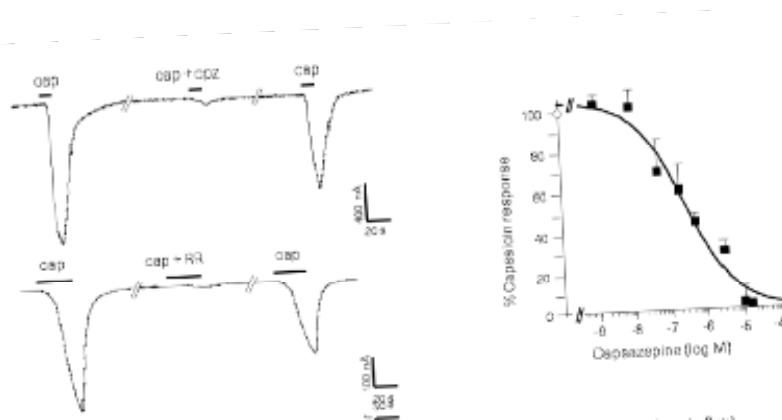


**FIG. 1**



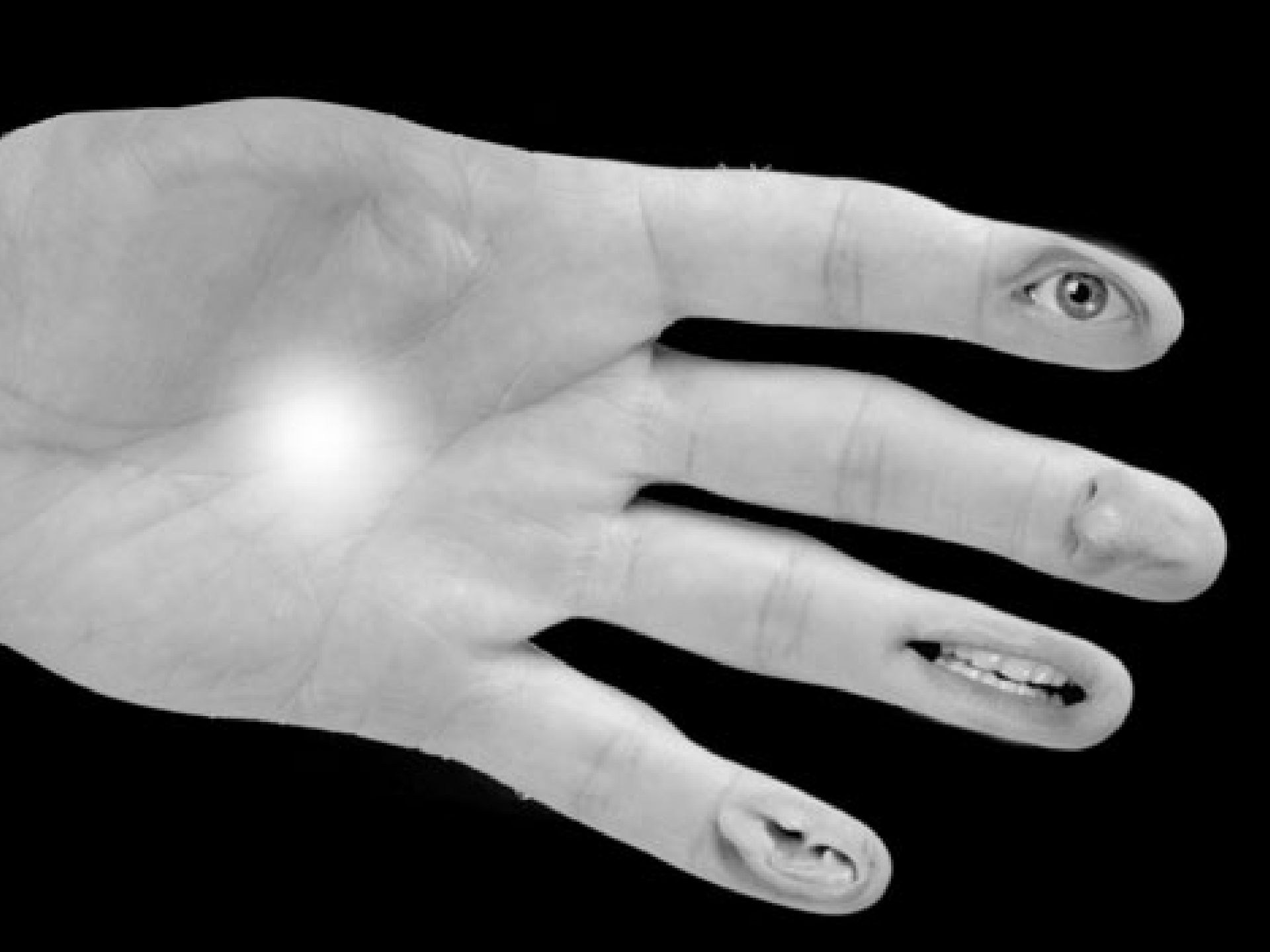
# What a Long, Strange Trp It's Been

9.013: Cell. and Mol. Neurobiology

Nathan Wilson

February 9, 2004





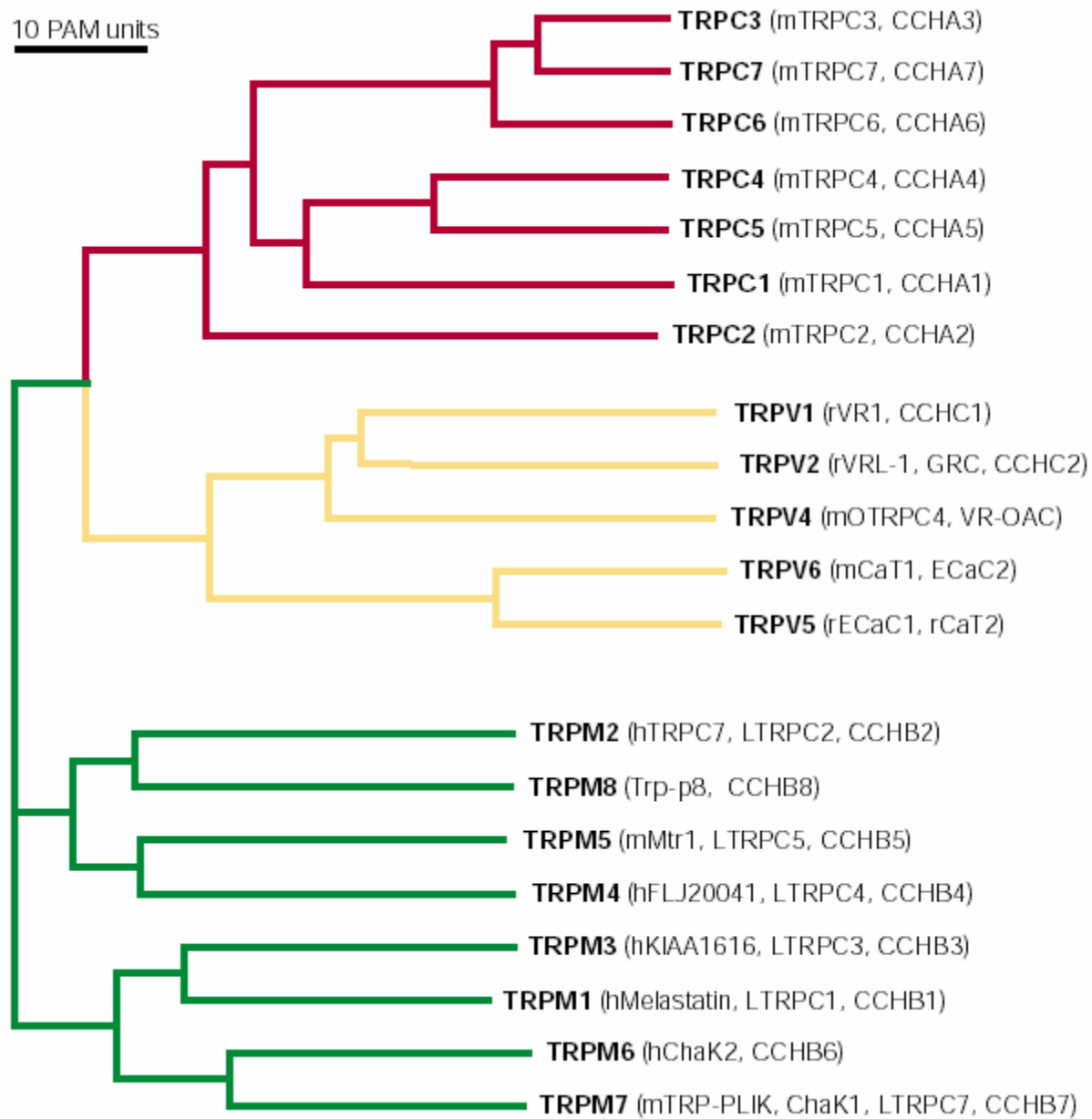


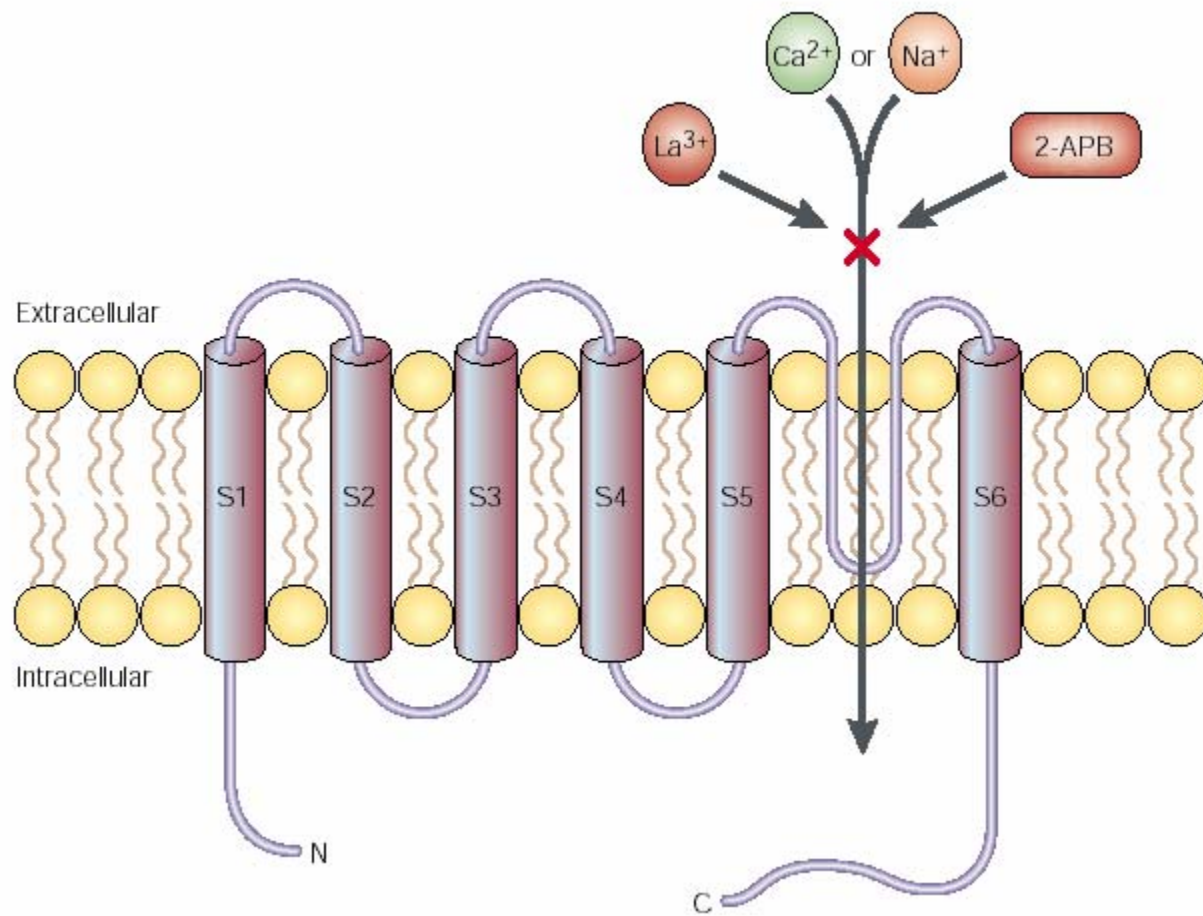
**“Human Vision”**  
**Visible Light Illumination**



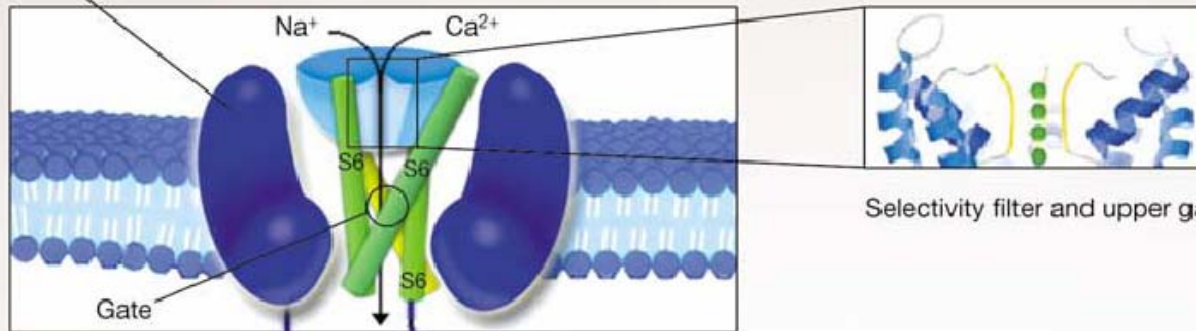
**“Honeybee Vision”**  
**Ultraviolet Illumination**

10 PAM units





S1-S4 transmembrane domains  
Weak voltage sensing

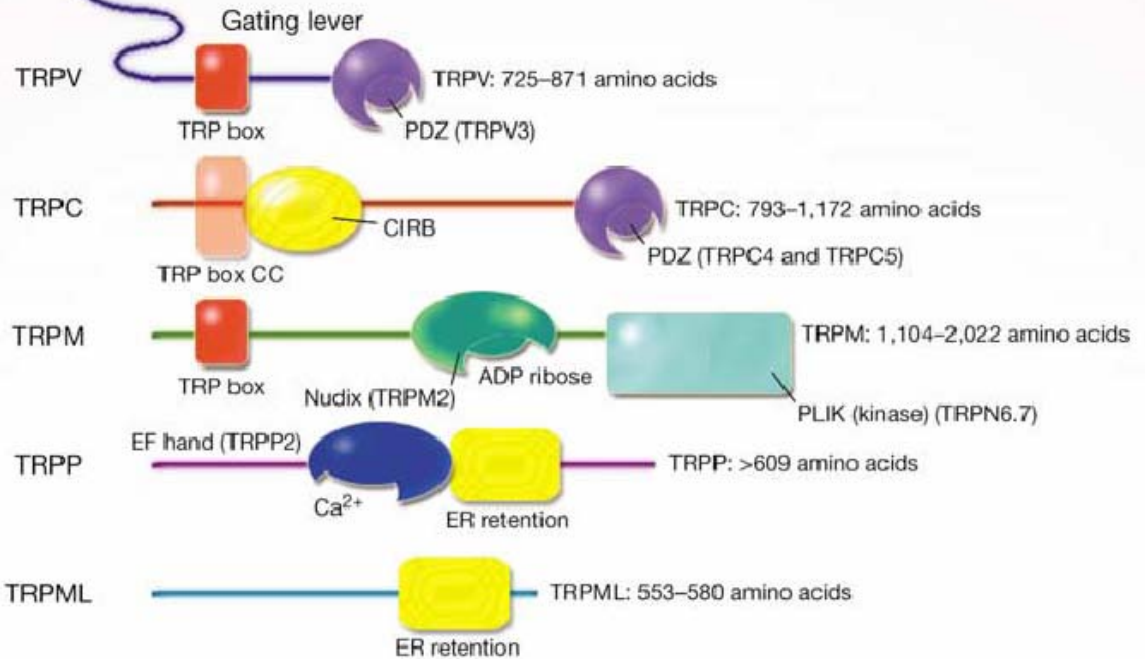


Selectivity filter and upper gate

Anchoring and/or protein interaction



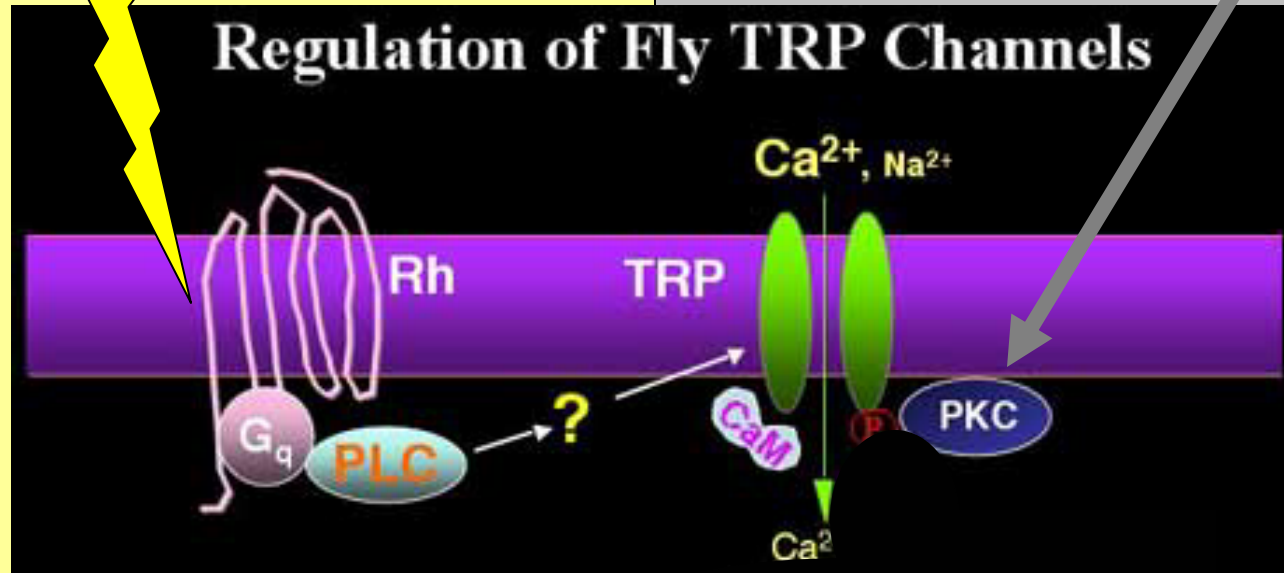
TRPM homology region





$h\nu$

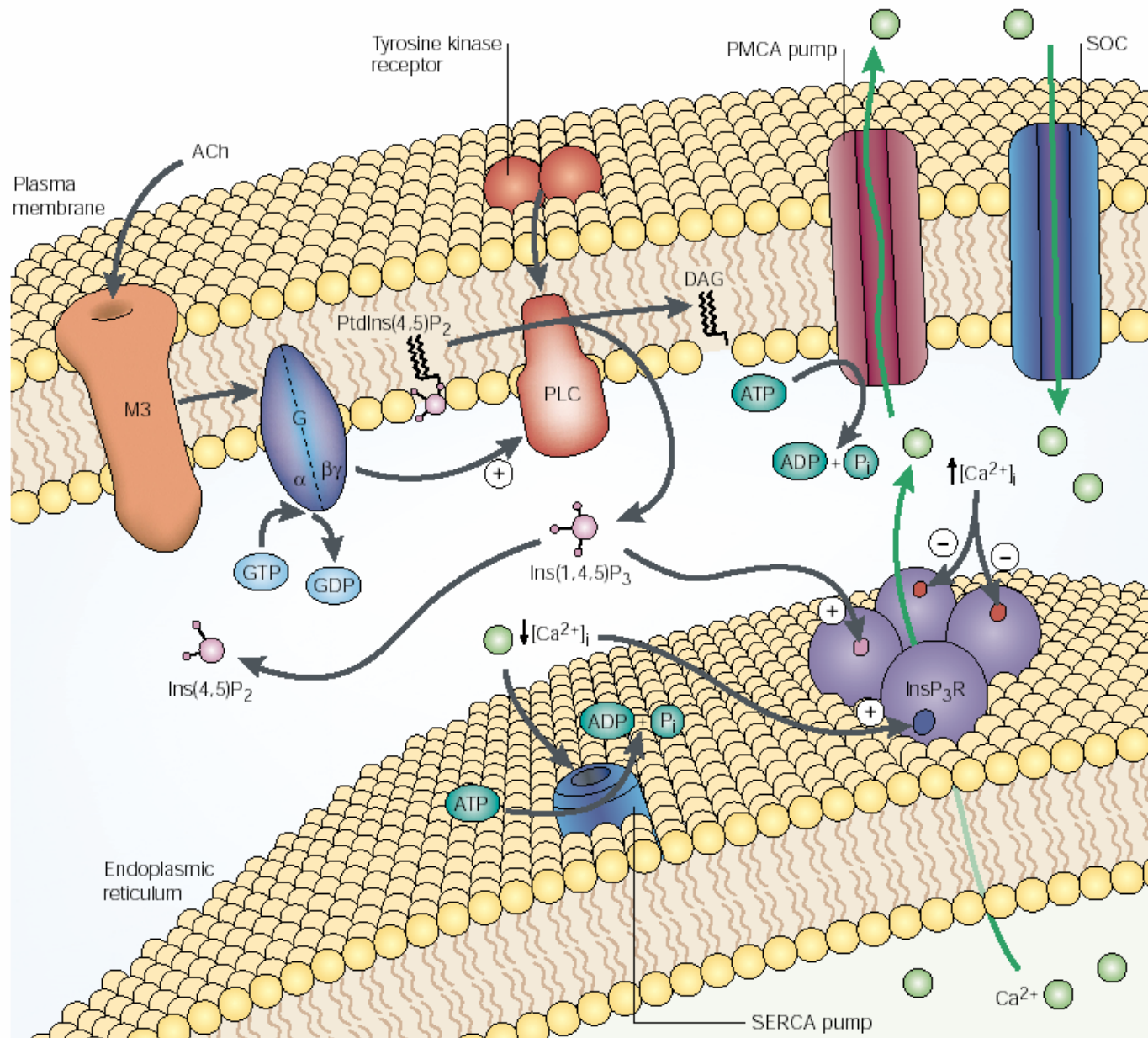
dark

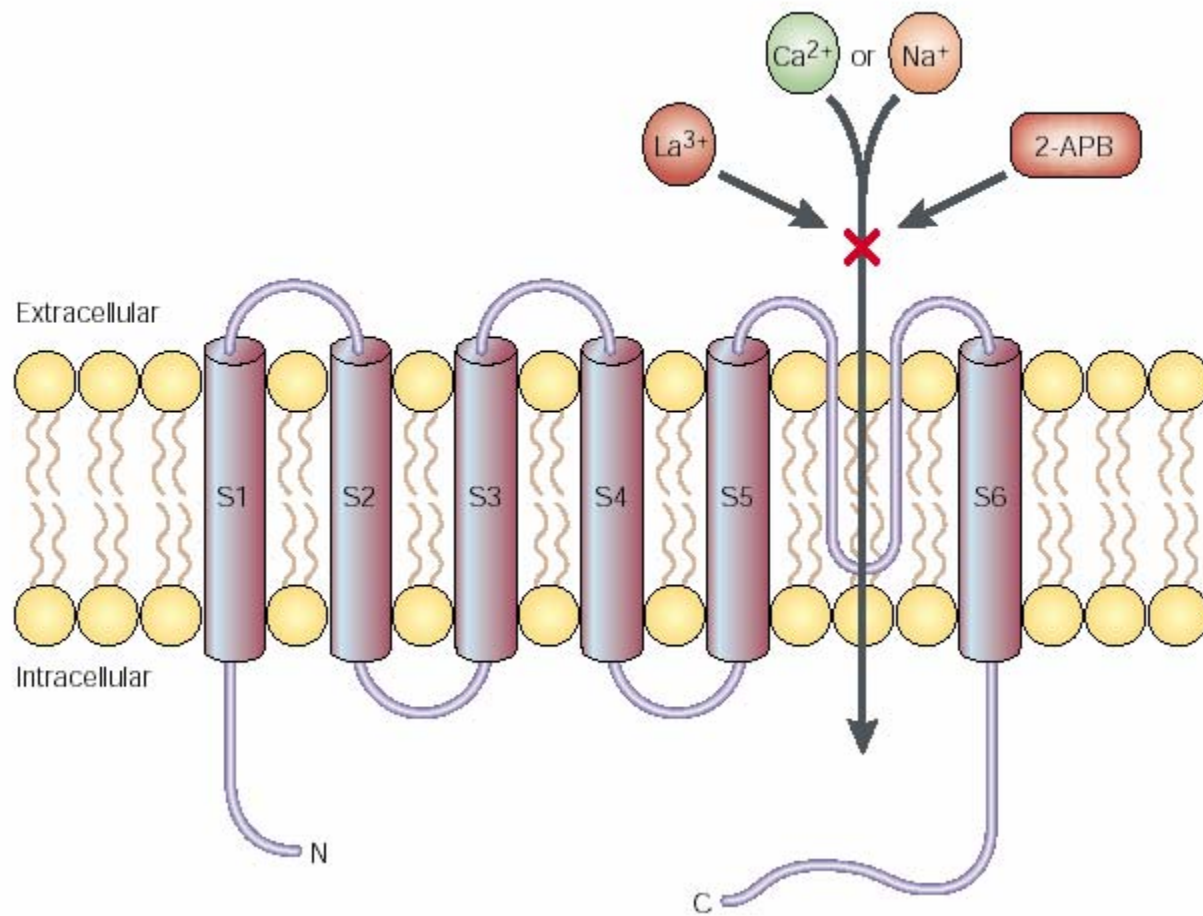


Rhodopsin activates  
G protein ( $\text{Gq}\alpha$ )  
which activates PLC

PLC breaks down  
 $\text{PIP}_2 \rightarrow \text{IP}_3$  & DAG  
which activate TRP  
which let in  $\text{Ca}^{++}$

$\text{Ca}^{++}$  activates PKC  
which deactivates  
TRP channel



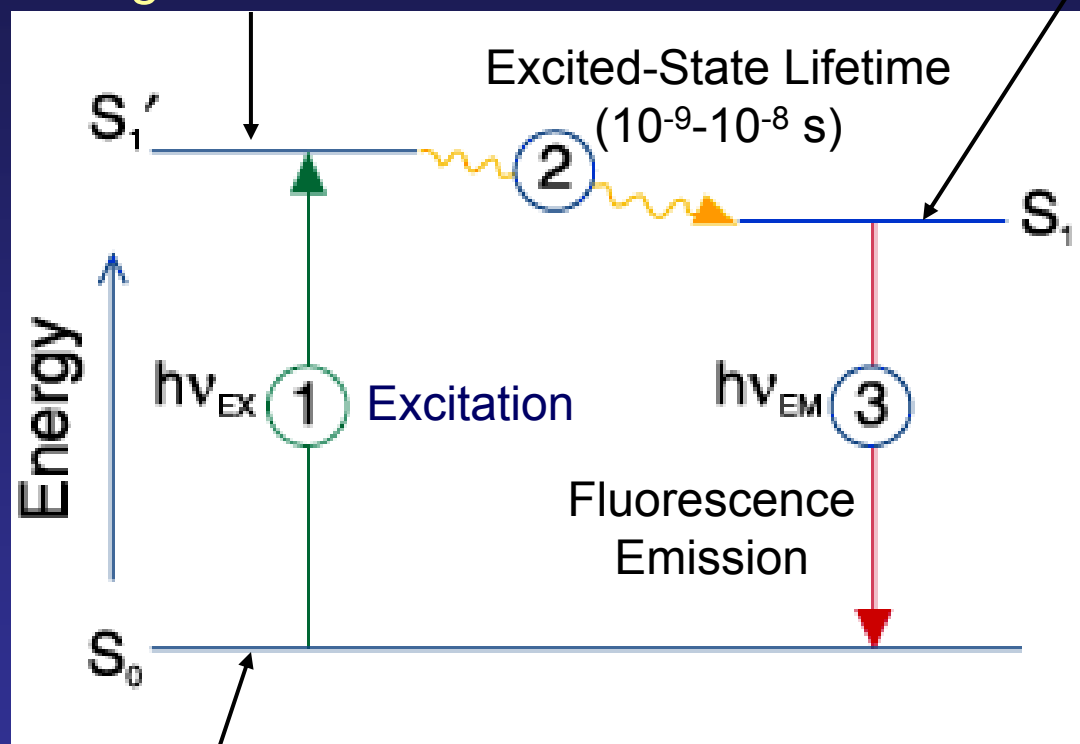


# Previously Known

- Locus of capsaicin sensitivity:  
Dorsal root ganglia
- Action of putative capsaicin receptor:  
trigger calcium influx into its cells.

# JABLONSKI DIAGRAM

Excited electronic singlet state      Singlet excited state

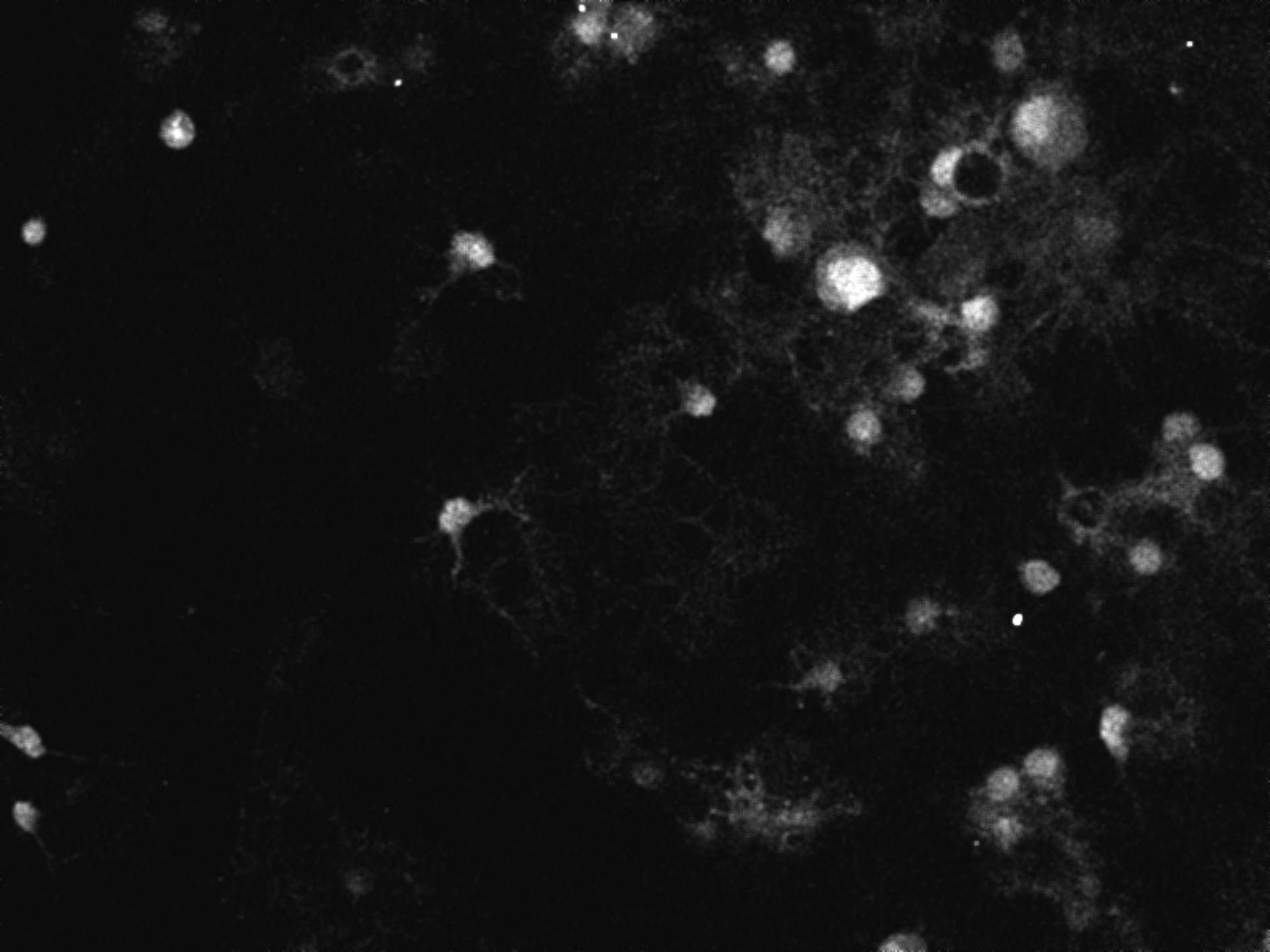


Ground state

**FLUORESCENCE QUANTUM YIELD**

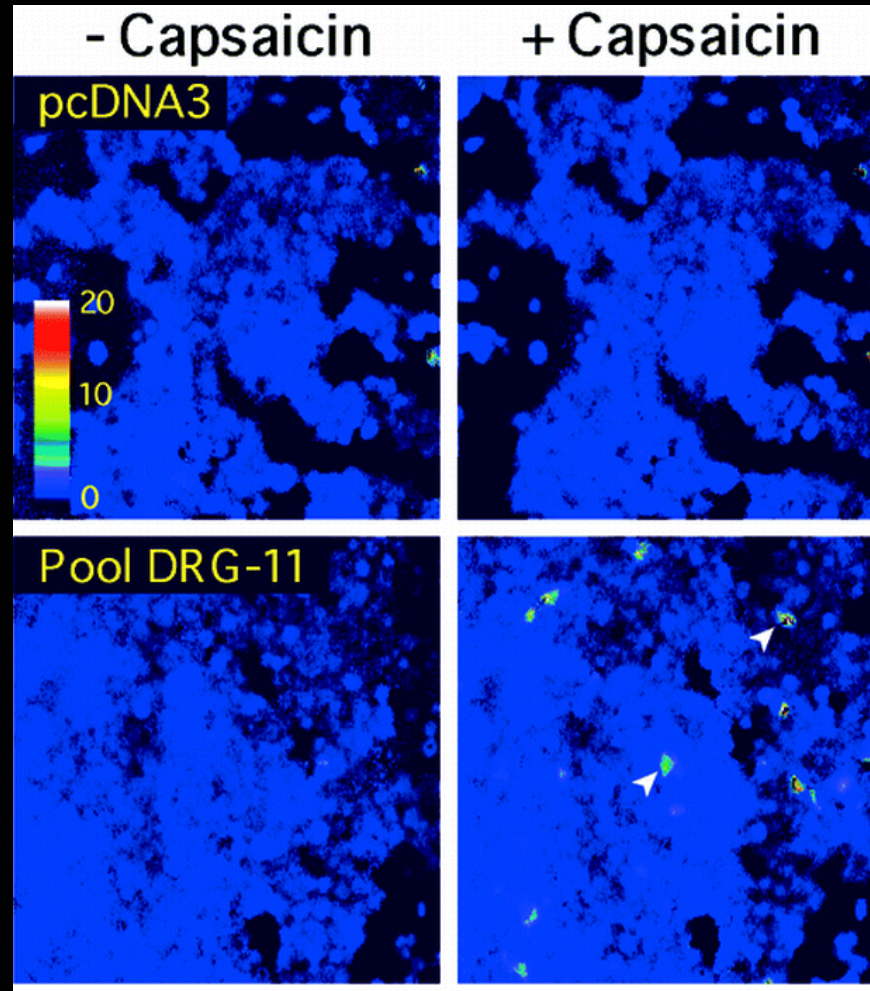
# fluorescence photons emitted (Stage 3)

# fluorescence photons absorbed (Stage 1)

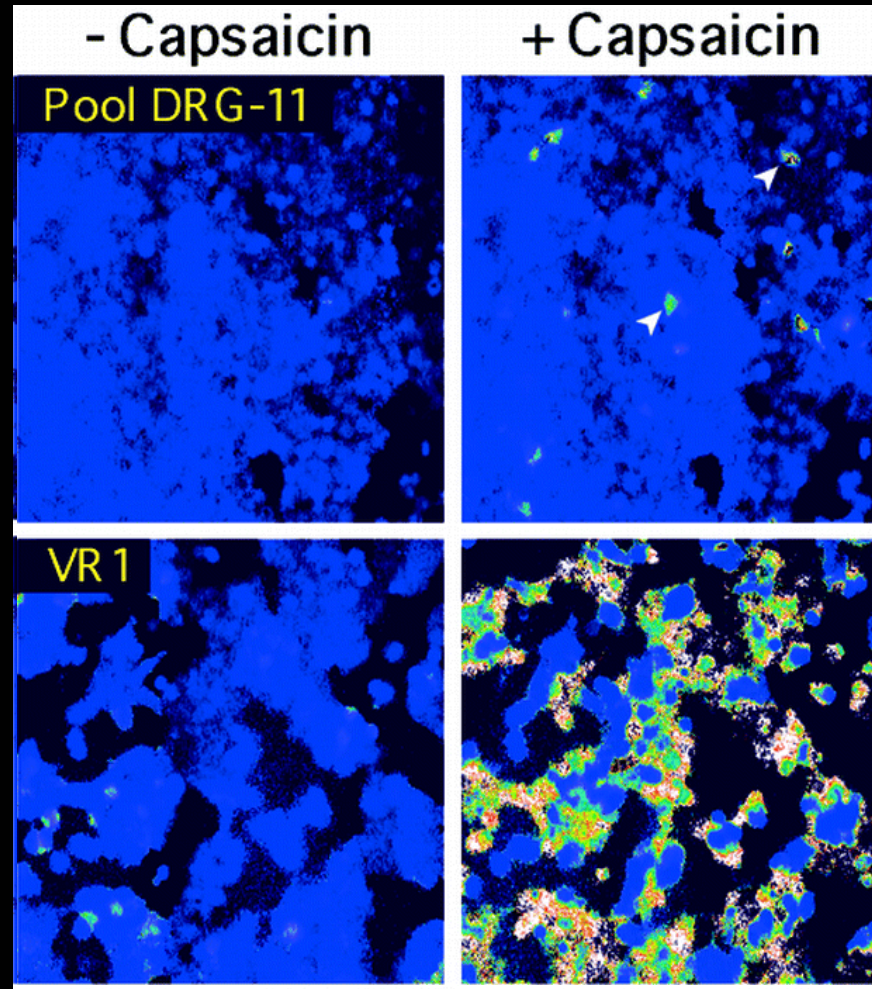




# Search for the Capsaicin Receptor: Expression Cloning



# Search for the Capsaicin Receptor: Expression Cloning





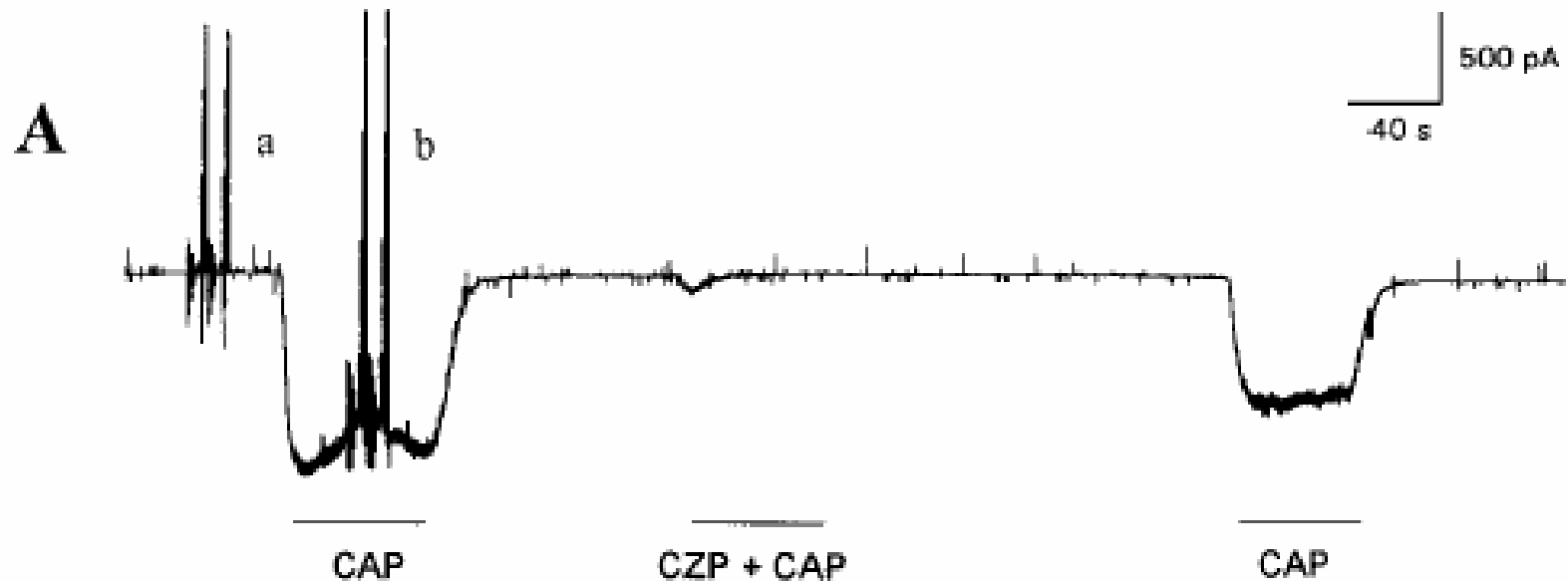
# Does it Work the Same?

## Previously Known

- **Nature** of receptor channel:  
**Non-selective cation channel**
- **Agonists** of receptor:  
include **capsaicin** and **resiniferatoxin**.
- **Antagonists** of receptor:  
include **capsazepine** and **rubidium red**.

Does it work the same?

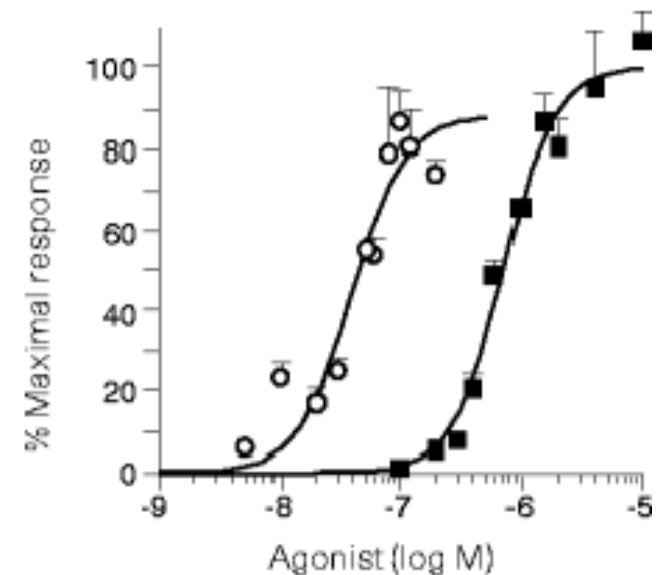
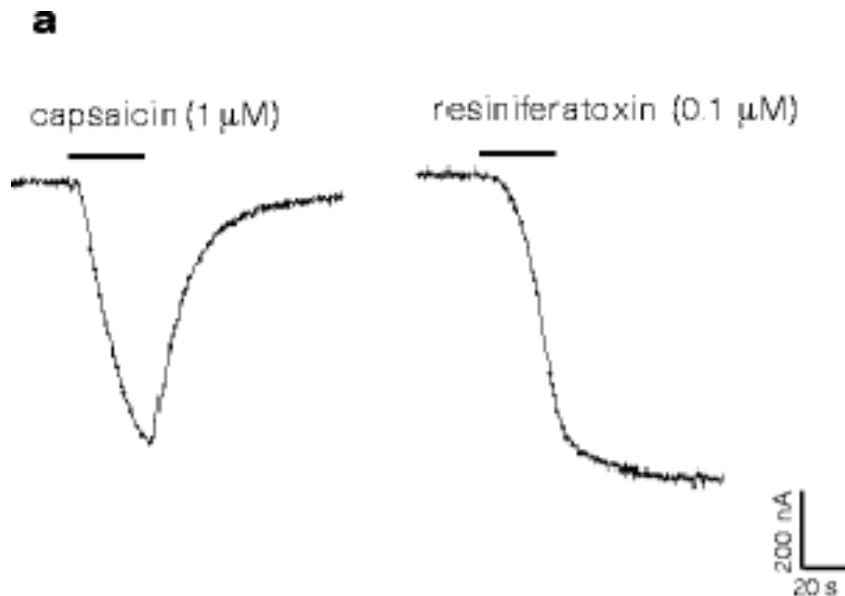
Does expression of the isolated protein confers capsaicin sensitivity?



(Oh et al., J. Neurosci., 1996)

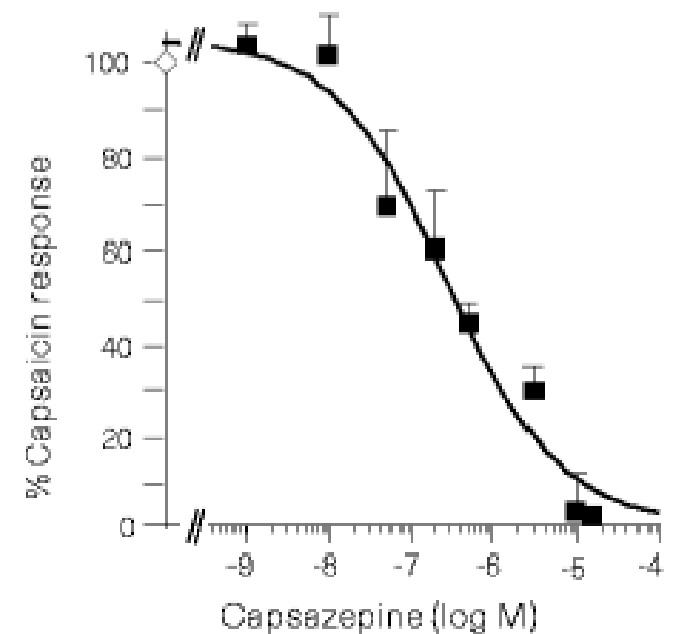
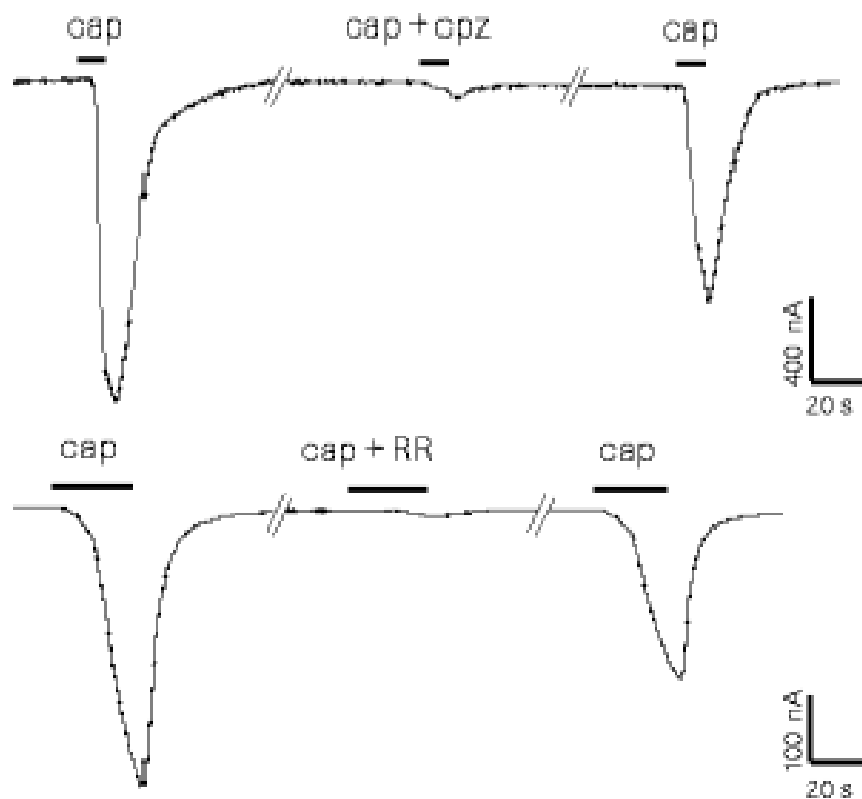
# Does it work the same?

## Expression of the isolated protein confers capsaicin sensitivity



# Does it work the same?

## Expression of the isolated protein confers antagonist sensitivity



Can VR1 confer that “je ne sais  
???” subtlety of chili experience?

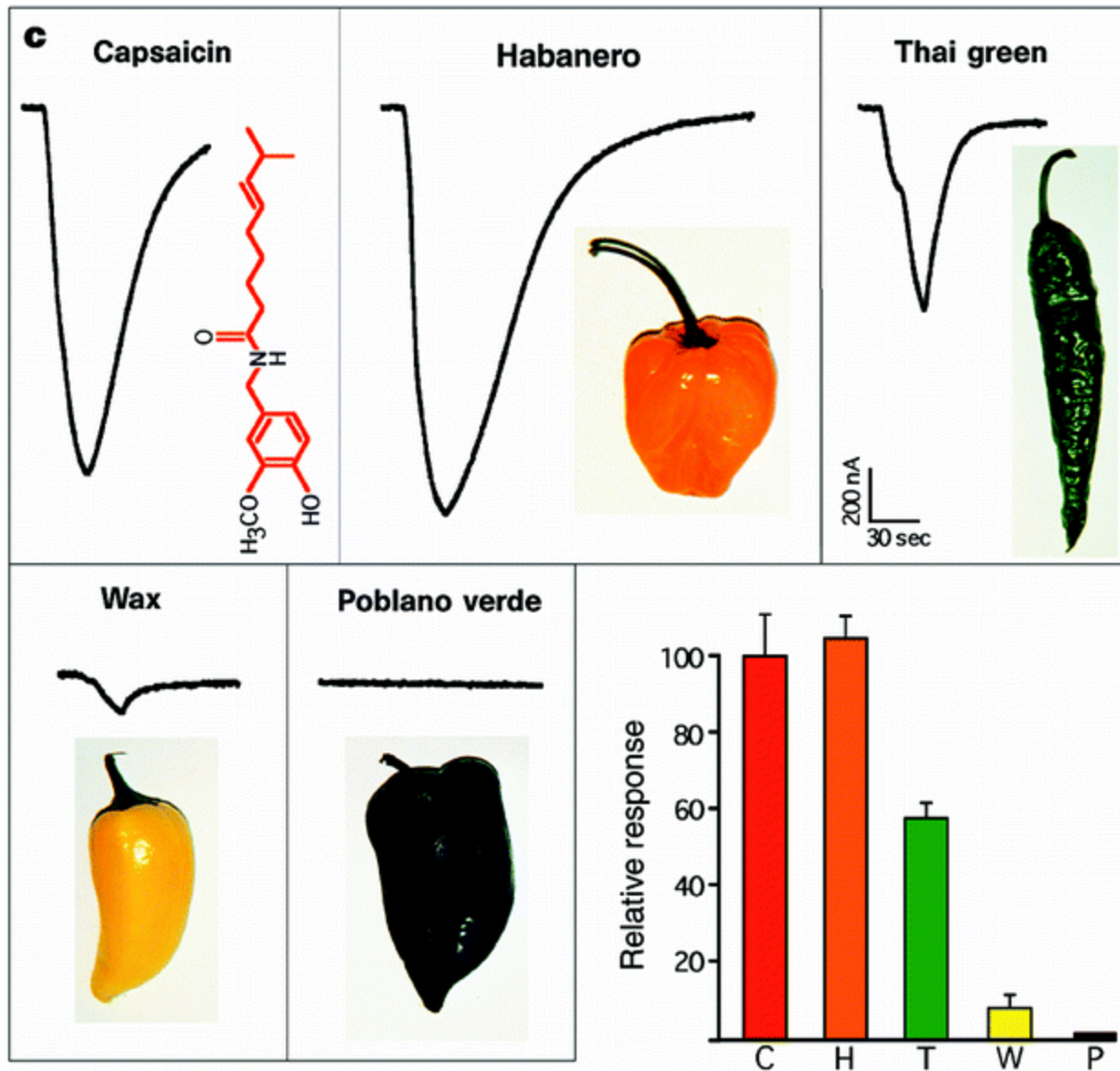


# PEPPERS

A COOKBOOK

BY ROBERT BERKLEY • PHOTOGRAPHS BY ERIC JACOBSON

# A More Rigorous Scale for Chilis

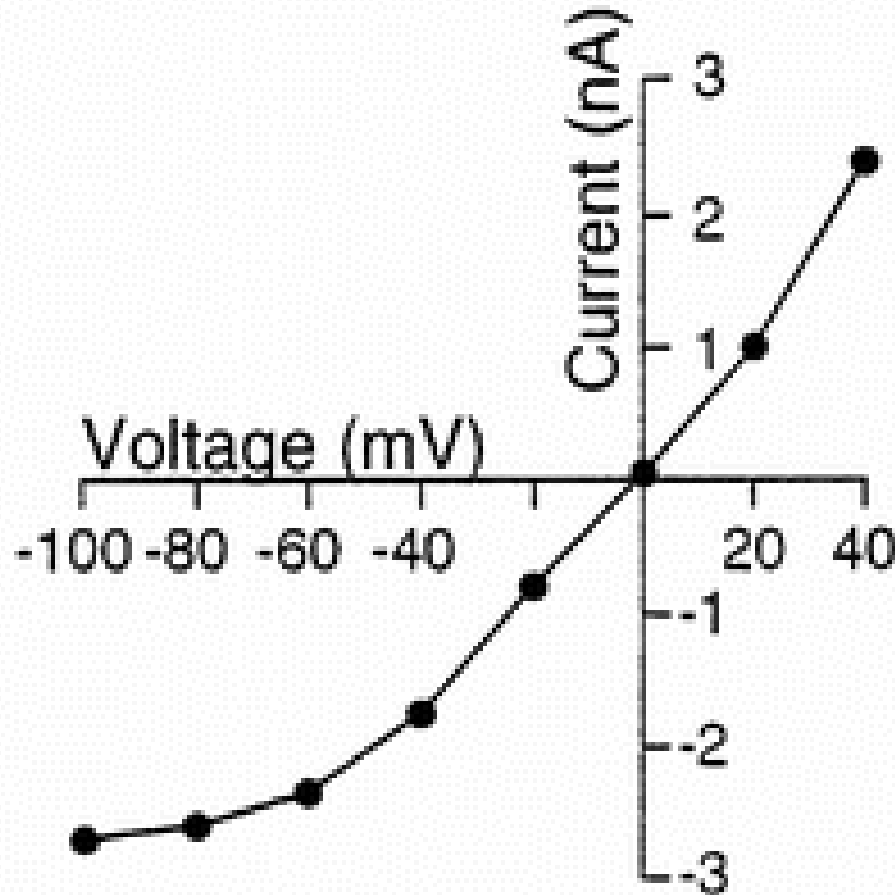


# Control: is it specific for the function in question?

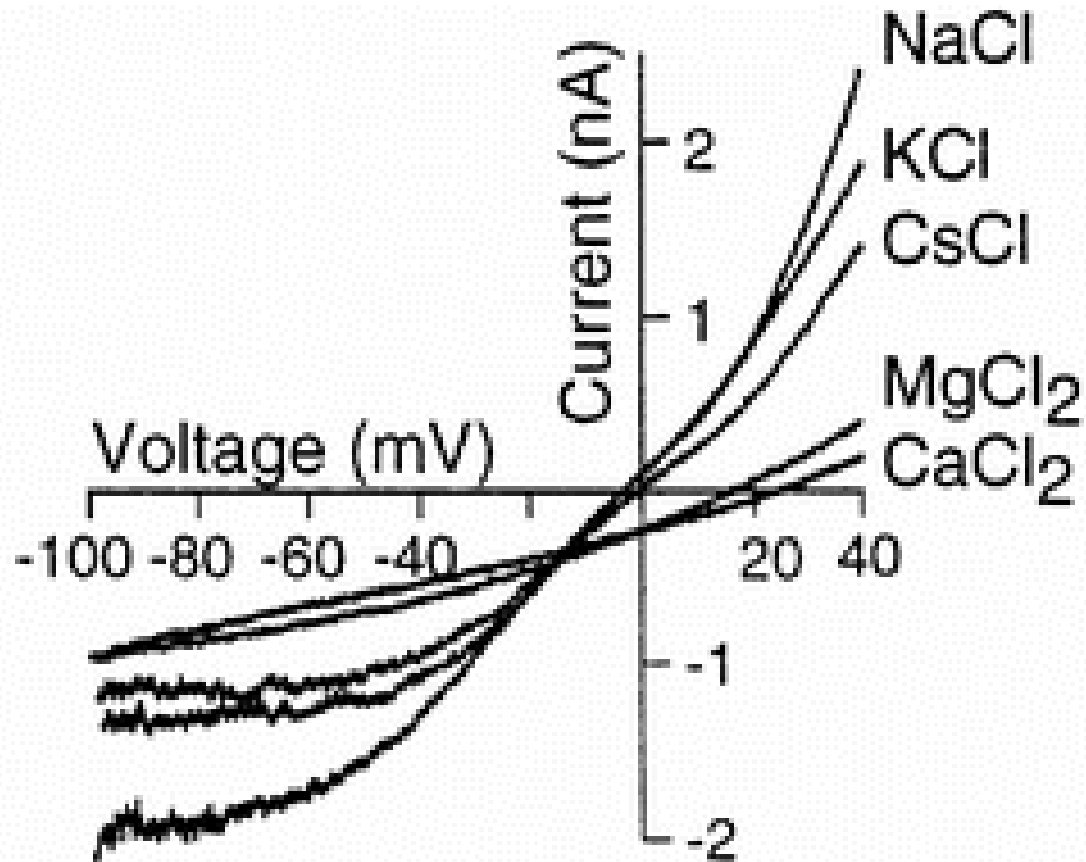
- Controls Tested:
  - ATP, serotonin, ACh, bradykinin, substance P, histamine, glutamate, hypertonic solution



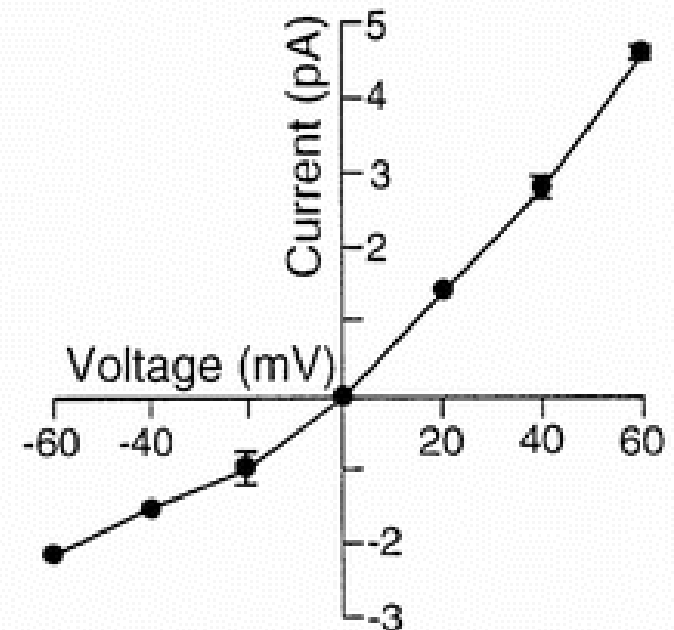
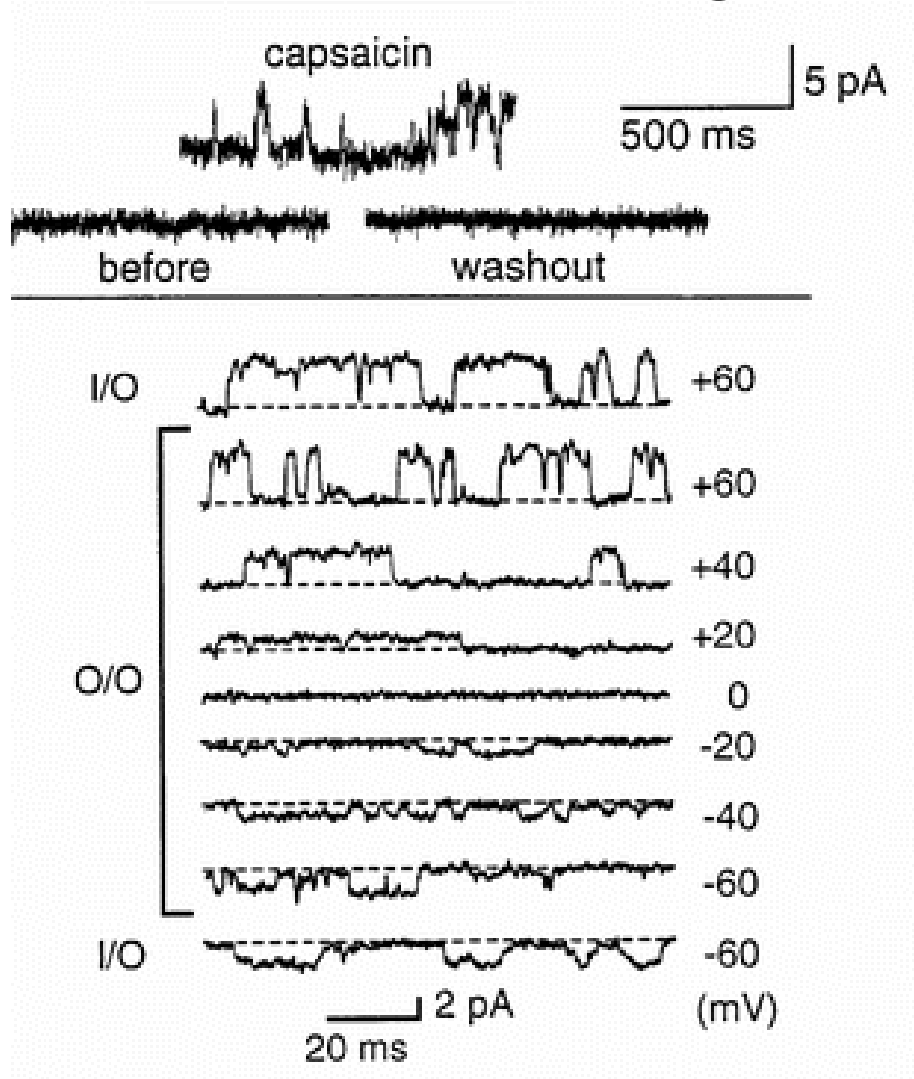
# “I-V Curve” for capsaicin currents during different holding voltages



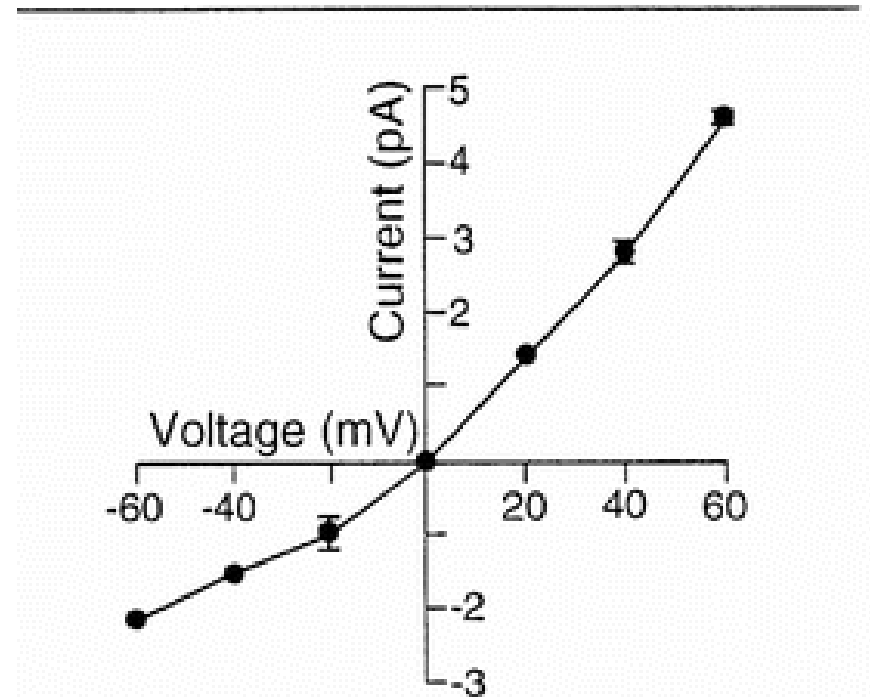
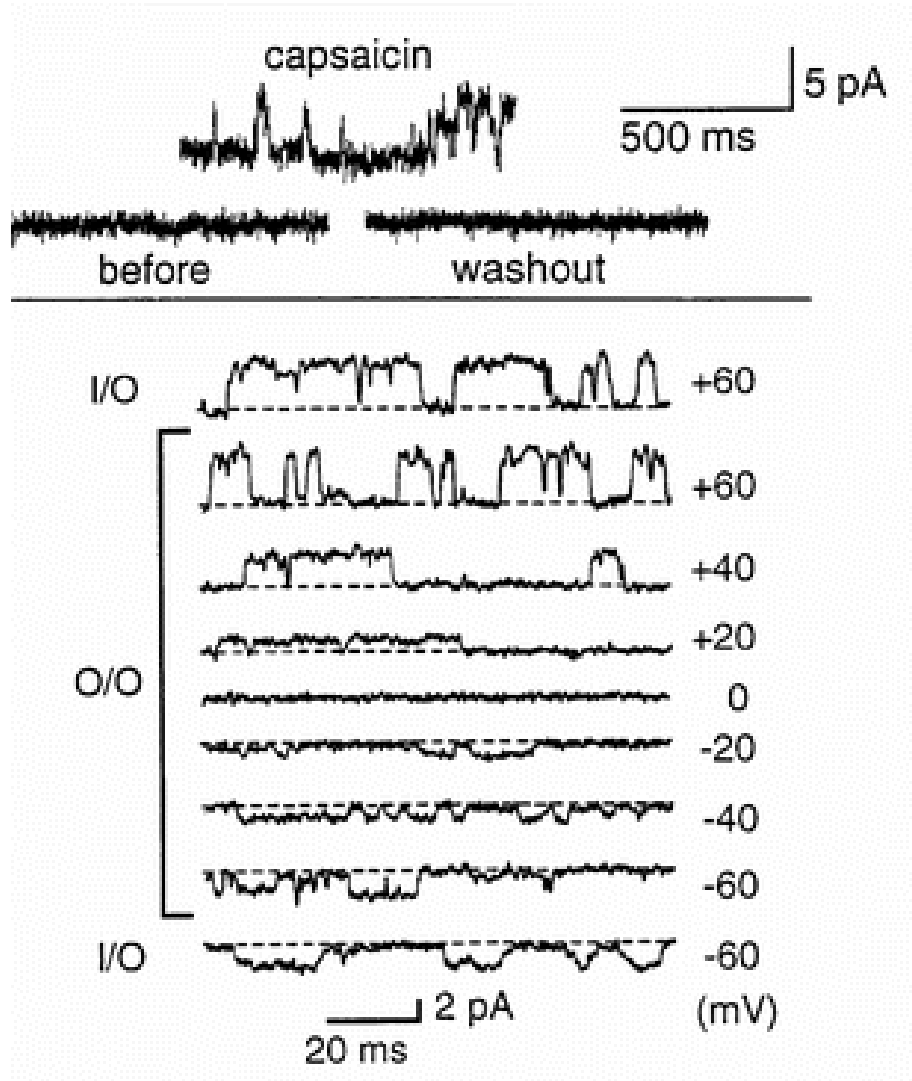
# Which Ions Carry the Charge?



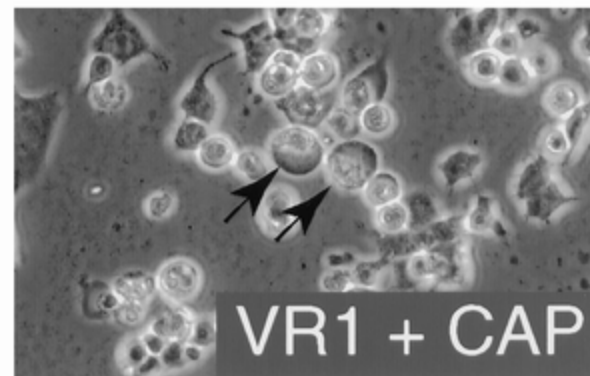
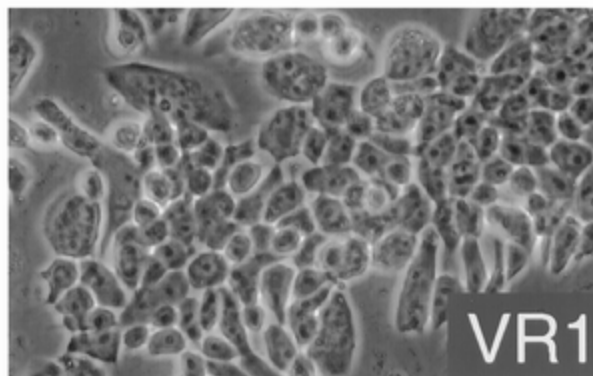
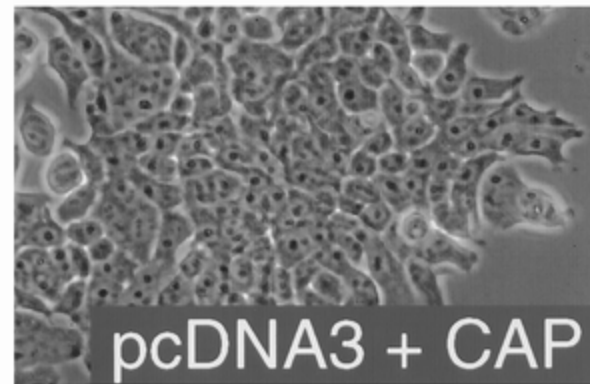
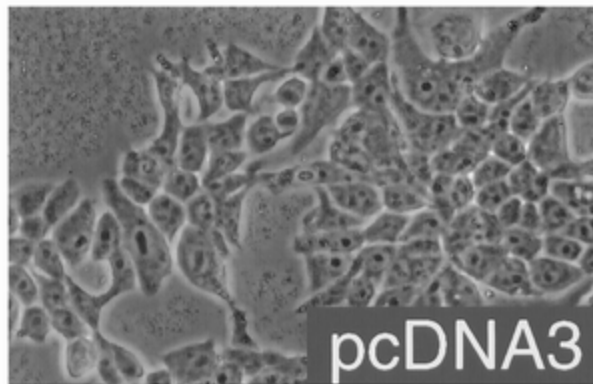
# Monitoring activity of single channels



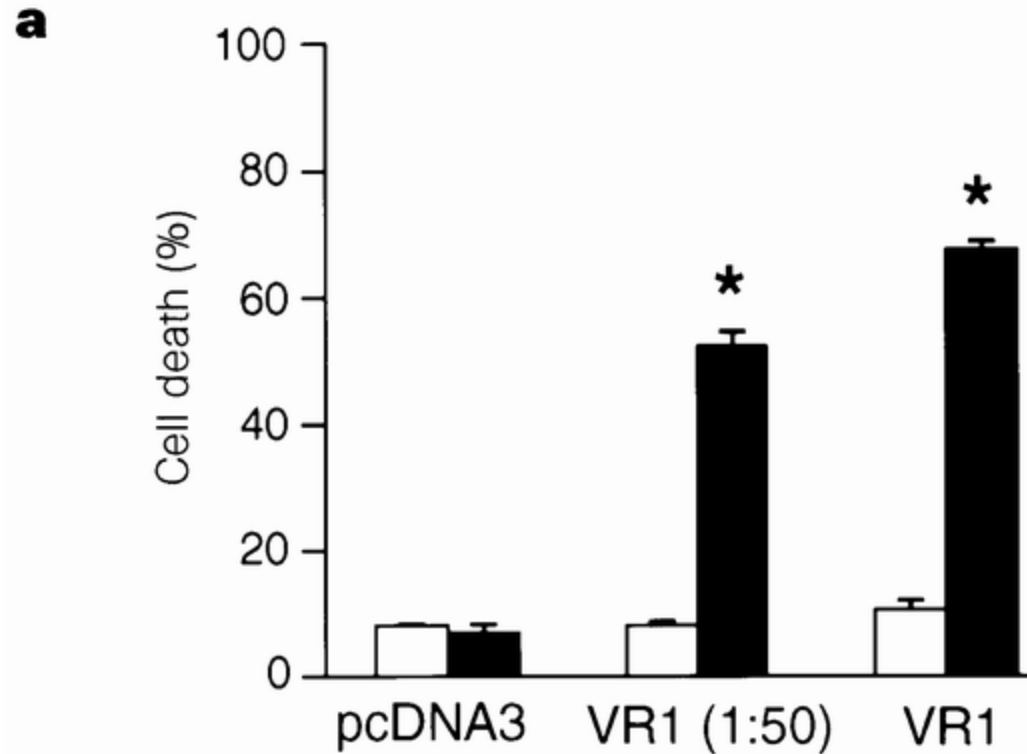
# Capsaicin works on either side of the membrane



The receptor, with capsaicin, is an effectively lethal accomplice



# The receptor, with capsaicin, is an effectively lethal accomplice



# a Predicted Amino Acid Sequence

MEQRASLDSEESPPQENSCLDPPDRDPNCKPPPVKPHIFTTRSR 46  
TRLFGKGDSEEASPLDCPYEEGGLASCPITVSSVLTIQRPDGPAS 93  
VRPSSQDSVSAGEKPPRLYDRRSIFDAVAQSNCQELESLLPFLQRSK 140  
KRLTDSEFKDPETGKTCLLKAMNLHNGQNDTIALLLDVARKTDSLK 187  
QFVNASYTDSYYKGQTALHIAIERRNMTLVTLLEVENGADVQAAANGD 234  
FFKKTGGRPGFYFGELPLSLAACTNQLAIVKFLQNSWQPADISARD 281  
SVGNTVLHALVEVADNTVDNTKFVTSMYNEILILGAKLHPTLKLEEIT 329  
NRKGLTPLALAASSGKIGVLAYILQREIHEPECRHLSRKFTWAYGPGP 376  
VHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHDMLLVEPLNRLLQ 423  
DKWDRFVKRIFYFNFFVYCLYMIIFTAAAYYRPVEGLPPYKLKNTVG 470  
DYFRVTGEILSVSGGVYFFFRGIQYFLQRRPSLKSLFVDSYSEILFFV 518  
QSLFMLVSVVLYFSQRKEYVASMVFSLAMGWTNMLYYTRGFQOMGI 564  
YAVMIEKMILRDLCRFMFVYLVFLFGFSTAVVTLIEDGKNNSLPMEST 612  
PHKCRGSACKPGNSYNSLYSTCLELFKFTIGMGDLEFTENYDFKAVF 659  
IILLLAYVILTYILLNMLIALMGETVNKIAQESKNIWKLQRAITILDTE 709  
KSFLKCMRKAFRSGKLLQVGFTPDGKDDYRWCFRVDEVNWTWNT 754  
NVGIINEDPGNCEGVKRTLFSLSLRSGRVSGRNWKNFALVPLLRDAST 801  
RDRHATQQEEVQLKHYTGSLKPEDAEEVFKDSMVPGEK 838

# Ankyrin repeats

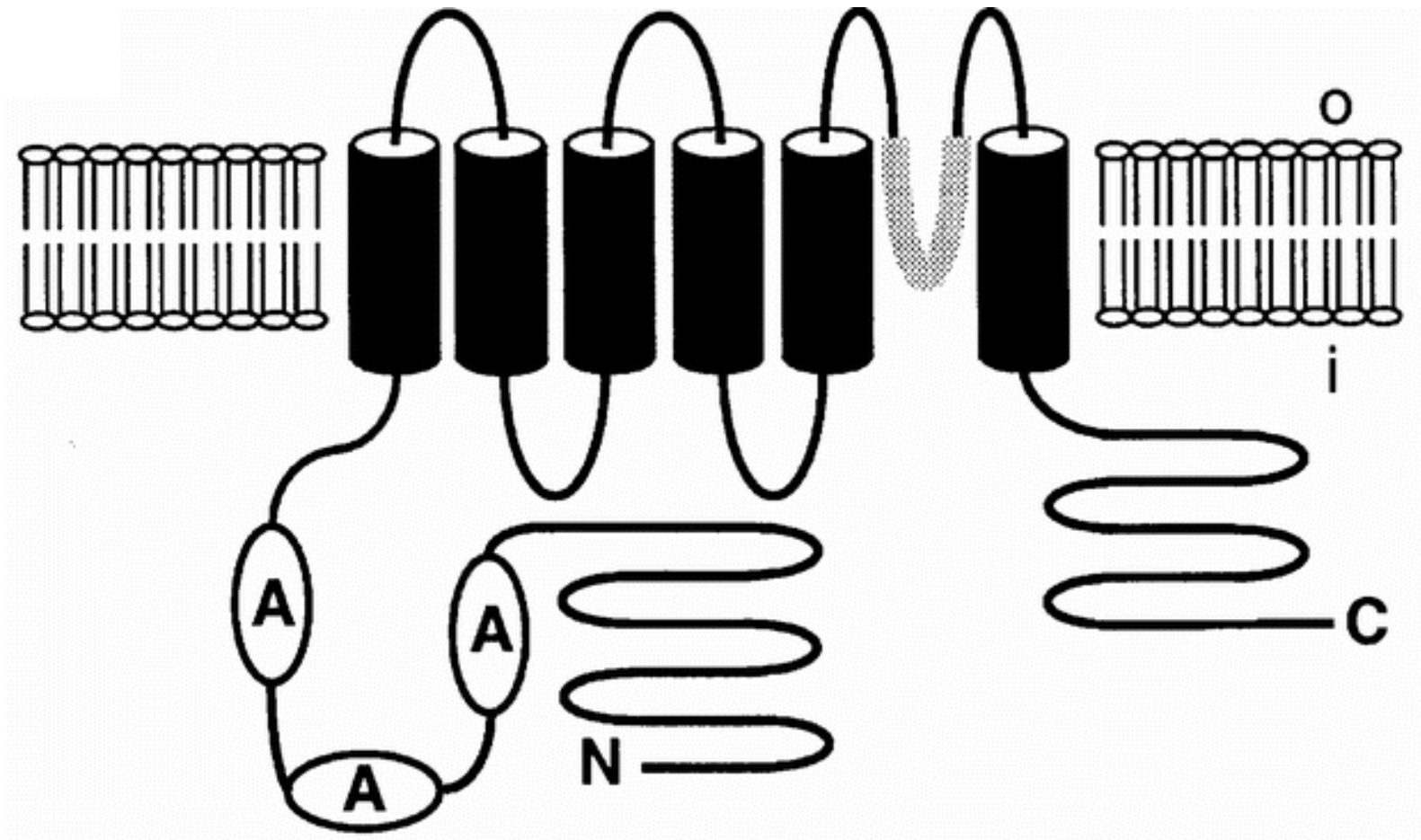
**a**

MEQRASLDSEESPPQENSCLDPPDRDPNCKPPPVKPHIFTTRSR 46  
TRLFGKGDSEEASPLDCPYEEGGLASCPITVSSVLTIQRPDGPAS 93  
VRPSSQDSVSAGEKPPRLYDRRSIFDAVAQSNCQELESLLPFLQRSK 140  
KRLTDSEFKDPETGKTCLLKAMLNHNGQNDTIALLLDVARKTDSLK 187  
QFVNASYTDSYYKGQTALHIAIERRNMTLVTLLEVENGADVQAAANGD 234  
FFKKTGKGRPGFYFGELPLSLAACTNQLAIVKFLQNSWQPADISARD 281  
SVGNTVLHALVEVADNTVDNTKFVTSMYNEILILGAKLHPTLKLEEIT 329  
NRKGLTPLALAASSGKIGVLAYILQREIHEPECRHLSRKFTWAYGPGP 376  
VHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHDMLLVEPLNRLLQ 423  
DKWDRFVKRIFYFNFFVYCLYMIIFTAAAYYRPVEGLPPYKLKNTVG 470  
DYFRVTGEILSVSGGVYFFFRGIQYFLQRRPSLKSLFVDSYSEILFFV 518  
QSLFMLVSVVLYFSQRKEYVASMVFSLAMGWTNMLYYTRGFQOMGI 564  
YAVMIEKMILRDLCRFMFVYLVFLFGFSTAVVTLIEDGKNNSLPMEST 612  
PHKCRGSACKPGNSYNSLYSTCLELFKFTIGMGDLEFTENYDFKAVF 659  
IILLLAYVILTYILLNMLIALMGETVNKIAQESKNIWKLQRAITILDTE 709  
KSFLKCMRKAFRSGKLLQVGFTPDGKDDYRWCFRVDEVNWTWNT 754  
NVGIINEDPGNCEGVKRTLFSLSLRSGRVSGRNWKNFALVPLLRDAST 801  
RDRHATQQEEVQLKHYTGSLKPEDAEVFKDSMVPGEK 838

The diagram shows the amino acid sequence of the Ankyrin protein, with positions 46, 93, 140, 187, 234, 281, 329, 376, 423, 470, 518, 564, 612, 659, 709, 754, 801, and 838 marked. Transmembrane domains (TM1 to TM6) are highlighted in black. A red arrow points to the sequence starting at position 234, indicating the start of the Ankyrin repeats. A black dot is located at position 187, and another black dot is located at position 376.



# Predicted Structure



# Predicted transmembrane domains

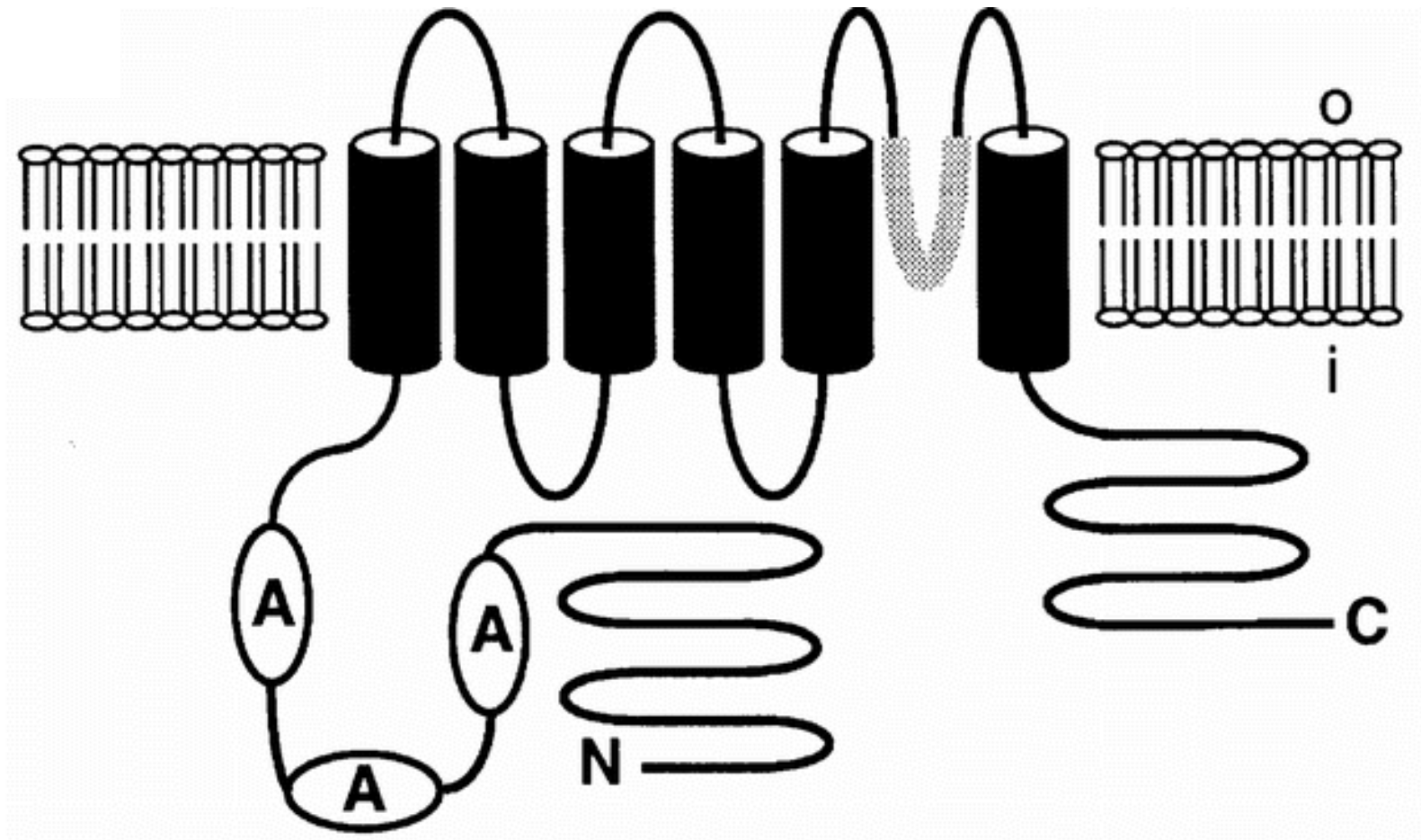
a

MEQRASLDSEESPPQENSCLDPPDRDPNCKPPPVKPHIFTTRSR 46  
TRLFGKGDSEEASPLDCPYEEGGLASCPITVSSVLTIQRPDGPAS 93  
VRPSSQDSVSAGEKPPRLYDRRSIFDAVAQSNCQELESLLPFLQRSK 140  
KRLTDSEFKDPETGKTCLLKAMNLHNGQNDTIALLLDVARKTDSLK 187  
QFVNASYTDSYYKGQTALHIAIERRNMTLVTLLEVENGADVQAAANGD 234  
FFKKTGGRPGFYFGELPLSLAACTNQLAIVKFLQNSWQPADISARD 281  
SVGNTVLHALVEVADNTVDNTKFVTSMYNEILILGAKLHPTLKLEEIT 329  
NRKGLTPLALAASSGKIGVLAYILQREIHEPECRHLSRKFTWAYGPG 376  
VHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHDMLLVEPLNRLLQ 423  
DKWDRFVKRIFYFNFFVYCLYMIIFTAAAYYRPVEGLPPYKLKNTVG 470  
DYFRVTGEILSVSGGVYFFFRGIQYFLQRRPSLXSLFVDSYSEILFFV 518  
QSLFMLVSVVLYFSQRKEYVASMVFSLAMGWTNMLYYTRGFQOMGI 564  
YAVMIEKMILRDLCRFMFVYLVFLFGFSTAVVTLIEDGKNNSLPMEST 612  
PHKCRGSACKPGNSYNSLYSTCLELFKFTIGMGDLEFTENYDFKAVF 659  
IILLLAYVILTYILLNMLIALMGETVNKIAQESKNIWKLQRAITILDTE 709  
KSFLKCMRKAFRSGKLLQVGFTPDGKDDYRWCFRVDEVNWTWNT 754  
NVGIINEDPGNCEGVKRTLFSLSLRSGRVSGRNWKNFALVPLLRDAST 801  
RDRHATQQEEVQLKHYTGSLKPEDAEEVFKDSMVPGEK 838

TM1  
TM2  
TM3  
TM4  
TM5  
TM6



# Predicted Structure



# Predicted pore loop region

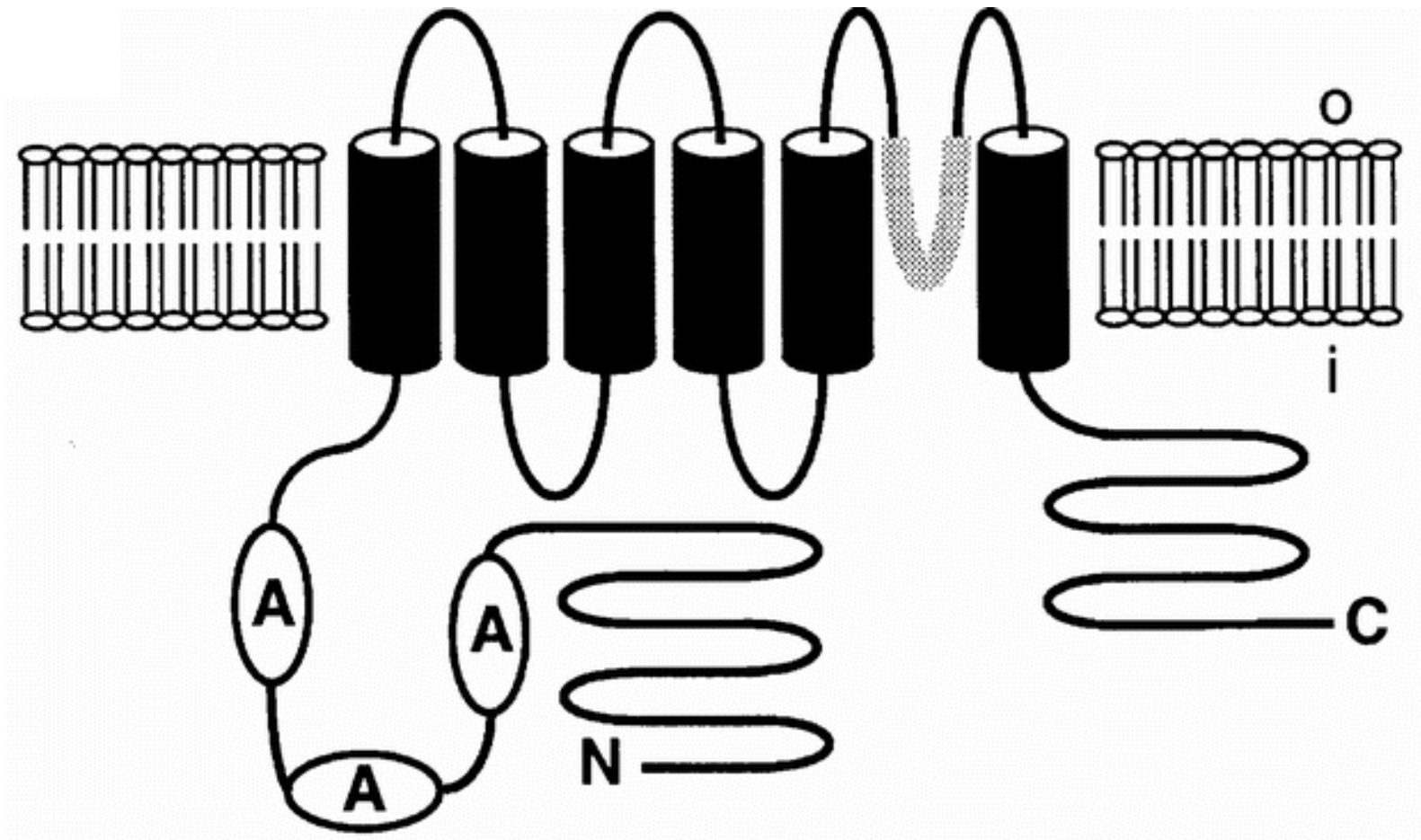
a

MEQRASLDSEESPPQENSCLDPPDRDPNCKPPPVKPHIFTTRSR 46  
TRLFGKGDSEEASPLDCPYEEGGLASCPITVSSVLTIQRPDGPAS 93  
VRPSSQDSVSAGEKPPRLYDRRSIFDAVAQSNOQELESLLPFLQRSK 140  
KRLTDSEFKDPETGKTCLLKAMNLHNGQNDTIALLLDVARKTDSLK 187  
QFVNASYTDSYYKGQTALHIAIERRNMTLVTLLEVENGADVQAAANGD 234  
FFKKTGGRPGFYFGELPLSLAACTNQLAIVKFLQNSWQPADISARD 281  
SVGNTVLHALVEVADNTVDNTKFVTSMYNEILILGAKLHPTLKLEEIT 329  
NRKGLTPLALAASSGKIGVLAYILQREIHEPECRHLSRKFTWAYYGP 376  
VHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHDMLLVEPLNRLLQ 423  
DKWDRFVKRIFYFNFFVYCLYMIIFTAAAYYRPVEGLPPYKLKNTVG 470  
DYFRVTGEILSVSGGVYFFFRGIQYFLQRRPSLSLSLFVDSYSEILFFV 518  
QSLFMLVSVVLYFSQRKEYVASMVFSLAMGWTNMLYYTRGFQOMGI 564  
YAVMIEKMILRDLCRFMFVYLVFLFGFSTAVVTLIEDGKNNSLPMEST 612  
PHKCRGSACKPGNSYNSLYSTCLELFKFTIGMGDLEFTENYDFKAVF 659  
IILLLAYVILTYILLNMLIALMGETVNKIAQESKNIWKLQRAITILDTE 709  
KSFLKCMRKAFRSGKLLQVGFTPDGKDDYRWCFRVDEVNWTWNT 754  
NVGIINEDPGNCEGVKRTLFSLSLRSGRVSGRNWKNFALVPLLRDAST 801  
RDRHATQQEEVQLKHYTGSLKPEDAEVFKDSMVPGEK 838

The diagram shows a protein sequence with six transmembrane domains (TM1-TM6) highlighted in black. A red vertical line with a downward arrow indicates a specific region of interest, likely the pore loop, which is highlighted in grey. The pore loop region is located between residues 612 and 659, specifically between the TM5 and TM6 domains. The sequence is presented in a standard one-letter amino acid code format, with residue numbers indicated on the right side of each line.



# Predicted Structure



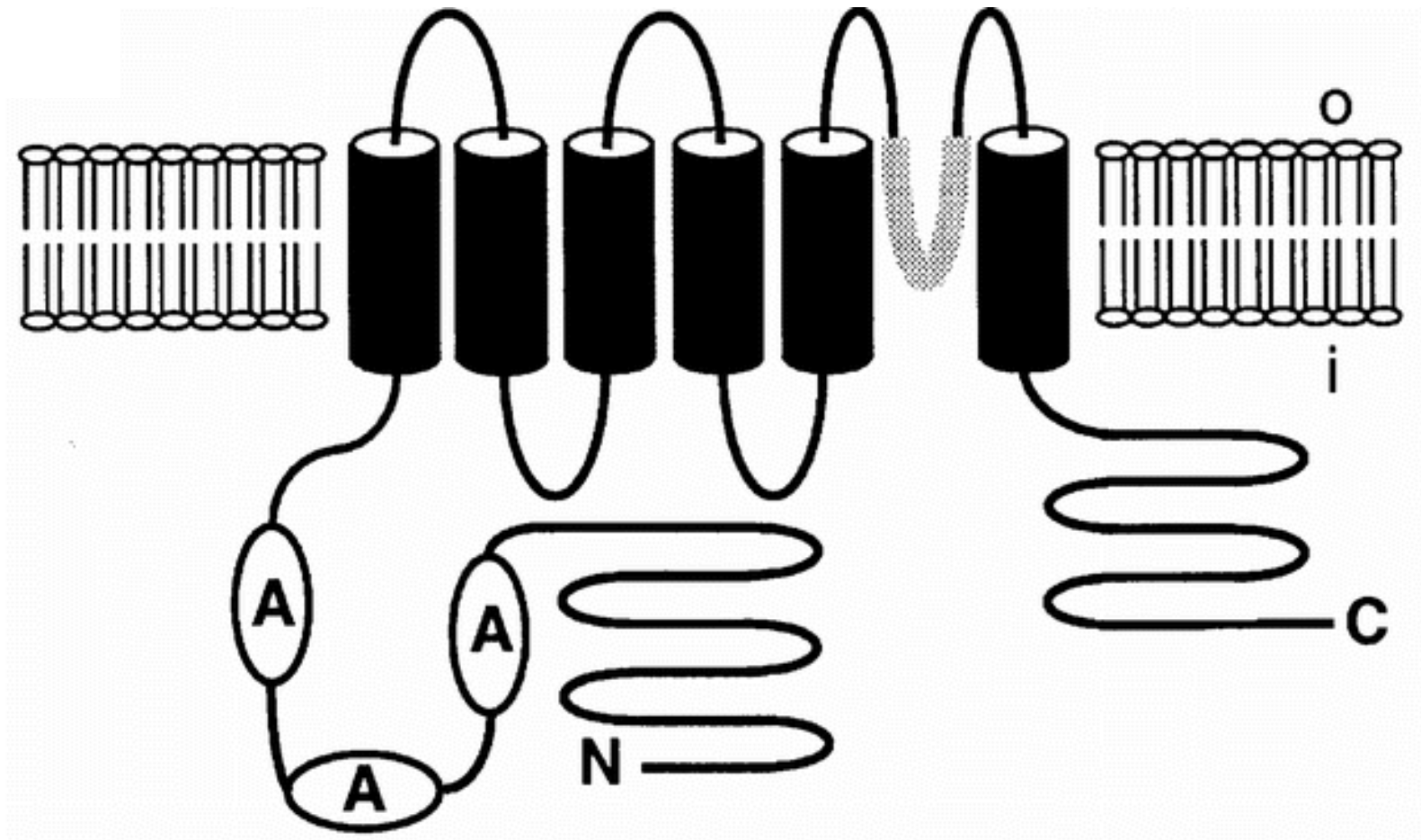
# Predicted PKA binding sites

a

MEQRASLDSEESPPQENSCLDPPDRDPNCKPPPVKPHIFTTRSR 46  
TRLFGKGDSEEASPLDCPYEEGGLASCPITVSSVLTIQRPDGPAS 93  
VRPSSQDSVSAGEKPPRLYDRRSIFDAVAQSNCOELESLLPFLQRSK 140  
KRLTDSEFKDPETGKTCLLKAMLNHNGQNDTIALLLDVARKTDSLK 187  
QFVNASYTDSYYKGQ TALHIAIERRNMTLVTLLEVENGADVQAAANGD 234  
FFKKTGGRPGFYFGELPLSLAACTNQLAIVKFLLQNSWQPADISARD 281  
SVGNTVLHALVEVADNTVDNTKFVTSMYNEILILGAKLHPTLKLEEIT 329  
NRKGLTPLALAASSGKIGVLAYILQREIHEPECRHLSRKFTWAYGP 376  
VHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHDMLLVEPLNRLLQ 423  
DKWDRFVKRIFYFNFFVYCLYMIIFTAAAYYHPVEGLPPYKLKNTVG 470  
DYFRVTGEILSVSGGVYFFFRGIQYFLQRRPSLKSLFVDSYSEILFFV 518  
QSLFMLVSVVLYFSQRKEYVASMVFSLAMGWTNMLYYTRGFQOMGI 564  
YAVMIEKMILRDLCRFMFVYLVFLFGFSTAVVTLIEDGKNNSLPMEST 612  
PHKCRGSACKPGNSYNSLYSTCLELFKFTIGMGDLEFTENYDFKAVF 659  
IILLLAYVILTYILLNMLIALMGETVNKIAQESKNIWKLQRAITILDTE 709  
KSFLKCMRKAFRSGKLLQVGFTPDGKDDYRWCFRVDEVNWTWNT 754  
NVGIINEDPGNCEGVKRTLFSLSLRSGRVSGRNWKNFALVPLLRDAST 801  
RDRHATQQEEVQLKHYYTGSCLKPEDAEVFKDSMVPGEK 838

TM1  
TM2  
TM3  
TM4  
TM5  
TM6

# Predicted Structure



# VR1 Resembles Store-Operated Channels

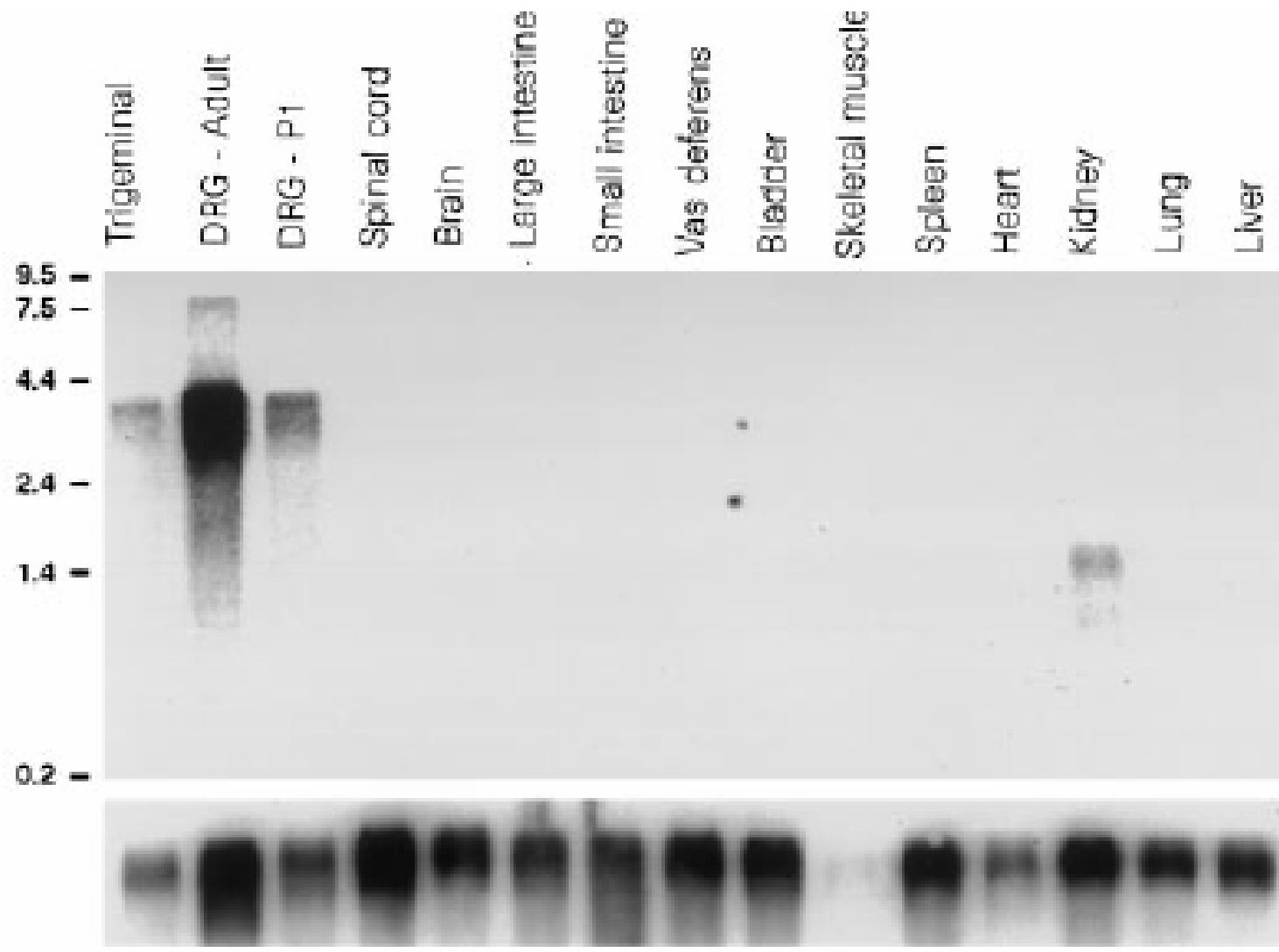
636 670

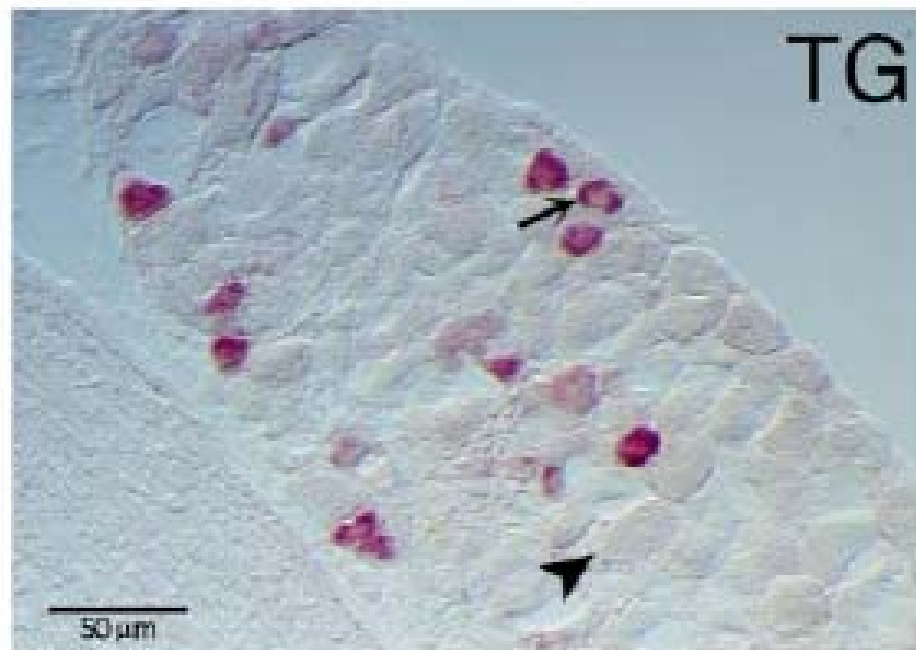
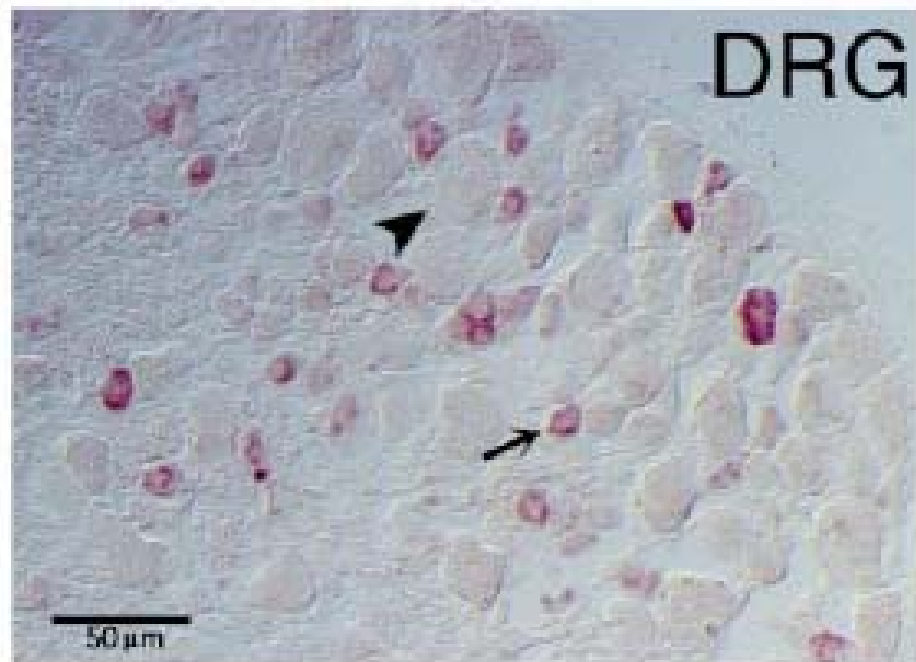
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E	L	F	K	F	T	I	G	M	G	E	L	-	-	-	A	F	Q	E	Q	L	H	F	R	G	-	M	V	L	L	L	L	L	-	A	Y	V	L	L	T
S	L	F	W	A	S	F	G	L	V	D	L	V	S	F	D	L	A	G	I	K	S	F	T	R	-	F	W	A	L	L	M	F	G	S	Y	S	V	I	N
S	L	F	W	A	S	F	G	L	V	D	L	V	S	F	D	L	A	G	I	K	S	F	T	R	-	F	W	A	L	L	M	F	G	S	Y	S	V	I	N
S	L	F	W	S	I	F	G	L	I	N	L	Y	V	T	N	V	K	A	Q	H	E	F	T	E	-	F	V	G	A	T	M	F	G	T	Y	N	V	I	S
R	T	F	I	M	T	I	G	E	F	S	V	L	Y	R	E	M	S	A	C	D	N	F	W	M	K	W	I	G	K	L	I	F	V	I	F	E	T	F	V

671  
Y I L L N M L I A L M G E T V N K I A Q E S K N I W K L Q R A I T I L  
Y I L L N M L I A L M S E T V N S V A T D  
I I V L L N M L I A M M S N S Y Q I I S E R A D V E W K F A R S Q L W M  
I I V L L N M L I A M M S N S Y Q I I S E R A D T E W K F A R S Q L W M  
L V V L L N M L I A M M N N S Y Q L I A D H A D I E W K F A R T K L W M  
S I L Q F N L L I A M M T R T Y E T I F L

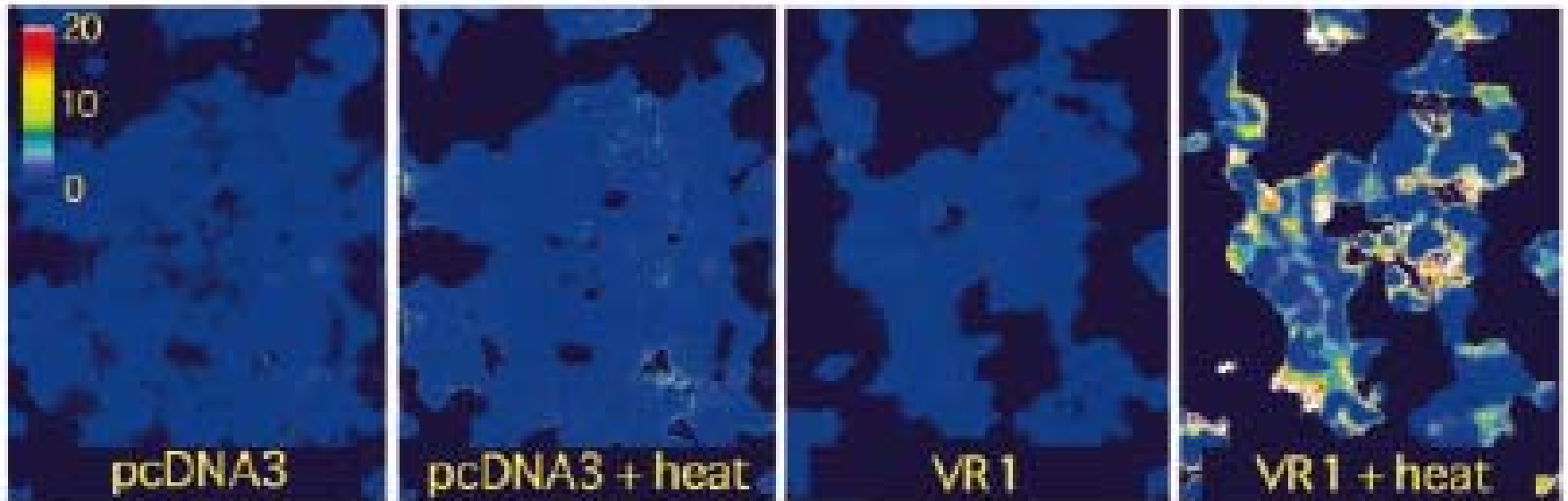
706



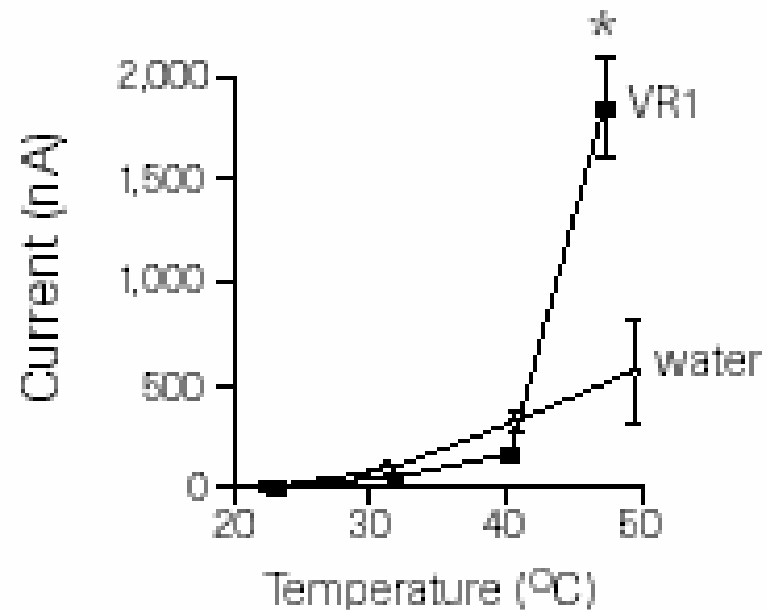
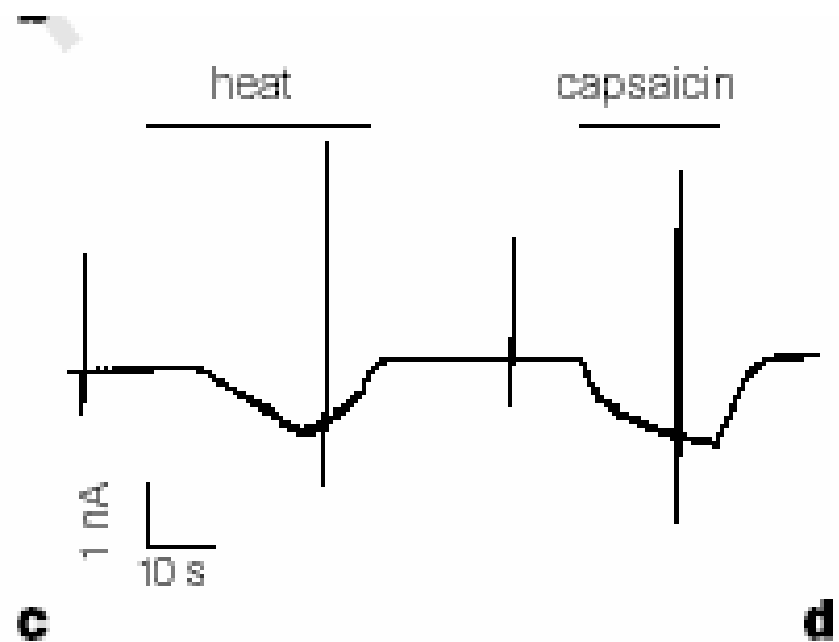


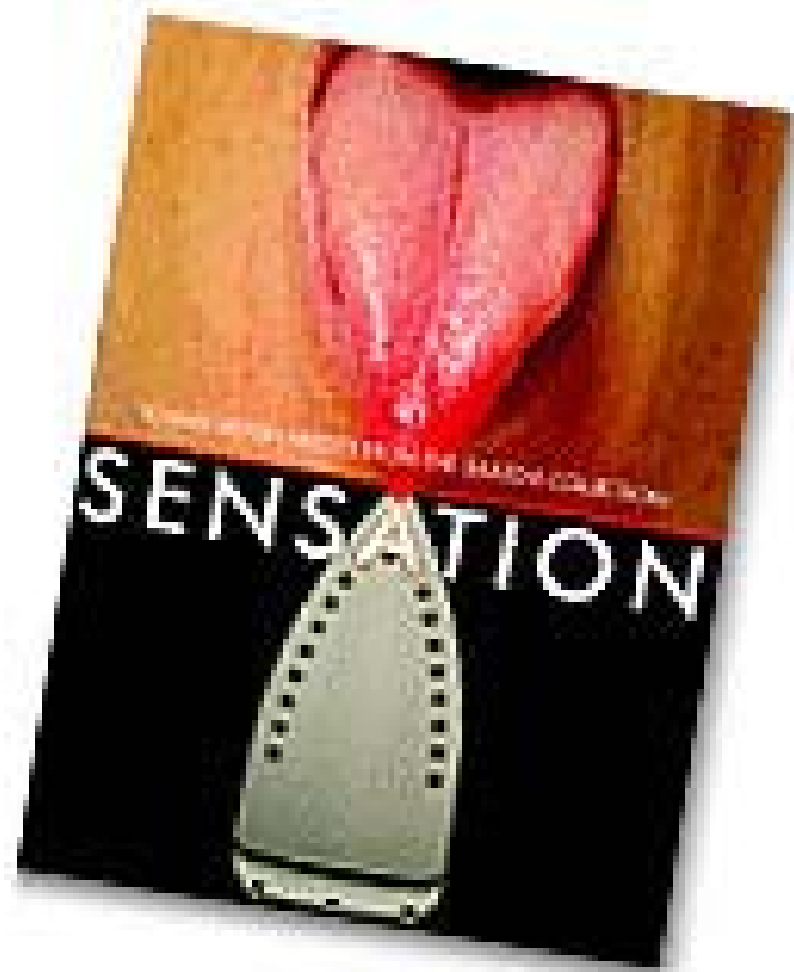


Heat also activates our putative receptor!

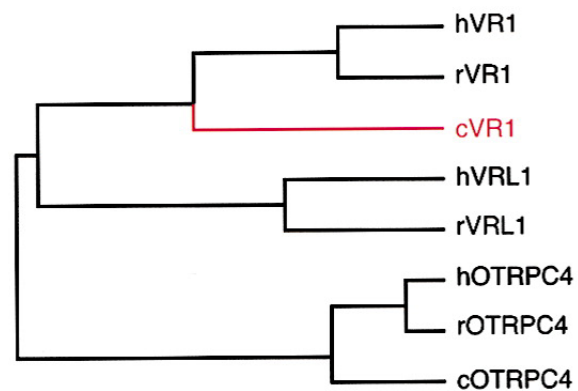
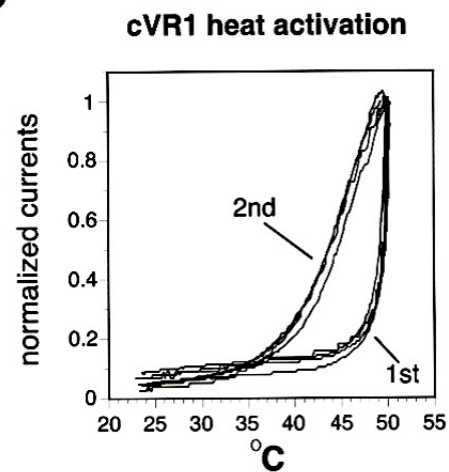
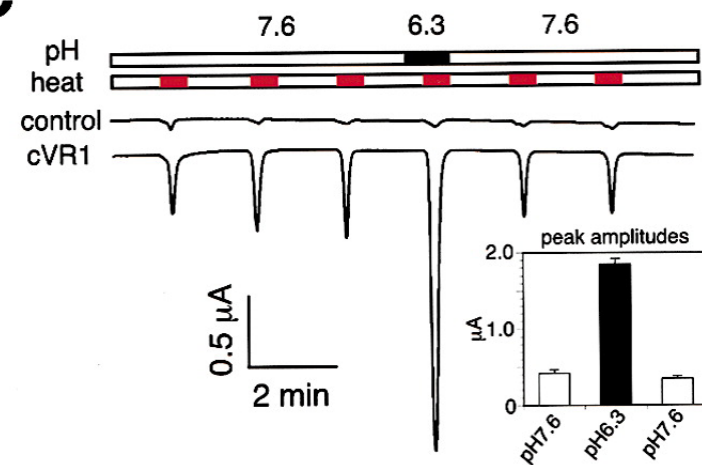
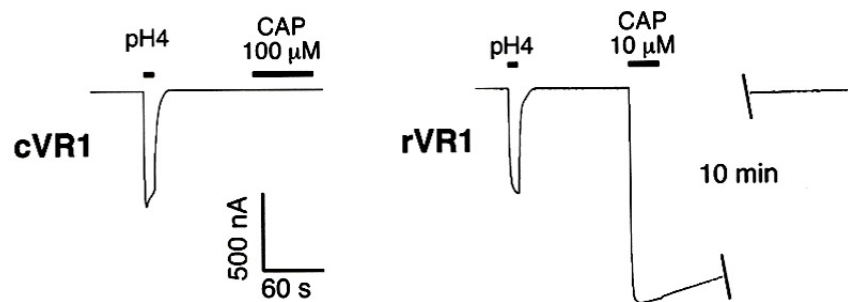
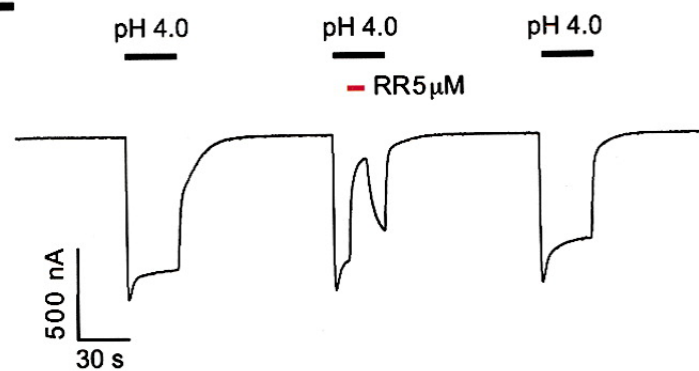


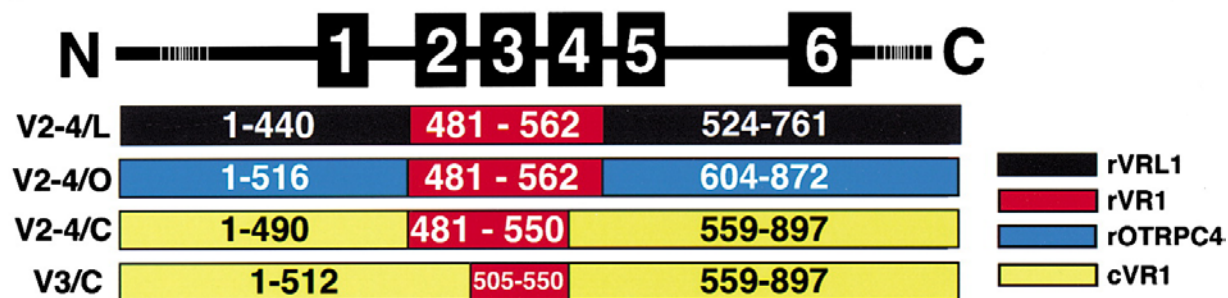
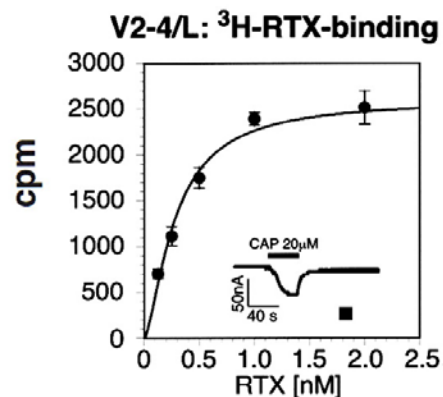
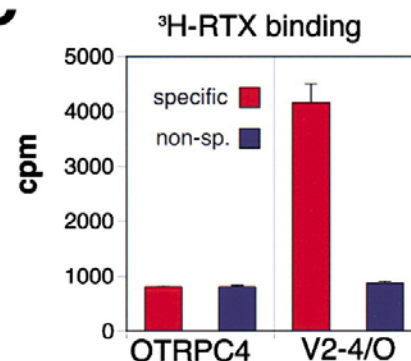
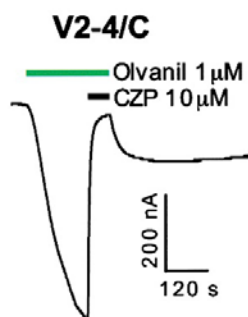
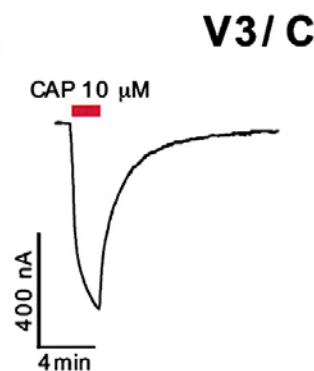
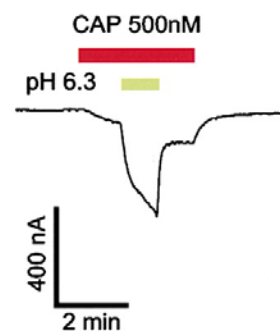
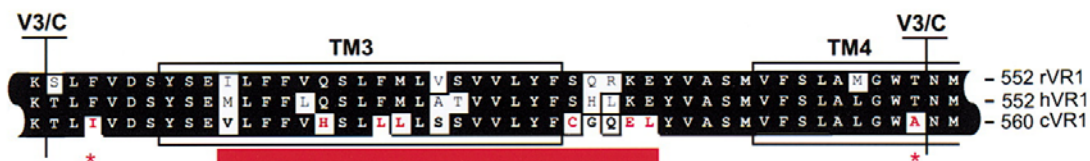
Heat and  
capsaicin are  
interchangeable  
for  
activating the  
VR1 receptor





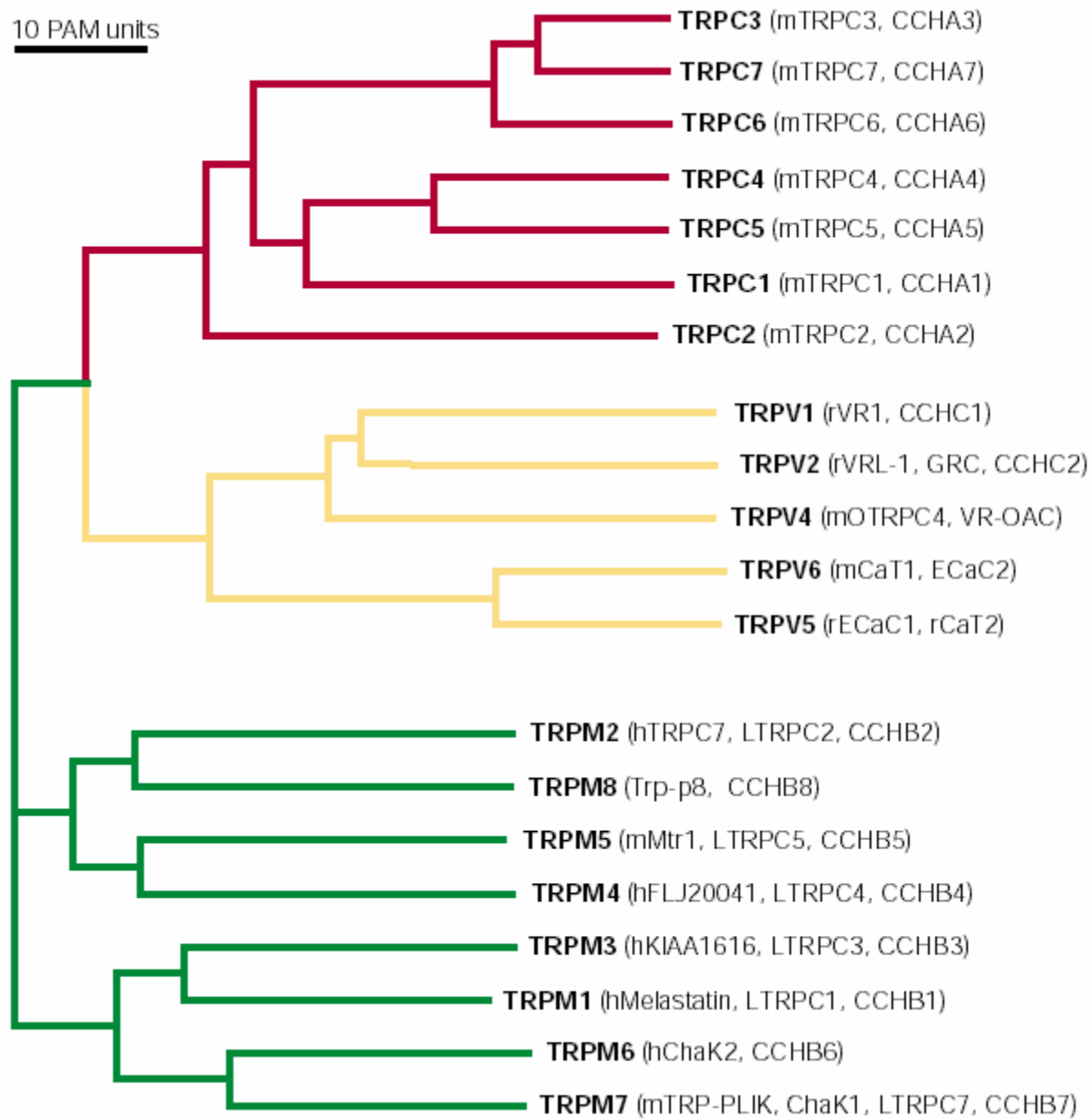


**A****B****C****D****E**

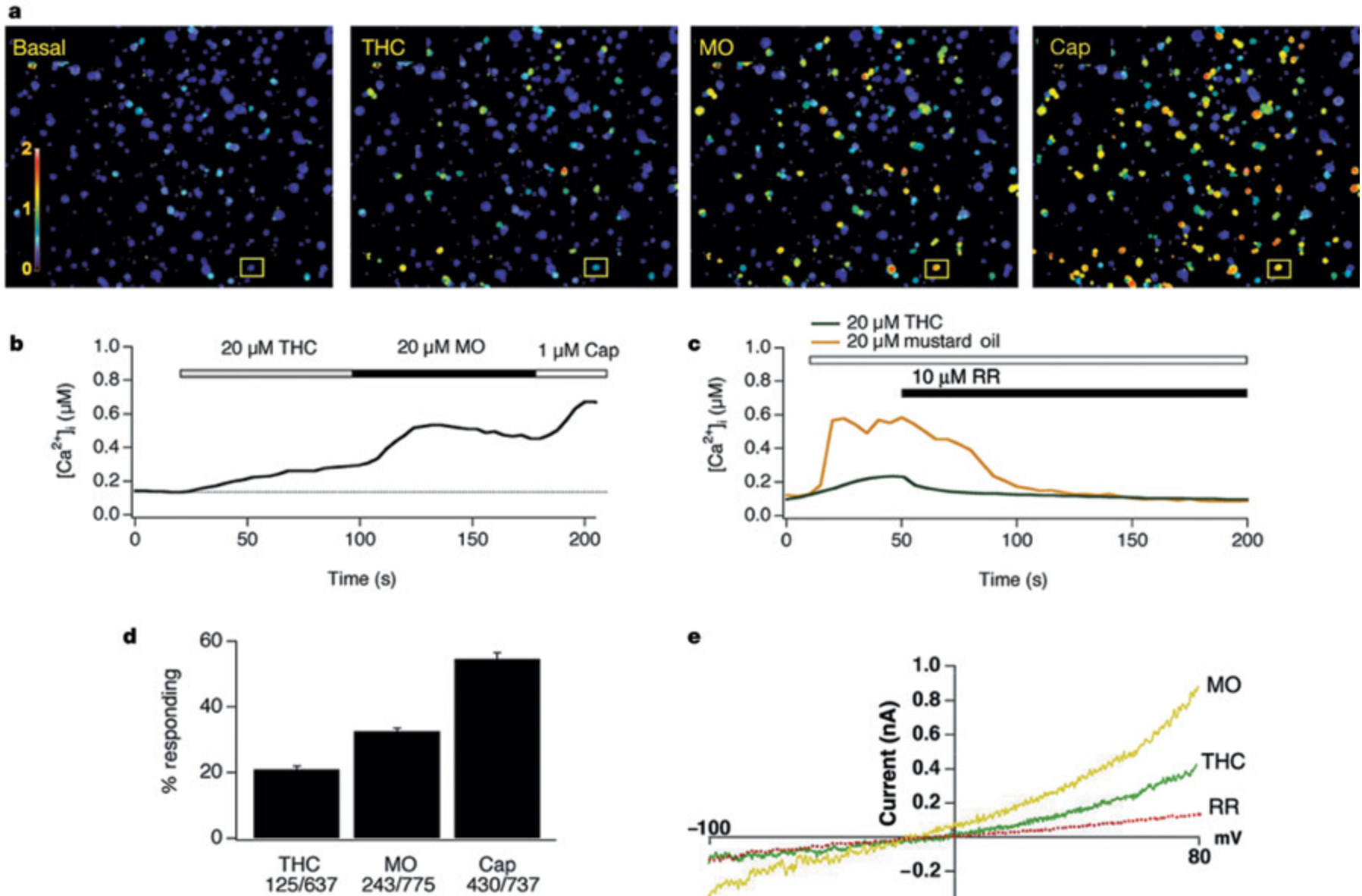
**A****B****C****D****E****V3/C****F**

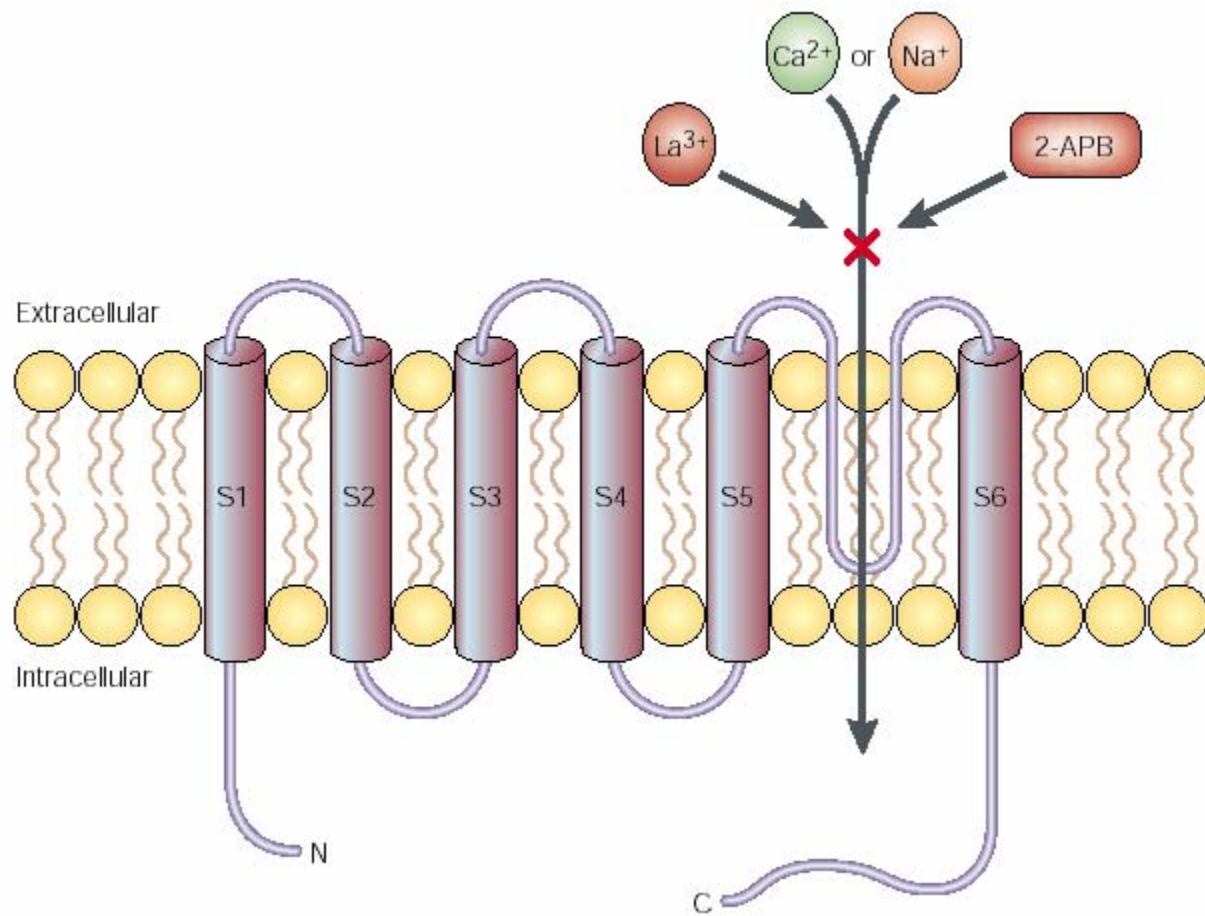


10 PAM units

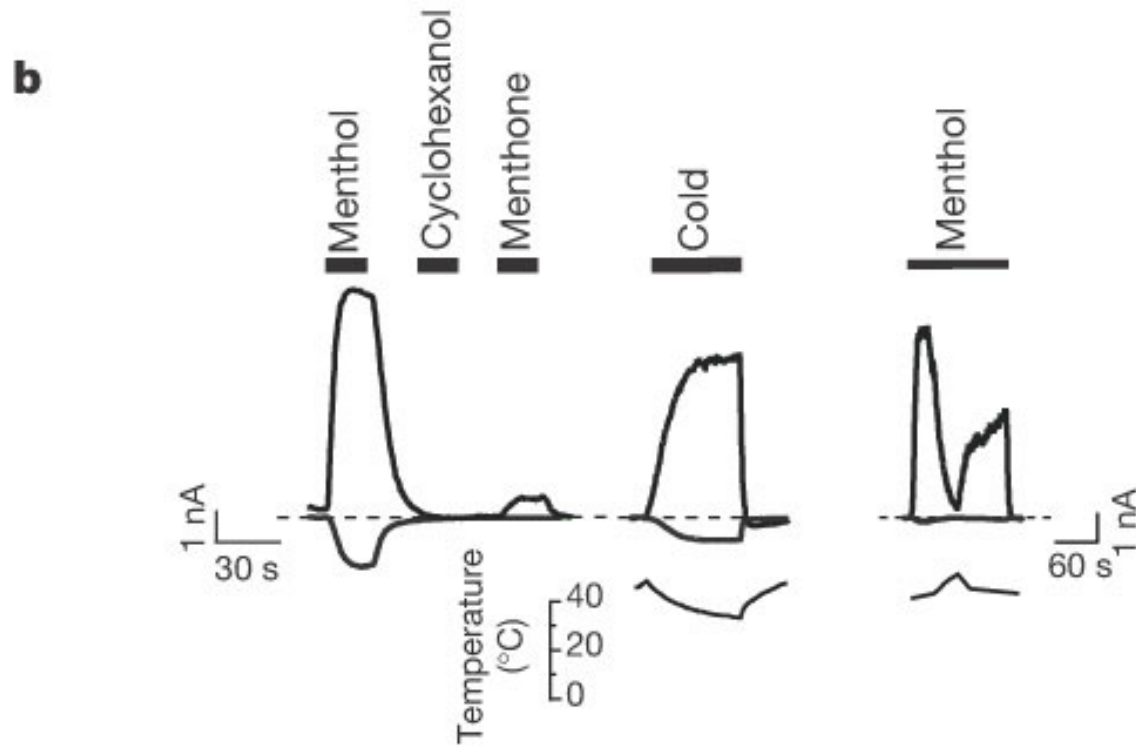
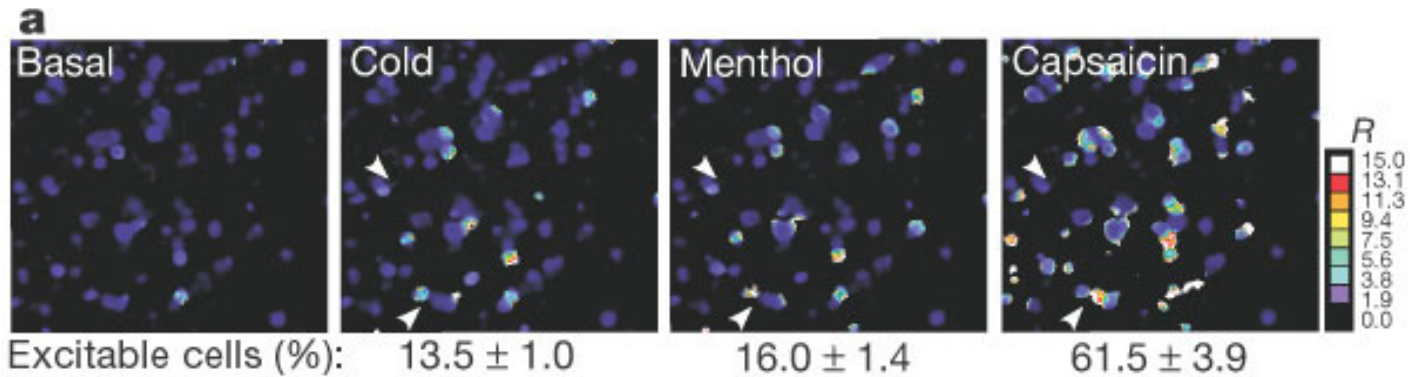


# Trp => Mustard Oil, THC

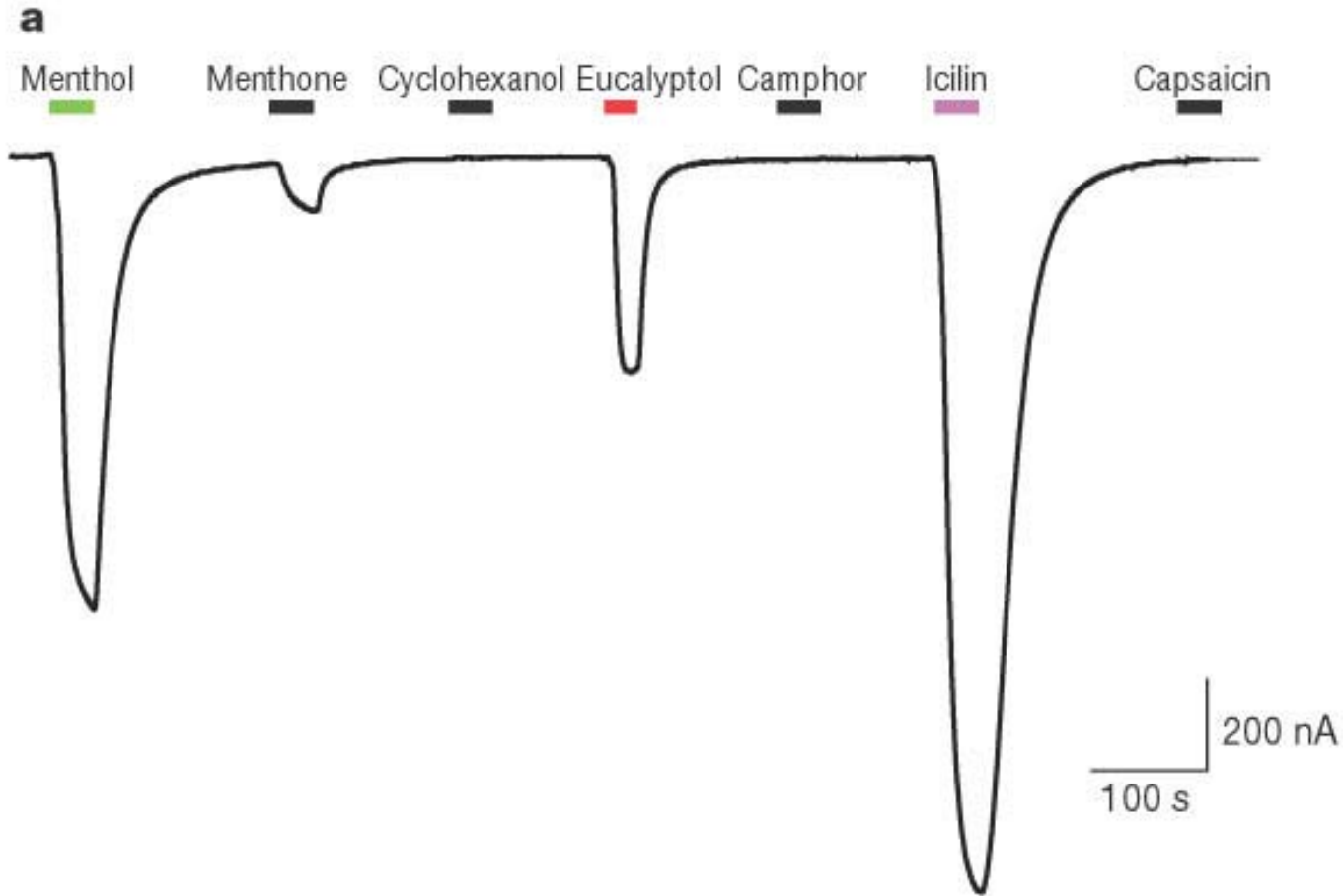




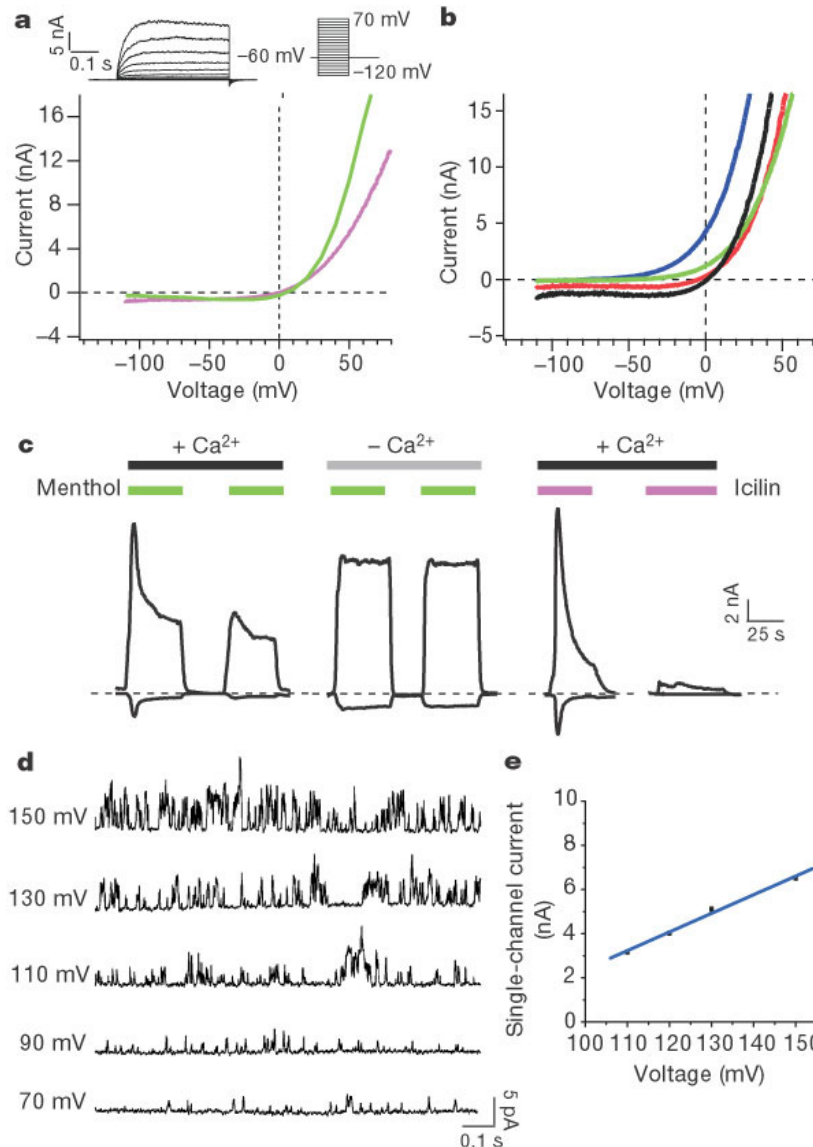
# 1. Calcium Imaging / Functional Cloning



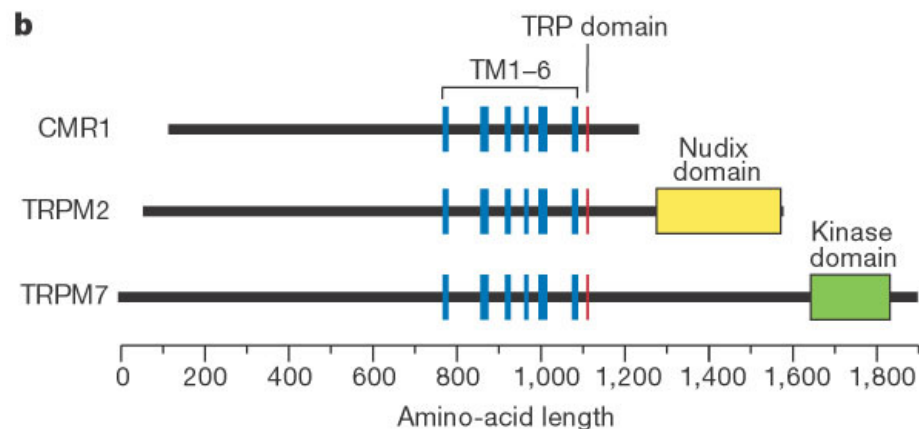
## 2. Recapitulate electrophys. sensitivity



# 3. Electrophys: Currents Same

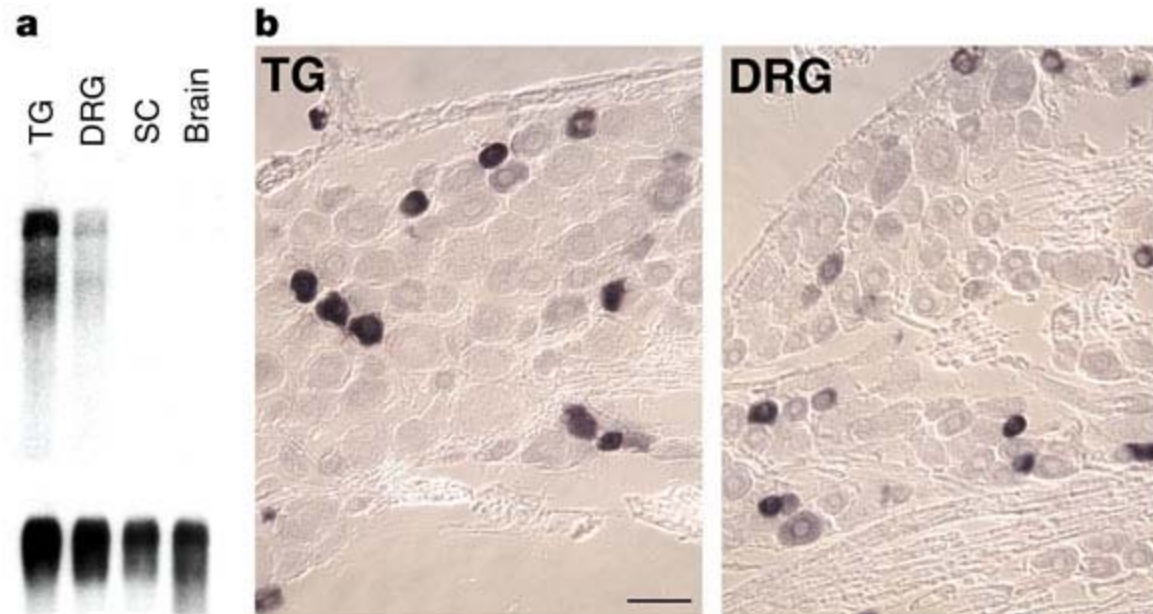


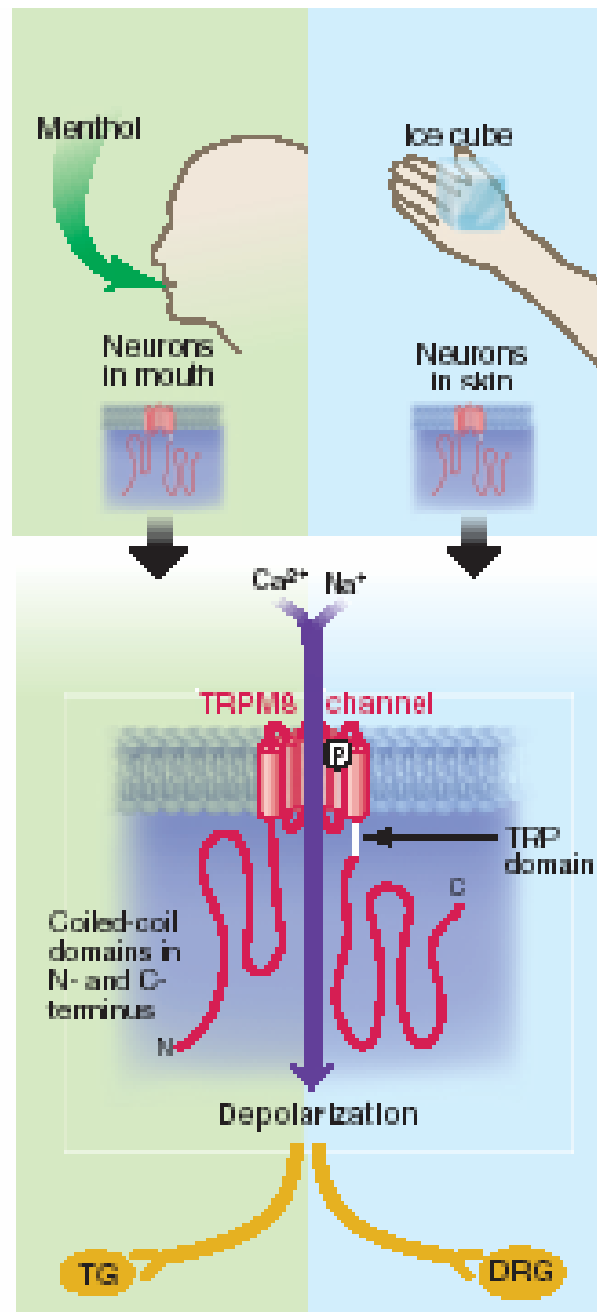
KRECVFFTRDSKAMESICKGQAQSQHIEGTQINQNEKWNKKHTKEFPT 100  
 DAFGDIQFETLGKKGKYLRSLCDTSETLYELLTQHWHLKTPNLVISVTG 150  
 GAKNFALKPRMRKIFSRLLIYIAQSKGAWILTGGTHYGLMKYIGEVVRDNT 200  
 ISRNSEENIVAIGIAAWGMVSNRDTLIRNCDEGHFSAQYIMDDFMRDPL 250  
 YILDNNHTHLLLVLDNGCHGHPTVEAKLRNQLEKYISERTSQDSNYGGKIP 300  
 IVCFAQGGGRETLKAINTSVKSKIPCVVVEGSGQIADVIALVEVEDVLT 350  
 SSMVKEKLVRFPLPRTVSRLPDEEIESWIKWLKEILESPLLTVIKMEEAG 400  
 DEVVSSAISYALYKAFSTNEQDKDNWNGQLKLLLEWNQLDLASDEIFTHD 450  
 RRWESADLQEVMTALIKDRPKFVRLFLENGNLQKFLTNEVLTLEFSTH 500  
 FSTLVYRNLQIAKNSYNDALLTFVWKLVANFRRSFWKEDRSSREDLDVEL 550  
 HDASLTTRHPLQALFIWAILQNKKELSKVIWEQTKGCTLAALGASKLLKT 600  
 LAKVKNDINAAGESEELANEYETRAVELFTECYSSDEDLAEQLLVYSCEA 650  
 WGSNCLELAVEATDQHFIAPQGVQNFSLKQWYGEISRDTKNWKIILCLF 700  
 IIPLVGCGLVSFRKKPIDKHKLLWYYVAFFTSPFVVFSWNVVIFYIAFLL 750  
 LFAYVLLMDPHSVPHTEPILYALVFVLCDEVQRQWYMGVNYFTDLWNV 800  
 MDTLGLFYFIAGIVFRLHSNKKSSLYSGRVIFCLDYIIFTLRLIHIFTVS 850  
 RNLGPKIIMLQRMILIDVFFFLFLFAVWMVAFGVARQGILRQNEQRWRWIF 900  
 RSVIYEPYLAMFGQVPSDVDSTTYDFSHCTFSGNESKPLCVELDEYNLPR 950  
 FPEWITIPLVCIYMLSTNILLVNLVAMFGYTVGIVQENNDQVWKFQRYF 1,000  
 LVQEYCNRLNIPFPFVVFAYFYFYMVVKCKCFKCCCKEKNTESSACCFRNEDN 1,050  
 ETLAWEGVMKENYLVKINTKANDNAEEMRHRFRQLDTKLNLDLKGLLKEIA 1,100  
 NKIK 1,104

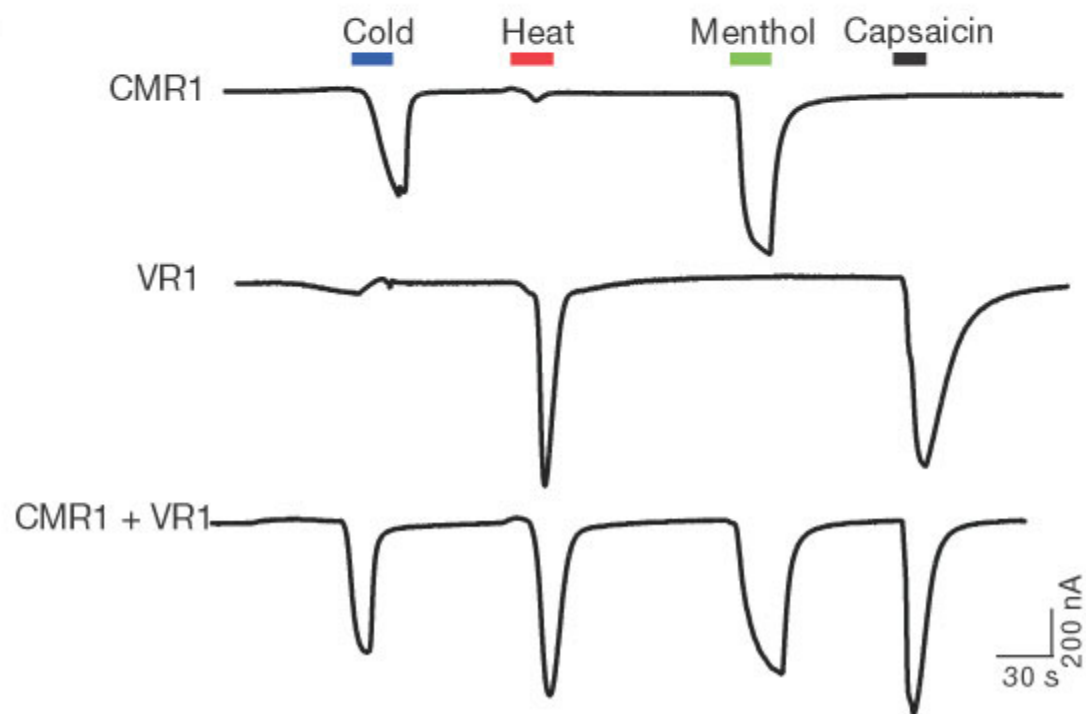
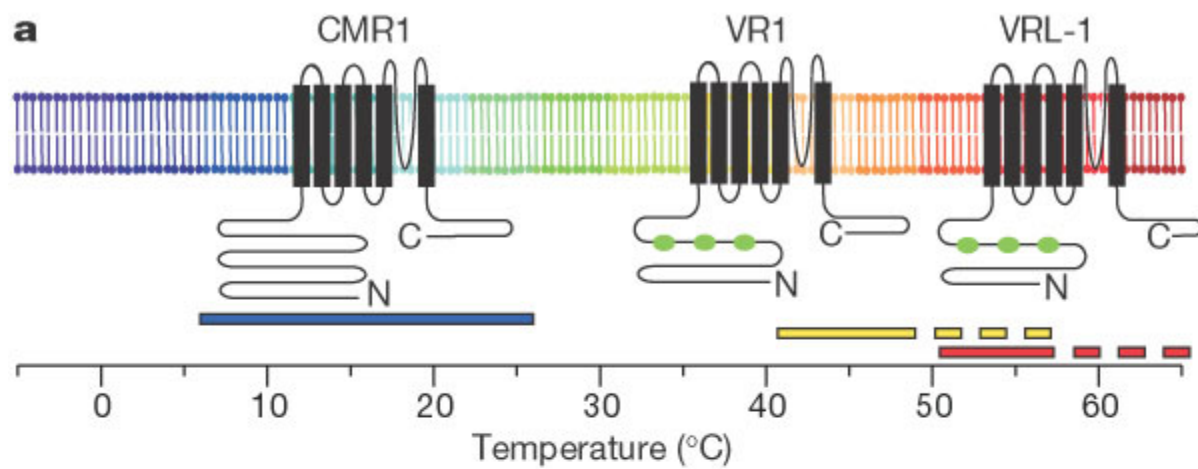




# Right Place, Makes Sense









# PEPPERS

A COOKBOOK

BY ROBERT BERKLEY • PHOTOGRAPHS BY ERIC JACOBSON