

FIGURE 1

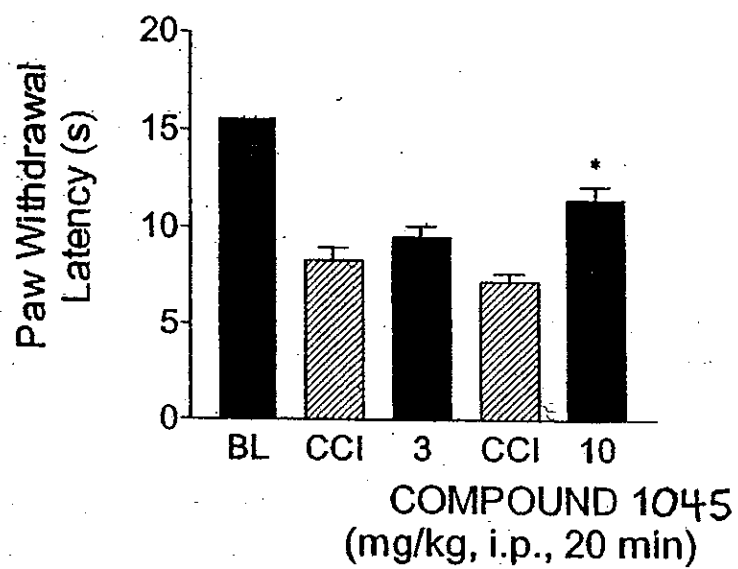


FIGURE 2

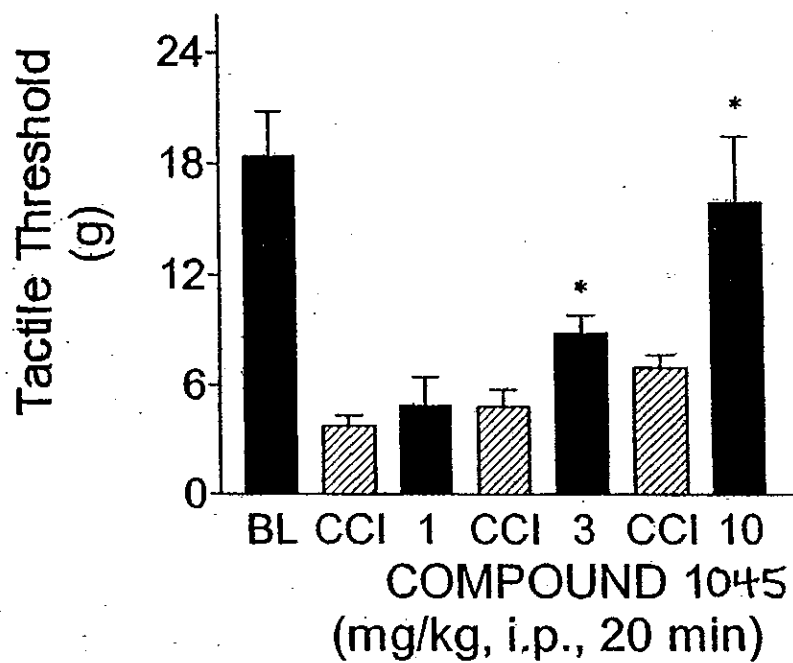


FIGURE 3

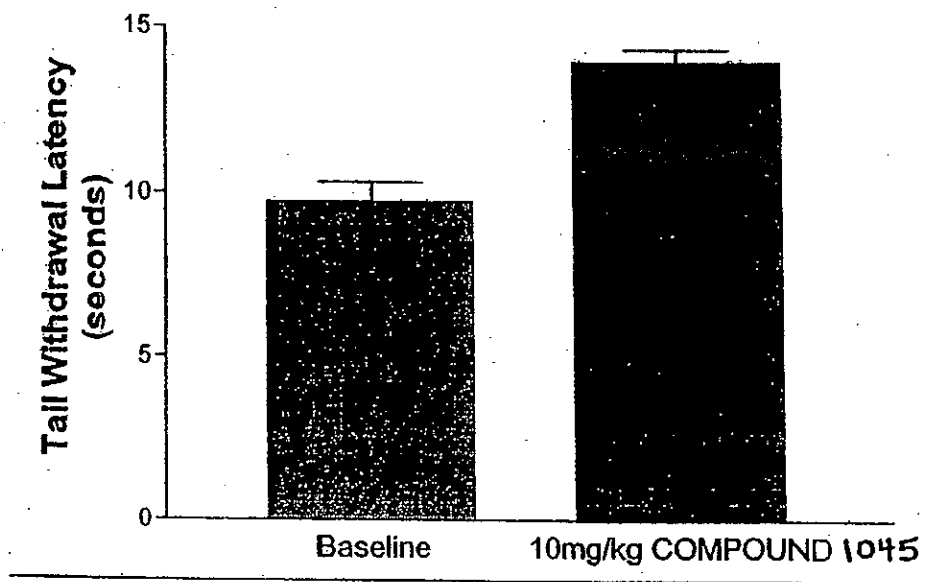


FIGURE 4

**Selective FF2 Receptor Agonists Attenuate
Phase II of Formalin-Induced Flinching in M-SD Rats**

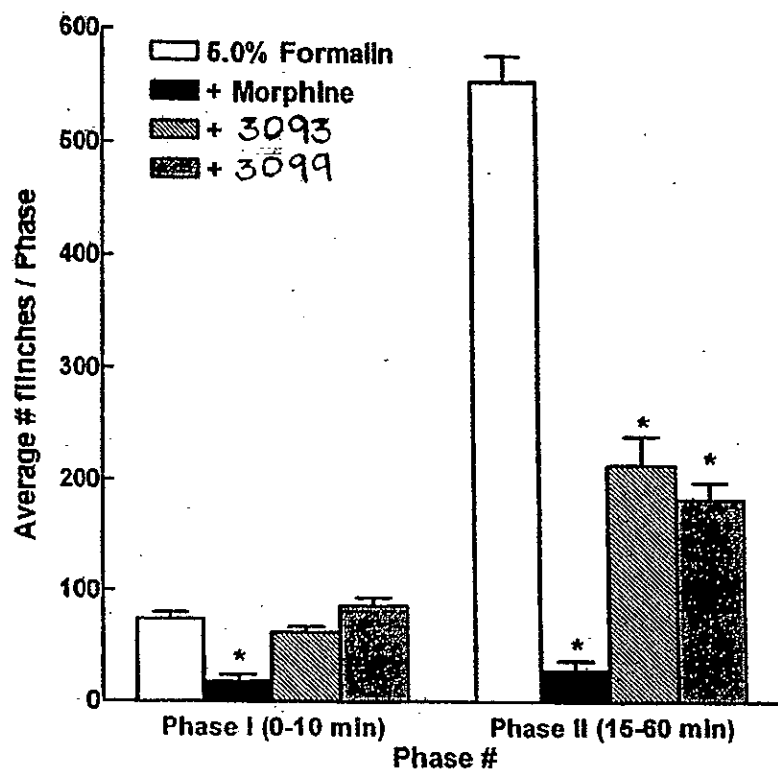


FIGURE 5

**Selective FF2 Receptor Agonists Produce a Dose-dependent
Reversal of Carrageenan-induced Thermal Hyperalgesia
in M-SD Rats**

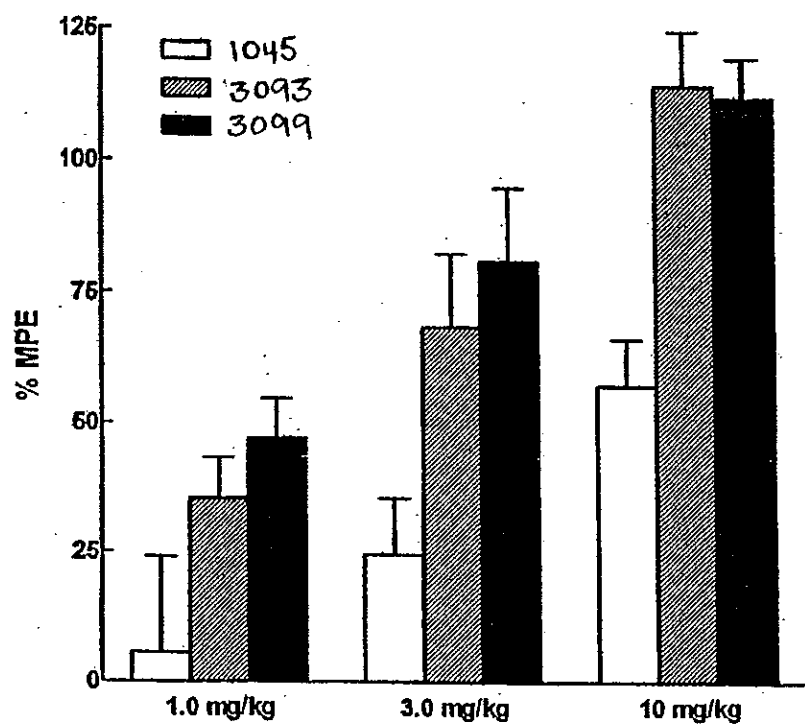


FIGURE 6

Selective FF2 Receptor Agonists Produce a Dose-dependent Reversal of L₅/L₆ SNL-induced Tactile Allodynia in M-SD Rats

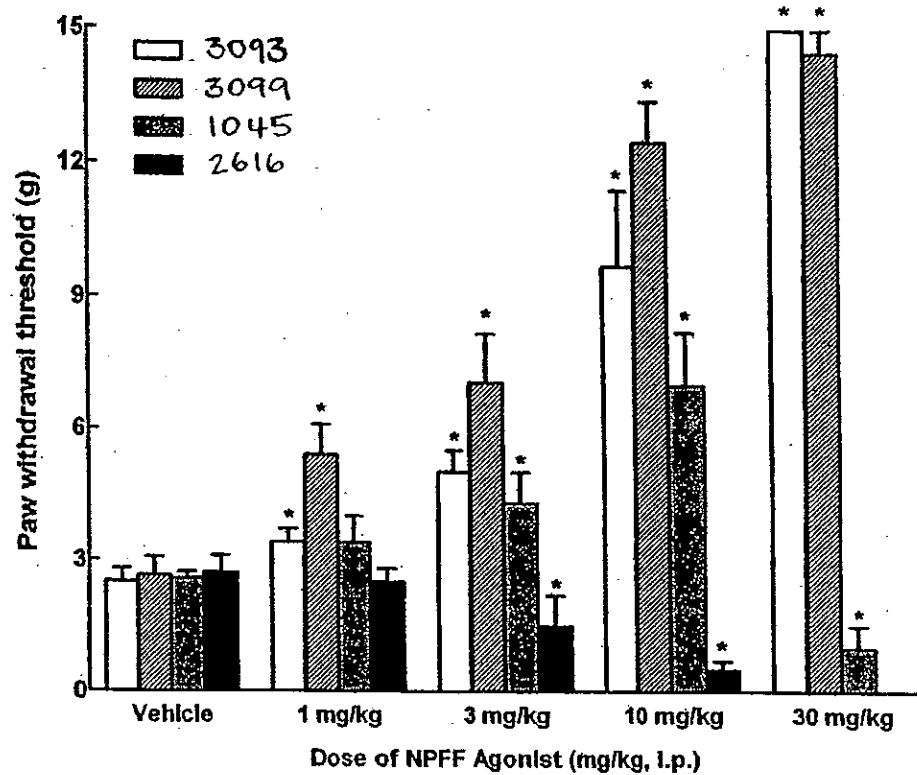


FIGURE 7

Oral administration of **3099**, a Selective NPFF FF2 Receptor Agonist,
Produces a Dose-dependent Reversal of
L₅/L₆ SNL-induced Tactile Allodynia in M-SD Rats

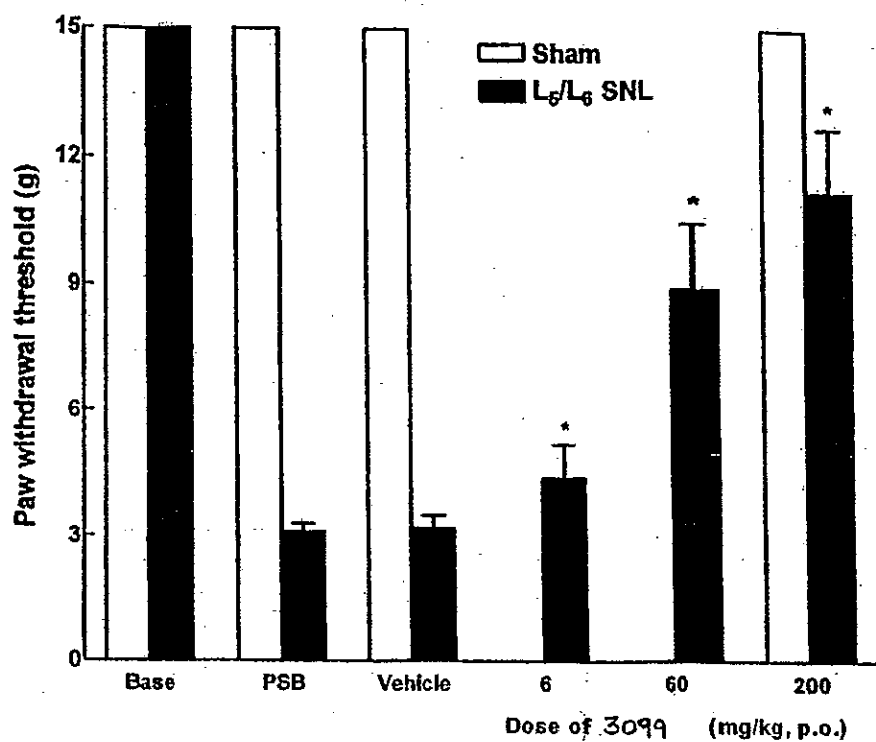
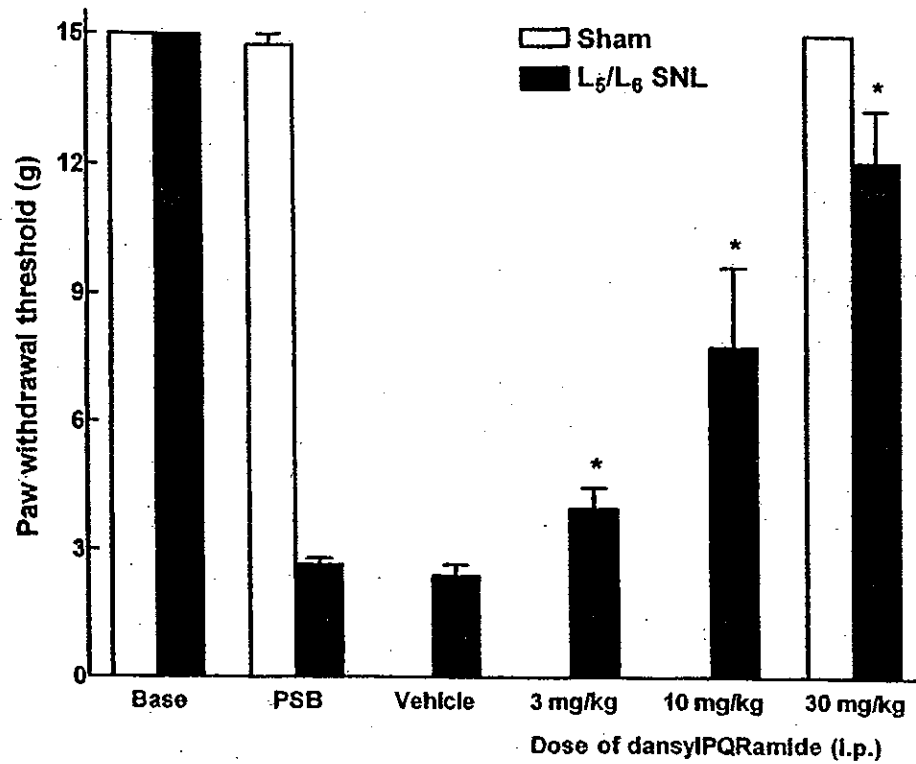


FIGURE 8

DansylPQRamide, a FF1 Receptor Antagonist, Produces A Dose-dependent Reversal of L₅/L₆ SNL-induced Tactile Allodynia in M-SD Rats



aaaaaaatta aaaataaaca aaaatgggtca taagatcata aacaatctta tgttgtataa 1500
 aaatacgtag agtgacttag acatgtttgc atgaataaat atatttctag agaacagtta 1560

<210> 2

<211> 420

<212> PRT

<213> Homo sapiens

<400> 2

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Trp	Asn	Val	Asn	Asp	Thr	Lys	His	His	Leu	Tyr	Ser	Asp	Ile	Asn	Ile
			20					25					30		
Thr	Tyr	Val	Asn	Tyr	Tyr	Leu	His	Gln	Pro	Gln	Val	Ala	Ala	Ile	Phe
		35					40					45			
Ile	Ile	Ser	Tyr	Phe	Leu	Ile	Phe	Phe	Leu	Cys	Met	Met	Gly	Asn	Thr
	50					55					60				
Val	Val	Cys	Phe	Ile	Val	Met	Arg	Asn	Lys	His	Met	His	Thr	Val	Thr
65					70				75					80	
Asn	Leu	Phe	Ile	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Leu	Val	Gly	Ile
				85					90					95	
Phe	Cys	Met	Pro	Ile	Thr	Leu	Leu	Asp	Asn	Ile	Ile	Ala	Gly	Trp	Pro
			100					105					110		
Phe	Gly	Asn	Thr	Met	Cys	Lys	Ile	Ser	Gly	Leu	Val	Gln	Gly	Ile	Ser
		115					120					125			
Val	Ala	Ala	Ser	Val	Phe	Thr	Leu	Val	Ala	Ile	Ala	Val	Asp	Arg	Phe
		130				135					140				
Gln	Cys	Val	Val	Tyr	Pro	Phe	Lys	Pro	Lys	Leu	Thr	Ile	Lys	Thr	Ala
145					150				155						160
Phe	Val	Ile	Ile	Met	Ile	Ile	Trp	Val	Leu	Ala	Ile	Thr	Ile	Met	Ser
				165					170					175	
Pro	Ser	Ala	Val	Met	Leu	His	Val	Gln	Glu	Glu	Lys	Tyr	Tyr	Arg	Val
			180					185					190		
Arg	Leu	Asn	Ser	Gln	Asn	Lys	Thr	Ser	Pro	Val	Tyr	Trp	Cys	Arg	Glu
		195					200					205			
Asp	Trp	Pro	Asn	Gln	Glu	Met	Arg	Lys	Ile	Tyr	Thr	Thr	Val	Leu	Phe
	210					215					220				
Ala	Asn	Ile	Tyr	Leu	Ala	Pro	Leu	Ser	Leu	Ile	Val	Ile	Met	Tyr	Gly
225					230					235				240	
Arg	Ile	Gly	Ile	Ser	Leu	Phe	Arg	Ala	Ala	Val	Pro	His	Thr	Gly	Arg
				245					250					255	
Lys	Asn	Gln	Glu	Gln	Trp	His	Val	Val	Ser	Arg	Lys	Lys	Gln	Lys	Ile
			260					265					270		
Ile	Lys	Met	Leu	Leu	Ile	Val	Ala	Leu	Leu	Phe	Ile	Leu	Ser	Trp	Leu
		275					280					285			
Pro	Leu	Trp	Thr	Leu	Met	Met	Leu	Ser	Asp	Tyr	Ala	Asp	Leu	Ser	Pro
		290				295					300				
Asn	Glu	Leu	Gln	Ile	Ile	Asn	Ile	Tyr	Ile	Tyr	Pro	Phe	Ala	His	Trp
305					310					315					320
Leu	Ala	Phe	Gly	Asn	Ser	Ser	Val	Asn	Pro	Ile	Ile	Tyr	Gly	Phe	Phe
				325					330					335	
Asn	Glu	Asn	Phe	Arg	Arg	Gly	Phe	Gln	Glu	Ala	Phe	Gln	Leu	Gln	Leu
			340				345					350			
Cys	Gln	Lys	Arg	Ala	Lys	Pro	Met	Glu	Ala	Tyr	Ala	Leu	Lys	Ala	Lys
		355				360					365				
Ser	His	Val	Leu	Ile	Asn	Thr	Ser	Asn	Gln	Leu	Val	Gln	Glu	Ser	Thr

aaaaaaatta aaaataaaca aaaatggtca taagatcata aacaatctta tgttgtataa 1500
 aaatacgttag agtgacttag acatgtttgc atgaataaat atatttctag agaacagtta 1560

<210> 2
 <211> 420
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu Asn Trp His Pro Ile
 1 5 10 15
 Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp Ile Asn Ile
 20 25 30
 Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala Ala Ile Phe
 35 40 45
 Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met Gly Asn Thr
 50 55 60
 Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His Thr Val Thr
 65 70 75 80
 Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu Val Gly Ile
 85 90 95
 Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala Gly Trp Pro
 100 105 110
 Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln Gly Ile Ser
 115 120 125
 Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Asp Arg Phe
 130 135 140
 Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile Lys Thr Ala
 145 150 155 160
 Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr Ile Met Ser
 165 170 175
 Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr Tyr Arg Val
 180 185 190
 Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp Cys Arg Glu
 195 200 205
 Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr Val Leu Phe
 210 215 220
 Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile Met Tyr Gly
 225 230 235 240
 Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His Thr Gly Arg
 245 250 255
 Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys Gln Lys Ile
 260 265 270
 Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu Ser Trp Leu
 275 280 285
 Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp Leu Ser Pro
 290 295 300
 Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His Trp
 305 310 315 320
 Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr Gly Phe Phe
 325 330 335
 Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln Leu Gln Leu
 340 345 350
 Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Ala Leu Lys Ala Lys
 355 360 365
 Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln Glu Ser Thr

370 375 380
Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys Ser Ala Glu
385 390 395 400
Lys Pro Gln Gln Glu Leu Val Met Glu Glu Leu Lys Glu Thr Thr Asn
405 410 415
Ser Ser Glu Ile
420