

## ***Can the absence of pain make you a hero?***

### ***Do we need pain?***

- *Pain is essential to minimize damage to the organism*
- *Pain leads to behaviour of damage avoidance and promotes tissue repair*

### ***Do we need analgesics?***

**YES!!!!**

## ***What problems are associated with current pain killers?***

**Effectivity?**

**Unwanted effects (side effects) e.g.:**

- *Respiratory suppression*
- *Drowsiness*
- *Itchiness*
- *Nausea/vomiting*
- *Constipation/gastrointestinal problems (e.g. ulcers)*

## ***Can the absence of pain make you a hero?***

nature

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### ARTICLES

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## **An *SCN9A* channelopathy causes congenital inability to experience pain**

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Pain is essential to minimize damage to the organism

Pain leads to behaviour of damage avoidance and promotes tissue repair

# Congenital indifference to pain (CIP)

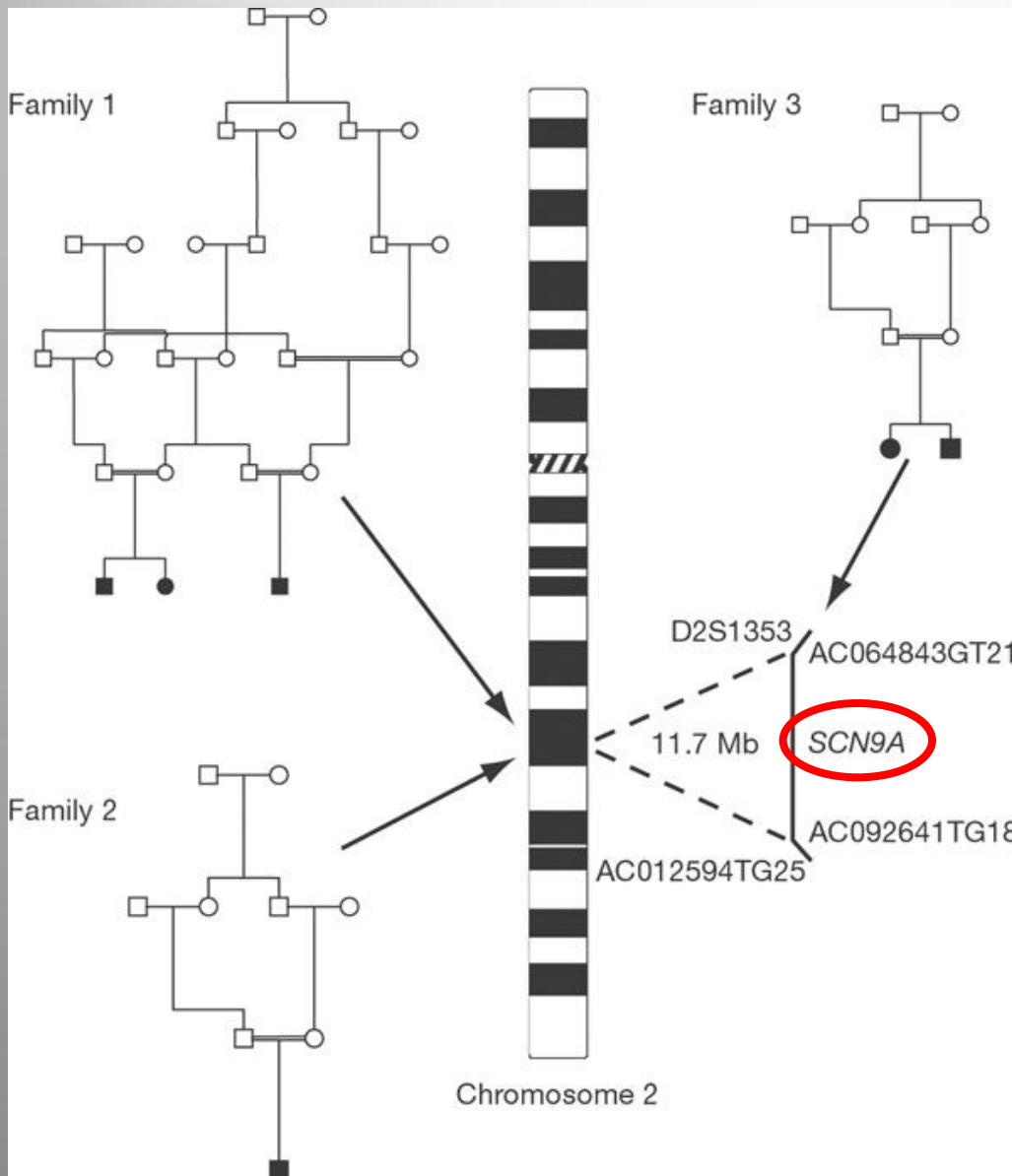
## Loss-of-function mutations in the $Na_v1.7$ gene

Table 1. Clinical features for CIP diagnosis

Clinical feature	CIP-14	CIP-10	CIP-8	CIP-32	CIP-5	CIP-26	CIP-33	CIP-38	CIP-102
Congenital onset and/or presenting in early childhood	Y	Y	Y	Y	Y	Y	Y	Y	Y
Lack of response to pain all over body on pinprick test	Y	Y	Y	Y	Y	Y	Y	Y	Y
Lack of response to visceral pain	Y	Y	Y	Y	Y	Y	Y	Y	Y
Other sensory modalities (tactile, thermal, vibratory) are normal	Y	Y	Y	Y	Y	Y	Y	Y	Y
Normal intelligence	Y	Y	Y	Y	Y	Y	Y	Y	Y
Normal deep tendon reflexes	UK	Y	ND	Y	Y	Y	Y	Y	Y
Normal nerve biopsy (myelinated and unmyelinated fibres)	Y	ND	Y	ND	ND	Y	Y	Y	ND
Normal motor and sensory nerve conduction velocities	Y	UK	UK	Y	Y	Y	Y	UK	Y
Normal autonomic function (e.g. tearing, blood pressure, sweating)	Y	Y	Y	Y	Y	Y	Y	Y	Y
Normal response to intradermal histamine injection	Y	ND	ND	ND	Y	UK	UK	Y	ND
Normal karyotype	ND	Y	Y	ND	ND	UK	UK	ND	UK

UK: unknown  
ND: not tested

In four families affected patients were offspring of known consanguineous mating

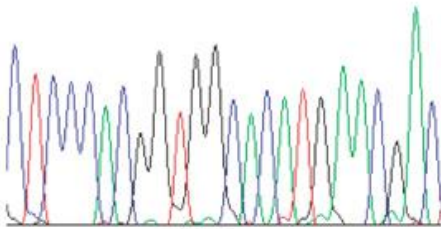


The gene SCN9A encodes for the voltage-gated Na<sup>+</sup> channel Na<sub>v</sub>1.7

Consanguineous family trees!

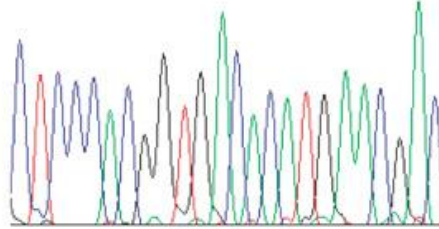
Family 1 mutation

C T C C C A C G G T G G C A C A T G A A C G A C



Wild type

C T C C C A C G G T G A C A C A T G A A C G A C



2691G→A

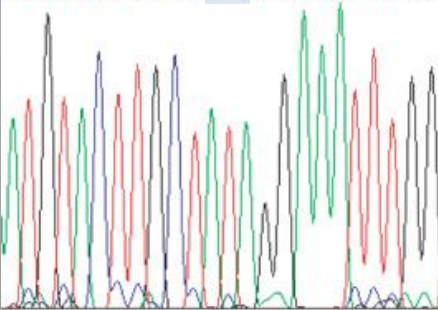
W897X

W=Trp=tryptophane

X=stop codon

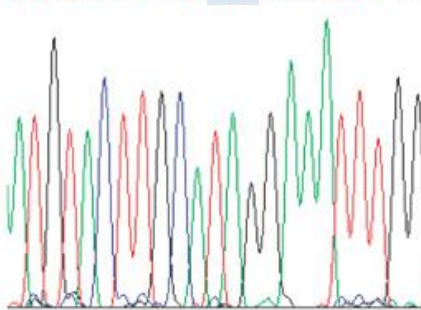
Family 2 mutation

A T G T A C T T G C T A T A G G A A A T T T G G



Wild type

A T G T A C T T G C A T A G G A A A T T T G G



2298delT

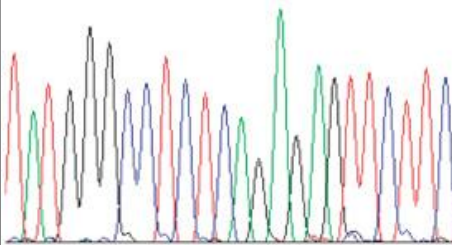
Frameshift I767X

I=Ile=isoleucine

S=Ser=serine

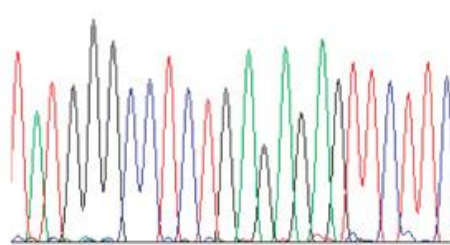
Family 3 mutation

T A T G G G C C T C T C A G A G A G T T C T T C



Wild type

T A T G G G C C T C T G A G A G A G T T C T T C

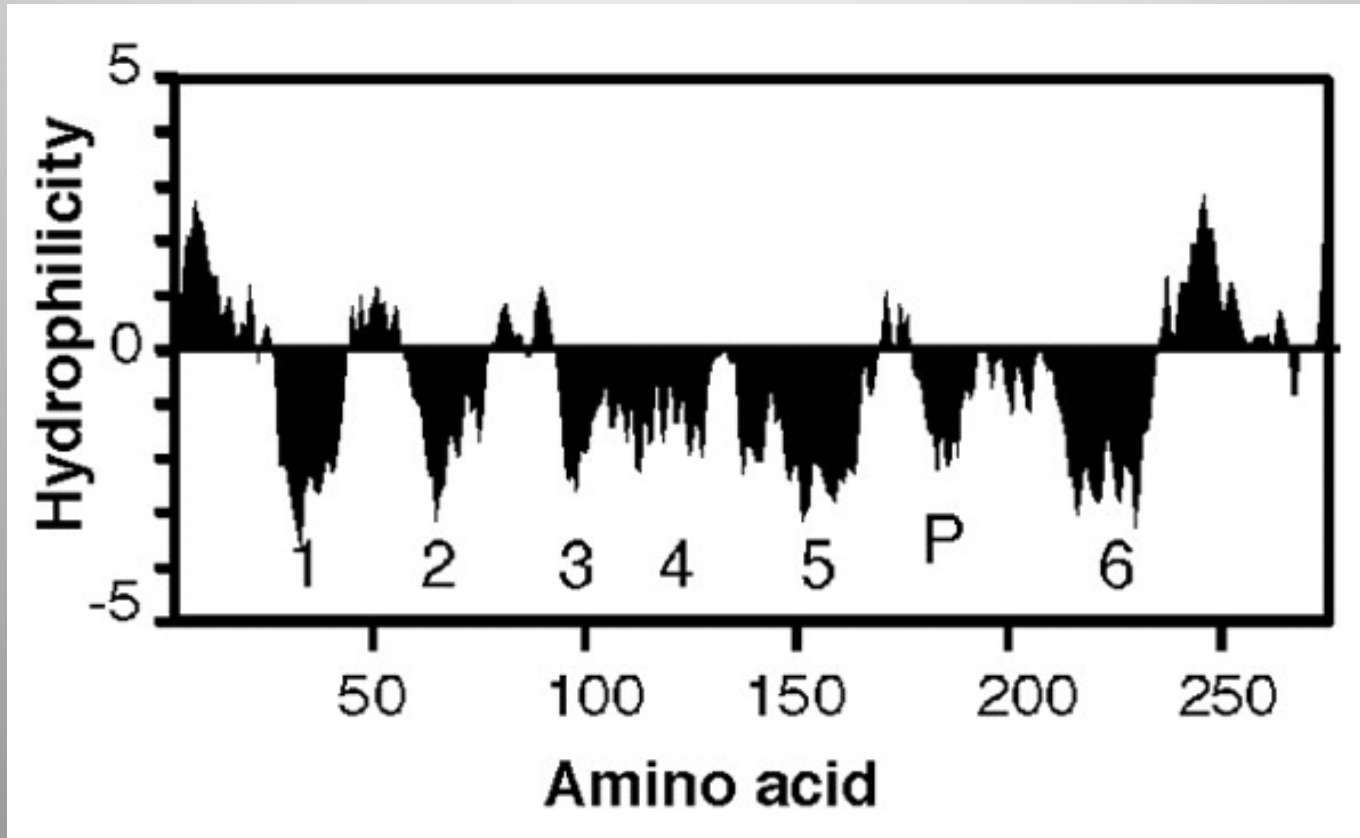


1376C→G

S459X

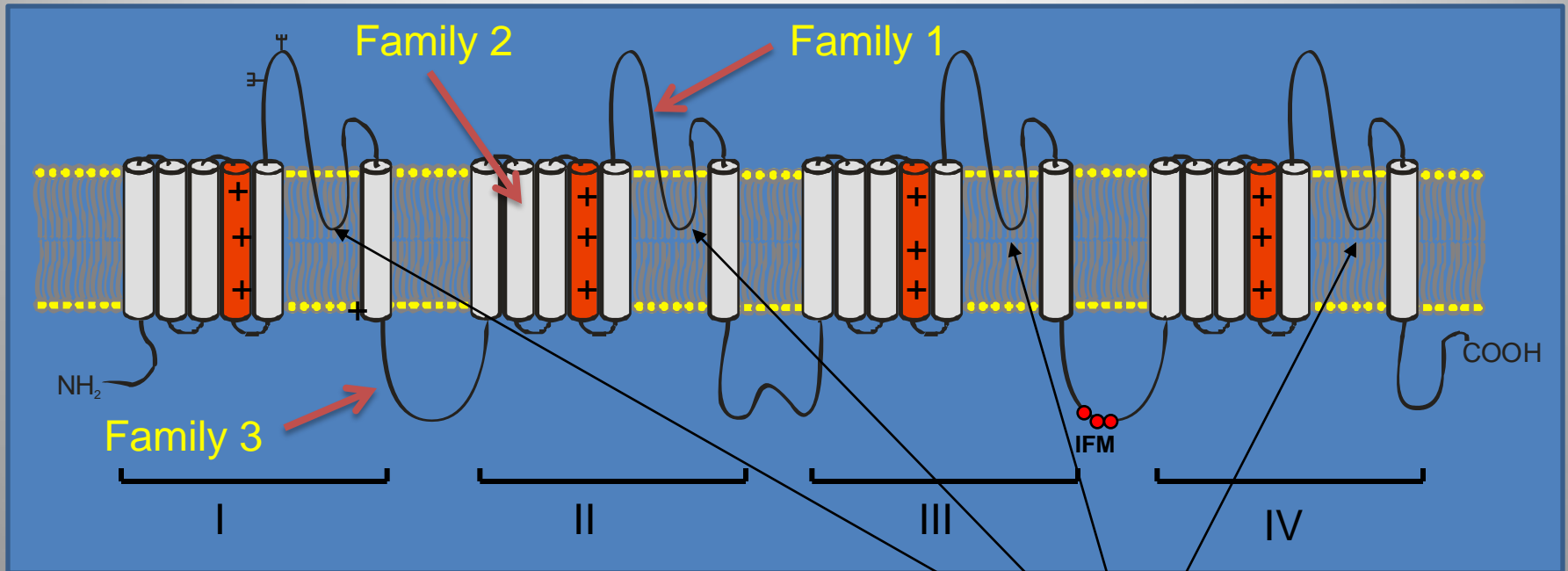
**Affected individuals are homozygous for mutation!**

A hydropathy plot allows to predict transmembrane segments of a membrane protein



Voltage-gated K channel

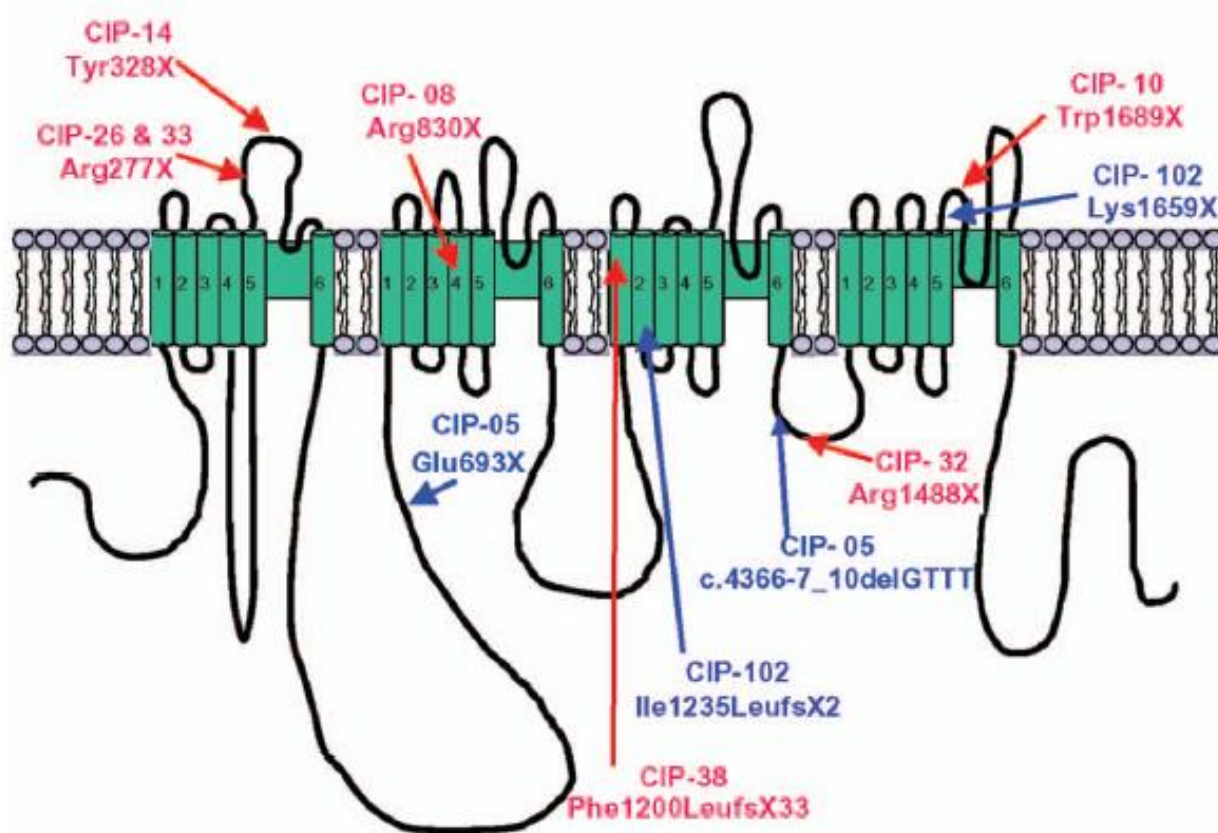
# Voltage-gated Na<sup>+</sup> channel topology ( $\alpha$ -subunit)



- Approx 2000 amino acid residues
- 4 repeats (I-IV)
- Extracellular glycosylation sites
- TM4: voltage sensor
- inactivation loop with IFM sequence

Selectivity filter





	Family	Exon	Allele		DNA sequence variation	Genotype	Description
			WT	MT			
<b>Homozygote</b> <span style="color: red;">—</span>	CIP-26	E6	C	T	c.829C>T	T, T	Nonsense mutation p.Arg277X
	CIP-33	E6	C	T	c.829C>T	T, T	Nonsense mutation p.Arg277X
	CIP-14	E8	C	A	c.984C>A	A, A	Nonsense mutation p.Tyr328X
	CIP-08	E15	C	T	c.2488C>T	T, T	Nonsense mutation p.Arg830X
	CIP-38	E19	A	-	c.3600delT	del T, del T	Frameshift causing p.Phe1200LeufsX33
	CIP-32	E24	C	T	c.4462C>T	T, T	Nonsense mutation p.Arg1488X
	CIP-10	E26	G	A	c.5067G>A	A, A	Nonsense mutation p.Trp1689X
<b>Compound Heterozygote</b> <span style="color: blue;">—</span>	CIP-05	E13	-	T	c.2076_2077insT	-, insT	Frameshift causing immediate STOP p.Glu693X
		Intron 23-24	-	-	c.4366-7_10delGTTT	-, del 4 bp	Splice-junction mutation
	CIP-102	E19	-	-	c.3703_3713del	-, del 11 bp	Frameshift causing p.Ile1235LeufsX2
	E26	A	T	c.4975A>T	A, T	Nonsense mutation p.Lys1659X.	

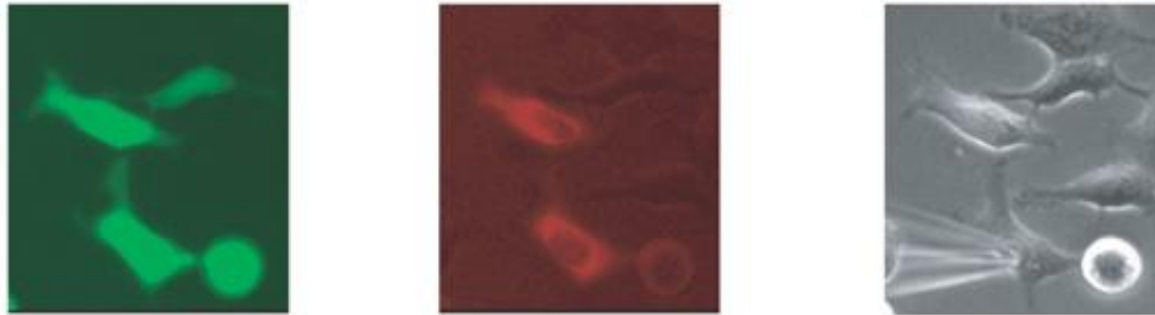


# Mutant analysis in heterologous expression system

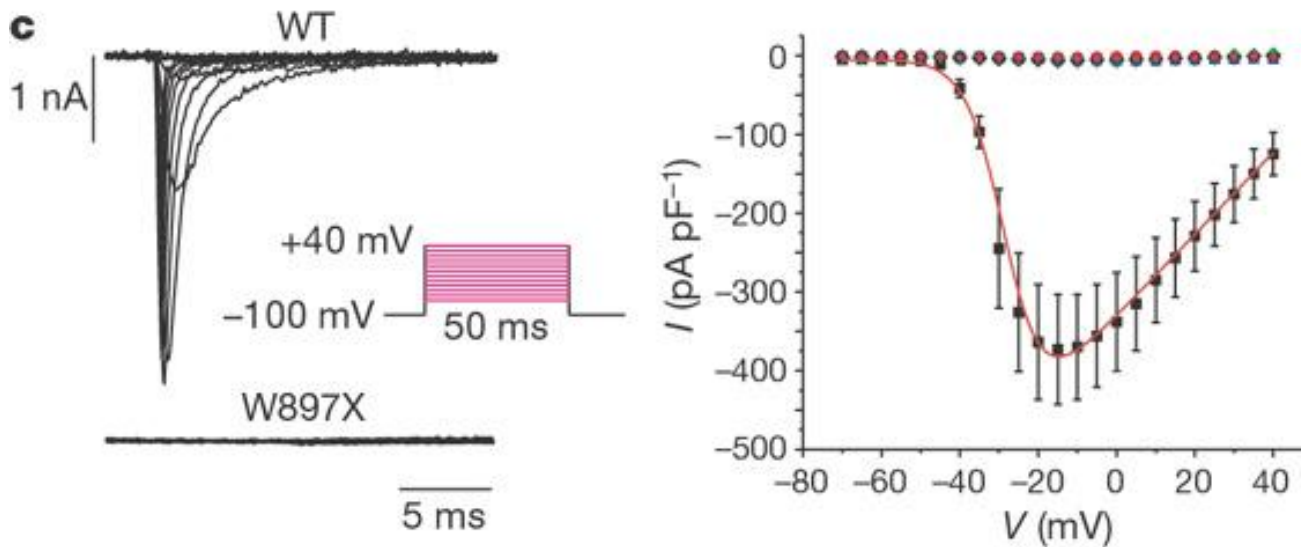
**a**



**b**



**c**



**Loss-of-Function mutation  
causes loss of pain sensation**

What does a Gain-of-Function  
mutation do?

**Table**  $\text{Na}_v1.7$  channelopathies

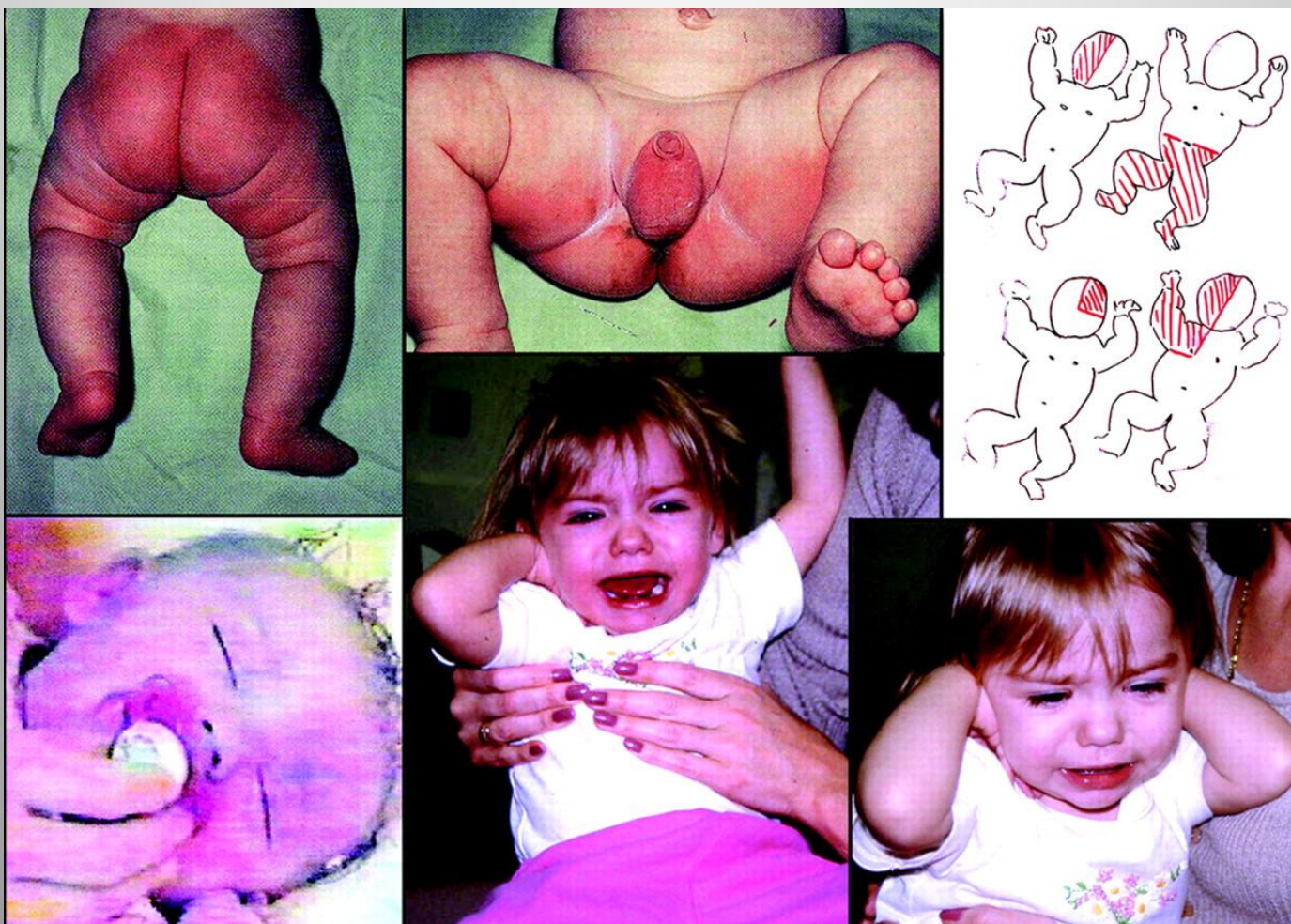
Disorder	Inheritance	Mutation	Clinical phenotype
Inherited erythromelalgia	Autosomal dominant	Missense mutations	Attacks of burning pain and redness in distal extremities; triggered by mild warmth and exercise
Paroxysmal extreme pain disorder	Autosomal dominant	Missense mutations	Episodic perirectal, ocular, and jaw pain accompanied by flushing and other autonomic abnormalities
Channelopathy-associated insensitivity to pain	Autosomal recessive	Nonsense mutations	Inability to sense pain

Waxman, S. G. *Neurology* 2007;69:505-507

# NEUROLOGY

**Paroxysmal extreme pain disorder (previously familial rectal pain syndrome)**  
C. R. Fertleman, C. D. Ferrie, J. Aicardi, N.A.F. Bednarek, O. Eeg-Olofsson, F. V. Elmslie, D. A. Griesemer, F. Goutières, M. Kirkpatrick, I. N.O. Malmros, M. Pollitzer, M. Rossiter, E. Roulet-Perez, R. Schubert, V. V. Smith, H. Testard, V. Wong and J. B.P. Stephenson

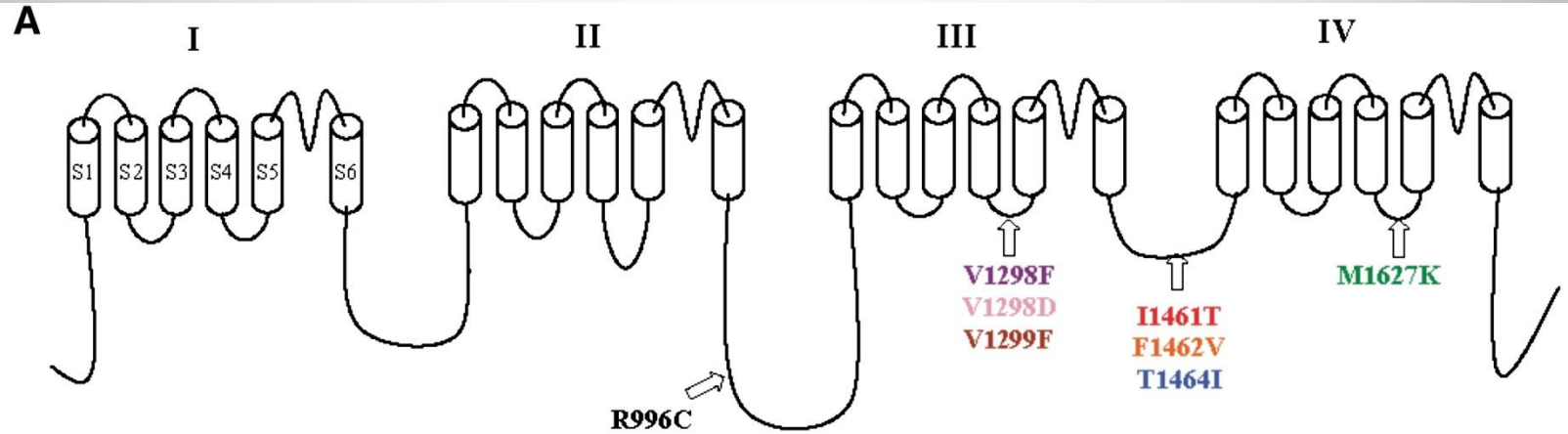
*Neurology* 2007;69:586-595  
DOI: 10.1212/01.wnl.0000268065.16865.5f



Fertleman, C. R. et al. Neurology 2007;69:586-595



# SCN9A mutations causing paroxysmal extreme pain disorder (PEPD)



**B**

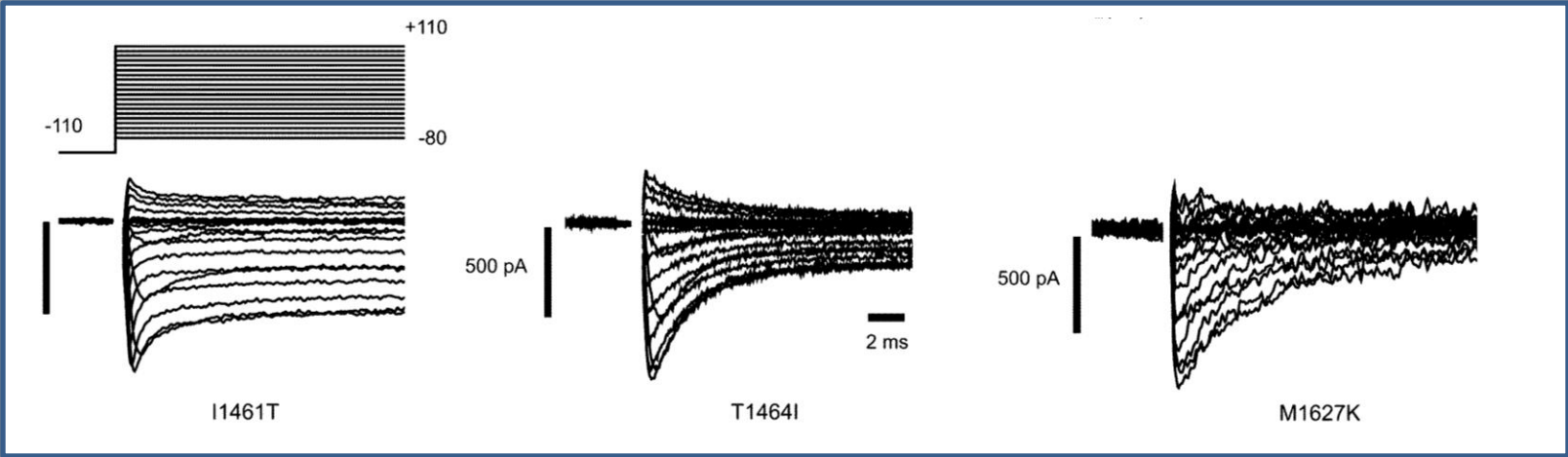
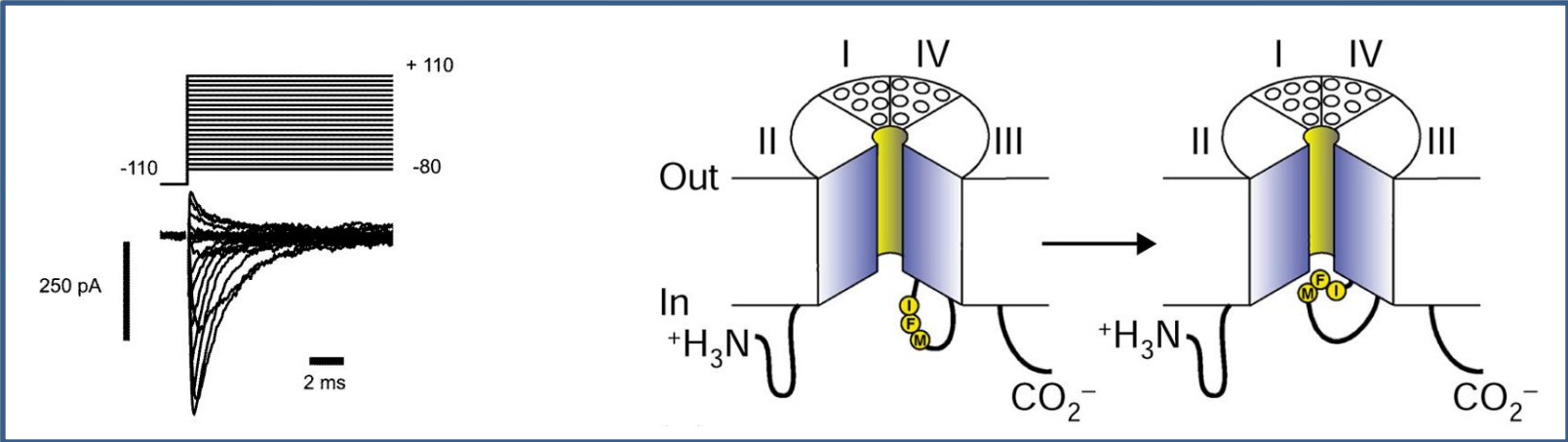
	i	ii	iii	iv
hNa <sub>v</sub> 1.7	NYVKQTLREFILKAF	SRFEGMRVVVNALIGA	LGG-QDIFMTEEQKK	RTLLFALMMSLPALFN
hNa <sub>v</sub> 1.1	AYVKRKIYEFIQQSF	SRFEGMRVVVNALLGA	FGG-QDIFMTEEQKK	RTLLFALMMSLPALFN
hNa <sub>v</sub> 1.2	DFVKRKIREFIQKAF	SRFEGMRVVVNALLGA	FGG-QDIFMTEEQKK	RTLLFALMMSLPALFN
hNa <sub>v</sub> 1.3	DYVKNKMRECFQKAF	SRFEGMRVVVNALVGA	FGG-QDIFMTEEQKK	RTLLFALMMSLPALFN
hNa <sub>v</sub> 1.4	GFAKAFLLGLLHGKI	SRFEGMRVVVNALLGA	LGG-KDIFMTEEQKK	RTLLFALMMSLPALFN
hNa <sub>v</sub> 1.5	RFVKRTTWD FCCGLL	SRFEGMRVVVNALVGA	LGG-QDIFMTEEQKK	RTLLFALMMSLPALFN
hNa <sub>v</sub> 1.6	AWTKLKVHAFMQAHF	SRFEGMRVVVNALVGA	FGG-QDIFMTEEQKK	RTLLFALMMSLPALFN
hNa <sub>v</sub> 1.8	VFGHRTKQALCSFFS	SRFEGMRVVVDALVGA	LGG-QDIFMTEEQKK	RTLLFALMMSLPALFN
hNa <sub>v</sub> 1.9	CFVRHTLEHFCHKWC	SQFEGMKVVVNALIGA	LGG-QDIFMTEEQKK	RTLLFALMMSLPALFN
mNa <sub>v</sub> 1.7	RFVKRTTWD FCCGLL	SRFEGMRVVVNALVGA	LGG-QDIFMTEEQKK	RTLLFALMMSLPALFN
rNa <sub>v</sub> 1.7	NYVKQTLREFILKSF	SRFEGMRVVVNALIGA	LGG-QDIFMTEEQKK	RTLLFALMMSLPALFN
DmNa <sub>v</sub> 2	SWVKRNIADCFKLIR	SRMQGMRVVVNALVQA	AGGSLEMFMTEDQKK	RTLLFALAMSLPALFN
CcNa <sub>v</sub> 1	DWTKRKATTKSQEEQ	SRFDGMKVVVNSLVHS	YEDGVGIFLTPGORN	ROLLETTIVKSAPALLN

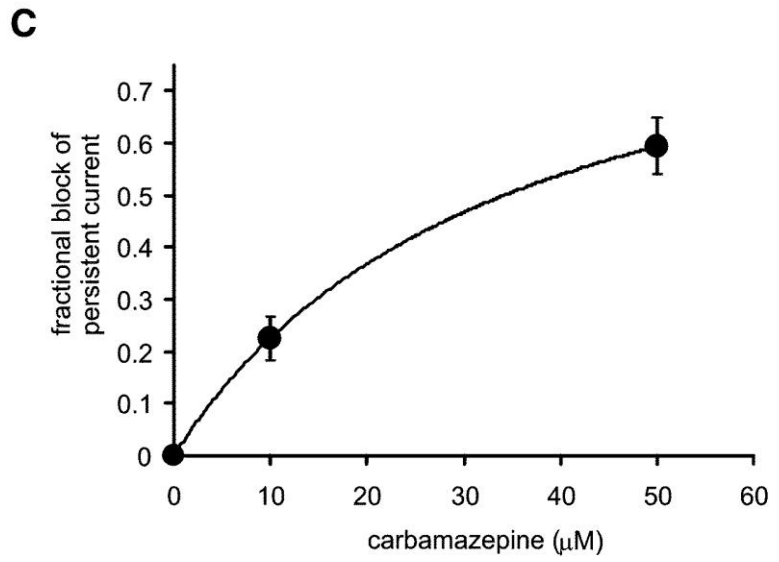
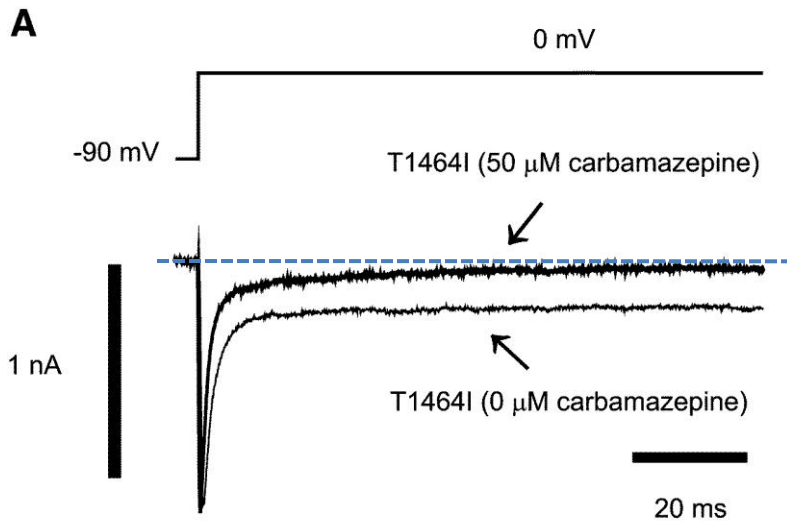
Conserved residues are highlighted in color: red (K, R, Q, E, D), green (S, F, G, M, R, V, V, N, A, L, I, G, A), blue (L, F, G, G, Q, D, I, F, M, T, E, E, Q, K, K), and orange (G, F, A, K, A, F, L, L, G, L, L, H, G, K, I, C, F, V, R, H, T, L, E, H, F, C, H, K, W, C, S, W, V, K, R, N, I, A, D, C, F, K, L, I, R, D, W, T, K, R, K, A, T, T, K, S, Q, E, E, Q).

Conserved motifs are indicated by triangles below the sequences:

- Red triangle under 'R' in hNa<sub>v</sub>1.7 (i)
- Red triangle under 'R' in hNa<sub>v</sub>1.7 (ii)
- Red triangle under 'R' in hNa<sub>v</sub>1.7 (iii)
- Blue triangle under 'R' in hNa<sub>v</sub>1.7 (iii)
- Green triangle under 'R' in hNa<sub>v</sub>1.7 (iv)

# SCN9A mutations causing PEPD affect inactivation





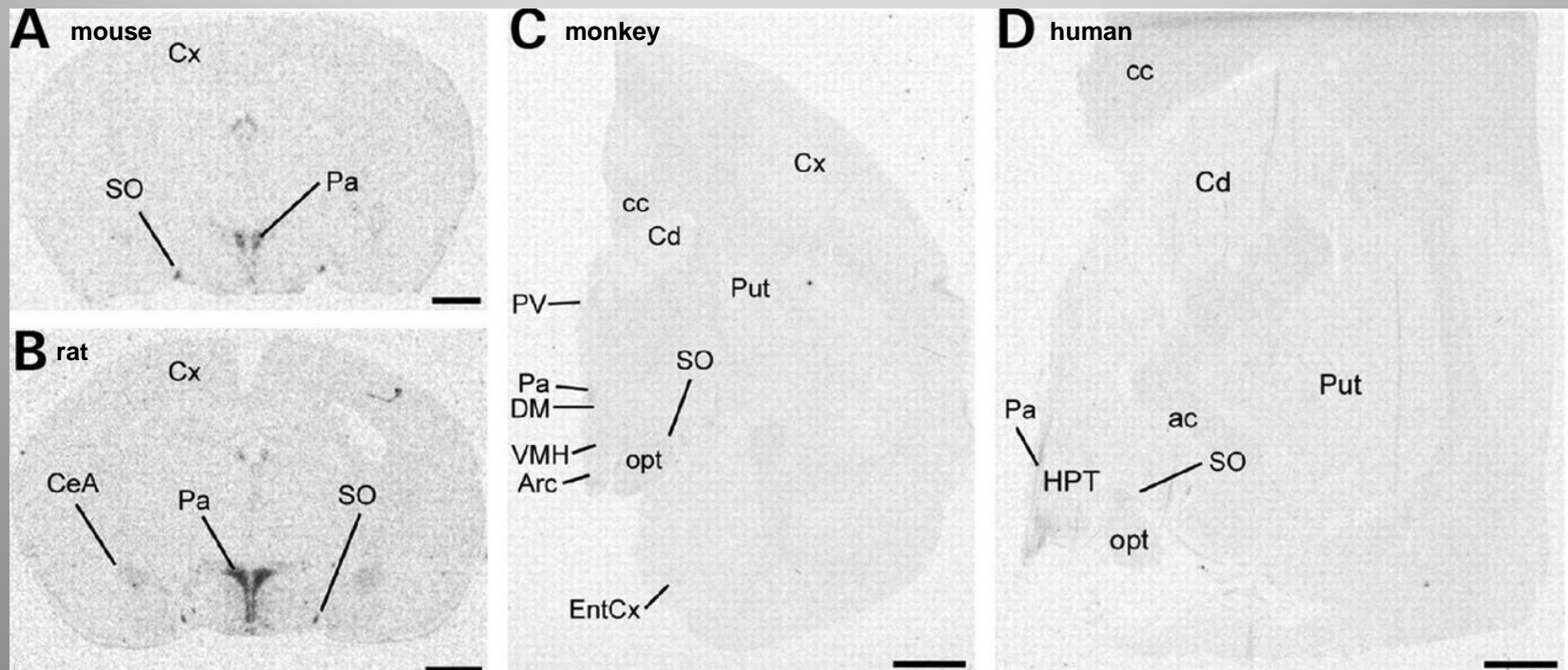
**The anti-epileptic drug carbamazepine blocks the persistent current of the PEPD mutation T1461I**



# Problems with animal models of SCNA9A loss of function

A global knockout in mice is lethal (animals do not feed)

- In rodents, but not primates, prominent *in situ* labelling in hypothalamus, pituitary and adrenal glands



**Table**  $\text{Na}_v1.7$  channelopathies

Disorder	Inheritance	Mutation	Effects on channel
Inherited erythromelalgia	Autosomal dominant	Missense mutations	Lower threshold for activation; slow deactivation; enhanced response to subthreshold stimuli
Paroxysmal extreme pain disorder	Autosomal dominant	Missense mutations	Impaired inactivation; enhanced persistent current
Channelopathy-associated insensitivity to pain	Autosomal recessive	Nonsense mutations	Loss of function of $\text{Na}_v1.7$

Now we know that SCN9A is essential for pain perception in humans.

So what!

What benefit do you see in the information gained from these studies?

## Further Reading

### Original Articles and Reviews

Cox et al. (2006) An SCN9A channelopathy causes congenital inability to experience pain. *Nature*. 444:894-8.

Goldberg et al. (2007) Loss-of-function mutations in the Nav1.7 gene underlie congenital indifference to pain in multiple human populations. *Clin Genet*. 71:311-9.

Ahmad et al. (2007) A stop codon mutation in SCN9A causes lack of pain sensation. *Hum Mol Genet*. 16:2114-21.

Waxman SG. (2007) Nav1.7, its mutations, and the syndromes that they cause. *Neurology*. 69:505-7.

Fertleman et al. (2007) Paroxysmal extreme pain disorder (previously familial rectal pain syndrome). *Neurology*. 69:586-95.

Fertleman et al. (2006) SCN9A mutations in paroxysmal extreme pain disorder: allelic variants underlie distinct channel defects and phenotypes. *Neuron* 52:767-774.

Jurkat-Rott, K. & Lehmann-Horn, F. (2005). Muscle channelopathies and critical points in functional and genetic studies. *The Journal of Clinical Investigation* 115:2000.

### Textbooks

Human Molecular Genetics 2. Strachan & Read. BIOS Scientific Publishers Ltd. Oxford

Ion Channels and Disease. Ashcroft, F.M. 2000. Academic Press, London