How to make a scientific research poster

Diana Schlamadinger
05/04/2011

A judge's perspective: Posters and abstracts

Judges typically spend ~ 5-10 minutes per poster – not enough time to absorb everything! This is how I assess a poster in this limited time:

1. Read title and coauthors.
2. Read abstract.
3. Scan introduction, look at figures. What are the molecules?
4. Scan methods, look at figures. What are the techniques?
5. Scan results, look at figures. What are the data, and how good is the quality?
6. Read discussion, focus on figures. What are the conclusions?
7. Scan references.
8. Listen to your 1-minute speech.

If I am running out of time, I read the abstract and look at the figures.

Your poster should be self-explanatory with only the title, abstract, figures, and one discussion paragraph.

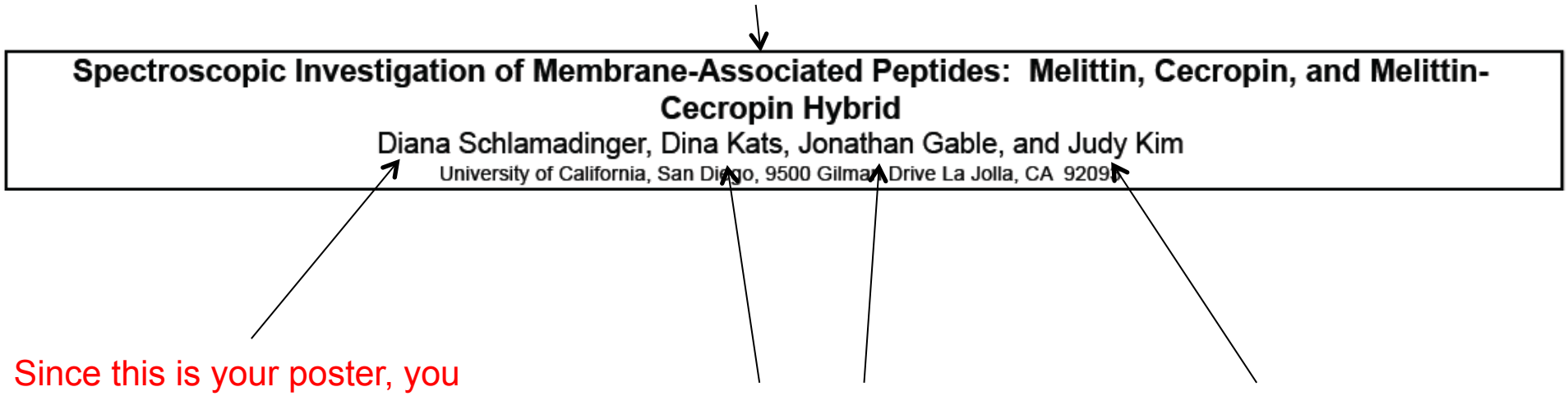
A judge's perspective: Posters and abstracts

The checklist that will be discussed in subsequent slides:

1. Is my title descriptive, and does it contain the necessary components?
2. Is my abstract concise and thorough?
3. Do I have well-defined headings that describe the layout of the poster?
4. Are my figures BIG, clear, and complete?
5. Do I include a reference section that typically has ~3-8 papers?
6. Is my Acknowledgements section complete?
7. Did I have at least one other person give me feedback on my poster?
8. Did I practice my 1-minute speech at least 3 times to colleagues/peers/friends?

What am I looking for in a title?

Title need not be a complete sentence. Be specific as possible.



Since this is your poster, you should be #1. If you are #2 or #3, I usually ask why.

Who else worked on the project, and what are affiliations? For example, is your work collaborative or independent?

Who provided the primary support scientifically and financially? Last author will tell me the principal investigator (PI).

The title should be complete and convey:

1. Your collaborators and PI
2. Location(s) where work was accomplished
3. Expertise, if appropriate (e.g. you did synthesis, and someone else did structure

What am I looking for in the abstract?

This is one of the most important parts of any presentation (oral and poster).

Abstract succinctly (<250 words) summarizes your motivation, experiments, findings, and discussion.

The abstract in a poster should be NO DIFFERENT from one in a paper or the one you submitted for your poster!

Abstract section is sometimes written as “Abstract and Background” to clarify that background information in abstract is sufficient for the poster (e.g. there is no separate background section).

Have at least two people (including your PI and other mentor) read your abstract.

Example of an abstract

Biochemistry **2001,** *40,* 13774−13778

Wavelength Dependent Cis-Trans Isomerization in Vision†

Judy E. Kim, Michael J. Tauber, and Richard A. Mathies*

Department of Chemistry, University of California, Berkeley, California 94720

Received August 6, 2001; Revised Manuscript Received October 1, 2001

Background motivation

ABSTRACT: The primary event in vision is the light-driven cis-trans isomerization of the 11-*cis*-retinal chromophore in the G-protein coupled receptor rhodopsin. Early measurements showed that this photoisomerization has a reaction quantum yield ϕ of ~0.67 [Dartnall (1936) *Proc. R. Soc. A 156*, 158−170; Dartnall (1968) *Vision Res. 8*, 339−358] and suggested that the quantum yield was wavelength independent [Schneider (1939) *Proc. Natl. Acad. Sci. U.S.A. 170*, 102−112]. Here we more accurately determine $\phi_{500} = 0.65 \pm 0.01$ and reveal that ϕ surprisingly depends on the wavelength of the incident light. Although there is no difference in the quantum yield between 450 and 480 nm, the quantum yield falls significantly as the photon energy is reduced below 20 000 cm^{-1} (500 nm). At the reddest wavelength measured (570 nm), the quantum yield is reduced by 5 ± 1% relative to the 500 nm value. These experiments correct the long-held presumption that the quantum yield in vision is wavelength independent, and support the hypothesis that the 200 fs photoisomerization reaction that initiates vision is dictated by nonstationary excited-state vibrational wave packet dynamics.

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Spectroscopic Investigation of Membrane-Associated Peptides: Melittin, Cecropin, and Melittin-Cecropin Hybrid

Diana Schlamadinger, Dina Kats, Jonathan Gable, and Judy Kim
University of California, San Diego, 9500 Gilman Drive La Jolla, CA 92093

ABSTRACT AND BACKGROUND

Both Melittin and Cecropin A have extensive biological relevance. Melittin, a 26 amino acid peptide and the main component of honeybee venom, is hemolytic and has been found to disrupt nearly all types of membranes.[1] Cecropin A, however, is a 37 amino acid antimicrobial peptide found in the Cecropia moth. This peptide is selective to the type of membrane with which it associates. Both of these peptides have very similar secondary structures, net charges, and one conserved tryptophan (W) residue known to be important to their activity. However, these peptides act very differently towards vesicles of varying lipid compositions. Furthermore, a hybrid peptide has been created that contains po… antimicrobial affects of parent peptides Cecropin A … found to be more effective at killing bacteria and is no…

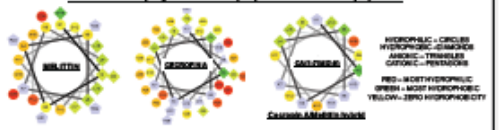
We have employed spectroscopic techniques to characterize the interaction between these peptides and biologically relevant membranes. The goal of these studies is to understand how the structure and local environment of these peptides varies in different environments that mimic cell membranes.

Lethal Concentrations (μM) of Cecropi…

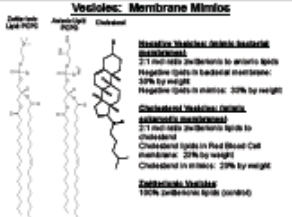
Peptide	E. Coli strain	P. Aeruginosa strain	B. Subt… strain			
Cecropin	0.3	2	4			
Melittin	0.8	3	0.2	0.2	0.5	4-8
CA(1-7)M(2-9)NH_2	1	4	0.5	0.5	0.5	>300

MATERIALS AND METHODS

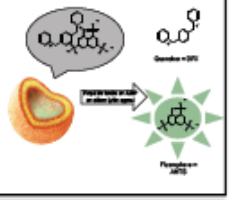
Helical wheel projections: Amphipathic membrane peptides



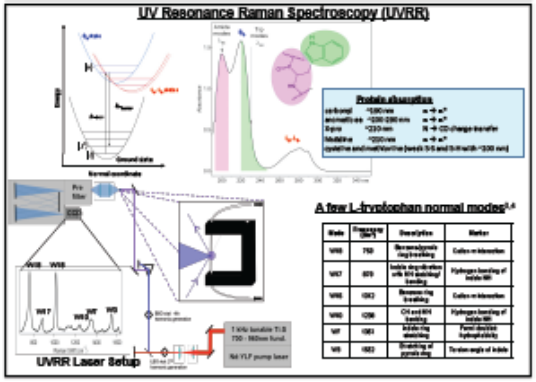
Vesicles: Membrane Mimics



Fluorescence Leakage Assay



UV Resonance Raman Spectroscopy (UVRR)

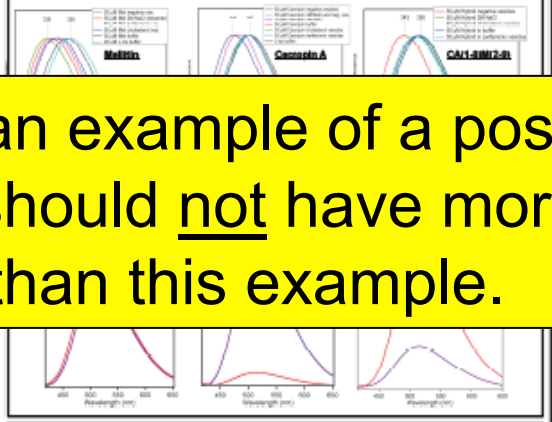


A few L-tryptophan normal modes[2,3]

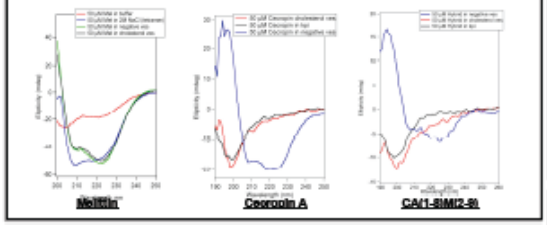
Mode	Frequency (cm^{-1})	Description	Marker
W18	750	Benzene/pyrrole ring breathing	Carbon-π interaction
W17	878	Indole deuteration with NH stretching/ bending	Hydrogen bonding of indole NH
W16	1012	Benzene ring breathing	Carbon-π interaction
W15	1256	CH and NH bending	Hydrogen bonding of indole NH
W7	1361	Indole ring stretching	Fermi doublet/ hydrophobicity
W6	1552	Stretching of pyrrole ring	Torsion angle of indole

RESULTS

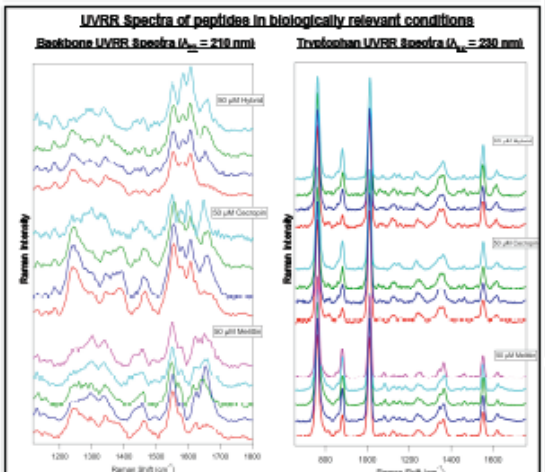
Tryptophan Fluorescence of the three peptides in different environments



Circular Dichroism: The changing secondary structure of membrane peptides



UVRR Spectra of peptides in biologically relevant conditions



Red is Buffer, Blue is zwitterionic vesicles, Green is cholesterol vesicles, Sky Blue is negative vesicles, and Pink is 2M NaCl.

DISCUSSION AND CONCLUSIONS

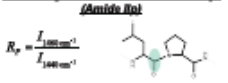
Fluorescence and Circular Dichroism to obtain basic structural information

Maximum fluorescence wavelength shifts when the fluorophore's environment changes. This results from a destabilization of the excited electronic state (mostly polar) when in…

Peptide	Environment	Flor. λ_{max}	CD structure	Leak % (10 μM)
Melittin/ Cecropin Hybrid	Buffer	350	Random coil	
	Zwitterionic Ves.	354		
	Cholesterol Ves.	355	Random coil	51
	Negative Ves.	343	α-helix	10
	Buffer	350	Random coil	
	Zwitterionic Ves.	357		
	Cholesterol Ves.	350	Random coil	8
	Negative Ves.	340	α-helix	50
	Buffer	355	Random coil/α-helix	
	Zwitterionic Ves.	343	α-helix	
	Cholesterol Ves.	346	α-helix	60
	Negative Ves.	336	α-helix	49
	2M NaCl (tetramer)	339	α-helix/ Random coil	

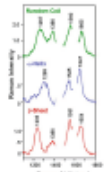
…): Structure of Backbone

H-bonding states of the X-Pro carbonyl (Amide III)



As H-bonding increases, R_p ↑
As H-bonding decreases, R_p ↓

Secondary Structure via UVRR[4]



Peptide	Environment	R_p	Structure
Melittin/ Cecropin Hybrid	Buffer	No Pro	Random coil
	Zwitterionic Ves.	No Pro	Random coil
	Cholesterol Ves.	No Pro	Random coil
	Negative Ves.	No Pro	α-helix
Cecropin	Buffer	3.1	Random coil
	Zwitterionic Ves.	3.3	Random coil
	Cholesterol Ves.	3.5	Random coil
	Negative Vesicles	1.0	α-helix
Melittin	Buffer	2.0	Random coil/α-helix
	Zwitterionic Ves.	1.3	α-helix
	Cholesterol Ves.	2.0	α-helix/ Random coil
	Negative Ves.	1.1	α-helix
	2M NaCl (tetramer)	1.3	α-helix

UVRR spectra (λ_{ex} = 230 nm) – Tryptophan Environment

Peptide	Environment	I_{W7}/I_{W6}	R_a	R_{HB}	R_{FD}
Melittin/ Cecropin Hybrid	Buffer	0.12	1.10	1.5	1.0
	Zwitterionic Ves.	0.22	1.01	1.4	1.1
	Cholesterol Ves.	0.22	1.14	2.0	1.0
	Negative Ves.	0.29	0.99	2.9	1.4
Cecropin	Buffer	0.14	1.09	1.7	1.0
	Zwitterionic Ves.	0.18	1.09	1.8	1.0
	Cholesterol Ves.	0.22	1.07	1.9	1.0
	Negative Vesicles	0.27	0.98	2.3	1.3
Melittin	Buffer	0.21	0.98	1.5	1.2
	Zwitterionic Ves.	0.31	1.02	1.3	1.3
	Cholesterol Ves.	0.34	0.98	1.4	1.4
	Negative Ves.	0.35	0.94	1.2	1.7
	2M NaCl (tetramer)	0.29	0.80	0.8	1.7

Cation-π Interactions

$R_a = \frac{I_{755\ cm^{-1}}}{I_{1000\ cm^{-1}}}$ $R_a \geq 1$, no cation-π; $R_a < 0.8$, cation-π

Hydrogen-bonding States of Indole N-H

$R_{HB} = \frac{I_{3396\ cm^{-1}}}{I_{3355\ cm^{-1}}}$

High R_{HB} = H-bonded
Low R_{HB} = no H-bond

Hydrophobicity

$R_{FD} = \frac{I_{1360\ cm^{-1}}}{I_{1340\ cm^{-1}}}$ High R_{FD} = Hydrophobic; Low R_{FD} = Hydrophilic

The data suggest that the hybrid peptide binds the negative vesicles better than Cecropin, but not as well as Melittin. Furthermore, the cholesterol is not required to deter binding. Negative lipids, however, are required for binding and create a hydrogen bonding environment for the tryptophan of all three peptides. The tryptophan of the Melittin tetramer, on the other hand, is buried in a hydrophobic core and has no opportunities to hydrogen bond.

ACKNOWLEDGEMENTS AND REFERENCES

Dr. Judy Kim, Jon Gable, Dina I. Kats and the Judy Kim Lab
Prof. Betsy Komives and Dr. Joseph Tsalkov for the use of CD instruments
UCSD Molecular Biophysics Training Grant, NIH

1) Raghuraman, H., et al. *Biosci. Rep.* **2007**, 27:189-223.
2) Andrew, D. et al. *FEBS* **1992**, 296: 190-194.
3) Harada, I., Takeuchi, H. Raman and Ultraviolet Resonance Raman Spectra of Proteins and Related Compounds; John Wiley and Sons, 1986; Vol. 13.
4) Schlamadinger, D. E.; Gable, J. E.; Kim, J. E. *J. Phys. Chem. B* **2009**, 113, 14783-14788.
5) Chi, Z., Chen, X. G., Holtz, J. S. W. and Asher, S.A. *Biochemistry* **1998**, 37, 2854-2864.

This is an example of a poster. Your poster should not have more text/ figures than this example.

Make headings BIG and BOLD. Include boxes/lines to separate sections.

Spectroscopic Investigation of Membrane-Associated Peptides: Melittin, Cecropin, and Melittin-

University of California, San Diego, 9500 Gilman Drive La Jolla, CA 92093

ABSTRACT AND BACKGROUND

ABSTRACT: Should tell me everything about the poster and your work

Lethal Concentrations (μM) of Cecropin A, Melittin, CA(1-7)M(2-9)NH_2

Peptide	E. Coli strain	P. Aeruginosa strain	B. Subtilis strain	S. Aureus strain	S. Pyogenes strain	Sheep Red Blood Cells
Cecropin	0.3	2	4	>200	4	>400
Melittin	0.8	3	0.2	0.2	0.5	4-8
CA(1-7)M(2-9)NH_2	1	4	0.5	0.5	0.5	>300

MATERIALS AND METHODS

Helical wheel projections: Amphipathic membrane peptides

METHODS: What are your molecules and techniques?

UV Resonance Raman Spectroscopy (UVRR)

A few L-tryptophan normal modes[1,4]

UVRR Laser Setup

RESULTS

Tryptophan Fluorescence of the three peptides in different environments

RESULTS: Show me the data!

Leakage Assay: Measuring the bilayer integrity in the presence of peptide

Circular Dichroism: The changing secondary structure of membrane peptides

Melittin | Cecropin A | CA(1-8M(2-9)

UVRR Spectra of peptides in biologically relevant conditions

Backbone UVRR Spectra (λ_{ex} = 210 nm) | Tryptophan UVRR Spectra (λ_{ex} = 230 nm)

Raman Intensity | Raman Shift (cm^{-1})

Red is Buffer, Blue is zwitterionic vesicles, Green is cholesterol vesicles, Sky Blue is negative vesicles, and Pink is 2M NaCl.

DISCUSSION AND CONCLUSIONS

DISCUSSION: Summarize findings in tables/figures. Interpret results here.

UVRR spectra (λ_{ex} = 210 nm): Structure of Backbone

H-bonding states of the X-Pro carbonyl (Amide III)

$R_P = \frac{I_{1660\ cm^{-1}}}{I_{1640\ cm^{-1}}}$

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ACKNOWLEDGEMENTS AND REFERENCES

Who helped you, what are your references?

Abstract/Background may include motivation

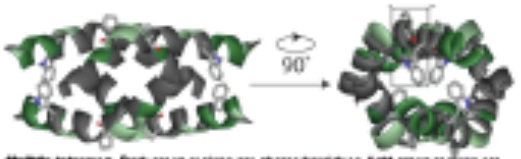
In addition to abstract you may want to include motivating

- statistics
- figures
- big picture questions

ABSTRACT AND BACKGROUND

Both Melittin and Cecropin A have extensive biological relevance. Melittin, a 26 amino acid peptide and the main component of honeybee venom, is hemolytic and has been found to disrupt nearly all types of membranes.[1] Cecropin A, however, is a 37 amino acid antimicrobial peptide found in the Cecropia moth. This peptide is selective to the type of membrane with which it associates. Both of these peptides have very similar secondary structures, net charges, and one conserved tryptophan (W) residue known to be important to their activity. However, these peptides act very differently towards vesicles of varying lipid compositions. Furthermore, a hybrid peptide has been created that contains portions from both peptides to increase the antimicrobial affects of parent peptides Cecropin A and Melittin. The hybrid peptide has been found to be more effective at killing bacteria and is not hemolytic like Melittin.

We have employed spectroscopic techniques to characterize the interaction between these peptides and biologically relevant membranes. The goal of these studies is to understand how the structure and local environment of these peptides varies in different environments that mimic cell membranes.



Melittin tetramer. Dark green regions are charged residues, light green regions are polar residues, and gray denotes hydrophobic residues (PDB: 2MLT).

Lethal Concentrations (μM) of Cecropin A, Melittin, CA(1-7)M(2-9)NH_2[3]

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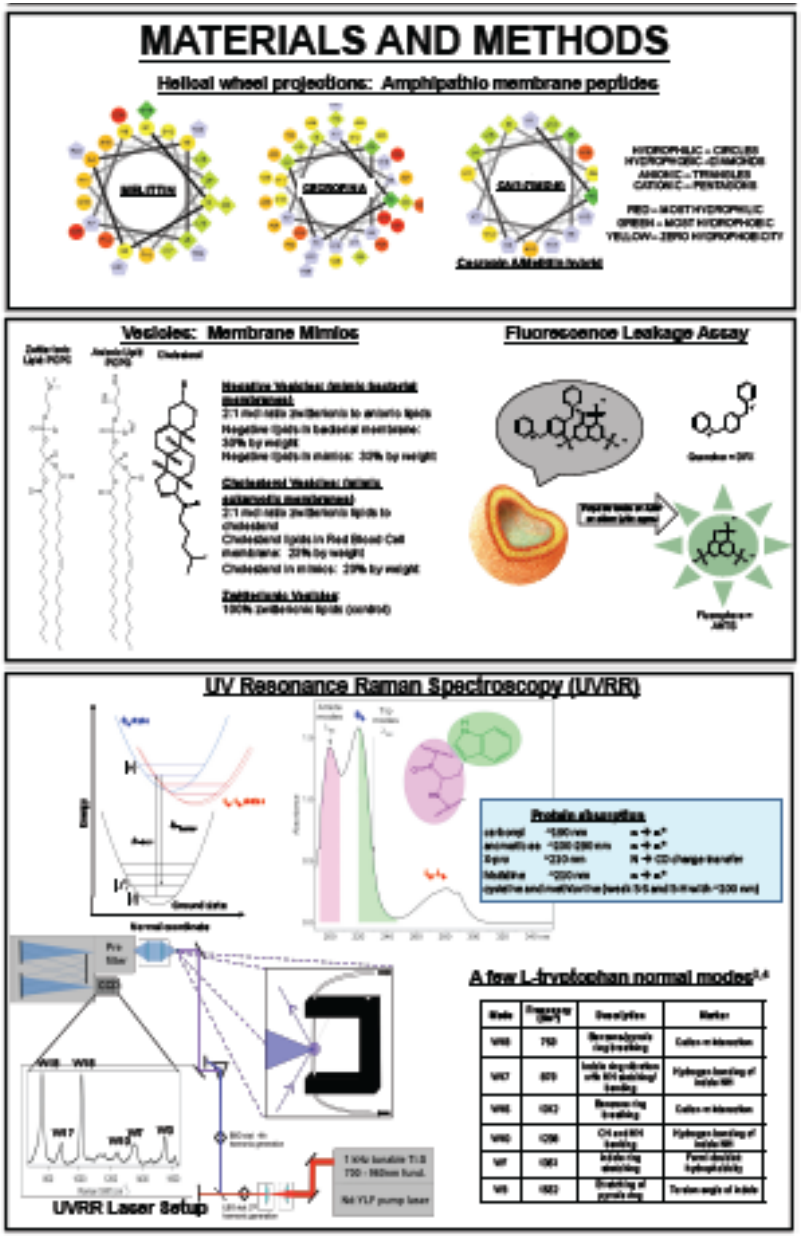
Melittin	0.8	3	0.2	0.2	0.5	4-8
CA(1-7)M(2-9)NH_2	1	4	0.5	0.5	0.5	>300

Methods – how you were able to obtain results

Chemicals, molecules drawn (ChemDraw!), assays, techniques

May include:

- proteins, molecules, biological assays
- synthetic requirements
- experimental setup diagrams
- laser diagrams



Spend the majority of your time on figures

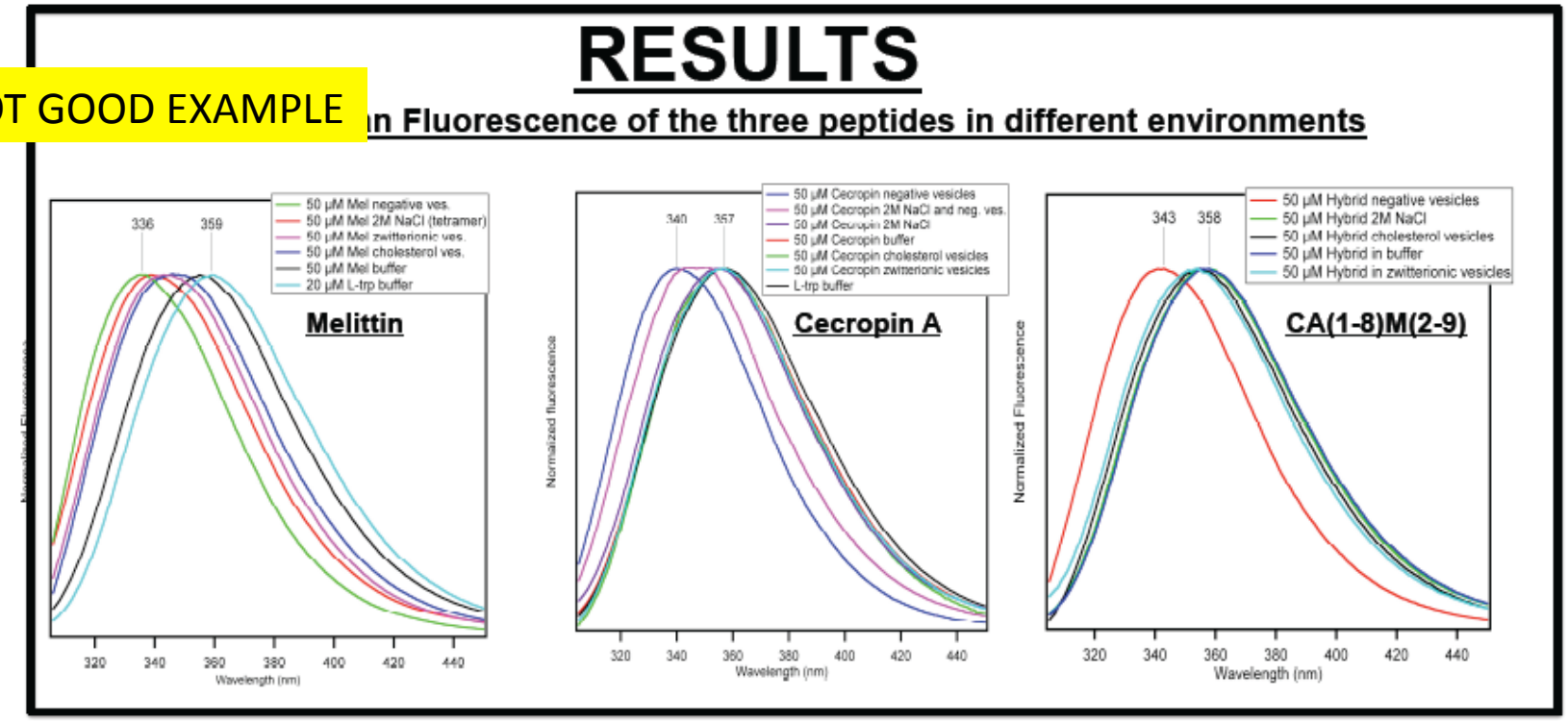
LABEL ALL AXES!

If possible, indicate points directly on the graph, not in legends.

Make everything as big as possible.

Provide subheadings to clarify the goals of the experiments.

NOT GOOD EXAMPLE



Spend the majority of your time on figures

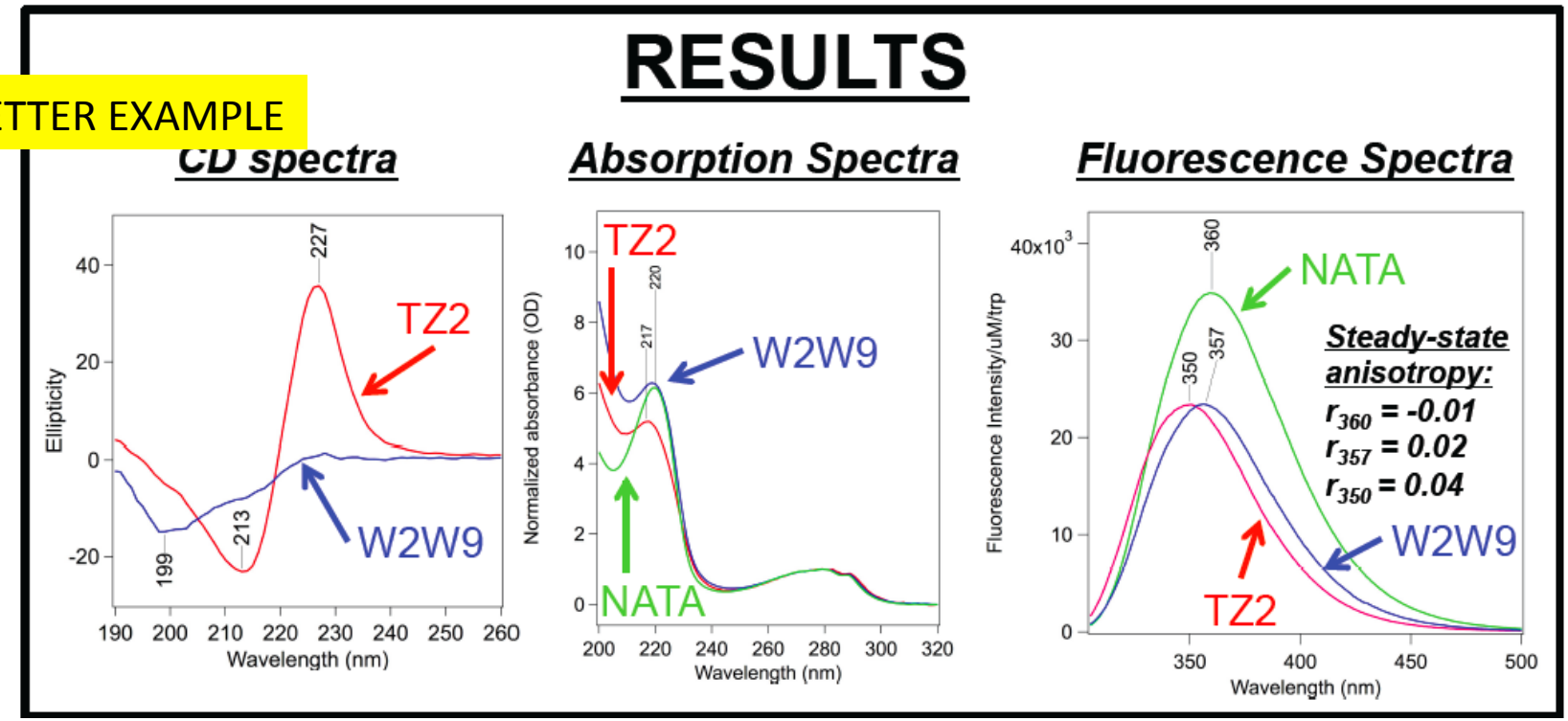
LABEL ALL AXES!

If possible, indicate points directly on the graph, not in legends.

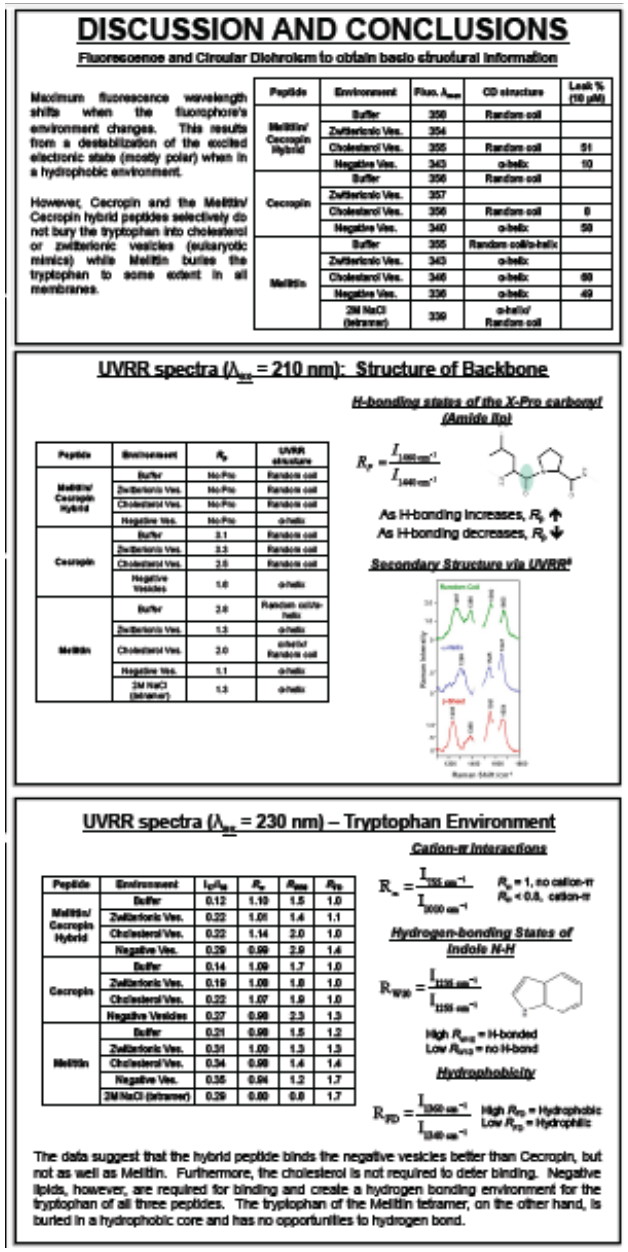
Make everything as big as possible.

Provide subheadings to clarify the goals of the experiments.

BETTER EXAMPLE



Discussion – what your results mean



DISCUSSION AND CONCLUSIONS

Fluorescence and Circular Dichroism to obtain basic structural information

Maximum fluorescence wavelength shifts when the fluorophore's environment changes. This results from a destabilization of the excited electronic state (mostly polar) when in a hydrophobic environment.

However, Cecropin and the Melittin/ Cecropin hybrid peptides selectively do not bury the tryptophan into cholesterol or zwitterionic vesicles (eukaryotic mimics) while Melittin buries the tryptophan to some extent in all membranes.

Peptide	Environment	Fluo. λ_{max}	CD structure	Leak % (10 μM)
Melittin/ Cecropin Hybrid	Buffer	356	Random coil	
	Zwitterionic Ves.	354		
	Cholesterol Ves.	355	Random coil	51
	Negative Ves.	343	α-helix	10
Cecropin	Buffer	356	Random coil	
	Zwitterionic Ves.	357		
	Cholesterol Ves.	356	Random coil	8
	Negative Ves.	340	α-helix	58
Melittin	Buffer	355	Random coil/α-helix	
	Zwitterionic Ves.	343	α-helix	
	Cholesterol Ves.	348	α-helix	68
	Negative Ves.	336	α-helix	49
	2M NaCl (tetramer)	339	α-helix/ Random coil	

UVRR spectra (λ_{ex} = 210 nm): Structure of Backbone

H-bonding states of the X-Pro carbonyl (Amide II')

$$R_Y = \frac{I_{1665\ cm^{-1}}}{I_{1640\ cm^{-1}}}$$

As H-bonding increases, R_Y ↑
As H-bonding decreases, R_Y ↓

Peptide	Environment	R_Y	UVRR structure
Melittin/ Cecropin Hybrid	Buffer	No Pro	Random coil
	Zwitterionic Ves.	No Pro	Random coil
	Cholesterol Ves.	No Pro	Random coil
	Negative Ves.	No Pro	α-helix
Cecropin	Buffer	3.1	Random coil
	Zwitterionic Ves.	3.3	Random coil
	Cholesterol Ves.	3.6	Random coil
	Negative Vesicles	1.6	α-helix
Melittin	Buffer	2.6	Random coil/α-helix
	Zwitterionic Ves.	1.3	α-helix
	Cholesterol Ves.	2.0	α-helix/ Random coil
	Negative Ves.	1.1	α-helix
	2M NaCl (tetramer)	1.3	α-helix

Secondary Structure via UVRR[3]

UVRR spectra (λ_{ex} = 230 nm) – Tryptophan Environment

Cation-π Interactions

$$R_\pi = \frac{I_{755\ cm^{-1}}}{I_{1000\ cm^{-1}}}$$

R_π = 1, no cation-π
R_π < 0.8, cation-π

Peptide	Environment	I_{σ}/I_{π}	R_Y	R_{WW}	R_{FD}
Melittin/ Cecropin Hybrid	Buffer	0.12	1.10	1.5	1.0
	Zwitterionic Ves.	0.22	1.01	1.4	1.1
	Cholesterol Ves.	0.22	1.14	2.0	1.0
	Negative Ves.	0.29	0.99	2.0	1.4
Cecropin	Buffer	0.14	1.09	1.7	1.0
	Zwitterionic Ves.	0.19	1.08	1.8	1.0
	Cholesterol Ves.	0.22	1.07	1.9	1.0
	Negative Vesicles	0.27	0.98	2.3	1.3
Melittin	Buffer	0.21	0.98	1.5	1.2
	Zwitterionic Ves.	0.31	1.00	1.3	1.3
	Cholesterol Ves.	0.34	0.98	1.4	1.4
	Negative Ves.	0.35	0.94	1.2	1.7
	2M NaCl (tetramer)	0.29	0.99	0.8	1.7

Hydrogen-bonding States of Indole N-H

$$R_{WW} = \frac{I_{1338\ cm^{-1}}}{I_{1358\ cm^{-1}}}$$

High R_{WW} = H-bonded
Low R_{WW} = no H-bond

Hydrophobicity

$$R_{FD} = \frac{I_{1360\ cm^{-1}}}{I_{1340\ cm^{-1}}}$$

High R_{FD} = Hydrophobic
Low R_{FD} = Hydrophilic

The data suggest that the hybrid peptide binds the negative vesicles better than Cecropin, but not as well as Melittin. Furthermore, the cholesterol is not required to deter binding. Negative lipids, however, are required for binding and create a hydrogen bonding environment for the tryptophan of all three peptides. The tryptophan of the Melittin tetramer, on the other hand, is buried in a hydrophobic core and has no opportunities to hydrogen bond.

Your data says about your system

Apply aspects of current research to your own

May include:

- tables not already presented in data
- how your data fits into currently existing data/literature
- be sure to cite where appropriate!

Make any text easy to read

Use large font size

Title: 90 pt. Arial
Subheadings: > 56 pt, Arial
Text: > 30 pt. Arial

Use **bold** and/or *italic* to make important points (subheadings and labels)

Greek symbols (“π” instead of “pi”)

PC: Character Map
Mac: Character Viewer
Both platforms: “Symbol” font
Different fonts will present symbol differently (e.g. π vs. π)

Don’t use obscure, hard to read fonts

References, acknowledgement, and feedback

References

Use journal format – see examples in *J. American Chemical Society, J. Physical Chemistry, Biochemistry*, etc. You can use superscripts in the poster like this.[1] Or you can use parenthesis like this (1). Punctuation comes before or after the citation, respectively

Acknowledgements

Co-authors listed in your title should not appear in acknowledgements! Who do you acknowledge? You should mention everyone who contributed to the work directly or indirectly. These could include **other members of your group, members from another group that gave you advice, labs or facilities that provided support** (e.g. Dr. Su from mass spec facility). Don't forget to include the **funding source**! If you don't know, ask your PI.

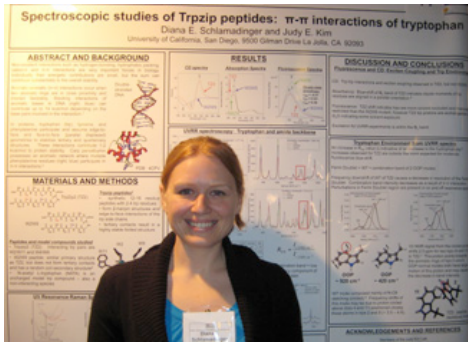
Finally, **get feedback** on your poster before it is printed. Send it to your PI and at least one other person in your lab.

The 1-minute speech

When asked about your poster, in 1 minute you should be able to summarize your abstract and state (as example):

"The goal of my research in the Kim group is to elucidate the molecular mechanisms of protein folding into membranes. We used a model integral membrane protein, Outer Membrane Protein A, and several mutations combined with vibrational spectroscopy to probe the folding reaction. Our data suggest that specific protein-lipid interactions, such as hydrogen-bonding with the lipid acyl group and cation-π interactions, are important to membrane protein stability. We have estimated the energetic contributions of these interactions with unfolding curves. Currently, we are probing the strength of these interactions for other types of membrane proteins, such as α-helical proteins and peptides."

Overall project goal ("membrane protein folding")
Molecules that were studied ("Outer membrane protein A + mutants")
Techniques ("vibrational spectroscopy")
Results ("hydrogen-bonding with lipid", "cation-π interactions", "energetic contributions")
Future directions ("α-helical proteins and peptides")
Practice the speech at least 3 times to people in your lab and your peers!



Most important advice: HAVE FUN!!!!