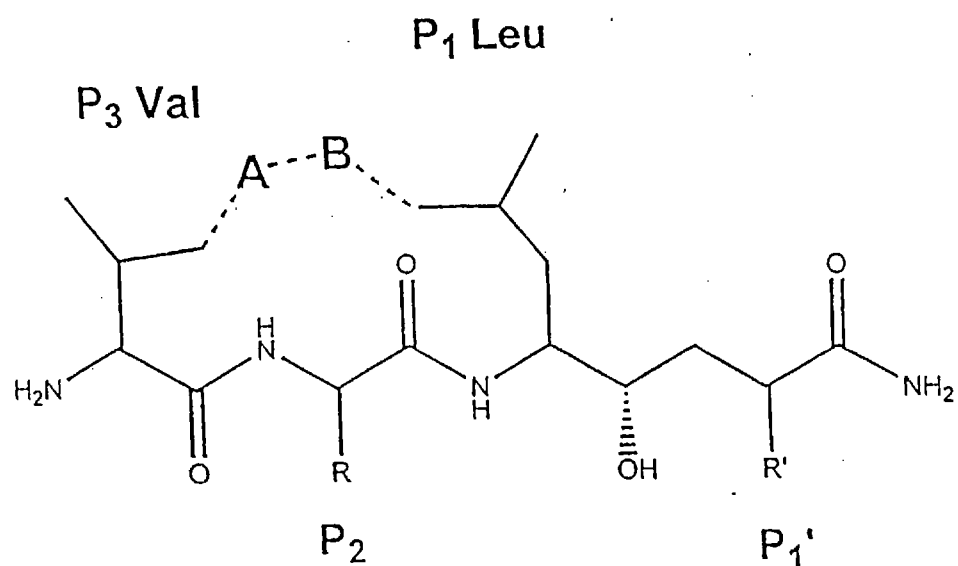




163163

Figure 1



G00002

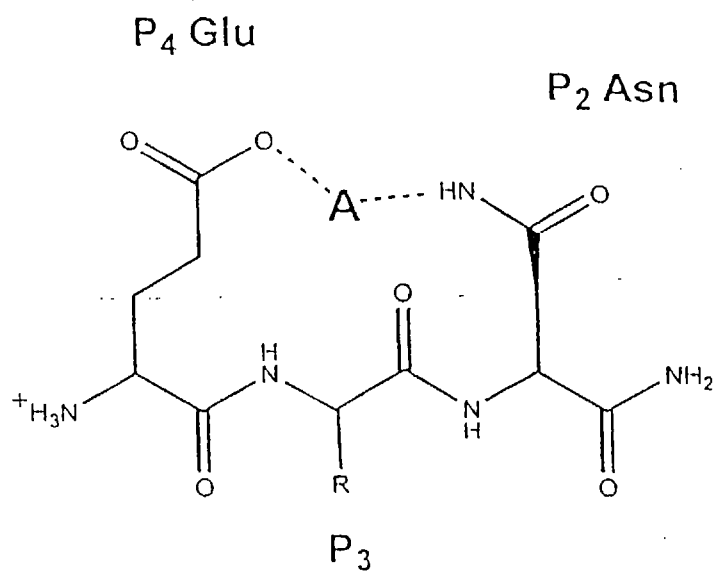


Figure 2

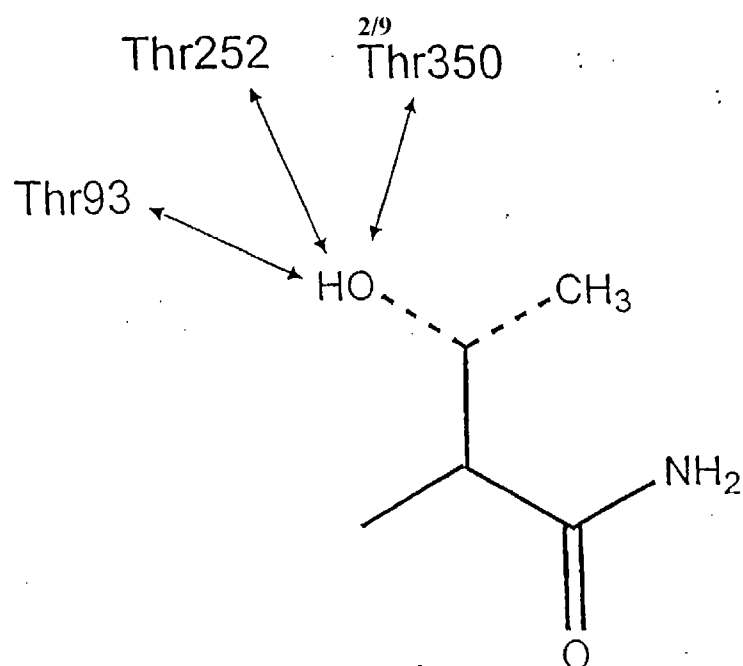


Figure 3

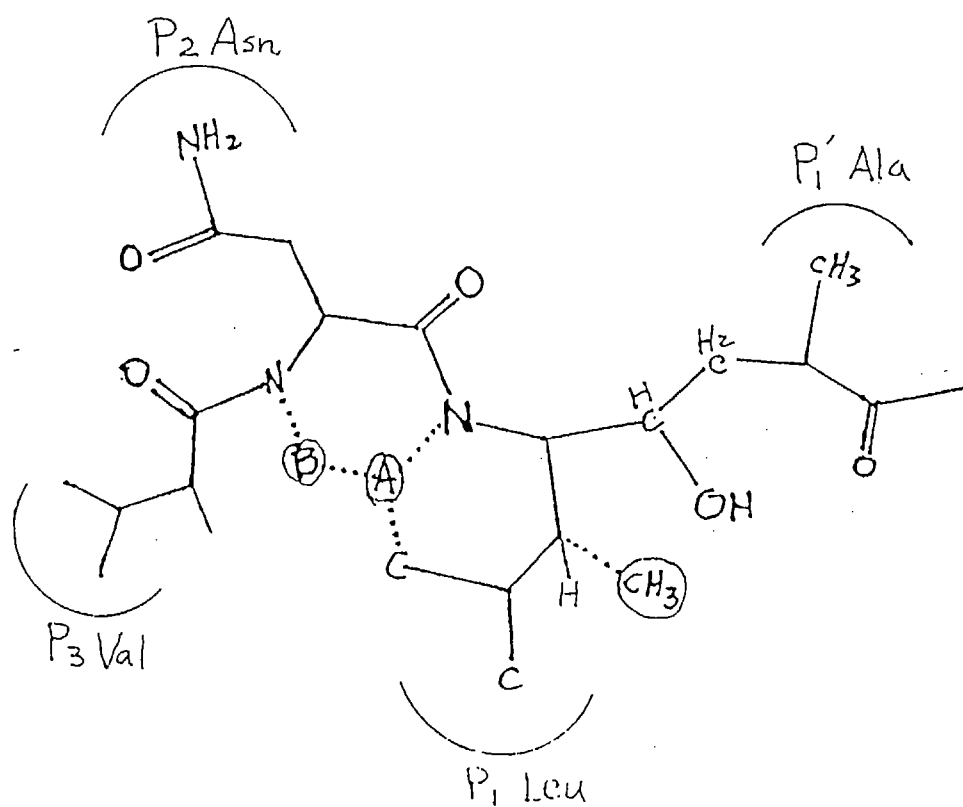


Figure 4

Memapsin 2 Specificity for Positions P₁'-P₄'

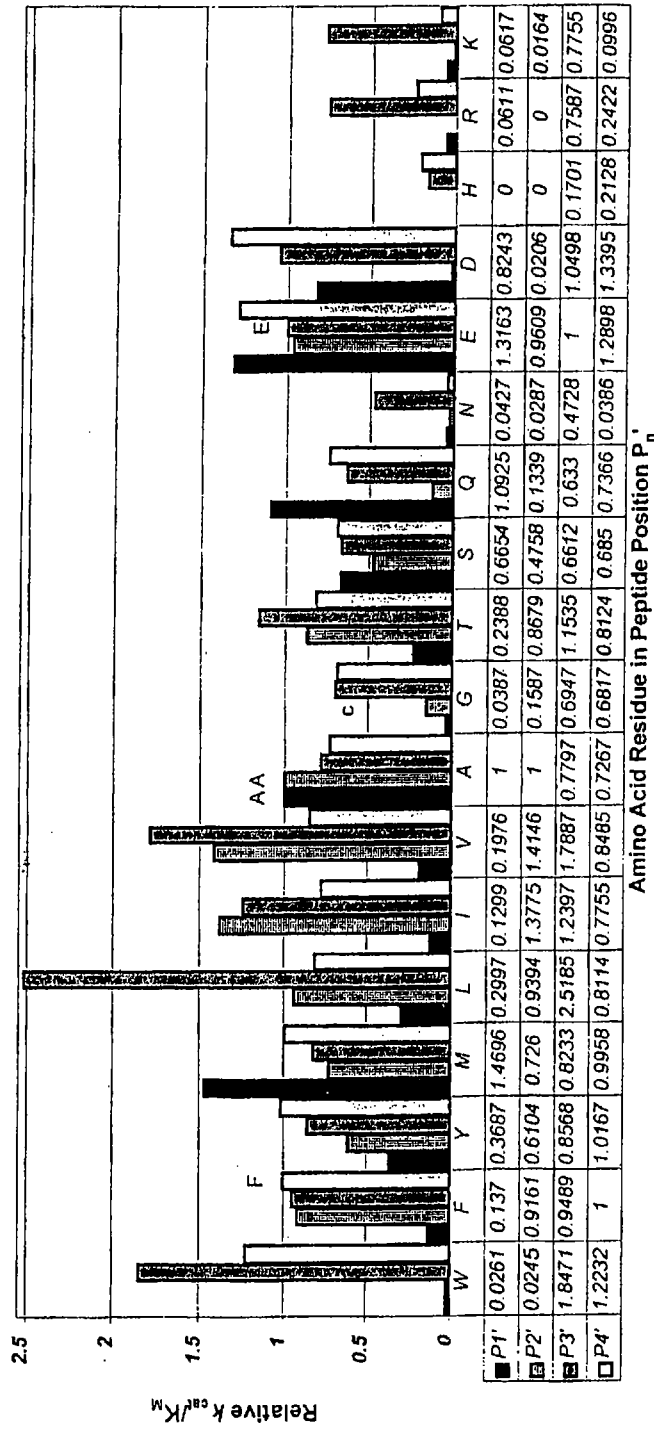


Figure 5

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ggctactacg tggagatgac cgtgggcagc ccccgcgaga cgctcaacat cctgggtggat 240
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cagaggcagc tgtccagcac ataccgggac ctccggaagg gtgtgtatgt gccctacacc 360
cagggcaagt ggggaagggga gctgggcacc gacctggtaa gcatcccca tggccccaac 420
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cagctttgtg gtgctggctt cccctcaac cagtctgaag tgctggcctc tgtcggaggg 660
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aaaaaaaaaa aa 3252

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Figure 6

Ala	Gly	Val	Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	1	5	10	15
Leu	Arg	Ser	Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	20	25	30	
Glu	Thr	Asp	Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	35	40	45	
Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	50	55	60	
Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	65	70	75	80
Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	85	90	95	
His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	100	105	110	
Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	115	120	125	
Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	130	135	140	
Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	145	150	155	160
Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	165	170	175	
Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	180	185	190	
His	Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	195	200	205	
Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	210	215	220	
Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	225	230	235	240

Figure 7A

Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	245	250	255
Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	260	265	270
Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	275	280	285
Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	290	295	300
Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	305	310	315
Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	325	330	335
Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	340	345	350
Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	355	360	365
Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	370	375	380
Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	385	390	395
Gly	Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	405	410	415
Ala	Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	420	425	430
Asn	Ile	Pro	Gln	Thr	Asp	Glu	Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	435	440	445
Met	Ala	Ala	Ile	Cys	Ala	Leu	Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	450	455	460
Cys	Gln	Trp	Arg	Cys	Leu	Arg	Cys	Leu	Arg	Gln	Gln	His	Asp	Asp	Phe	465	470	475
Ala	Asp	Asp	Ile	Ser	Leu	Leu	Lys									485		

Figure 7B

Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	Gly	Ser	Met	Ala	1	5	10	15
Gly	Val	Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	20	25	30	
Arg	Ser	Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	35	40	45	
Thr	Asp	Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	50	55	60	
Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	65	70	75	80
Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	85	90	95	
Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	100	105	110	
Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	115	120	125	
Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	130	135	140	
Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	145	150	155	160
Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	165	170	175	
Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	180	185	190	
Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	195	200	205	
Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	210	215	220	
Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	225	230	235	240

Figure 8A

Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	
				245					250					255		
Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	
			260					265					270			
Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	
		275					280					285				
Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	
	290					295					300					
Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	
305					310					315					320	
Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	
				325					330					335		
Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	
			340					345					350			
Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	
		355					360					365				
Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	
	370					375					380					
Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	
385					390					395					400	
Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	
				405					410					415		
Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	
			420					425					430			
Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	
		435					440					445				
Ile	Pro	Gln	Thr	Asp	Glu	Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met	
	450					455					460					
Ala	Ala	Ile	Cys	Ala	Leu	Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys	
465					470					475					480	
Gln	Trp	Arg	Cys	Leu	Arg	Cys	Leu	Arg	Gln	Gln	His	Asp	Asp	Phe	Ala	
				485					490					495		
Asp	Asp	Ile	Ser	Leu	Leu	Lys										
			500													

Figure 8B

1 MAQALPWLLL WMGAGVLP AH GTQHGIRLPL RSGLGGA PLG LRLPRETDEE
51 PEEPGRRG SF VEMVDNLRGK SGQGYV VEMT VGSP PQTLNI LVDTGSSNFA
101 VGAAPHPFLH RYYQRQLSST YRDLRKG VYV PYTQ GKWEGE LGTDLV SIPH
151 GPNVTVRANI AAITESDKFF INGSNW EGIL GLAYAEIARP DDSLEPFFDS
201 LVKQTHVPNL FSLQLCGAGF PLNQSEVLAS VGGSMIIGGI DHSLYTGSLW
251 YTPIRREWYY EVIIVRVEIN GQDLKMDCKE YNYDKSIVDS GTTNLRLPKK
301 VFEAAVKS IK AASSTEKFPD GFWLGEQLVC WQAGTTPWNI FPVISLYLMG
351 EVTNQSFRIT ILPQQYL RPV EDVATSQDDC YKFAISQSST GTVMGAVIME
401 GFYVVFD RAR KRIGFAVSAC HVHDEFRTAA VEGPFVTLDM EDCGYNIPQT
451 DESTLMTIAY VMAAICALFM LPLCLMVCQW RCLRCLRQQH DDFADDISLL
501 K

Figure 9