

# About OMICS Group

OMICS Group International is an amalgamation of [Open Access publications](#) and worldwide international science conferences and events. Established in the year 2007 with the sole aim of making the information on Sciences and technology 'Open Access', OMICS Group publishes 400 online open access [scholarly journals](#) in all aspects of Science, Engineering, Management and Technology journals. OMICS Group has been instrumental in taking the knowledge on Science & technology to the doorsteps of ordinary men and women. Research Scholars, Students, Libraries, Educational Institutions, Research centers and the industry are main stakeholders that benefitted greatly from this knowledge dissemination. OMICS Group also organizes 300 [International conferences](#) annually across the globe, where knowledge transfer takes place through debates, round table discussions, poster presentations, workshops, symposia and exhibitions.

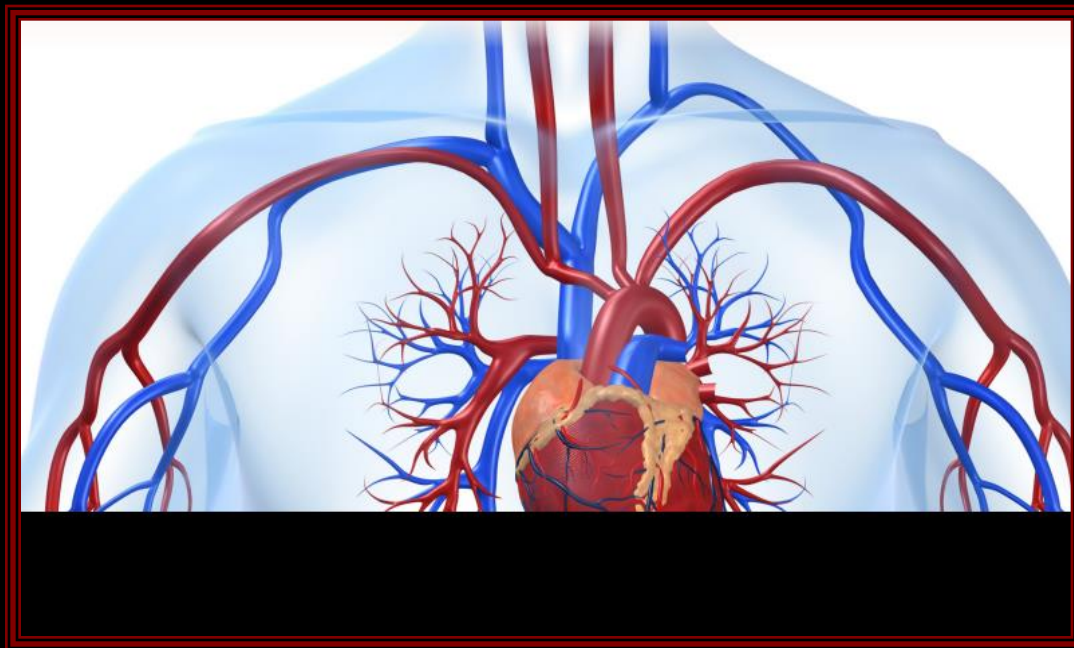
# About OMICS Group Conferences

OMICS Group International is a pioneer and leading science event organizer, which publishes around 400 open access journals and conducts over 300 Medical, Clinical, Engineering, Life Sciences, Pharma scientific conferences all over the globe annually with the support of more than 1000 scientific associations and 30,000 editorial board members and 3.5 million followers to its credit.

OMICS Group has organized 500 conferences, workshops and national symposiums across the major cities including San Francisco, Las Vegas, San Antonio, Omaha, Orlando, Raleigh, Santa Clara, Chicago, Philadelphia, Baltimore, United Kingdom, Valencia, Dubai, Beijing, Hyderabad, Bengaluru and Mumbai.

# **Ion channels phosphorylopathy:**

## **A link between genomic variations and heart arrhythmia**



**3<sup>rd</sup> International Conference on  
Clinical & Experimental Cardiology  
April 15-17, 2013**

**Saverio Gentile, Ph.D  
Loyola University Chicago, USA**

gene name

hERG-1: human ether-a-go-go-related gene 1

Protein name:

Kv11.1: Voltage-gated potassium channel 11.1

gene name

CACNA1C: calcium channel, voltage-dependent, L type, alpha 1C subunit

Protein name:

Cav 1.2; L-type

Brain

Hypophysis

Pancreas

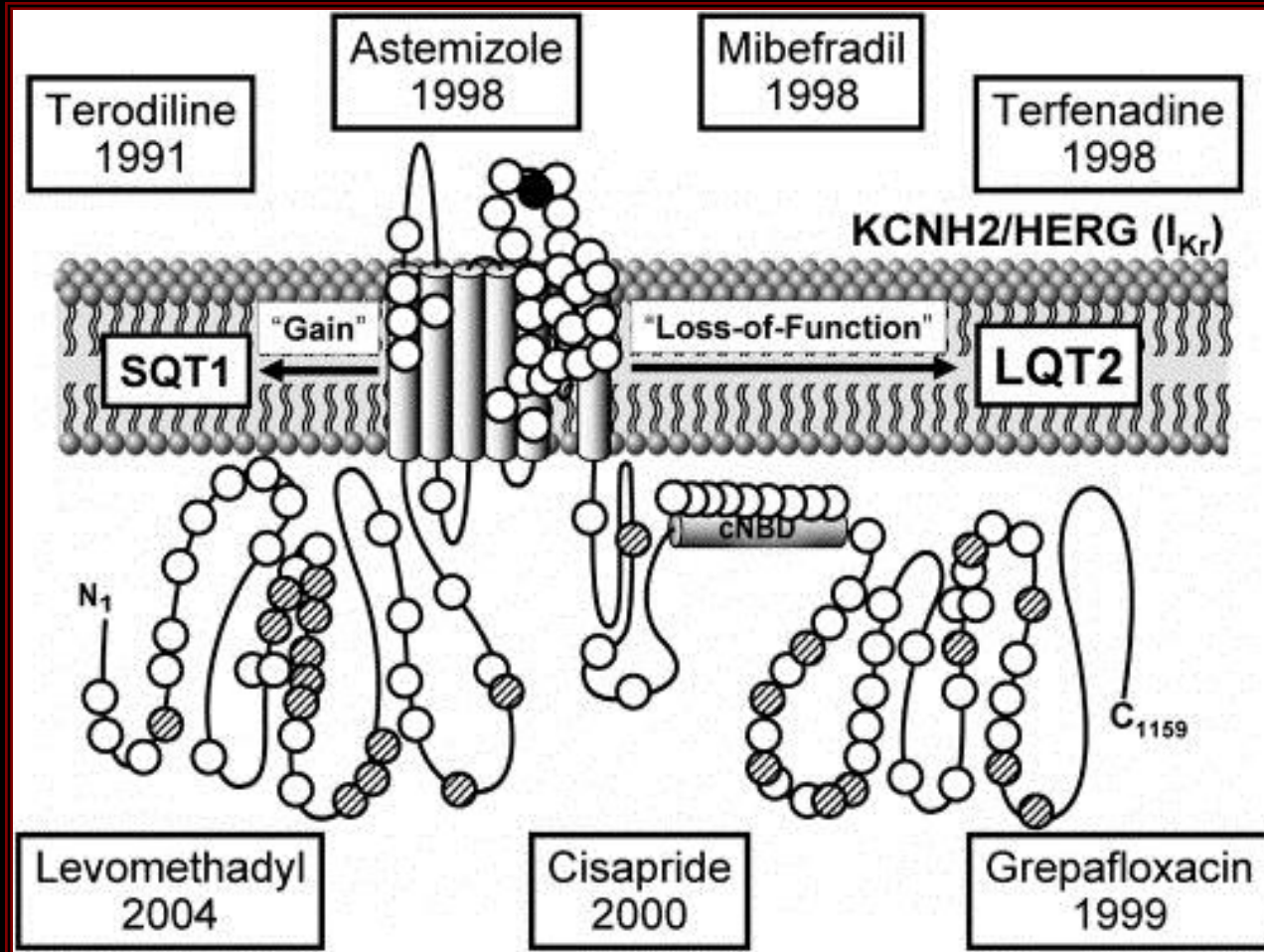
Intestine



Tissues

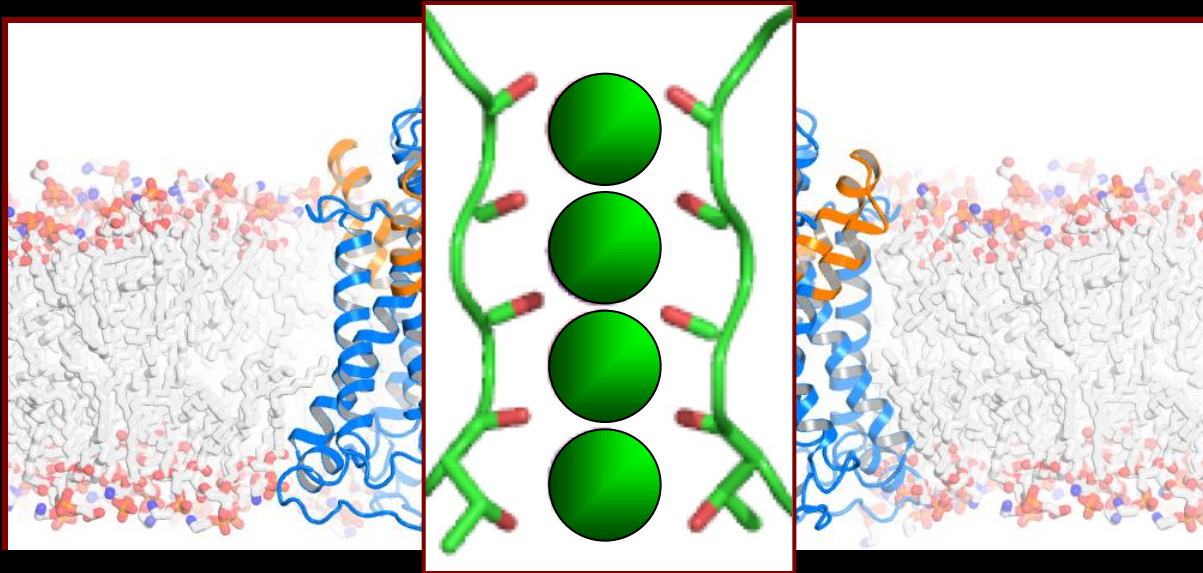
Heart

More than 290 mutations on Kv11.1 channel are associated with Long QT syndrome



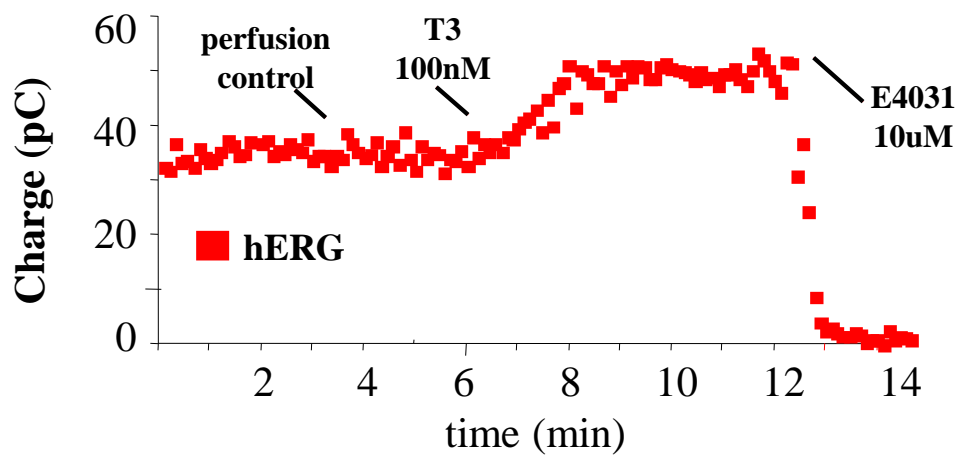
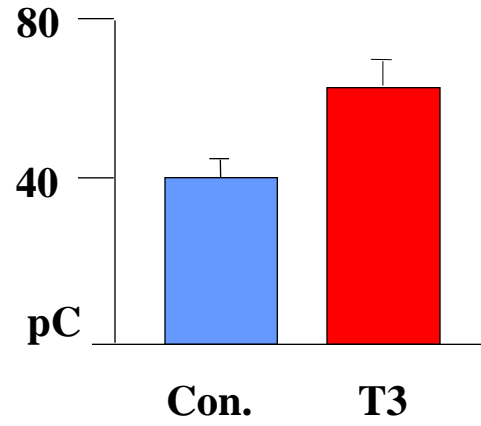
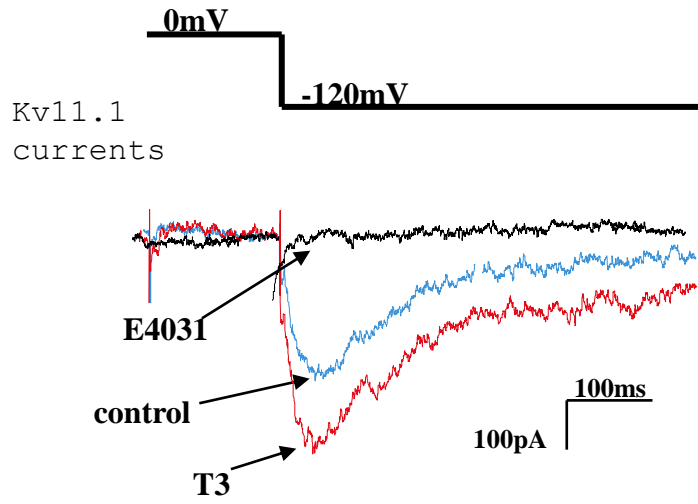
Drug-induced torsades de pointes: The evolving role of pharmacogenetics

Patrick T. Fitzgerald, MDa, Michael J. Ackerman, MD, PhD Heart Rhythm, 2005

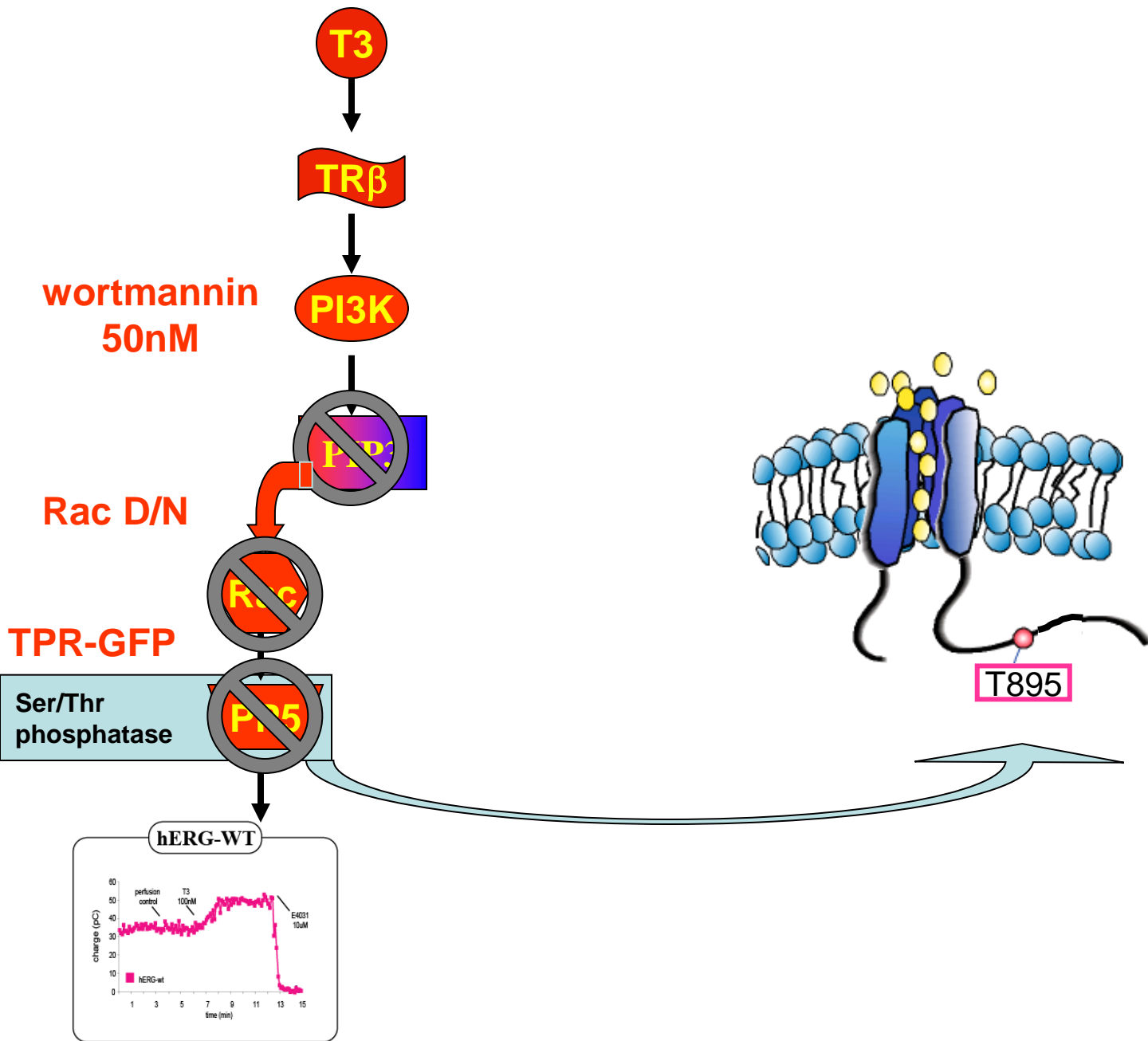


Ribbon representation of the Kv1.2-Kv 2.1 paddle chimera tetramer (PDB 2R9R, K<sup>+</sup> ions shown as green spheres) viewed from the side with the extracellular solution above. <http://lab.rockefeller.edu/mackinnon/>

# T3 stimulates hERG1 channel activity

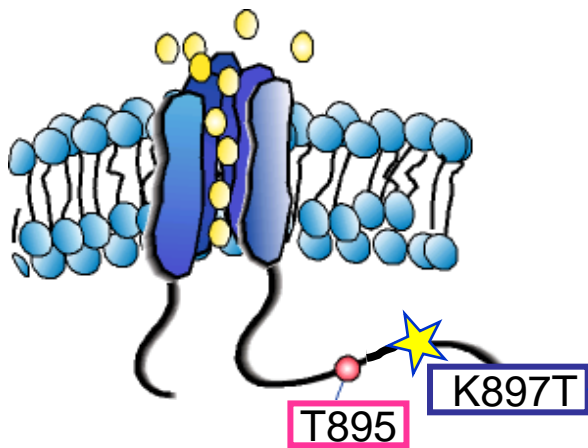


# T3 regulates hERG-K897T through PI3K but not through Rac and PP5

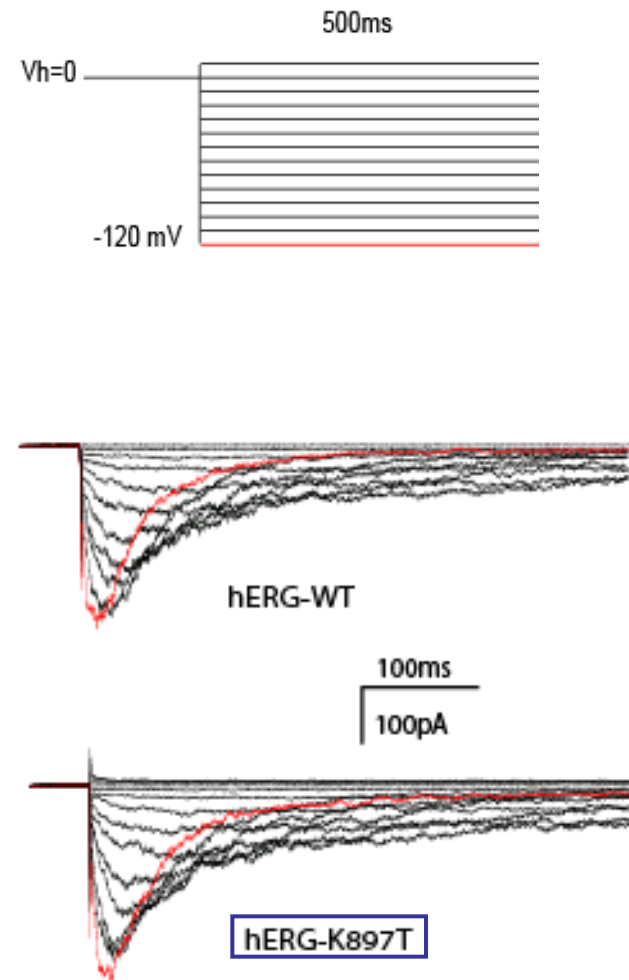




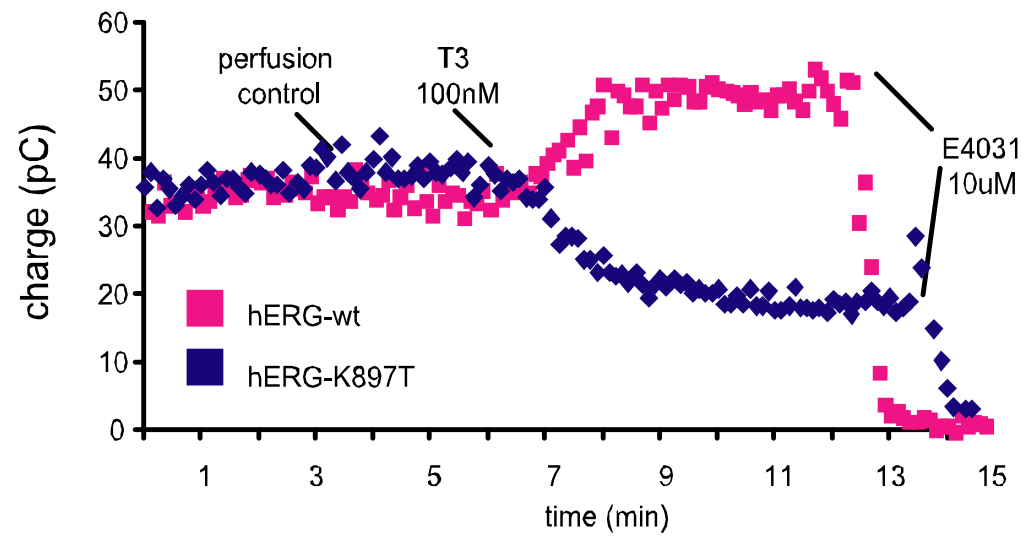
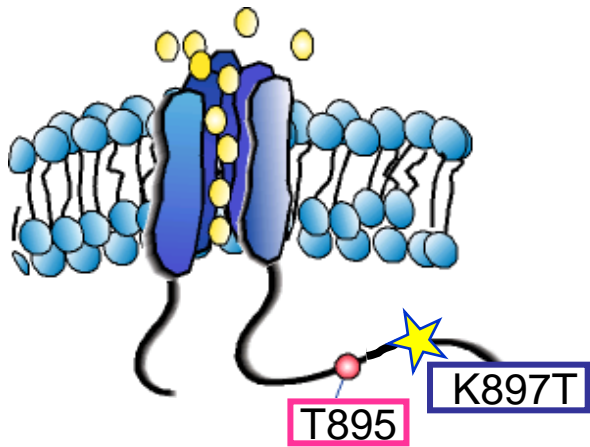
# The LQT2-related K897T hERG variant is not different from WT hERG



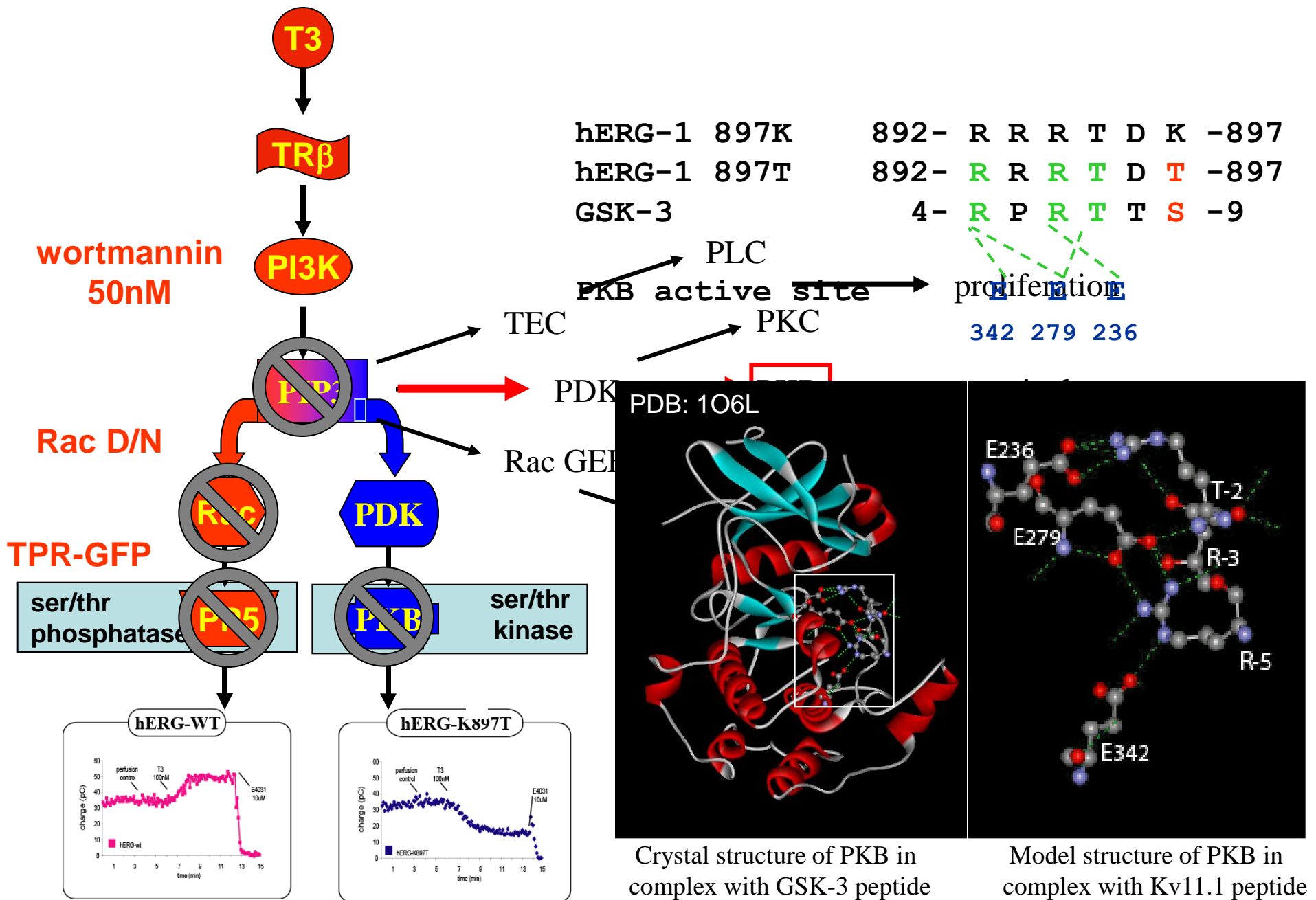
**hERG-SNP K897T is associated with cardiac ventricular arrhythmia and sudden death**

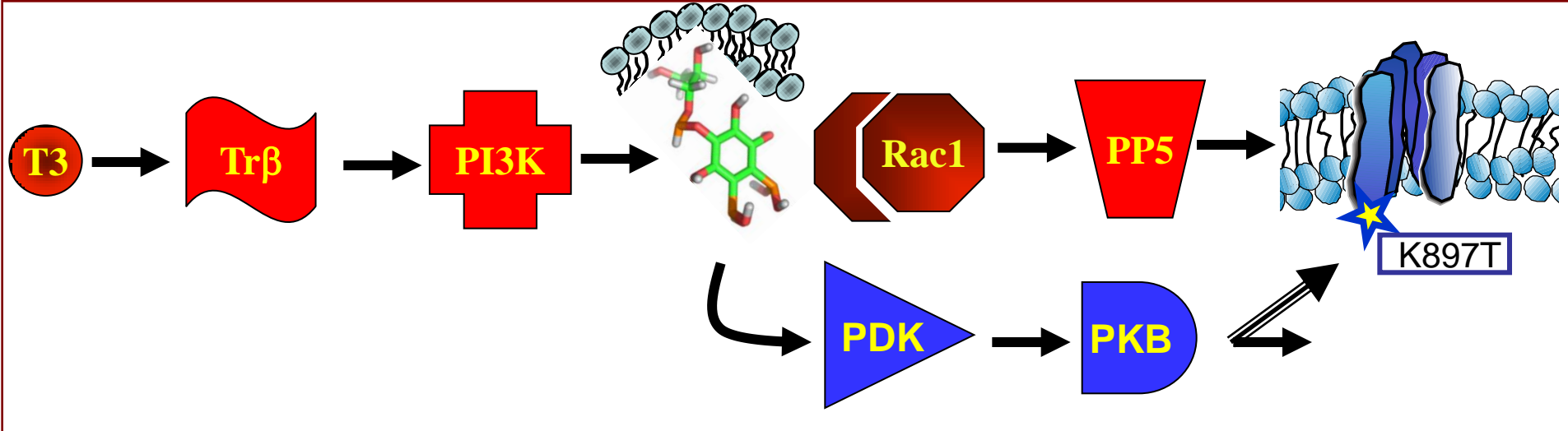


# T3 inhibits hERG1-K897T activity



# T3 regulates hERG-K897T through PI3K but not through Rac and PP5





## Conclusion

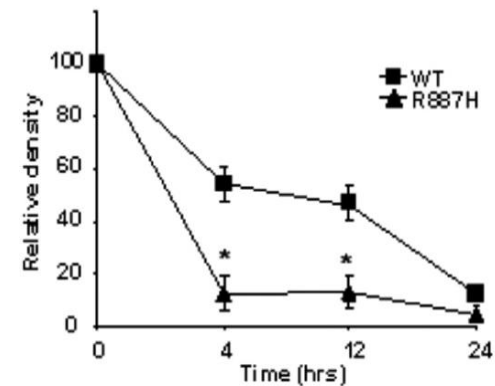
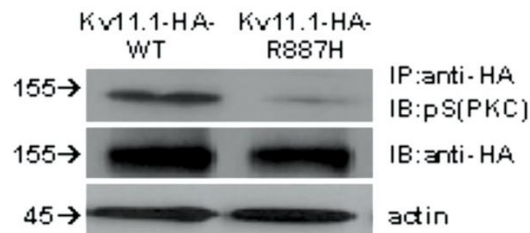
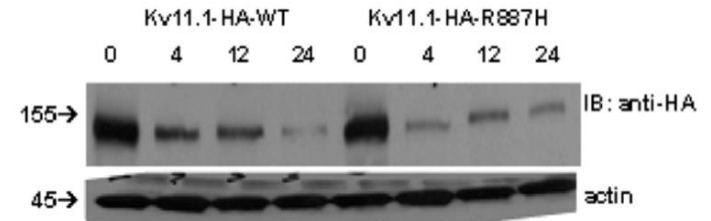
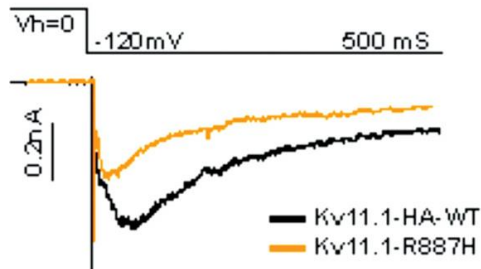
**-Kv11.1-897T is a substrate for PKB  
(Phosphorylation by creating a phosphosite)**

**-Inhibition of Kv11.1 by PKB links a  
human SNP to a fatal cardiac phenotype**

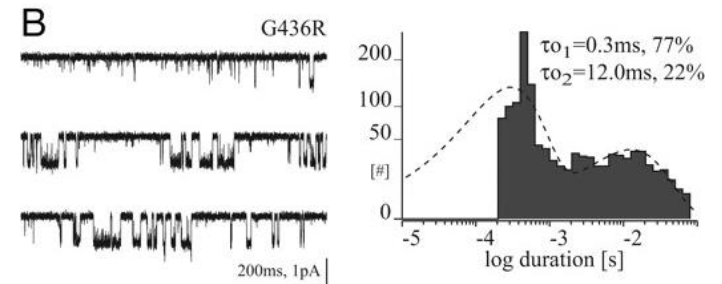
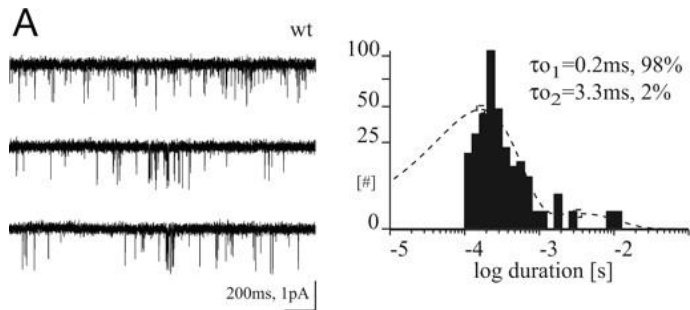
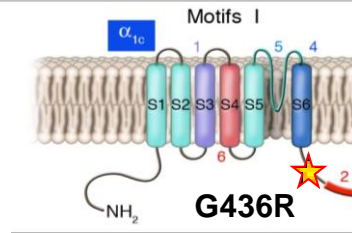
# Long QT2 Mutation on the Kv11.1 Ion Channel Inhibits Current Activity by Ablating a Protein Kinase C Consensus Site.

Donovan, Lansu, Williams, Denning, and Saverio Gentile  
 MOLECULAR PHARMACOLOGY 2012, Vol. 82, No. 3

PKC motif	R-R-X-S-hyd-R/K
Kv11.1-WT	887-R-K-L-S- F -R
Kv11.1-R887H	887-H-K-L-S- F -R
pS (PKC)	-R-K-X-S-hyd-R/K

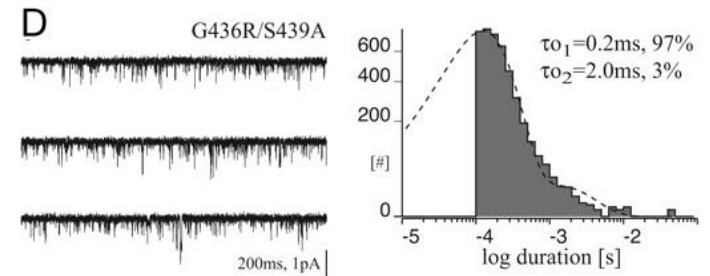
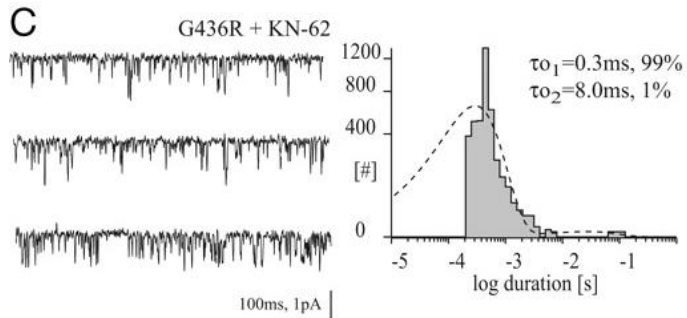


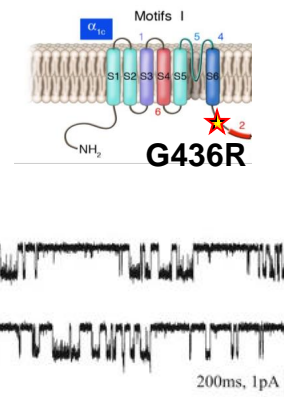
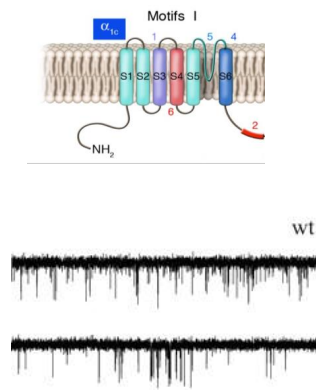
# Timothy syndrome mutation creates a CAMKII consensus site



**CAMKII**                    **-R-x-x-S/T**  
**A) CaV1.2.....436-G-W-D-S-439**

KN-62= CAMKII inhibitor





Calcium  
TOXICITY

## Conclusion

We propose that aberrant phosphorylation, or “phosphorylopathy,” of the CaV1.2 channel protein contributes to the excitotoxicity associated with LQT8

# Ion channel Phosphorylopathies:

## Mutations that creates or disrupts phosphorylation sites on ion channels

**Kv11.1 Ion channel malfunction and Cardiac arrhythmia**

1

Creation of kinase consensus site by adding a phosphorylatable residue

PKB motif									
hERG-1 897K	892-	R	R	R	T	D	K	-897	
hERG-1 897T	892-	R	R	R	T	D	T	-897	

2

Disruption of kinase consensus site by removing a docking residue

PKC motif									
Kv11.1 887R	887-	R	K	L	S	F	R	-892	
Kv11.1 887H	887-	H	K	L	S	F	R	-892	

**CaV1.2 Ion channel malfunction and Cardiac arrhythmia**

3

Creation of kinase consensus site by adding a docking residue

CAMKII motif									
Cav1.2 406G	406-	G	W	D	S			-409	
Cav1.2 409R	406-	R	W	D	T			-409	



# Ion channels phosphorylopathy:

## A link between genomic variations and heart arrhythmia

Gene	Protein	SNP	PO4	Kinase	Disease
CACNA1C	Cav1.2	S1545P	-60%	CAMKII	Timothy
KCNH2	Kv11.1	K897T	+94%	PKB	LQT2
KCNH2	Kv11.1	R176W	-94%	PKA	LQT2
KCNH2	Kv11.1	T474I	-90%	PKA	LQT2
KCNQ1	Kv7.1	G179S	+73%	GSK3	LQT1
KCNQ1	Kv7.1	Y184S	+80%	CAMKII	LQT1
KCNQ1	Kv7.1	S566F	-76%	CAMKII	LQT1
KCNQ1	Kv7.1	W392R	+75%	CAMKII	LQT1
KCNQ1	Kv7.1	A525T	+67%	PKA	LQT1
KCNQ1	Kv7.1	R583C	-91%	CAMKII	LQT1
KCNQ2	Kv7.2	N780T	+99%	CAMKII	MYOK,EPI
KCNJ1	Kir1.1	S219R	-79%	PKA	Bartter Syn.
KCNJ13	Kir1.4	T175I	-90%	CAMKII	Bartter Syn.
KCNJ12	Kir2.2	S15L	-99%	GSK3	Not reported
TRPC6	TRPC6	P15S	+96%	CK1	GMS
TRPV4	OTRPC4	P19S	+94%	CK2	Not reported



Thanks (a lot) to:

Mr. Alexander J. Donovan

Research Assistant

2010-2011

Now Ph.D Student in the  
Chemistry Department @ UIC

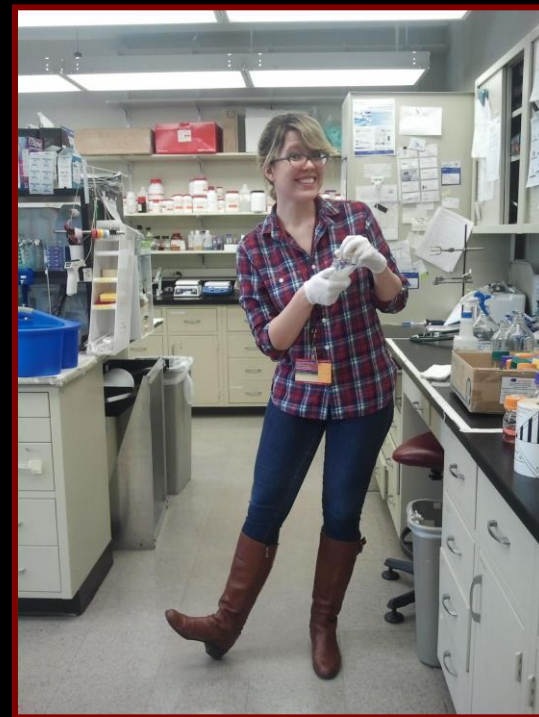


Miss. Katherine Lansu

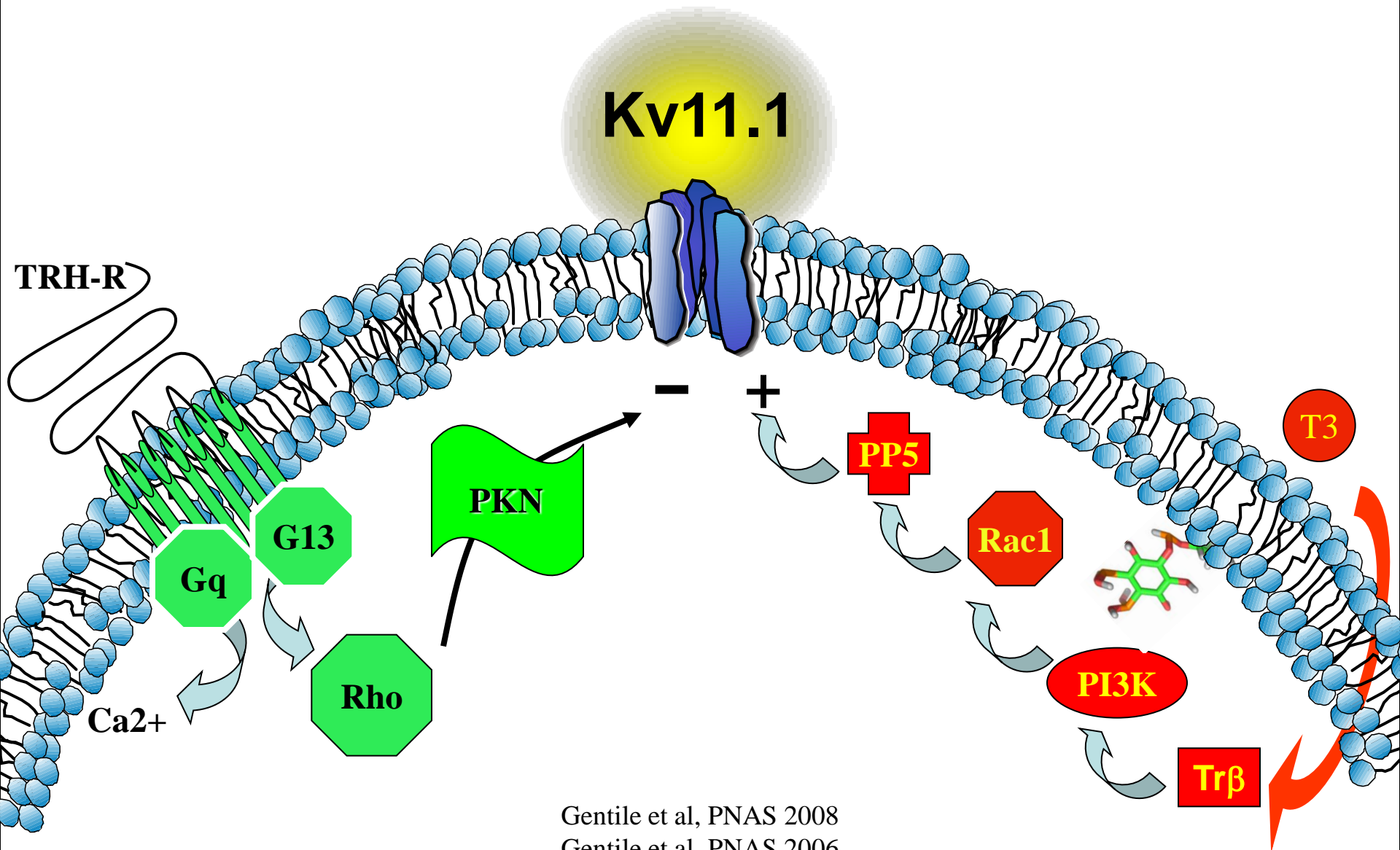
Research assistant

2011-2012

Now Ph.D Student @ UNC



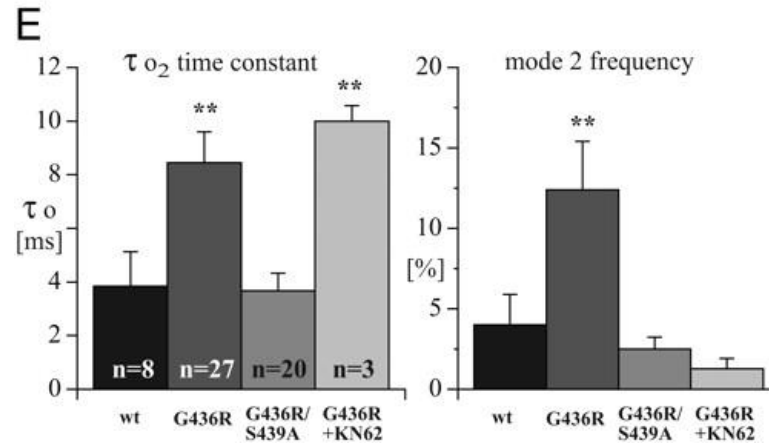
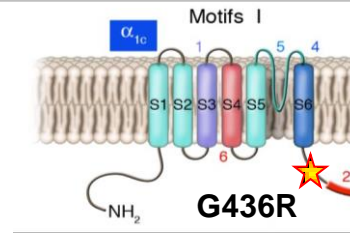
# T3/TRH-dependent regulation of hERG1 channel activity



Gentile et al, PNAS 2008

Gentile et al, PNAS 2006

# Timothy syndrome mutation creates a CAMKII consensus site



**CAMKII**      **-R-x-x-S/T**  
**CaV1.2**.....**436-G-W-D-S-439**  
**CaV1.2**.....**436-R-W-D-S-439**  
**CaV1.2**.....**436-R-W-D-A-439**

Summary of the values for the long open times,  $\tau_{o2}$ , as well as the frequency of mode 2 openings from the indicated number of patches expressing each construct.

# Ion channel Phosphorylopathies:

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**CaV1.2 Ion channel malfunction and Cardiac arrhythmia**

3

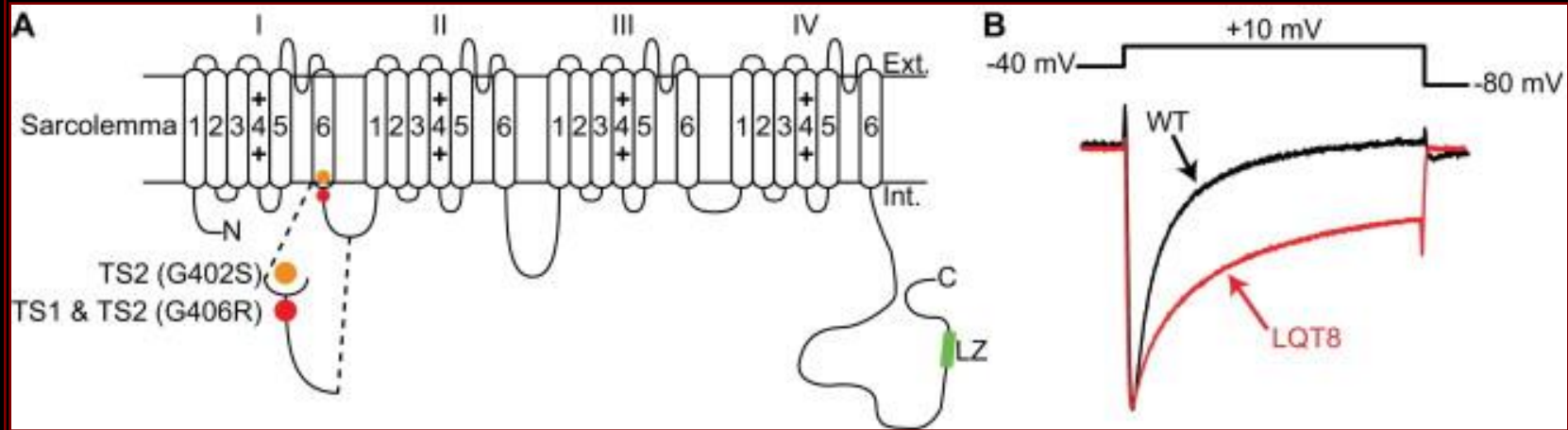
Creation of kinase consensus site by adding a docking residue

CAMKII motif									
Cav1.2 406G	406-	G	W	D	S	-409			
Cav1.2 409R	406-	R	W	D	T	-409			

gene name

CACNA1C: calcium channel, voltage-dependent, L type,  
alpha 1C subunit

Protein name:  
Cav 1.2; L-Type

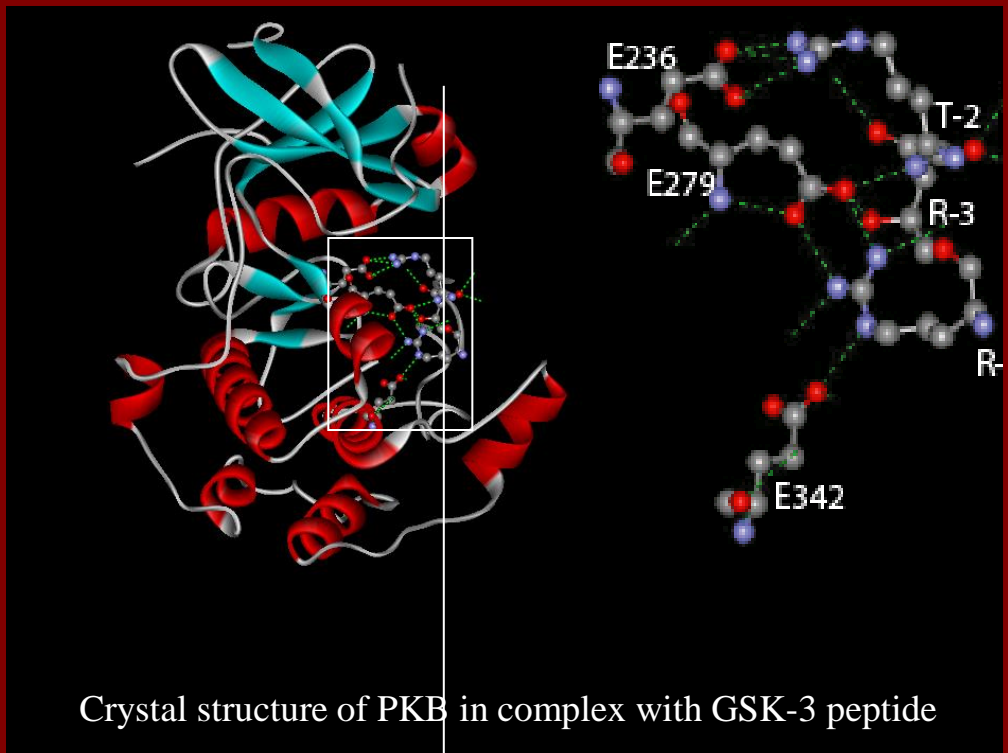


### L-Type Ca<sup>2+</sup> Channel Function During Timothy Syndrome

Rose E. Dixon, Edward P. Cheng, Jose L. Mercado, Luis F. Santana

Trends in Cardiovascular Medicine Volume 22, Issue 3, April 2012, Pages 72–76

# Phosphorylation requires recognition of a specific kinase signature





**Thanks' for your kind attention!!!!!!**



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International

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