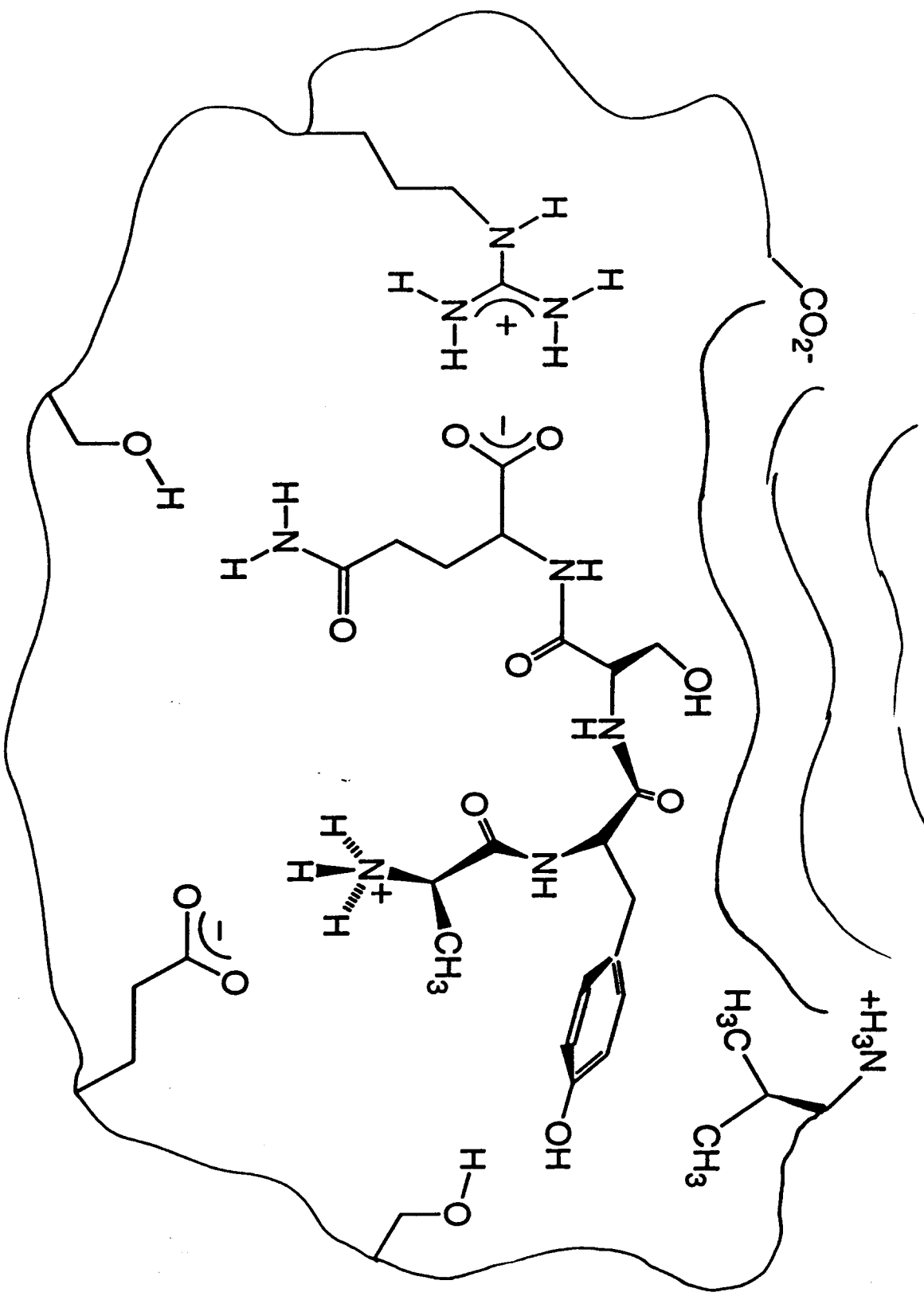


Mimicreceptor

Pseudoreceptor

Water

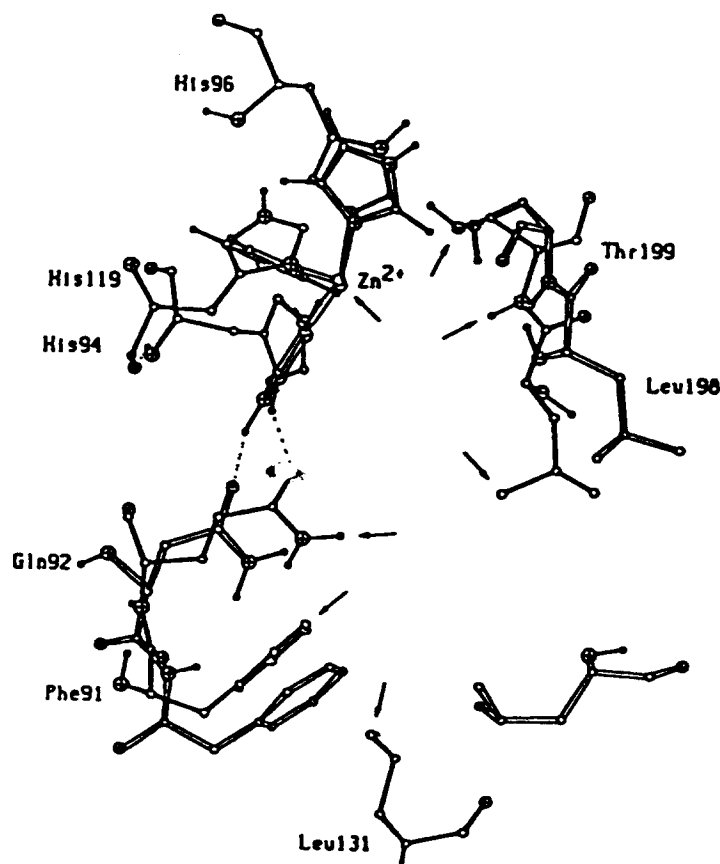


Pseudoreceptors and Minireceptors

- o Flexible comparison of pharmacophore elements
- o Mechanistic insights
- o Selectivity by evaluating multiple receptors or subtypes
- o $\Delta E_{\text{bind}}(\text{rel})$ ($\Delta G_{\text{bind}}(\text{rel})$) via Free Energy Perturbation
- o 3-D searches as for enzyme X-ray structures
- o *De novo* design

Minireceptor Enzyme Validation

- o Simulate active site of Human Carbonic Anhydrase (2. Å resolution) with four potent docked sulfonamide inhibitors and the program YAK
- o Nine residues targeted including the catalytic Zn



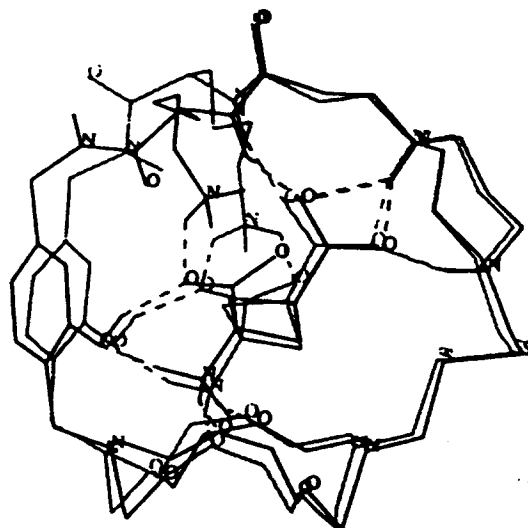
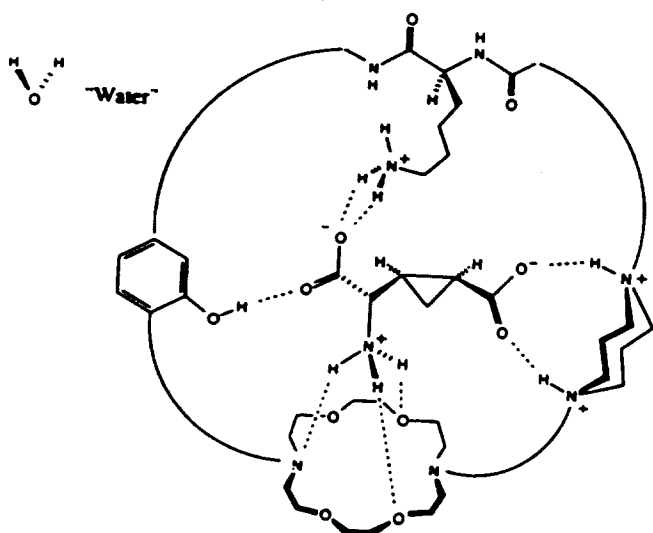
- o Five of nine residues sited within 0.7 Å of X-ray positions; mean deviation for all nine 1.7 Å. For Thermolysin and 3 phosphorimidate inhibitors, average deviation of 1.3 Å for 12 AA side chains

(Snyder, J.P.; Rao, S.N., Koehler, K.F.; Vedani, A. in "3D QSAR in Drug Design," Ed. H. Kubinyi, ESCOM, Leiden, 1993, pp 336-354)

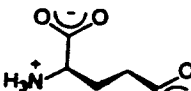
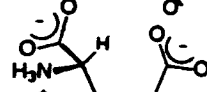
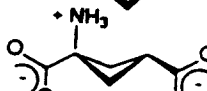
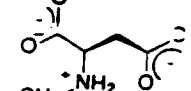
NMDA Agonists Glutamic Acid Receptors

Schematic representation of the pseudoreceptor constructed around SRS-CPG. Curved lines correspond to molecular spacers between the key binding groups.

Comparison of the AMBER optimized *cis*-2,4-MG pseudoreceptor complexes before and after the F transformation MGA → S-GLU → MGA.



Comparison of experimental and predicted free energies of binding for NMDA agonists relative to (S)-glutamic acid:
 $\Delta\Delta G_{\text{binding}} (\Delta G_{\text{agonist}} - \Delta G_{\text{S-GLU}})$, kcal/mol, 277°K

	$K_i(\mu\text{M})^{277}$	ΔG_{exp}	$\Delta\Delta G_{\text{exp}}$	$\Delta\Delta G_{\text{calc}}$	$\Delta\Delta G_{\text{calc}}$
				H_2O	$\text{DE}(\Delta r)$
	S-Glu	0.036	1.8	0.0	
	R-Glu	2.7	-0.55	2.4	16.9
	SRS	0.009	2.6	-0.76	-2.0
	RSR	0.055	1.6	0.23	-3.1
	SSR	0.15	1.0	0.79	9.2
	RRS	1.7	-0.29	2.1	4.4
	MGA	0.052	1.6	0.20	—
	NMDA	3.3	-0.66	2.5	—

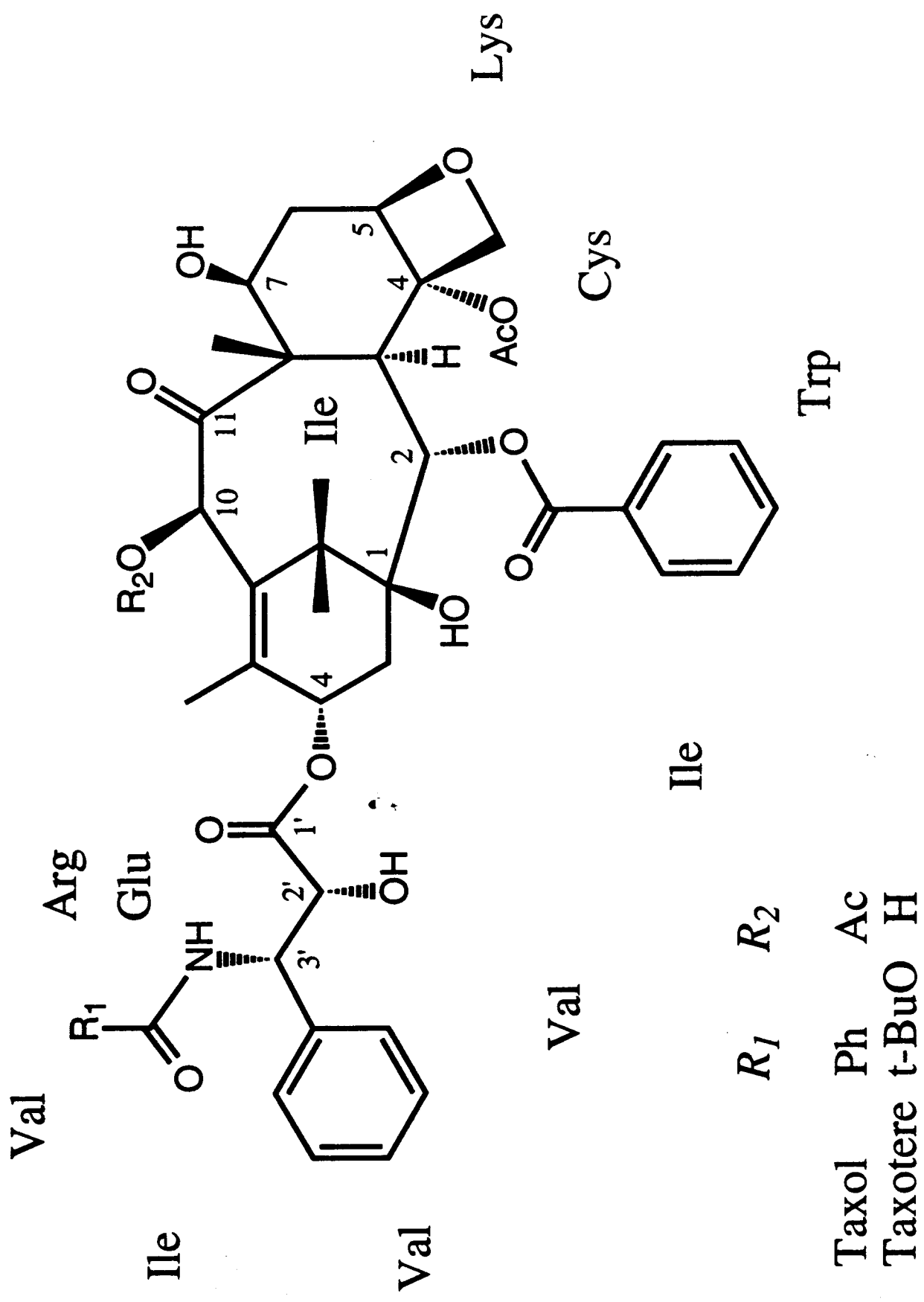
(Snyder, J.P.; Rao, S.N., Koehler, K.F.; Pellicciari, R. in "Trends in Receptor Research," Eds. P. Angeli, U. Gulini, W. Quaglia, Elsevier, 1992, pp 367-403)

Taxol and Taxotere

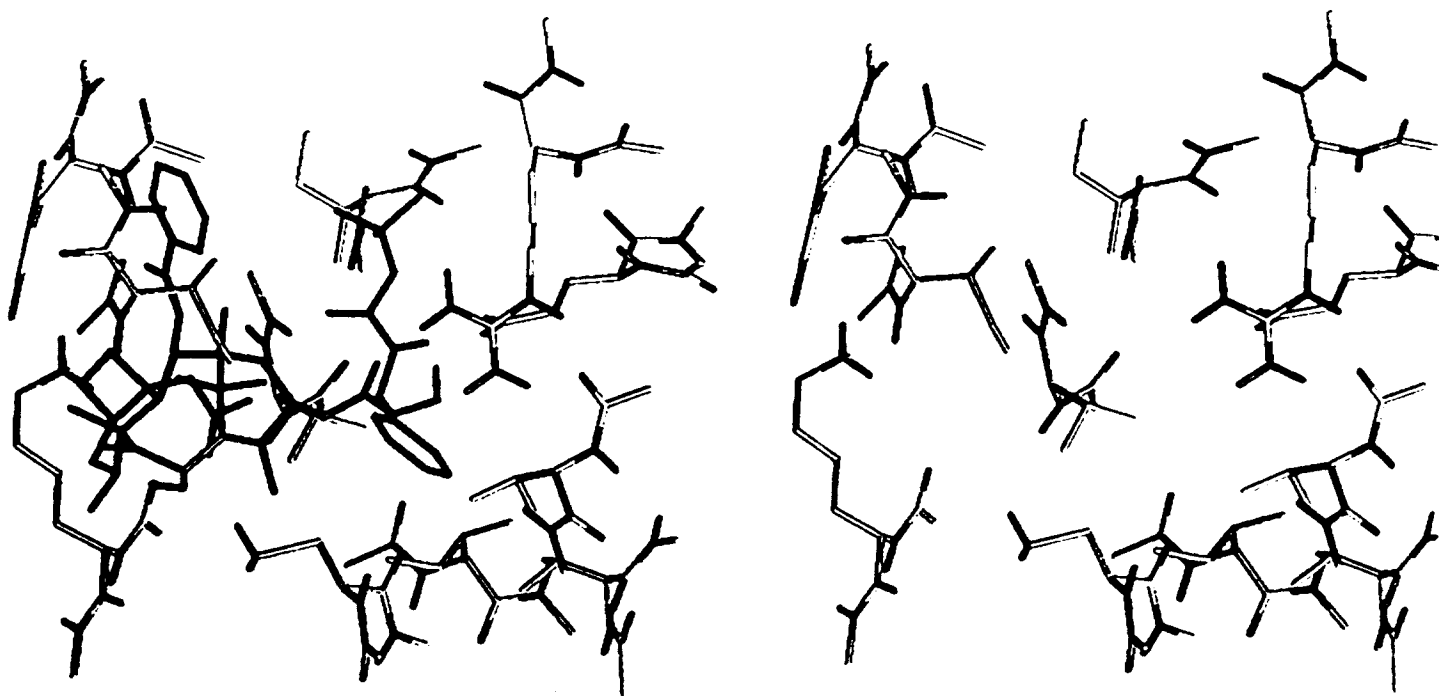
- o Isolated in limited quantities from the Western Yew tree and related species
- o Exciting antitumor lead in early clinical trials:
 - Drug refractory, advanced ovarian cancer
 - Metastatic breast cancer
 - Non-small cell lung cancer
 - Head and neck cancer
- o Unique mechanism of antimitotic action: promotes assembly and stability of microtubules
- o Total synthesis in 1994:
 - R. Holton et al, *J.Am.Chem.Soc.* 1994, 116, 1597
 - K.C. Nicolaou et al, *Nature* 1994, Feb. 17, 631
- o Considerable SAR available
- o No simple and bio-effective analogs known

Receptor Building and Design Templating

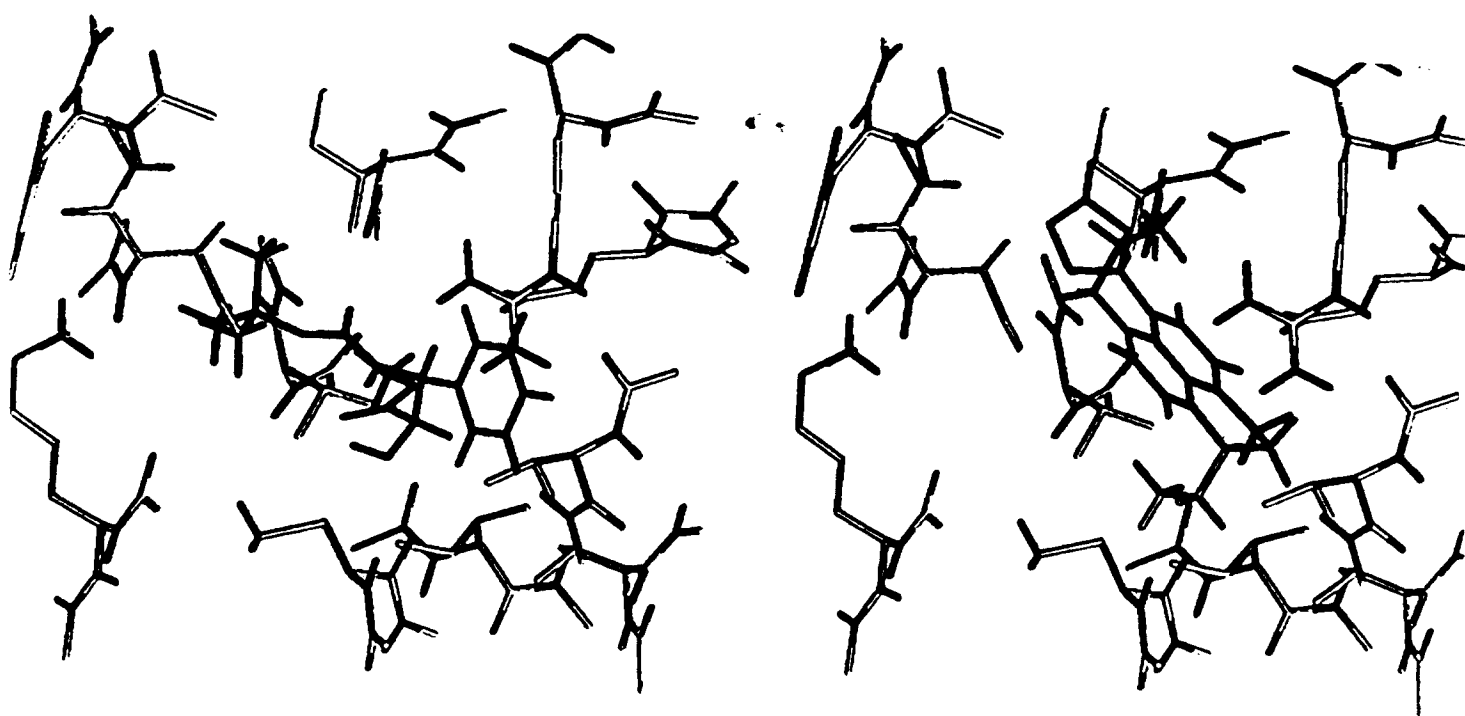
- o Use taxotere/taxol conformations believed to be bioactive (Williams et al, *Tetrahedron* 1993, 49, 6545; *Can. J. Chem.* 1994, 72, 252)
- o Taxotere surrounded by 11 amino acid side chains in accord with 31 β -tubulin N-terminal AA's (Rao et al *J. Biol Chem.* 1994, 269, 3132) and known taxane SAR
- o AA's linked and resulting *pseudoreceptor* optimized with the AMBER force field
- o AA's capped and resulting *minireceptor* optimized with AMBER
- o Evacuated taxotere cavity searched with the *de novo* design tool LEAPFROG (Tripos)



Taxol Ph Ac
 Taxotere t-BuO H



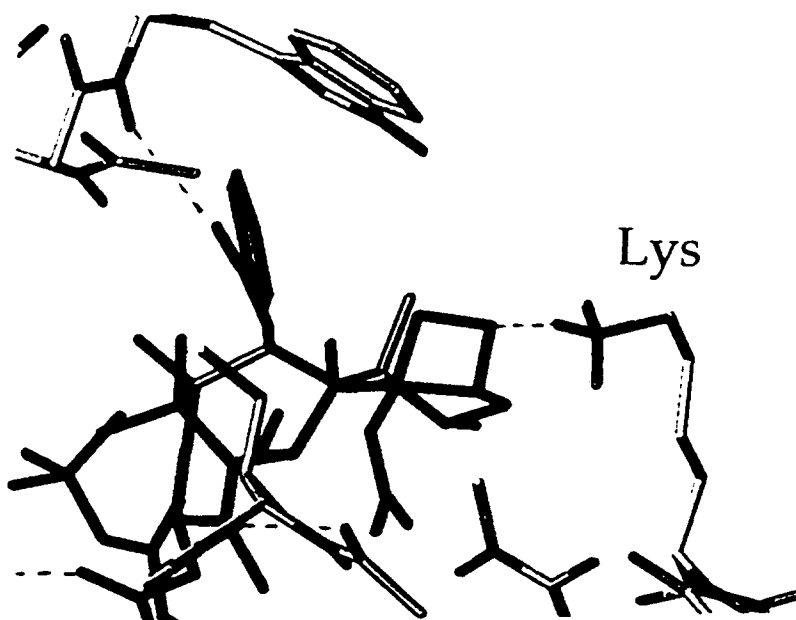
Taxol/Taxotere capped minireceptor showing taxotere optimized interactions (left); receptor cavity (right)



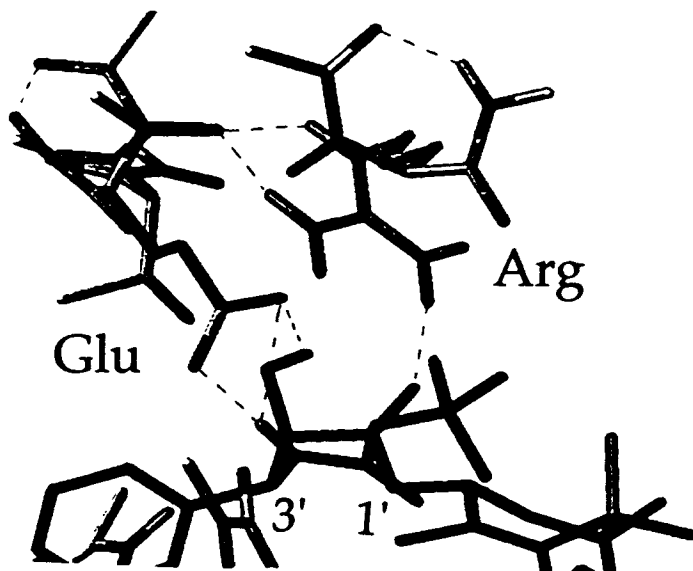
Minireceptor binding two Leapfrog generated ligands derived from *de novo* design

Taxol/Taxotere capped minireceptor; Key interactions between side chains and three important ligand centers

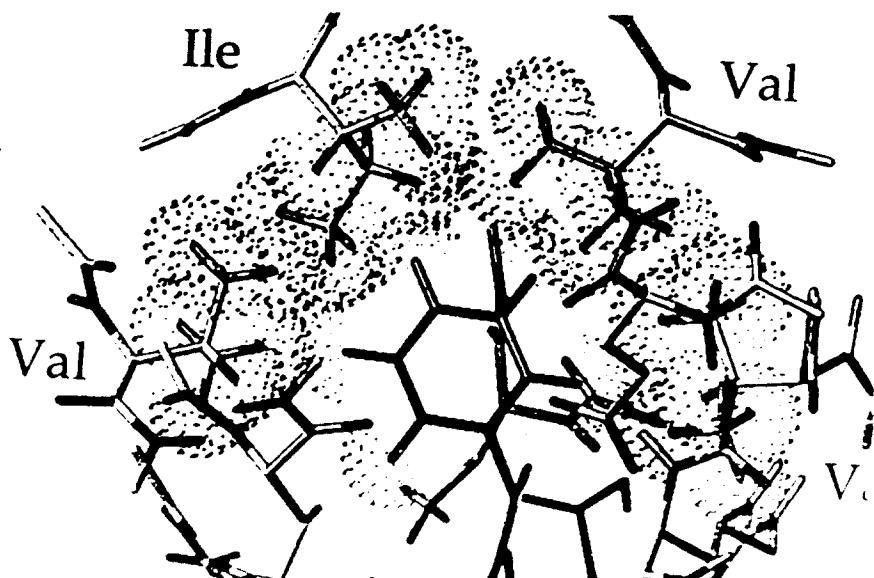
H-bond between Lys and O of oxetane ring

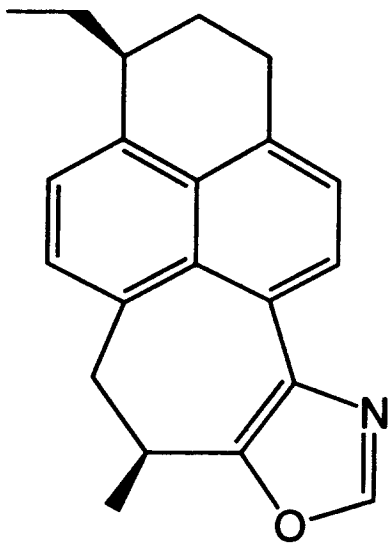
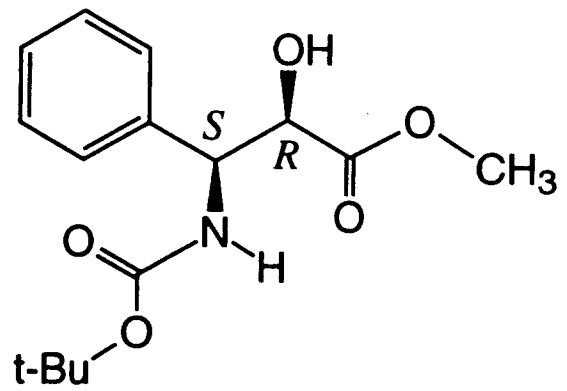


H-bonds between Glu/Arg and the hydrophilic groups on the C1'-C3' side chain of taxotere

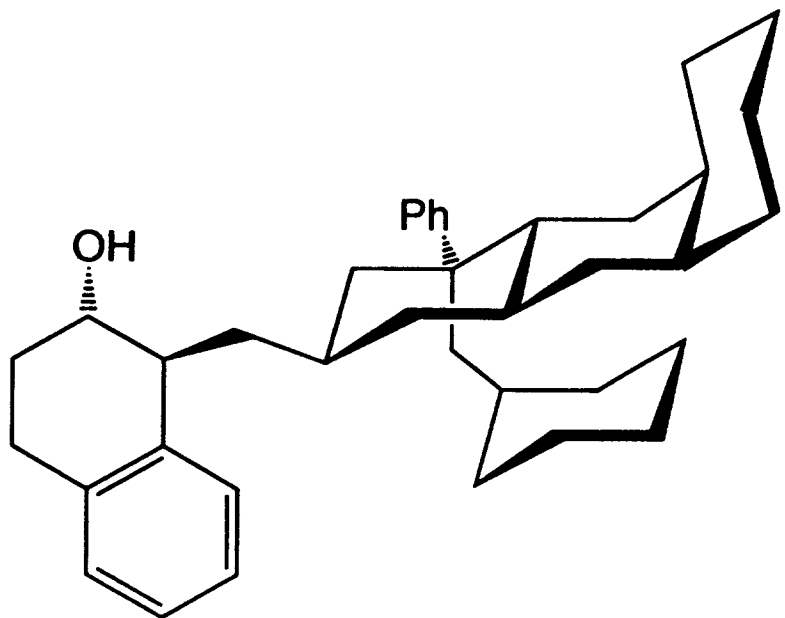


Hydrophobic pocket for Phenyl at C3' (Ile and 3 Val's)





LeapFrog Structures (Cramer, Tripos)



Conclusions

- o Mini- and pseudoreceptor construction facile and realistic
- o Semiquantitative prediction possible
- o Unique 3-D molecular design feasible
- o GrowMol design* and database screening underway

* Bohacek, R.S.; McMartin, C. *J.Am.Chem.Soc.* 1994, 116, 5560)

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