

# Peptides as leads for medicinal chemistry - the Ups and Downs of Peptidomimetic Research.

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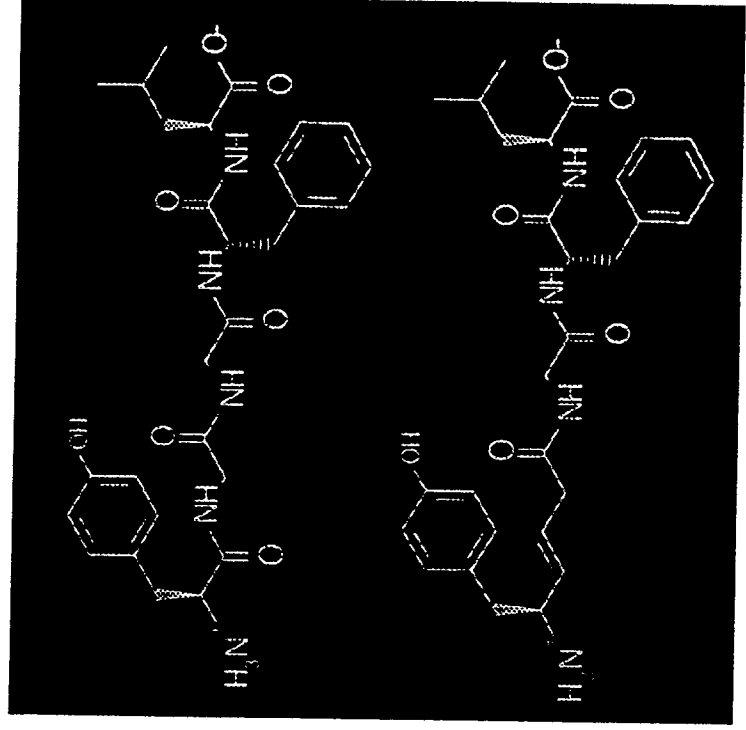
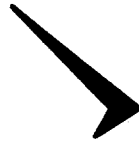
e-mail: [mmh1203@ggr.co.uk](mailto:mmh1203@ggr.co.uk)



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# Enkephalins

- Replacement of amide bonds by carbon carbon double bonds
- Stable to amino peptidase
- Higher logP



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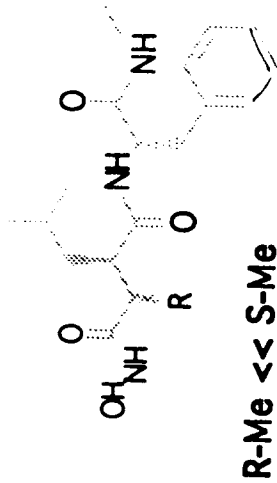
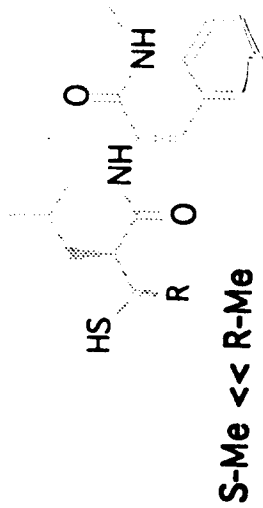
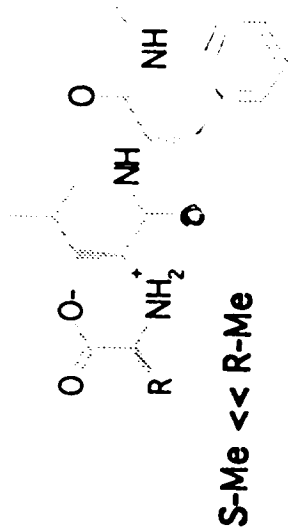
# Angiotensin II - attempt 1

- Asp-Arg-Val-Tyr-Ile-His-Pro-Phe
- analogues based on His-Pro-Phe
- synthesis failed
- selected screening based on lipophilic acids
- no success
  - lack of capacity
  - lack of samples

**X**

# Collagenase Inhibition

- Collagenase model based on Thermolysin
- Potency enhancement of Methyl
- Conformational analysis
- identification of solvent "direction" ✓
- in vitro problems X
- X-ray structure
  - confirms TLN homology
  - Bioactive conformation correct



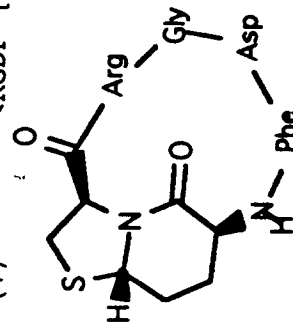
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# Fibrinogen antagonists

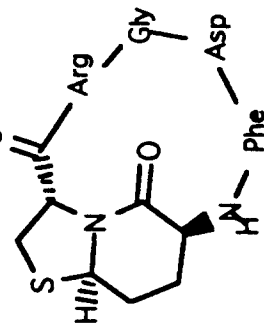
- constrained cyclic RGD peptides
- non-peptide "antagonists"

Cyclic RGD peptides and their Fibrinogen antagonist activity

Compound	Sequence <sup>a</sup>	Activity <sup>b</sup> 1.0 (standard)
(1)	GRGDS	>44
(2)	<RBDFG>	>25
(3)	<RGD-(Me)FG>	0.4
(4)	<RGDFG>	0.7
(5)	<RGDF-[D]PF>	0.9
(6)	<RGDF-[C65]>	0.02
(7)	<RGDF-[t65]>	



(6)



(7)

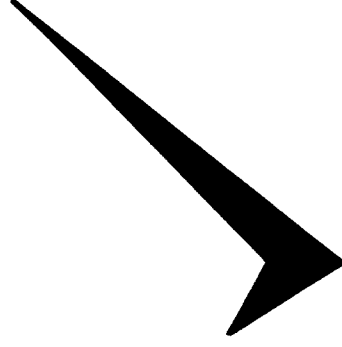
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# Fibrinogen - the Jewel in the Crown

- Linear Peptide
- Cyclic constraints
- Rapid identification of non-peptide lead
- Development of potent non peptide

- GR144053

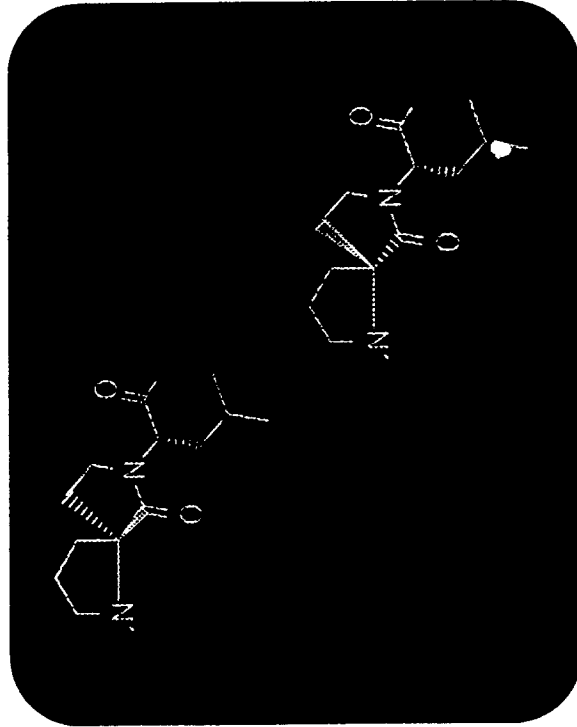
- .....



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## Early NK1 work

- Ava-Phe-Phe-(XY)-Met-NH<sub>2</sub> based on SP(6-11)
- XY = Gly-Leu Substance P



(R)-spirolactam  
Agonist

(S)-spirolactam  
Antagonist

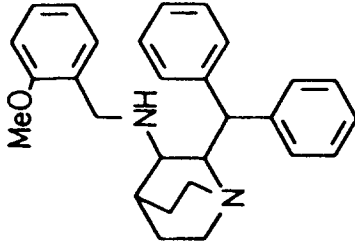
Ward et al J.Med.Chem 1990,3,1848

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# NK1 antagonism

- peptide dead end?
- loss of interest in NK1?
- Pfizer lead

– high throughput screening success



## • reasons for failures of peptide approach?

- antagonists don't bind at same sites as agonist despite competitive antagonism
- mutation information

» JBC vol 267, 25664-25667 (1992),

» Biochem v33, 3007, 1994

# X

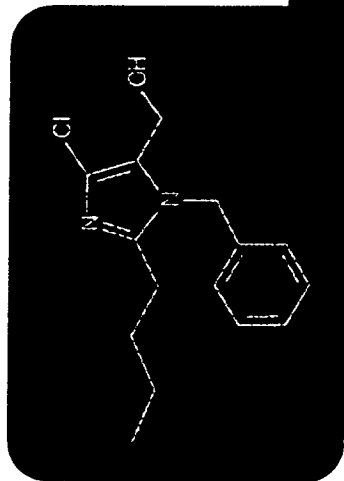
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# Angiotensin II - attempt 2

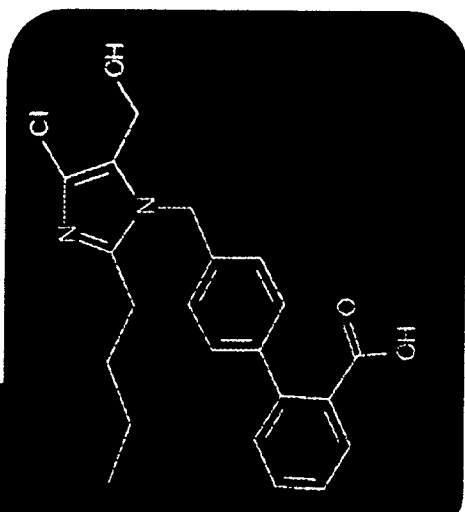
- Takeda patent

- "weak" All antagonism - pKb 5.7
- high throughput screening



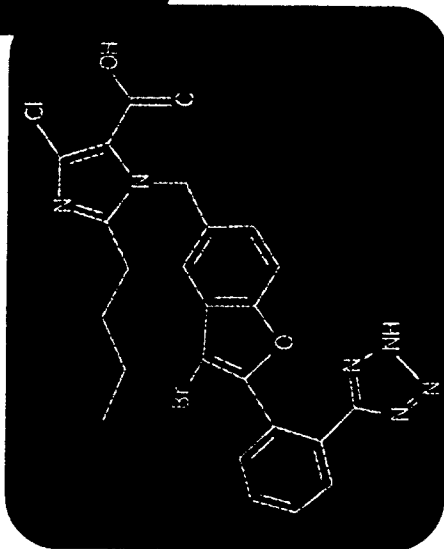
- Dupont add acid group

- potent All antagonism



- Glaxo - GR117289

- » pKb 9.8



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# Non peptide All and NK1 antagonists

- Input from peptidomimetic work?
- Would we have got where we are without learning the hardway through peptides?
- Can we tell in advance?
- 7TMs vs enzymes?
  - Renin, HIV-Protease!!
- where to next?



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# Chemical libraries

eg Chiron work:

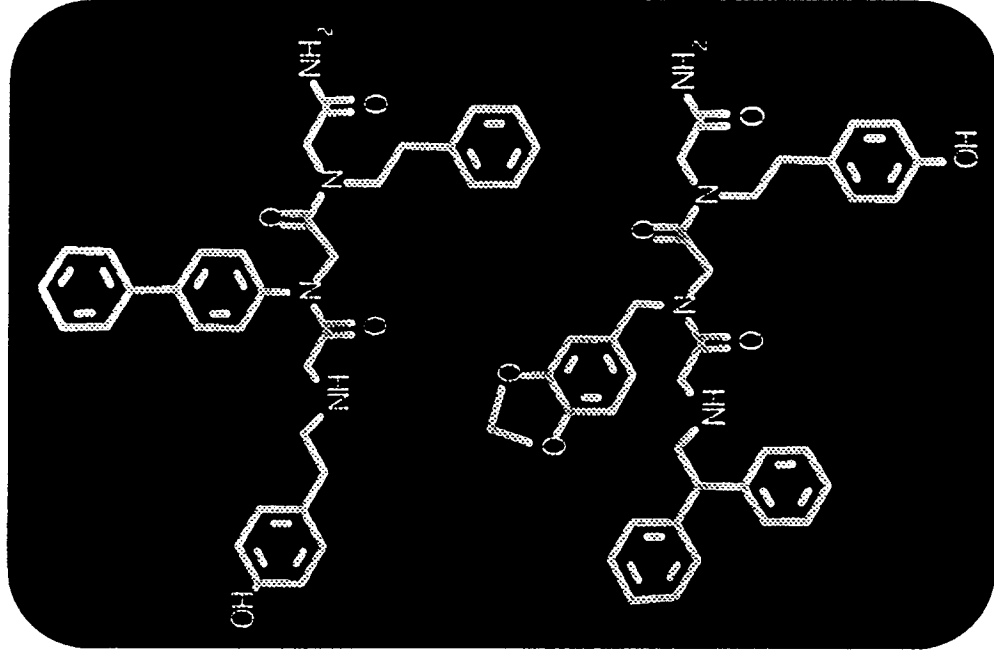
JMedChem 1994,37,2679

18 mixtures of ca. 204 PEPTOID trimers  
screening and "decoding" identified:

»  $K_i=5nM$  at  $\alpha_2$  adrenergic receptor

»  $K_i=6nM$  at m-specific opiate receptor

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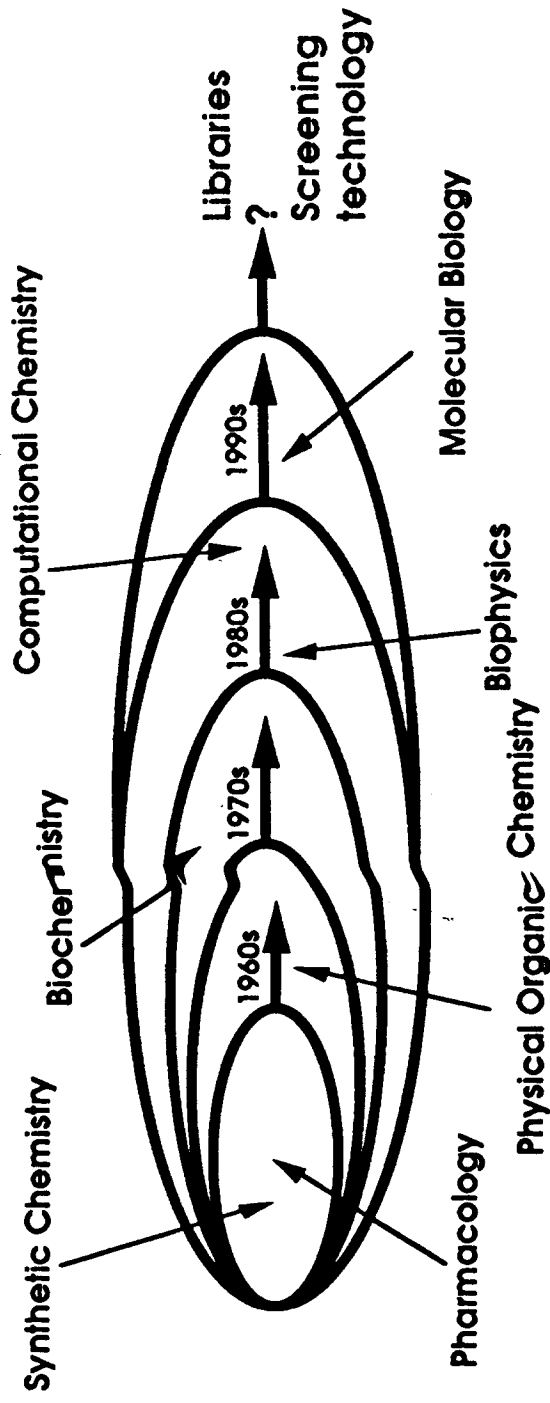


## Libraries (cont'd)

- yet more peptides? **X**
- Chiron results suggest peptoids are not peptides?
  - different physicochemical properties
  - metabolically more stable
- non peptide libraries?
  - benzodiazepines etc
- Capacity of screening?
- Information explosion? **X**



# Modern Medicinal Chemistry ✓



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## Summary

- Peptides and peptidomimetics make useful tools for exploring biology
- No *a priori* way of knowing that the peptidomimetic approach will lead to a good drug
- Need to short circuit traditional methodology with use of "inspired" High Throughput screening of compound collections to make the strategic jump of peptide to true non-peptide
- Gaps in compound collections will be filled by libraries

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