presentation clearer and more effective. A plain-language summary of Student A's research and the original transcript are provided below.

Summary:
Cancer happens when cells grow too much and form tumors. One protein that may be involved is MAGE-B2, which appears in many cancers and is linked to poorer patient outcomes. To better understand MAGE-B2, we studied which proteins it connects with inside cells. Using lab methods, we pulled MAGE-B2 out of healthy cells and found about 200 proteins that might interact with it. We then tested a smaller group more carefully and discovered that MAGE-B2 strongly binds to several proteins that control cell growth, including ELAB1, PHB, and PRMT5. These results suggest that MAGE-B2 may help cancer cells grow by working with these proteins. Next, we plan to block these proteins in cancer cells to see if that slows down tumor growth and points to new treatment options.

Sample language Drawn from the presentation	**Actual Language** Used in the presentation
Research Question / Problem	
"Today I'm going to talk about my research on [topic]." "So what does [key term or variable] have to do with [broader issue]?"	"Today I'm going to be talking to you about my research in melanoma antigen Gene b2 (MAGE-B2) and my project entitled uncovering MAGE-B2 function using unbiased proteomics and interactome analysis." "So what does MAGE-B2 have to do with cancer?"
Significance / Background	
"So it's important to understand what [key concept] is." "This gives us an opportunity to better understand how [phenomenon] works or affects [something]." "So why focus on [specific target]? There are a few main reasons for that."	"So MAGE-B2 falls under the category of cancer biology or cancer research." "So of course, it's important to understand what is cancer." "So this provides us an opportunity to better understand how it plays into cancer phenotypes and possibly give us a way that where we can target it in therapies and hopefully create better outcomes for patients." "So why choose MAGE-B2 out of all of these different options, and there are three main reasons for that."
Methods	
"So to explore [topic], we first wanted to [main action]." "To do this, we used [method or tool]." "From there, we moved on to [next step or procedure]."	"So to begin with, we wanted to generate a library of proteins that we know to specifically interact with MAGE-B2." "So to do this, we did an unbiased discovery of binding partners from MAGE-B2 using a tang of affinity purification." "So first, we did a primary pull down the GFP IP... and then doing a secondary pull down to enrich from MAGE-B2..." "So we used a subtractive analysis with just a general GFPIP pulldown..." "From there, we moved into an in vivo colormunal precipitation to further validate these targets." "So to do this, we co transfected, again, AGK, so healthy cells..."
Results	
"So here we can see that [finding]." "Interestingly, we found that [unexpected or notable result]." "So this is a summary of what we have so far."	"So interestingly, of those 200 or so proteins that we got from our subtractive analysis, a large amount of them were post transcriptional regulators." "So here we can see that PHB and E lab one were our strongest binders." "And again, we can see here that the results of our in vitro experiment are reiterated with ELAB one and PHB being our two strongest binders above background." "Interestingly though, PRMT five also showed a significant amount of binding above background where in our in vitro analysis it had not."
Conclusions / Future Directions	
"As we move forward, we plan to continue exploring [specific targets or directions]." "Our next step is to [action]." "If we can show [goal or hypothesis], then we'll move into [next phase]." "That's a summary of our research so far. Thank you."	"But as we move forward with our experiment, we continue to we plan to continue to investigate PHB, e lab one and PRMT Five." "Our initial plan is to continue in healthy cells." "If we can show or recapitulate this idea in those healthy cells, then we plan to move forward into cancerous cell lines..." "That is a summary of our research as we have it thus far. Thank you."

Transcript:

Hello. My name is XXX. Today I'm going to be talking to you about my research in melanoma antigen Gene b2 (MAGE-B2) and my project entitled uncovering MAGE-B2 function using unbiased proteomics and interactome analysis. So MAGE-B2 falls under the category of cancer biology or cancer research. So of course, it's important to understand what is cancer. So cancer is the unchecked over proliferation of cells leading to tumorigenesis and cancer phenotypes, and is generally caused by one of two things. The first is the loss of activation in tumor suppressor genes which are responsible for down regulating cellular proliferation, and the second is the up regulation of oncogenes, which are responsible for up regulating cellular proliferation. So effects on either one of these two things can lead to an imbalance in the cellular proliferation process, which leads to the cancer phenotypes that we see.

So what does MAGE-B2have to do with cancer? So MAGE-B2 is a Cancer-testis antigens or CTA, meaning that it is only expressed aberrantly in cancers or in testes cells, so only in germlines or in cancers. So this provides us an opportunity to better understand how it plays into cancer phenotypes and possibly give us a way that where we can target it in therapies and hopefully create better outcomes for patients. So how can we sub categorize MAGE-B2? MAGE-B2 is an X chromosomally located type one mage, meaning that it falls under the general definition of a cancer tested antigen, and it can further be sub classified by its b sub family. So you can see here the dendrogram of the MAGE family.

So why choose MAGE-B2 out of all of these different options, and there are three main reasons for that. The first is that MAGE-B2 is one of the less well understood melanoma antigen genes. The primary ones currently understood and researched are MAGE A3, A4, C1, and C2.

Secondly, MAGE-B2 is an exemplary member of the gene family. So as I told you, it's a true cancer testes antigen only expressed in germline and cancers. And as you can see in this graph here, it has a high penetrance in a wide variety of cancers, giving us an opportunity to uniquely investigate these cancers in particular and lung cancers. Over 50% of patients express MAGE-B2. It also has penetrance in melanomas, colorectal cancers and even ovarian cancers. And the final reason to choose MAGE-B2 is that it is a cancer biomarker [and its expressions correlates with poor patients prognosis] in and of itself. In this data that we mined from online databases, we can see that patients of cancers that express MAGE-B2 have poor health outcomes than those that have MAGE-B2 non expressing cancers. So patients that had MAGE-B2 had poor survival outcomes.

So how do we actually explore MAGE-B2? So to begin with, we wanted to generate a library of proteins that we know to specifically interact with MAGE-B2. So just generally, create a library so we can begin to understand the interacting with MAGE-B2 and start to paint a picture of how MAGE-B2 actually interacts in cancers. So to do this, we did an unbiased discovery of binding partners from MAGE-B2 using a tang of affinity purification [tandem affinity purification]. So we did this in AGK cells, so healthy human embryonic kidney cells, due to their stability and low background protein expression, which will help us get this unbiased library of proteins that we can begin to use for our interactive analysis. So first, we did a primary pull down the GFP IP for cleaving with a 3c protease, and then doing a secondary pull down to enrich from MAGE-B2 using s agarose beads, this gave us a wide pool of different proteins that we suspect to work with MAGE-B2. However, we can't be sure that they were specific to MAGE-B2, so we used a subtractive analysis with just a general GFPIP pulldown in order to give us a library of about 200 proteins which we now suspect to be specific MAGE-B2. So interestingly, of those 200 or so proteins that we got from our subtractive analysis, a large amount of them were post transcriptional regulators, meaning that they have the ability to play a role in this cancer regulation that we suspect MAGE-B2 to be a part of this further supports our hypothesis that MAGE-B2 plays a role in this cancer over proliferation, which ultimately means that possibly it plays a role that we can target in therapies. So now that we have those 200 or so targets, we chose about 10 to 20 to continue to explore in our research. And of those 10 to 20, we started with four in an in vitro target validation experiment. So those four that we had chosen were ELAB one, PHB, PCMT 1 and PRMT 5. And in order to explore them, we started with an in vitro target validation. In order to do this, we used PCs to make tagged target proteins and split them into two different experiments. The first being a GST control pull down, and the second being a GST may be MAGE-B2 pull down. With the idea being with the GST control pull down, we can ensure that the background binding GST is not what's causing the pull down. So here we can see that PHB and E lab one were our strongest binders. Even though ELAB one had some background binding, those two still had a significant amount of binding above background, warranting further exploration.

PCMT one and PRMT Five both had relatively low levels of binding, but we decided to move forward with them anyways, due to the residual materials we still have, making it easier for us. From there, we moved into an in vivo colormunal precipitation to further validate these targets. So to do this, we co transfected, again, AGK, so healthy cells with p i, R, E, S, P, R, O, flag, H, v2 and our PCs two. MYC tagged target proteins. We cultured them for 72 hours. We harvested them and lysed them in order to get our protein mixture. And then again, using western blot analysis, we were able to get this diagram. Here, we used Alpha tubulin as a housekeeping protein to ensure that the transfection of our cells did not negatively affect the health of the cells or the protein expression to ensure that we have an unbiased in vivo co IP. And again, we can see here that the results of our in vitro experiment are reiterated with ELAB one and PHB being our two strongest binders above background. Interestingly though, PRMT five also showed a significant amount of binding above background where in our in vitro analysis it had not. So this is a summary of what we have thus far. But as we move forward with our experiment, we continue to we plan to continue to investigate PHB, e lab one and PRMT Five. Our initial plan is to continue in healthy cells. So continue in ATK cells using KDKO, so knock down, knock out analyzes using s i, RNA mediation, in order to see if we can begin to affect the cellular proliferation in healthy cells by regulating these proteins that we hypothesize to be important in that process. If we can show or recapitulate this idea in those healthy cells, then we plan to move forward into cancerous cell lines such as HCT 116 which is a colorectal cell line, in order to see if we can answer the true question that lies at the heart of our research is, can we affect cancer phenotypes using these target proteins in our knowledge of MAGE-B2, that is a summary of our research as we have it thus far. Thank you.

The Poster Presentation from Student B

Student B's presentation includes many useful expressions that clearly signal transitions and sections. As a result, the structure of the talk is easy to follow, even when the content becomes complex. This example further illustrates how clear transition phrases make a presentation more accessible to a broad audience. From this transcript, we identified additional sample language that contributes to effective poster presentations. A plain-language summary of Student B's research and the original transcript are provided below.

Summary:

This study conducted a preliminary analysis of existing quantitative data of patients with psychosis—a mental health condition that affects how people perceive reality. Specifically, the researcher aimed to explore potential patterns and possible racial differences reflected in the numbers. Results showed that most assessments took place in inpatient settings. Black patients were given higher scores for hallucination symptoms, while White patients were given higher scores for anxiety symptoms. These differences have raised potential hypotheses and questions about potential racial bias in how patients are scored in the US healthcare system.

Sample language Drawn from the presentation	**Actual Language** Used in the presentation
Research Question / Problem	
"I'm basically doing a preliminary investigation into..." "I just basically want to lay a foundation of..." "I also was pretty curious about..." "I also was interested in looking at ...."	"I'm basically doing a preliminary investigation into the dimensional scores associated with psychosis." "I just basically want to lay a foundation of what this data has to offer, and you know what it looks like in different patient populations as well." "And I also was pretty curious about if there were possible racial disparities in how these patients were being scored." "I also was interested in looking at the co-occurring ICD codes."
Significance / Background	
"There hasn't been too much work that's been done on ..."	"And so with these quantitative numbers, you know, physicians are just more able to keep track of, you know, what is exactly is happening with their patients, and it also gives them a better idea of the clinical trajectories, and also just a better understanding of the neurobiological mechanisms that are associated with these patients who are diagnosed with psychosis. And so a lot of hospitals have begun to use this quantitative data. But there hasn't been too much work that's been that's been done, actually, on this, on this type of data, and there actually hasn't been any work that has been done from a researcher standpoint here at the VUMC."
Methods	
"That just leads me to my methods, where I..." "I also summarized key statistics across these different demographics..." "Here I move into the regression testing for ..."	"And so that just leads me to my methods, where I just extracted the demographic information from patients with these dimensional assessments." "And I also summarized key statistics across these different demographics, such as sex and race." "And here I move into the hormone regression testing for possibe racial bias."
Results	
"Moving on to the results..." "That brings me to my next point..." "I also included a table just to show ...." "Additionally, what I found with the regression testing is that..."	"And so, moving on to the results. Here's just a quick summary table of all the patients that have dimensional scores recorded here at VUMC." "And that brings me to my next point, just we want to see what type of scores are these patients actually getting." "And I also included a table just to show where these assessments were mainly taking place." "And additionally, what I found with the logistic regression testing is that black, black reported patients... were scored higher within the hallucinations symptom and white reported patients were actually scored higher in the anxiety symptom domain."
Conclusions / Future Directions	
"With all these results in mind, it seems that..." "And that basically concludes my research..."	"And so with all this, with all these results in mind, it seems that a lot of these dimensional assessments are happening in an inpatient setting..." "And that basically concludes my research here at VUMC."

Transcript:

How's it going? Everyone? My name is XXX, and I'm here to present my research on the dimensional analysis of psychosis here at VUMC.

And so psychosis has a lot of different domains of symptoms such as like positive symptoms, impaired cognition, hallucinations and etc. And you know, keeping track of all these different symptoms and their different severities are pretty hard, and so physicians basically came up with a quantitative dimensional analysis to help physicians keep track of what exactly what's going wrong inside these patients with psychosis. And so they created a scale alongside, in accordance to the DSM five, where they're rating these different buckets of symptoms on a scale of zero to four, with zero being and the symptom is absent, and four being the symptom is the most severe. And so with these quantitative numbers, you know, physicians are just more able to keep track of, you know, what is exactly is happening with their patients, and it also gives them a better idea of the clinical trajectories, and also just a better understanding of the neurobiological mechanisms that are associated with these patients who are diagnosed with psychosis. And so a lot of hospitals have begun to use this quantitative data. But there hasn't been too much work that's been that's been done, actually, on this, on this type of data, and there actually hasn't been any work that has been done from a researcher standpoint here at the VUMC. And so that's where I that's where just I come in. I'm basically doing a preliminary investigation into the dimensions school dimensional scores associated with psychosis, and I just basically want to lay a foundation of what this data has to offer, and you know what it looks like in different patient populations as well. And so that just leads me to my methods, where I just extracted the demographic information from patients with these dimensional assessments. And I also summarized key statistics across these different demographics, such as sex and race. And I also was pretty curious about if there were possible racial disparities in how these patients were being scored. And just to see if perhaps there was a like, just to see if there was like, a source of racial bias within these scores as well.

And so, moving on to the results. Here's just a quick summary table of all the patients that have dimensional scores recorded here at VUMC. And I used a de-identified electronic health record called the synthetic derivative, which is widely used here by researchers here at UMC. And I split these patients into three different buckets, basically saying, Oh, this first bucket has patients that have one to five different assessments, and then the second bucket is six to six to 10 different assessments, and third bucket is patients that have 1010, or more assessments that were performed. And so that basically gives a better idea of how long these patients have actually stayed here at VUMC. And I also stratified by age, sex and race.

And that brings me to my next point, just we want to see what type of scores are these patients actually getting. And so I actually stratified the different scores and visualized them using a history of them just to see the distribution of scores across these different symptom domains.

And I also was interested in looking at the co-occurring ICD codes. And so ICD codes are these universal codes that are used by all hospitals to better keep track of the specific diagnoses that each patient has, and based on this table, it seems that most of these patients that have these dimensional scores are diagnosed with schizophrenia or other schizoaffective disorders.

And here I move into the hormone regression testing for possible racial bias, and so I stratified. I stratified patients by either black or white, and I wanted to see if there were any differences in scores.

And moving on, I also stratified the same distribution of scores across race, and so that just gives a better showing of how these scores are different across black and white reported patients.

And I also included a table just to show where these assessments were mainly taking place.

And so with all this, with all these results in mind, it seems that a lot of these dimensional assessments are happening in an inpatient setting, as opposed to like an outpatient or an emergency room visit.

And additionally, what I found with the logistic regression testing is that black, black reported patients in the EHR were scored higher within the hallucinations symptom and white reported patients were actually scored higher in the anxiety symptom domain. And you know that basically raises a lot of potential hypotheses and questions about, you know, is there racial bias here at VUMC?

And, you know, is there, are there possible disparities in, you know, how these patients are actually being scored? And that, as a reflect that itself is just a reflection of, you know, racialized racialization in healthcare, which is widely spread throughout the United States, and that basically concludes my research here at VUMC.