

# **DRUG DISCOVERY**

**Edward A. Sausville, M.D., Ph.D.**  
**Associate Director for Clinical Research**  
**Greenebaum Cancer Center**  
**University of Maryland at Baltimore**

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# OUTLINE OF PRESENTATION

- \* ***General Introduction***
- \* Definition of Drug Targets
- \* Generating Diversity
- \* Definition of Lead Structures
- \* Qualifying Leads for Transition to Early Trials

# DRUG DISCOVERY: WHERE HAS IT WORKED?

Majority of Drug Targets:	% Top Sales
- G-Protein Coupled Receptors	18
- Nuclear (Hormone) Receptors	10
- Ion Channels	16
- Enzymes	~50

## Problem:

How to choose target likely to succeed especially if directed at new target (e.g. protein-protein interactions)?

# DRUG DISCOVERY: A SUCCESSION OF STYLES

Antiquity to 1960s:

Mixtures of natural products vs. bioassays  
(e.g., digitalis, rauwolfia, penicillins, anthracyclines,  
vinca, taxol, camptothecins)

1930s to present:

Pure compounds vs. bioassays  
(e.g., sulfas, diuretics, hypoglycemics, antiHBP)

1960s to present:

Pure compounds vs. pure enzymes  
(e.g., ACE inhibitors, cholesterol-lowering statins,  
RT and protease inhibitors)

1980s to present:

Combinatorial methods to bring mixtures of compounds  
vs. many targets

# WHY COMPOUNDS FAIL AND SLOW DOWN IN DEVELOPMENT

## Reasons for failure

- \* Toxicity, 22%
- \* Lack of efficacy, 31%
- \* Market reasons, 6%
- \* Poor biopharmaceutical properties, 41%

## Reasons for slowdown

- \* Synthetic complexity
- \* Low potency
- \* Ambiguous toxicity finding
- \* Inherently time-intensive target indication
- \* Poor biopharmaceutical properties

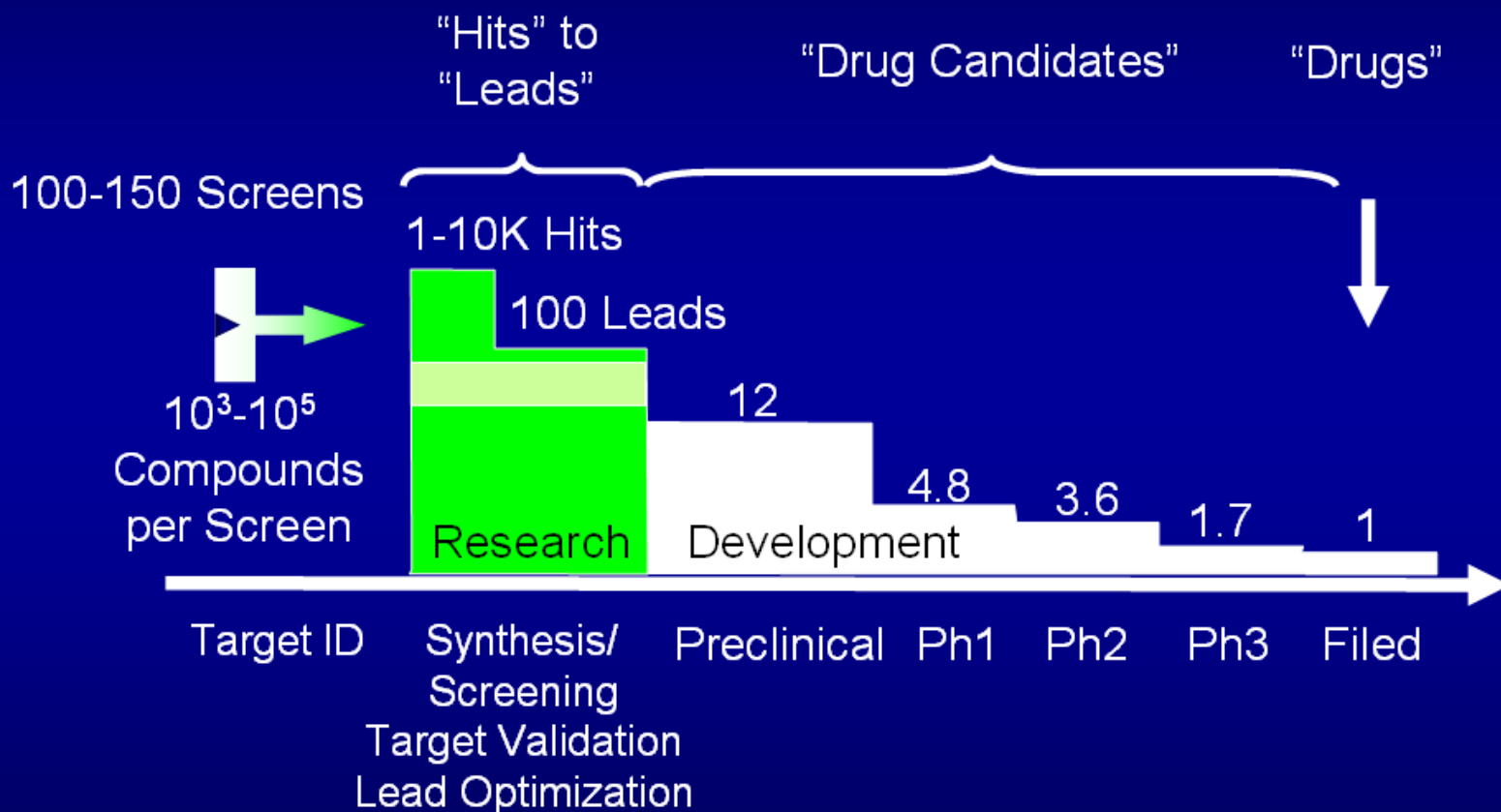
Modern Drug Discovery

January/February 1999

*Modern Drug Discovery*, 1999, 2 (1), 55-60.

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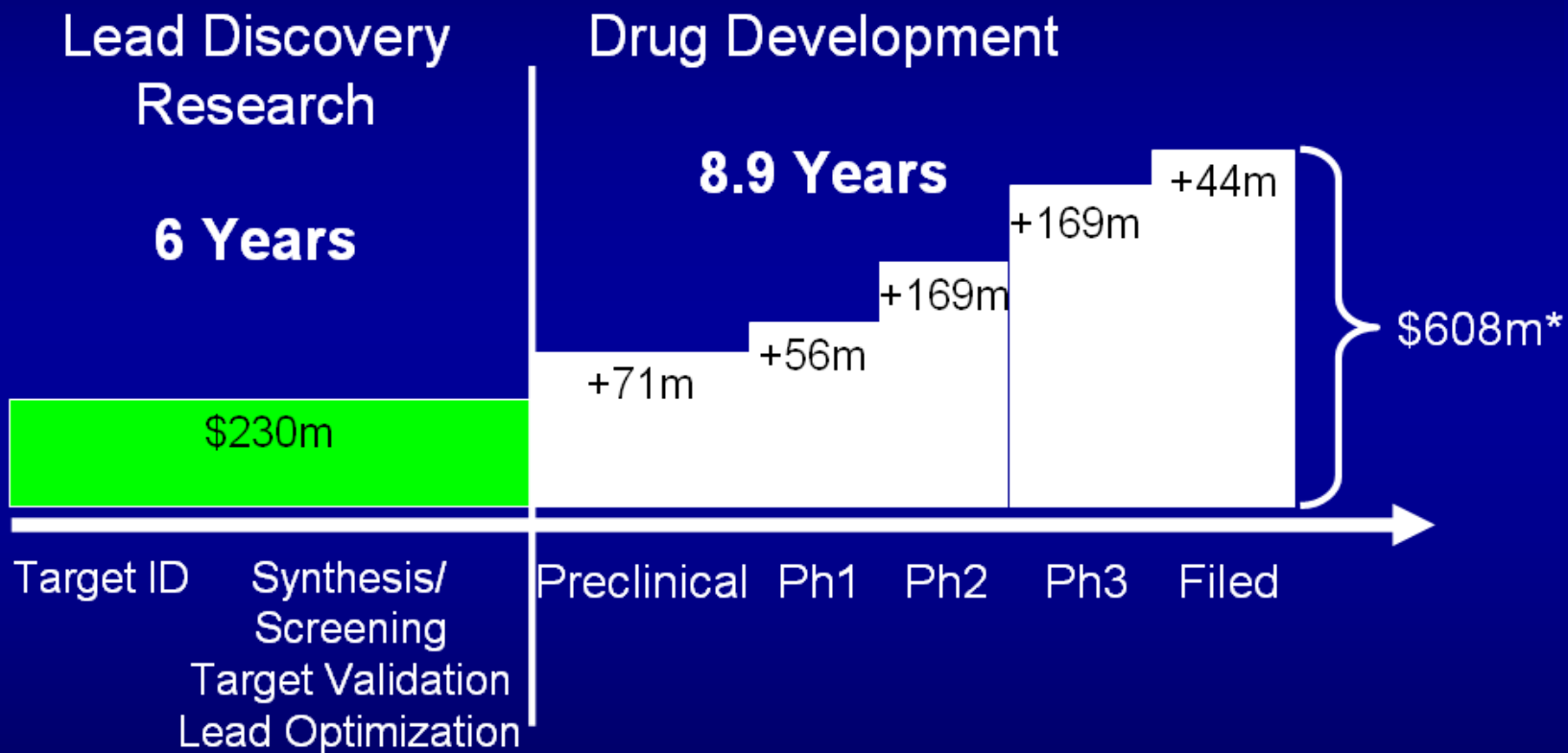
# TRADITIONAL PHARMACEUTICAL R&D Suffers High Attrition\*



\* Tufts CSDD, H&Q 1998; The Pfizer Journal, 1/2000

# TRADITIONAL PHARMACEUTICAL R&D

## Costly\* and Time Consuming\*\*



\* Lehman Brothers, 1997; \*\* Tufts CSDD

# OUTLINE OF PRESENTATION

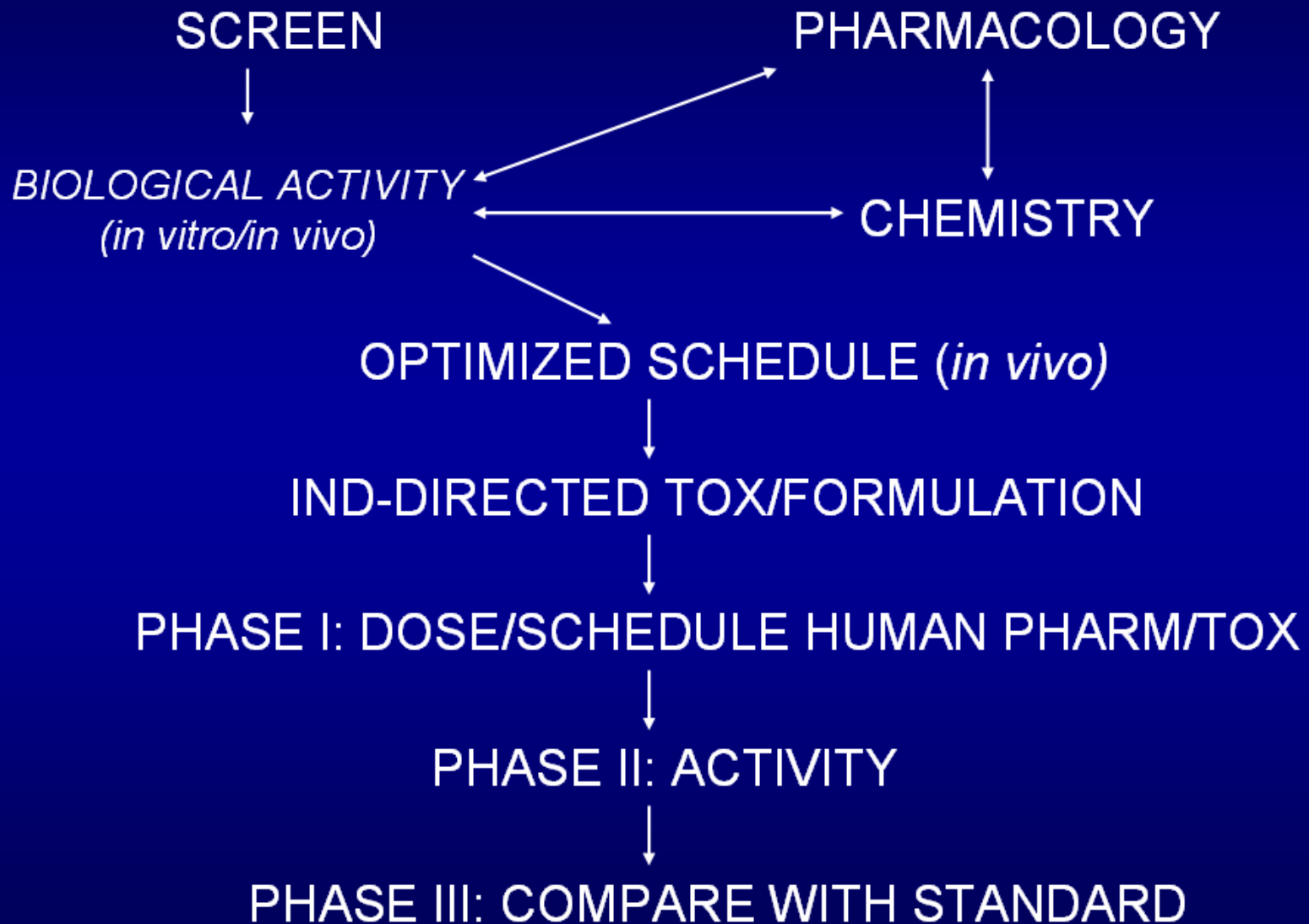
- \* General Introduction
- \* ***Definition of Drug Targets***
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- \* Qualifying Lead for Transition to Early Trials



# TWO CONTRASTING DRUG- DISCOVERY “PHILOSOPHIES”

- \* “EMPIRICAL”: Recognize initial drug lead by functionally useful effect
  - E.g. : penicillin (anti-bacterial effect)
  - rauwolfia (anti-hypertensive)
  - taxol (anti-tumor)
  - digoxin (cardiotonic / antiarrhythmic)
- \* “RATIONAL”: Recognize drug by design or screen against biochemical target’s function
  - E.g.: HIV-protease inhibitor (anti-infection)
  - metoprolol (anti-hypertensive)
  - methotrexate (anti-tumor)

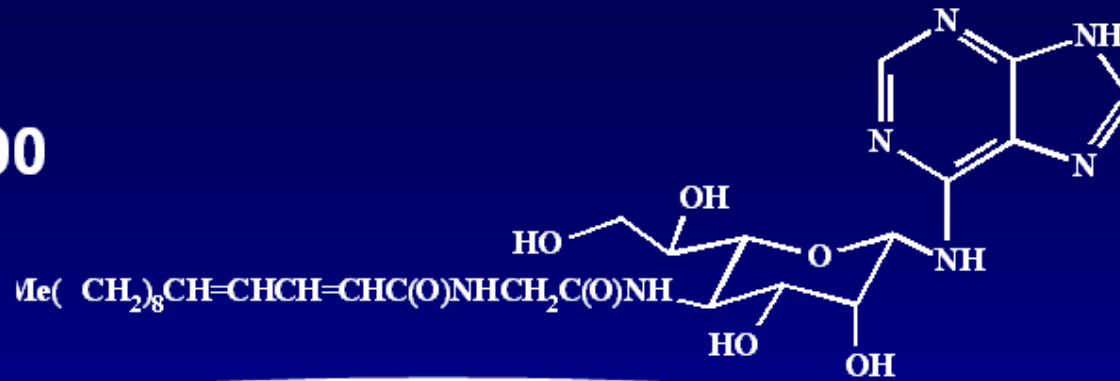
# “EMPIRICAL” DRUG DISCOVERY



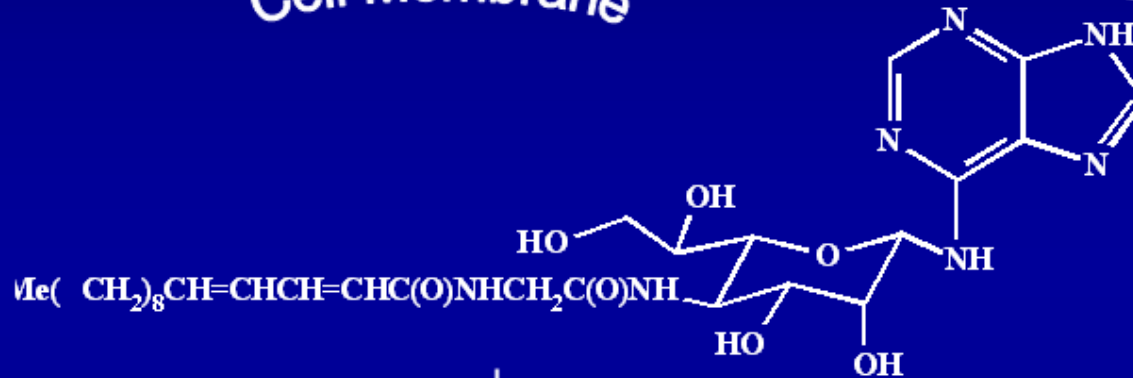
# PROBLEMS WITH EMPIRICAL MODELS

- \* Lead optimization difficult without known biochemical target--How to optimize?
- \* Value of screen depend on predictive value of screening model with biology of disease
  - E.g.: acid hypo-secretion or H2 receptor binding assay  
HIGHLY correlate with useful anti-ulcer Rx
  - Counter E.g.: anitumor activity in > 33% mouse models of cancer have at best 50% chance of >1 P2 trial for non=targeted cancer Rx's
- \* Divorced from mechanism: an intriguing lead must be "deconvolutedh

# KRN5500



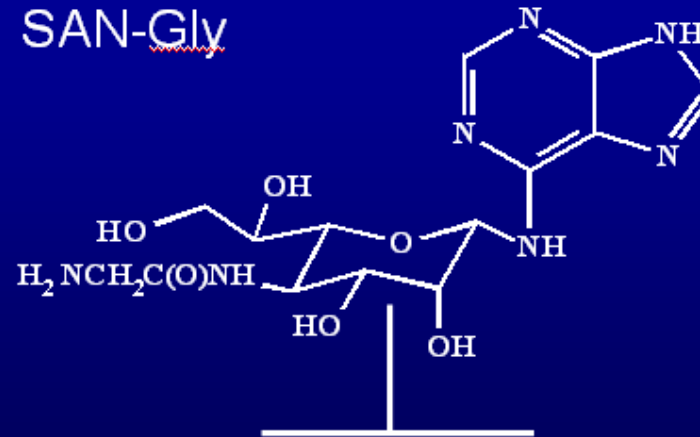
Cell Membrane



Deacylation

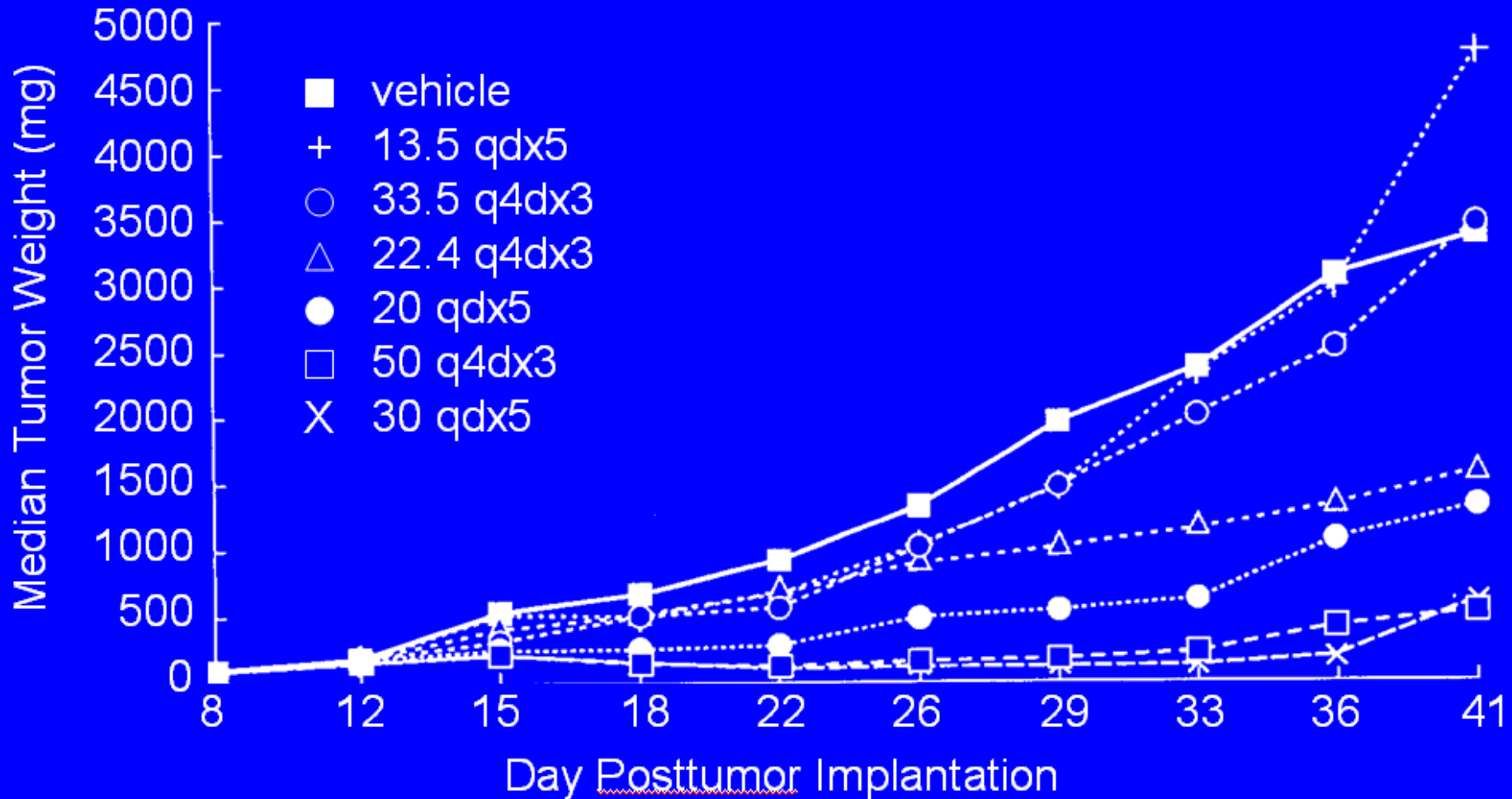


SAN-Gly

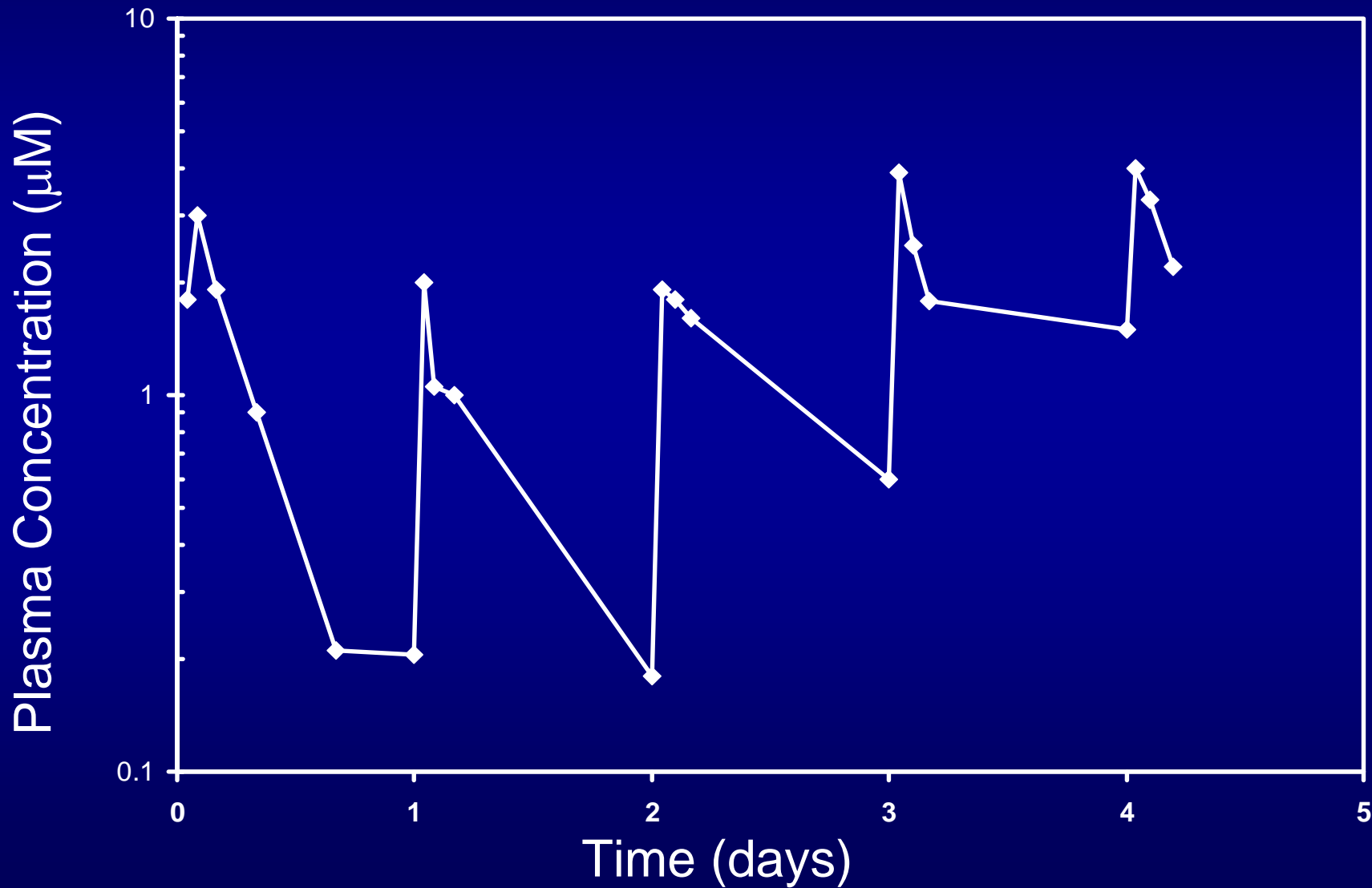


Protein Synthesis

# EFFECT OF KRN5500 ON COLO-205 ATHYMIC MOUSE XENOGRAFTS



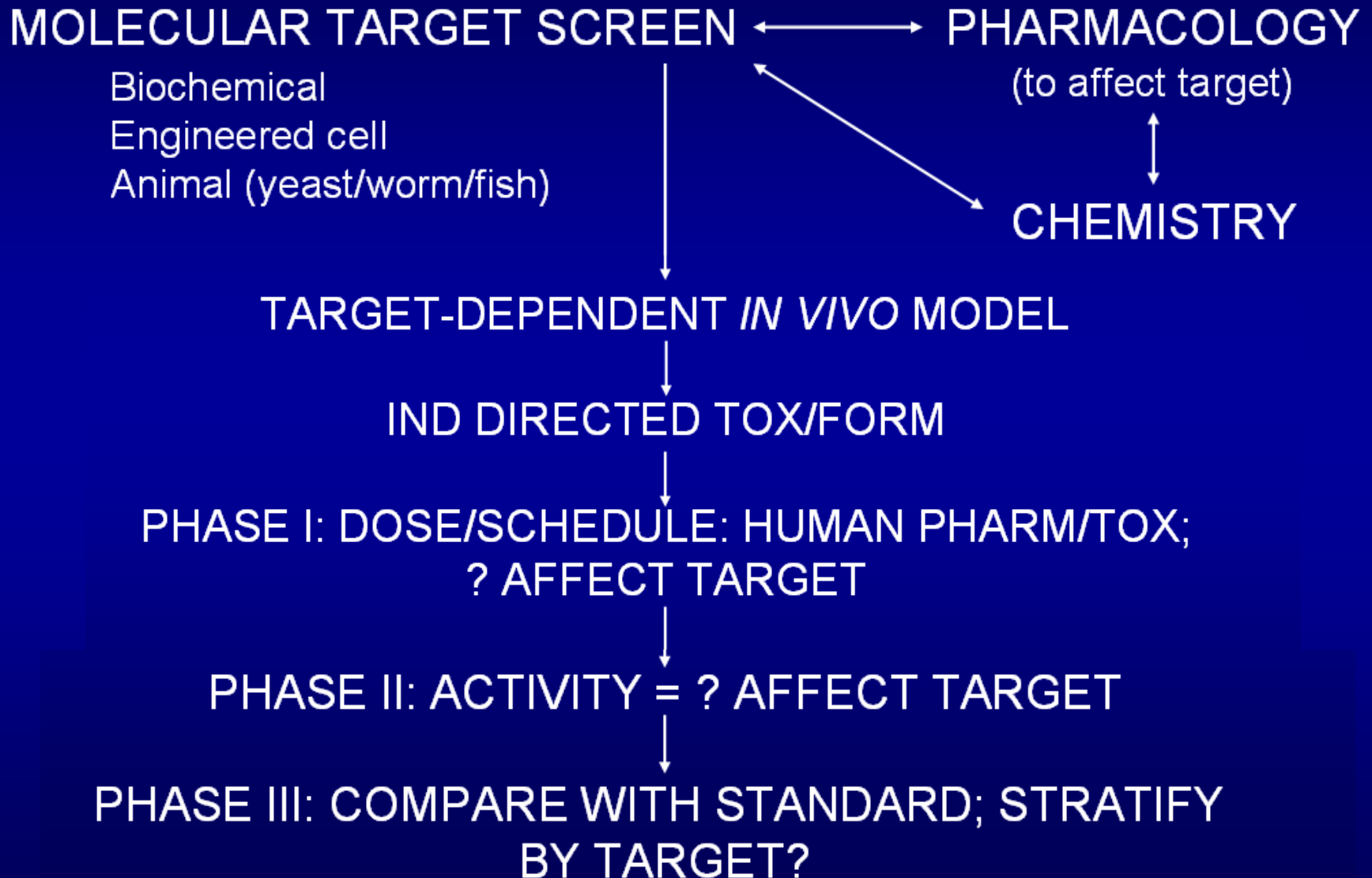
# KRN5500 PLASMA CONCENTRATIONS ON EFFECTIVE SCHEDULE(20 MG/KG/D) IN MICE



# SUMMARY OF KRN-5500 PHASE I

- \* 26 patients as IV once per day over 5 days
- \* Dose limiting toxicity = interstitial pneumonitis
- \* MTD = 2.9 mg/M<sup>2</sup>/d x 5
- \* Achieve only 0.75 - 1 μM at 3.7 mg/M<sup>2</sup>/d x 5
- \* 4/6 patients with >25% incr C<sub>max</sub> have grade 4 toxicity

# “RATIONAL” DRUG DISCOVERY





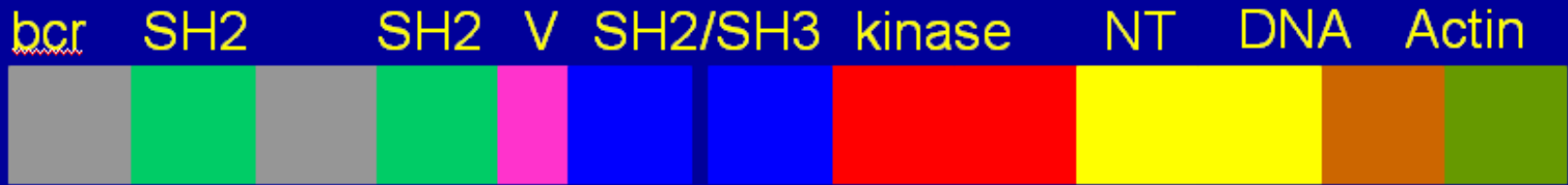
# **bcr-abl AS TARGET: RATIONALE**

- \* Apparently pathogenetic in t9:Q22 (Ph+) CML/ALL
- \* Absence in normal tissues
- \* Modulate signal transduction events downstream

Maintenance of chronic phase

Adjunct to bone marrow transplantation

# bcr-abl FUSION PROTEIN



**Phosphorylation of  
other substances**

# EXAMPLE OF "RATIONAL" APPROACH: bcr-abl directed agents

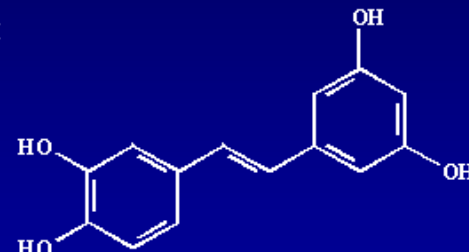
Natural  
product  
empiric lead



erbstatin



lavendustin

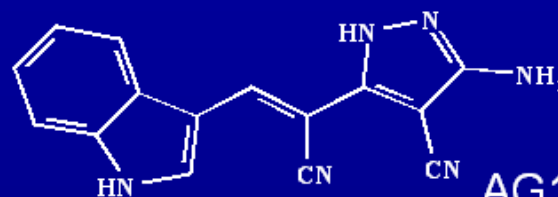


piceatannol

1st generation  
synthetic

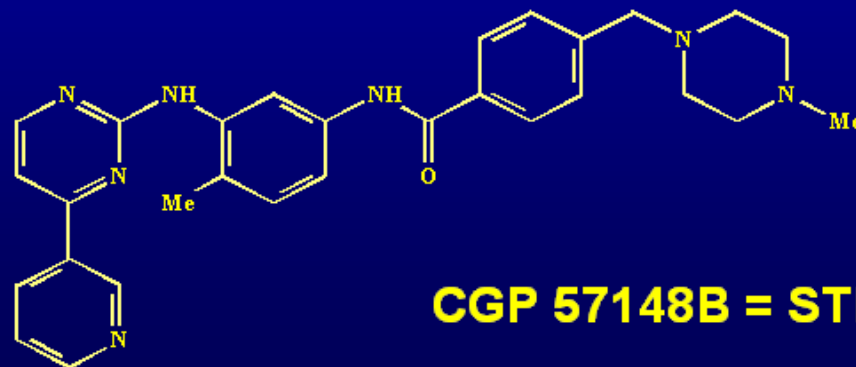


AG957



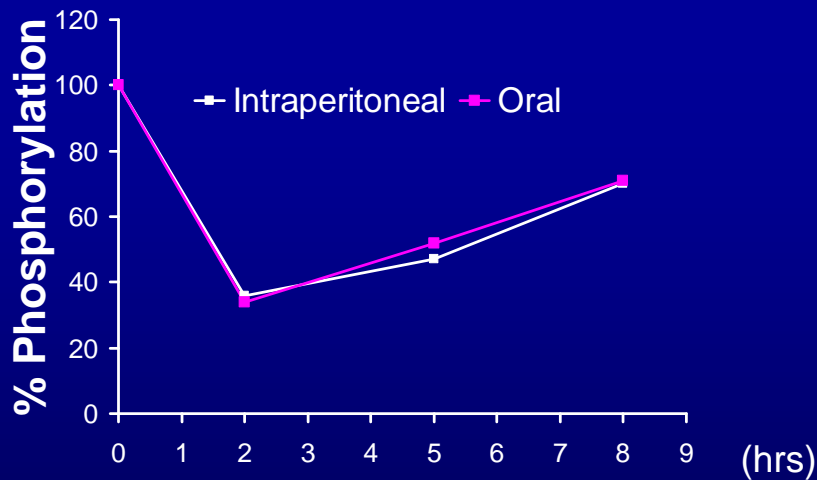
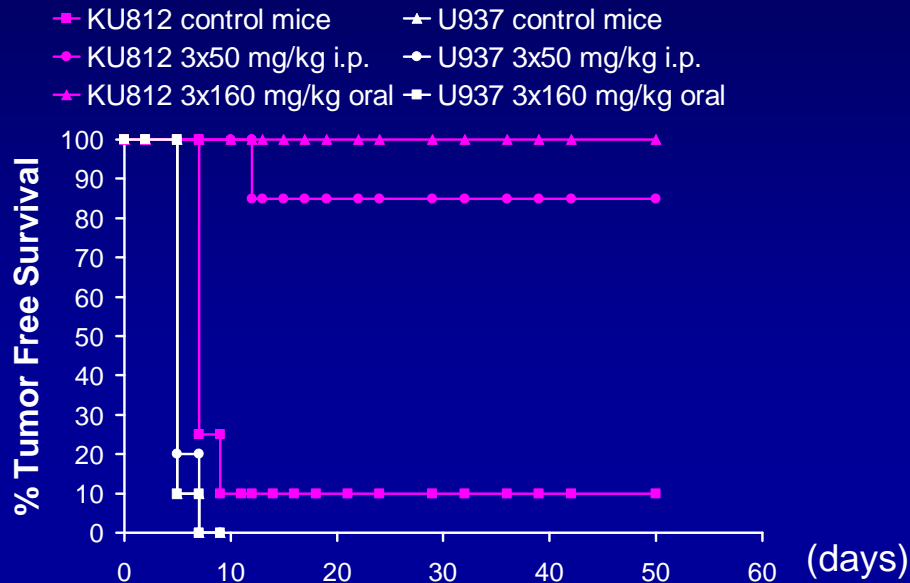
AG1112

2nd generation  
synthetic;  
in clinic

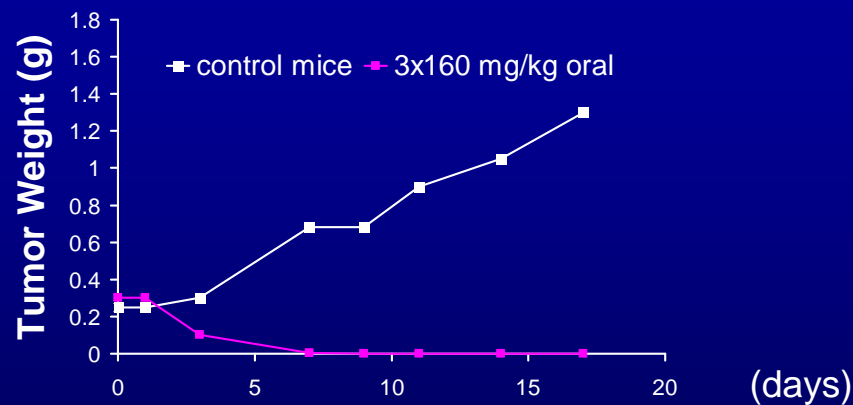


**CGP 57148B = STI571**

# STI571: An oral in vivo bcr-abl kinase inhibitor



Tyr phosphorylation *in vivo*

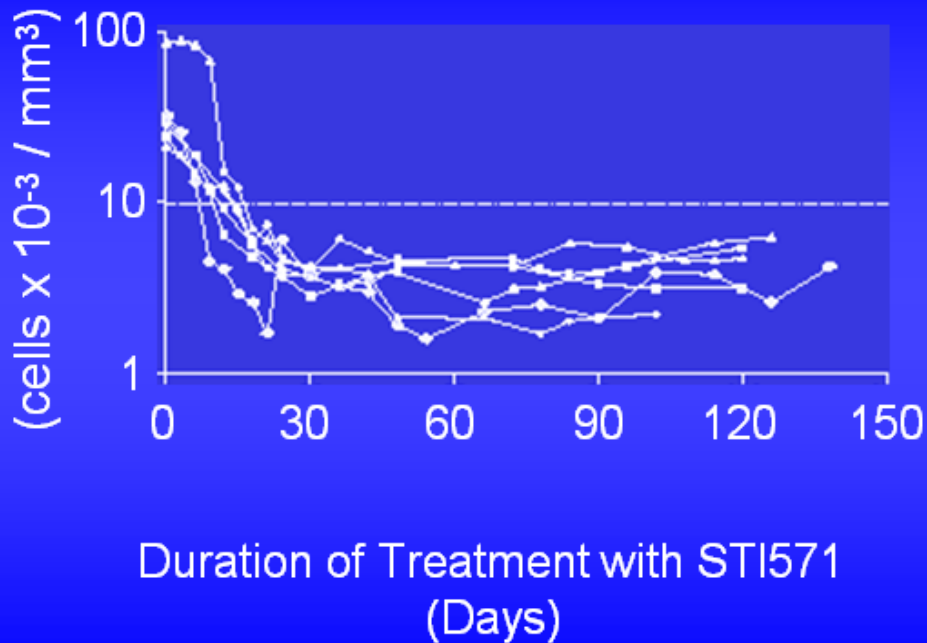


Antitumor activity *in vivo*

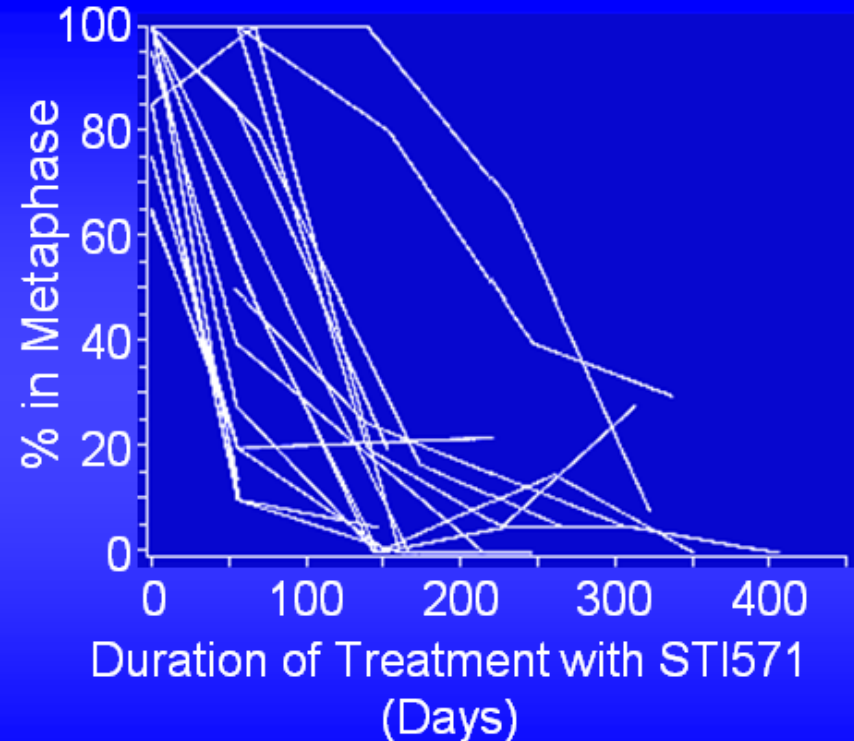
# EFFICACY AND SAFETY OF A SPECIFIC INHIBITOR OF THE BCR-ABL TYROSINE KINASE IN CHRONIC MYELOID LEUKEMIA

BRIAN J. DRUKER, M.D., MOSHE TALPAZ, M.D., DEBRA J. RESTA, R.N., BIN PENG, PH.D.,  
ELISABETH BUCHDUNGER, PH.D., JOHN M. FORD, M.D., NICHOLAS B. LYDON, PH.D., HAGOP  
KANTARJIAN, M.D.,  
RENAUD CAPDEVILLE, M.D., SAYURI OHNO-JONES, B.S., AND CHARLES L. SAWYERS, M.D.

## White Cell Count



## Ph Chromosome + Cells



# MOLECULAR TARGET DEFINITION - HOW TO?

- **BIOLOGY:**

- \* Cytogenetics → Breakpoints → Molecules (bcr-abl)
- \* “Positive” selection from tumor DNA → Active oncogenes  
(signal transduction)
- \* Tumor gene expression profiling (CGAP)

- **“RETROFIT” ACTIVE MOLECULES:**

- \* Binding partners (geldanamycin, rapamycin, fumagillin)
- \* Computational algorithm (molecule ↔ target)
  - COMPARE
  - Cluster analysis

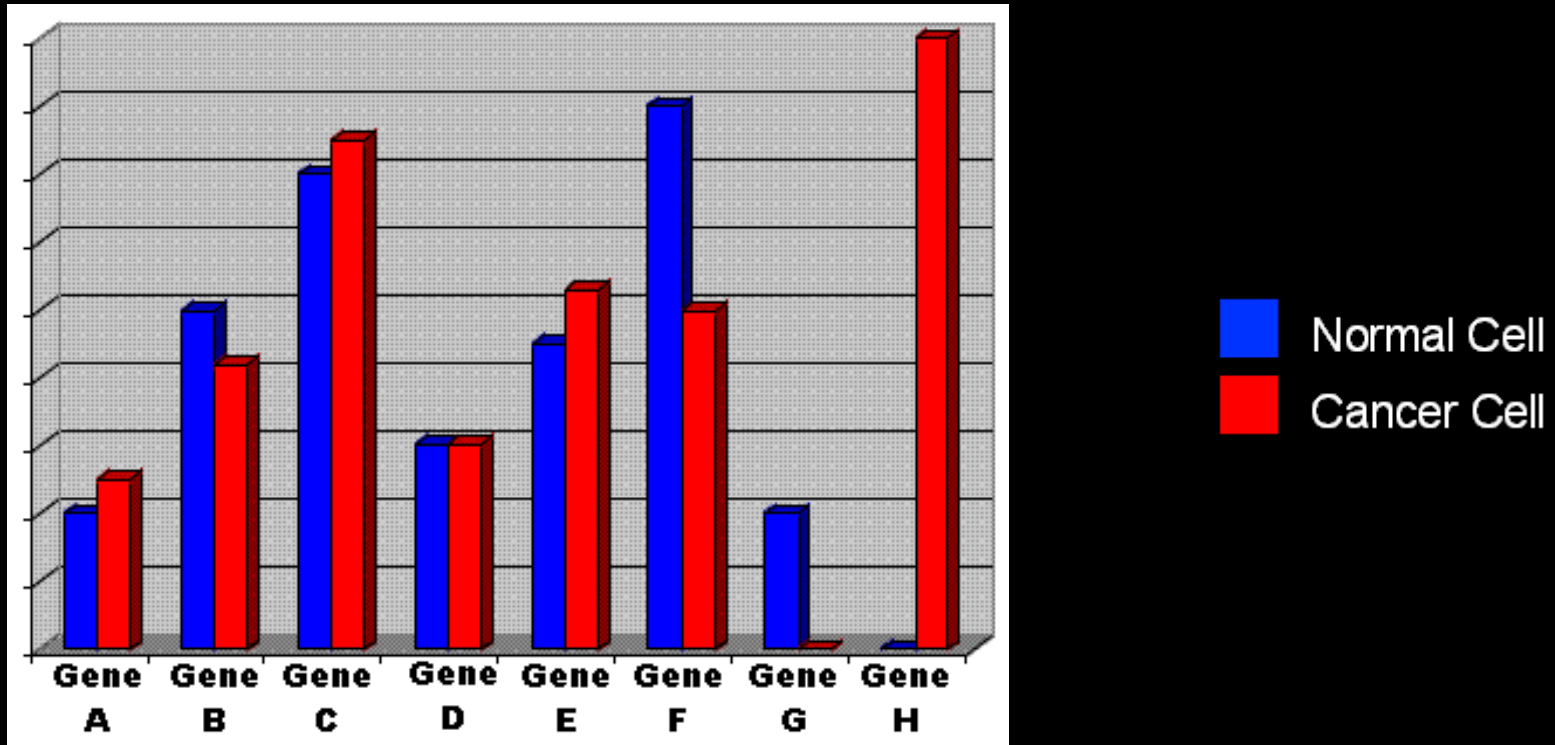
- **“CLASSICAL:”**

- \* Cell metabolism / Biochemistry
- \* Suggest single targets → Inefficient; Medicinal Chemistry possible

- **CHEMICAL GENETICS:**

- \* Libraries of molecules and precisely defined organisms

## Gene Expression: The Cell's Fingerprint



Establishing for a cell the repertoire of genes expressed, together with the amount of gene products produced for each, yields a powerful "fingerprint". Comparing the fingerprints of a normal versus a cancer cell will highlight genes that by their suspicious absence or presence (such as Gene H ) deserve further scientific scrutiny to determine whether such suspects play a role in cancer, or can be exploited in a test for early detection.

NATIONAL CANCER INSTITUTE

NCBI

NINDS

NIDCR

NIAID

CIT

CGAP INITIATIVES:



The Cancer Genome Anatomy Project



HUMAN  
TUMOR GENE  
INDEX



MOLECULAR  
FINGER-  
PRINTING



CANCER  
CHROMOSOME  
ABERRATION  
PROJECT



GENETIC  
ANNOTATION  
INITIATIVE

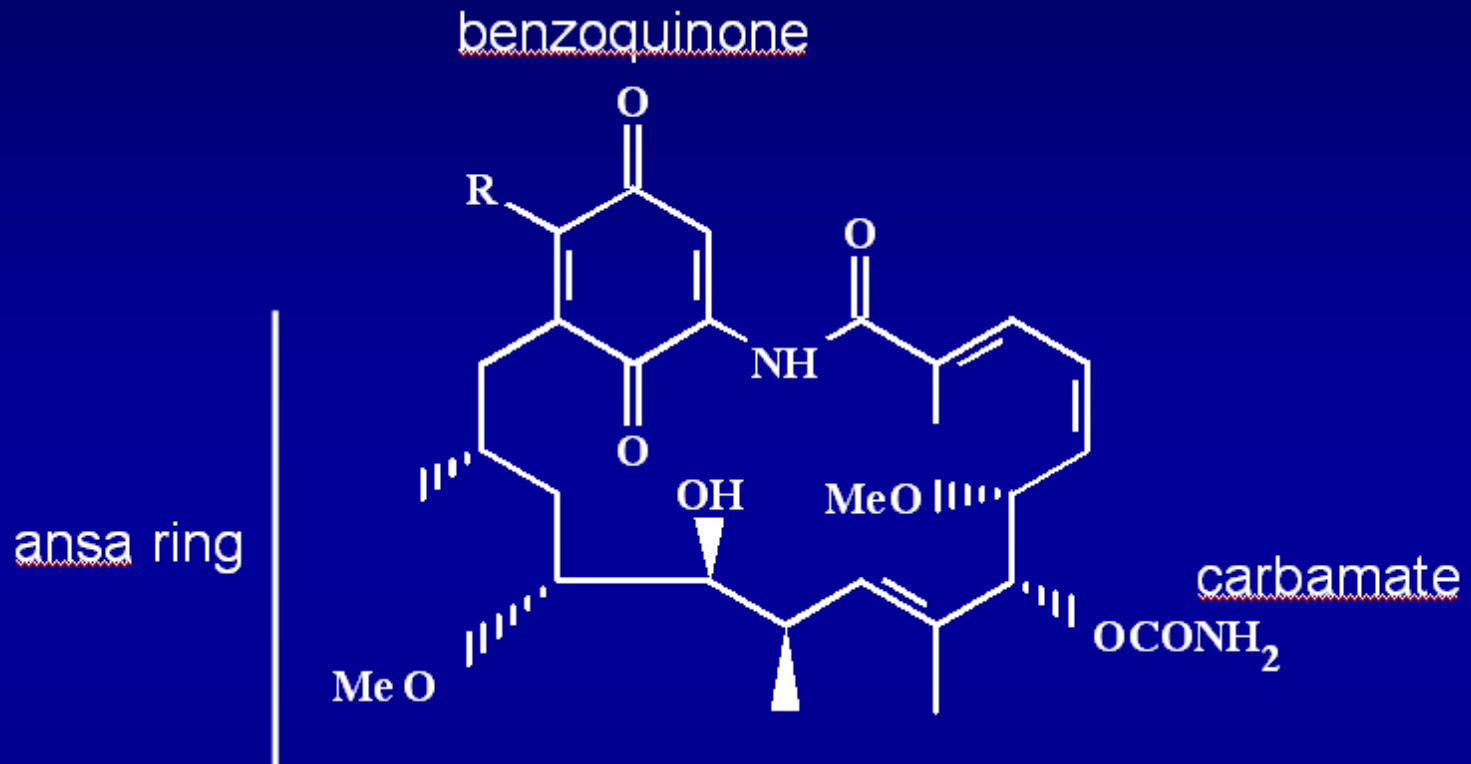


MOUSE  
TUMOR GENE  
INDEX





# GELDANAMYCIN: EXAMPLE OF BINDING PARTNER DEFINING TARGET



	<b>NSC</b>	<b>R</b>
Geldanamycin	122750	<u>OMe</u>
17-AAG	330507	NHCH <sub>2</sub> CH=CH <sub>2</sub>

# BENZOQUINOID ANSAMYCINS

## INITIAL CELL PHARMACOLOGY - I

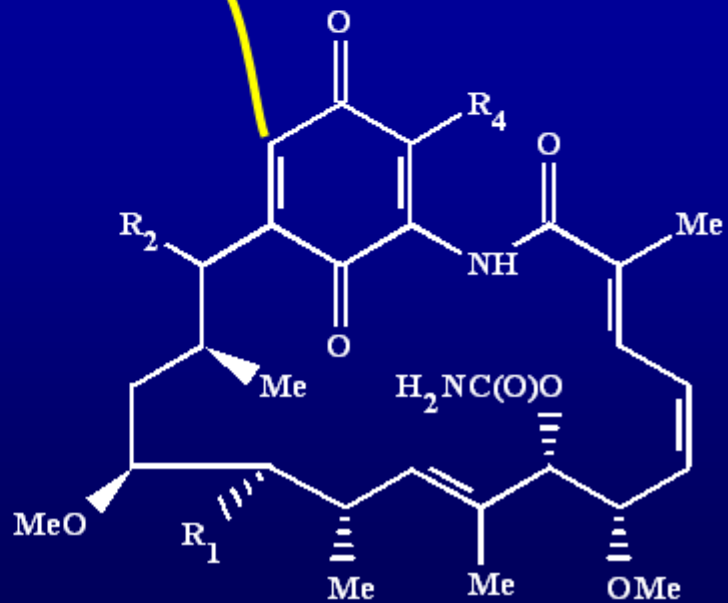
- \* “Reverse” transformed phenotype of src-transformed rat kidney cell line
  - decrease tyrosine phosphorylation of pp60src
  - not inhibit pp60 immune complex kinase directly but these were inhibited from drug-treated cells (Uehara et al, MCB 6: 2198, 1986)
  - thus alter “intracellular environment” of src
- \* Decrease steady state phosphorylation levels to 10% of control
  - decrease steady state level of pp60src by 30%
  - accelerate turnover of pp60src

(Uehara et al, Cancer Res 49: 780, 1989)

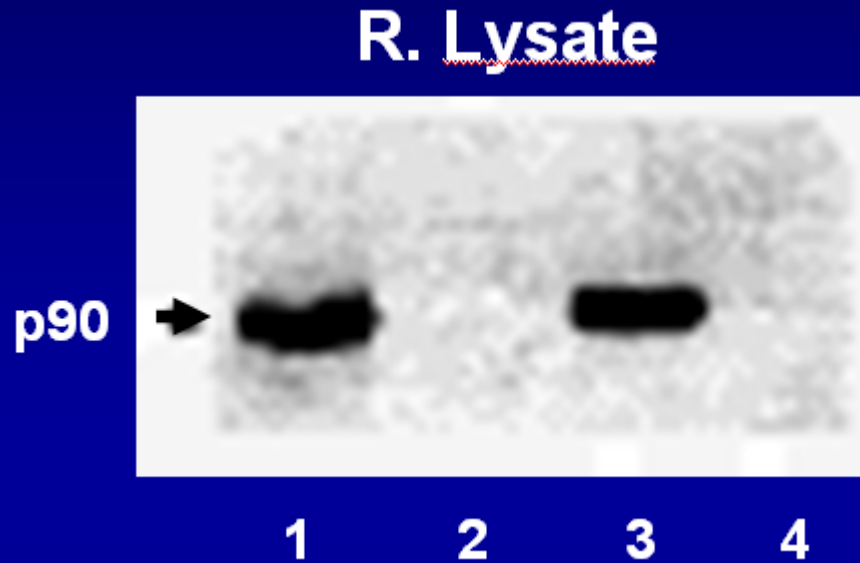


Bead

18 Atom Spacer



# GELDANAMYCIN BEADS IDENTIFY HSP90 AS BINDING PARTNER

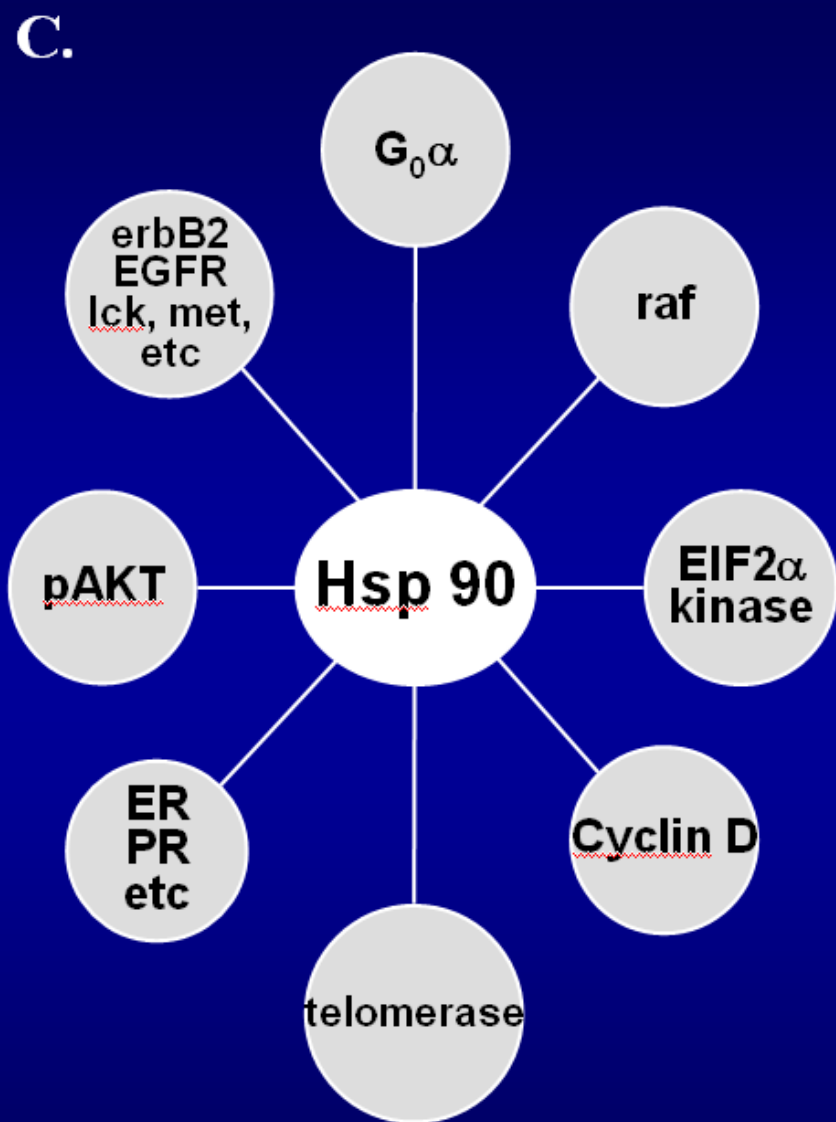
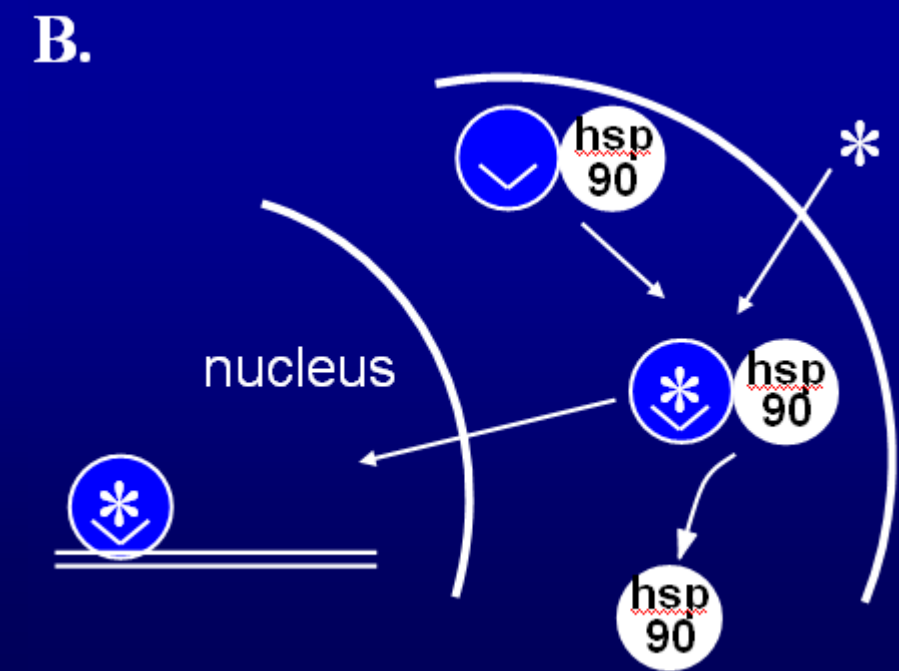
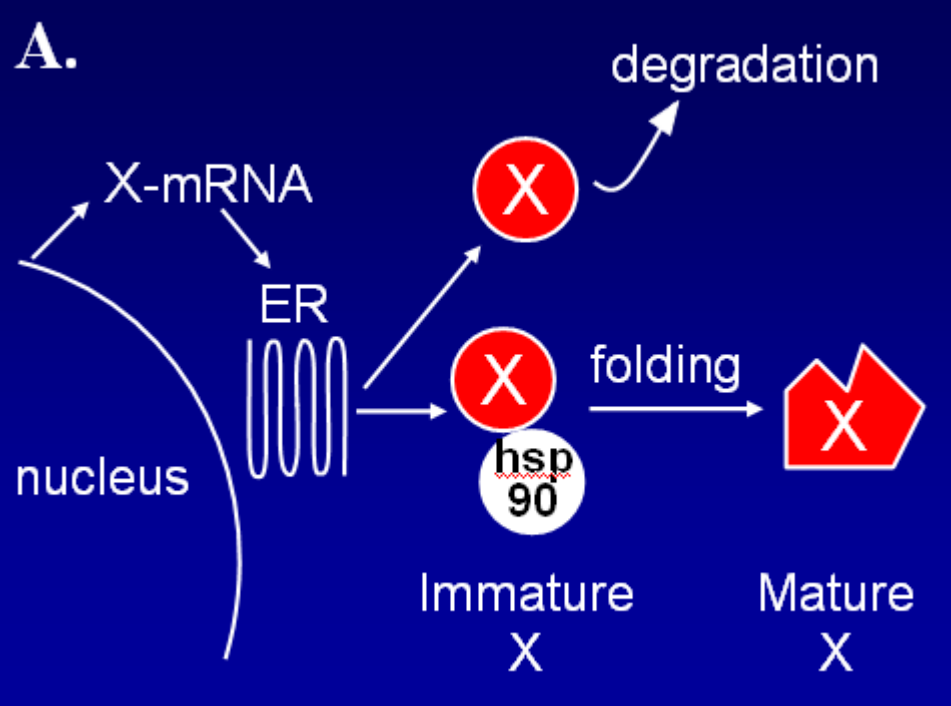


1) Bead-Geld

3) Bead-Geld + Geldampicin

2) Bead-Geld + Geld

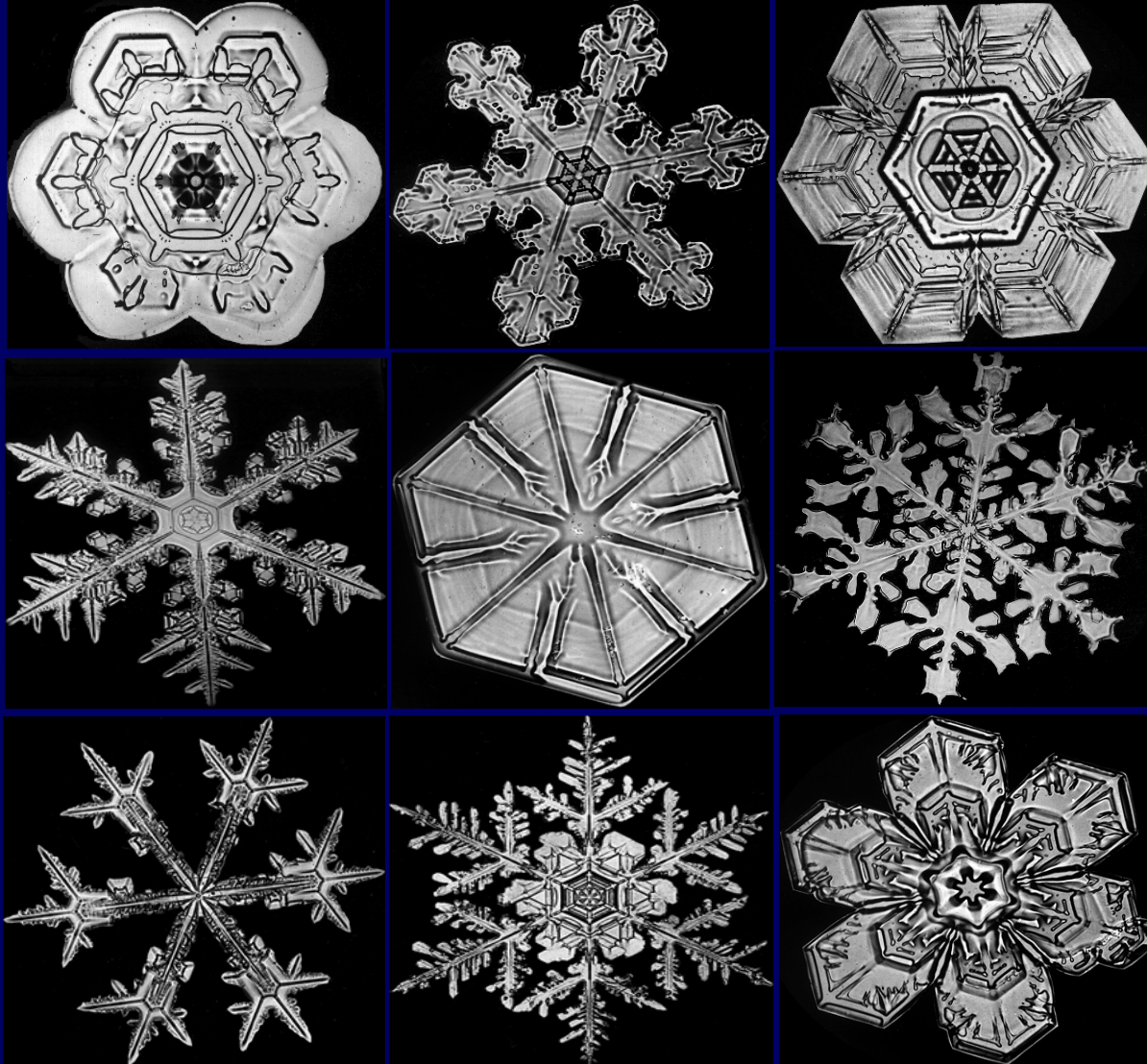
4) Bead



# OUTLINE OF PRESENTATION

- \* General Introduction
- \* Definition of Drug Targets
- \* ***Generating Diversity***
- \* Definition of Lead Structures
- \* Qualifying Lead for Transition to Early Trials

# Diversity



It is estimated that there are  $10^{40}$  compounds in all of "chemical space". Since the Big Bang, there have only been  $10^{17}$  seconds.

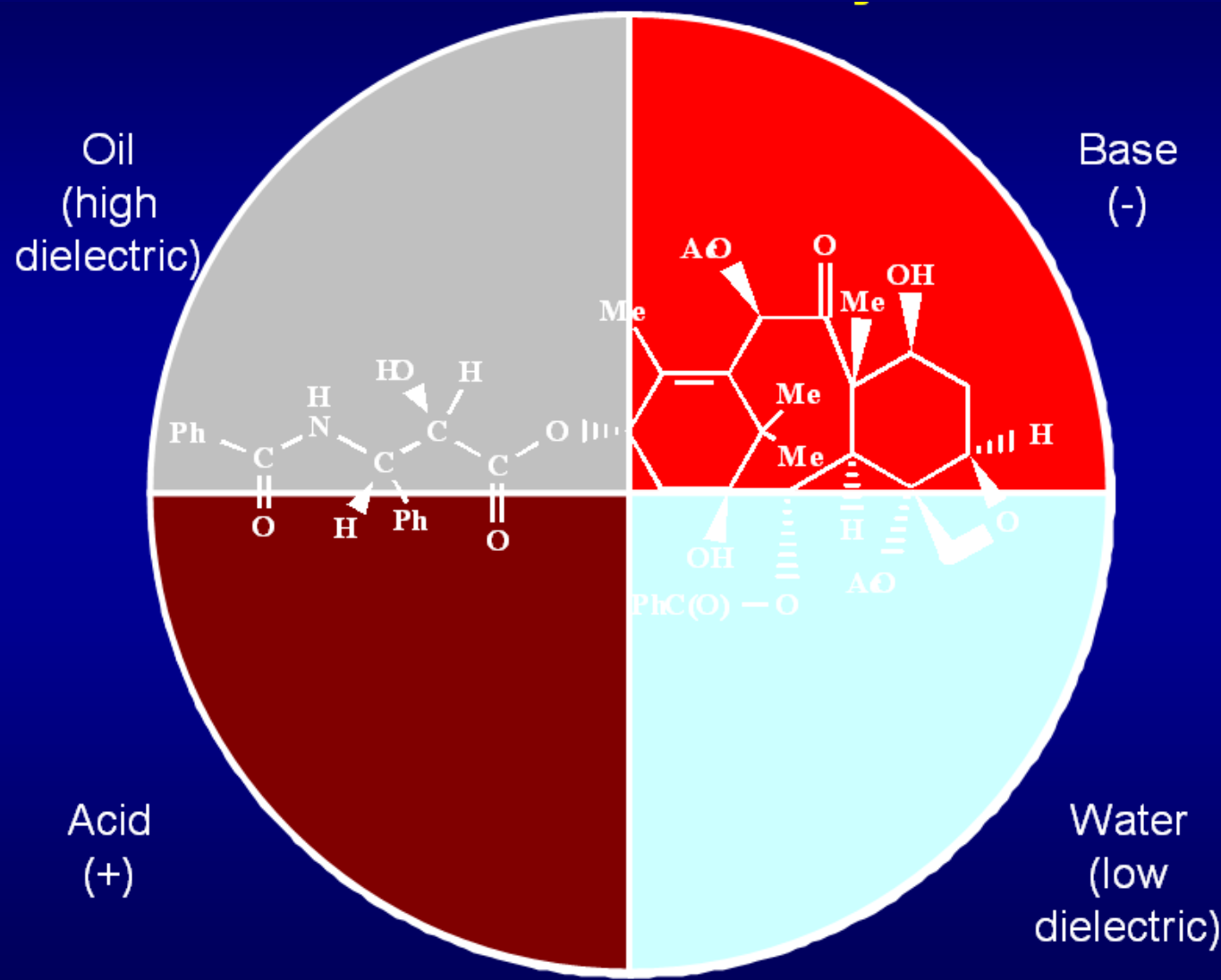
- Peter Wipf



# SOURCES OF DIVERSITY

- \* “Natural Products” = entities derived from plants, animals, bacteria, etc. May have “ethnopharmacognosy” to suggest use
  - “pure compound” collections
  - extracts: aqueous/organic
  - genetically altered producer organisms
- \* Target non-selected chemical compound libraries
  - peptide / protein
  - non-peptide
- \* Target-directed chemical compound libraries
  - “classical” medicinal chemistry / bona fide crystal structure - derived
  - “docked” lead structures into model

# Natural Products: Unique arrays of the four “elements” which make a really useful drug



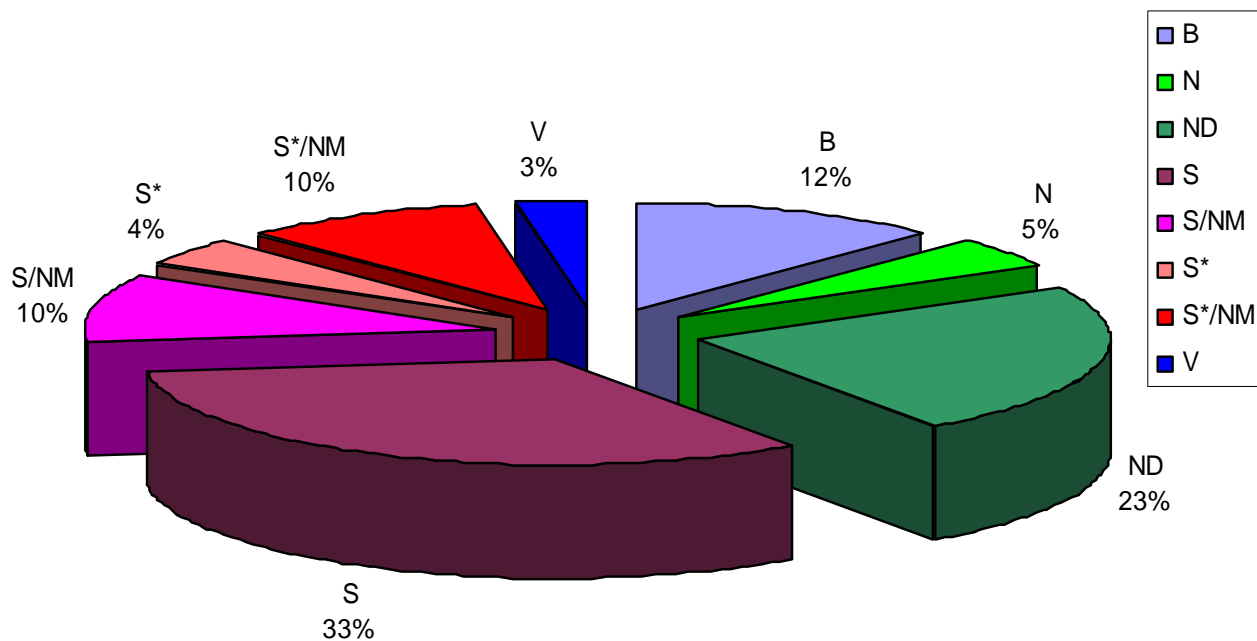
# Sources of "Modern Drugs"

If one looks at the current drug scene from a chemical perspective (data from 1981 - 2002) then the following slides show reasonable approximations of the sources of drugs currently approved, World-wide, by the FDA or equivalent body.

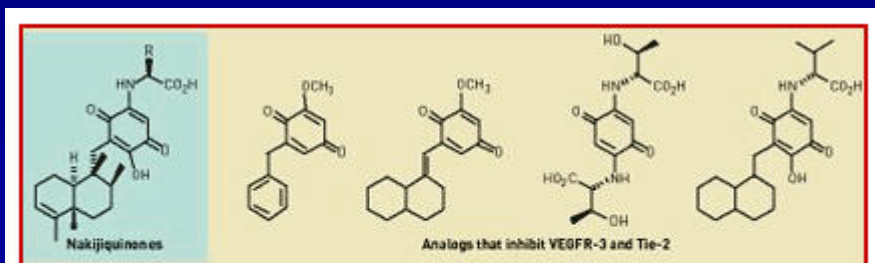
Codes are:

N	Natural Product
ND	Natural Product Derivative
S*	Natural Product Pharmacophore
S	Synthetic Compound
B/V	Biological / Vaccine
(NM)	Natural Product Mimic as a subdivision

# Sources of Drugs (1981-2002); Extended Subdivisions n = 1031



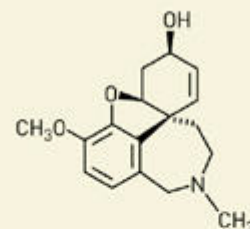
# EXAMPLES OF NP LEAD GENERATION OF NOVEL SCAFFOLDS



**GUIDED BY NATURE** A compound library developed around nakijiquinones, which are natural inhibitors of the receptor tyrosine kinase called Her-2/Neu, produced analogs that inhibit two other receptor tyrosine kinases, VEGFR-3 and Tie-2.

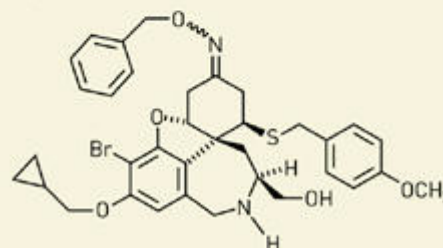
## NATURE LEADS

A library based on a natural product ...



Galanthamine, an antiedementia drug

... turns up a new compound with a different activity



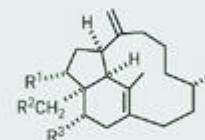
Secramine, a galanthamine-based molecule that blocks protein trafficking

## INSECT CHEMISTRY

Nasute termites ...

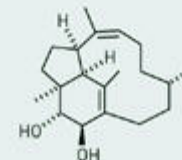


... are rich in trinervitane compounds



$R^1, R^2, R^3 = \text{OH}$   
 $R^1, R^2 = \text{OH}; R^3 = \text{H}$   
 $R^1 = \text{OAc}; R^2, R^3 = \text{OH}$   
 $R^1 = \text{OH}; R^2, R^3 = \text{OAc}$   
 $R^1, R^2, R^3 = \text{OAc}$

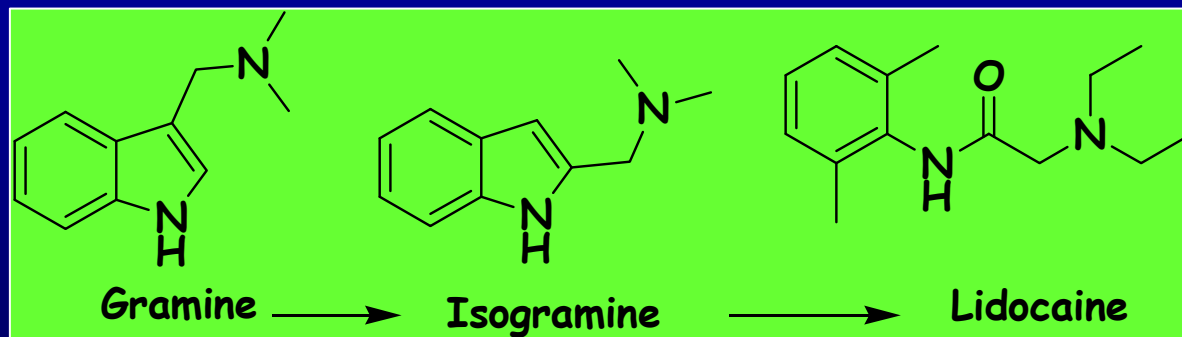
Ac = acetyl



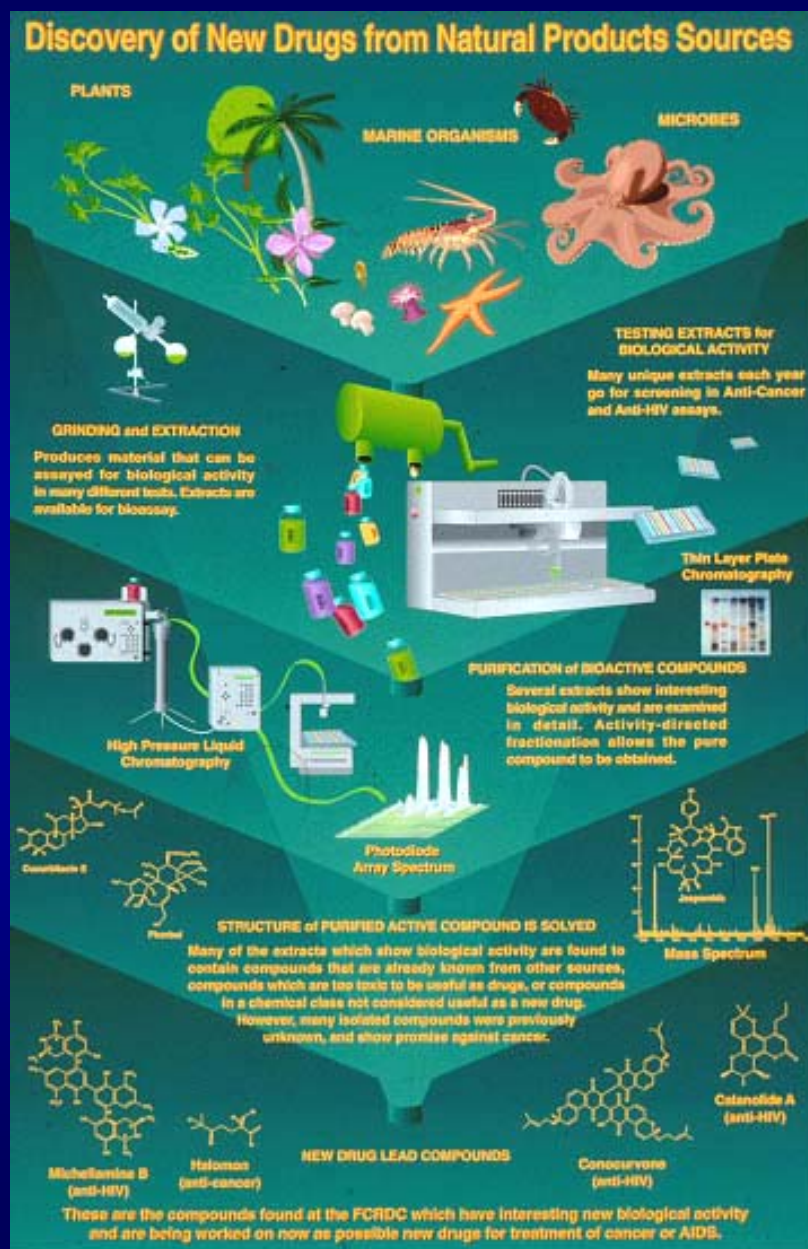
CSIRO PHOTO

# Discovery of Lidocaine

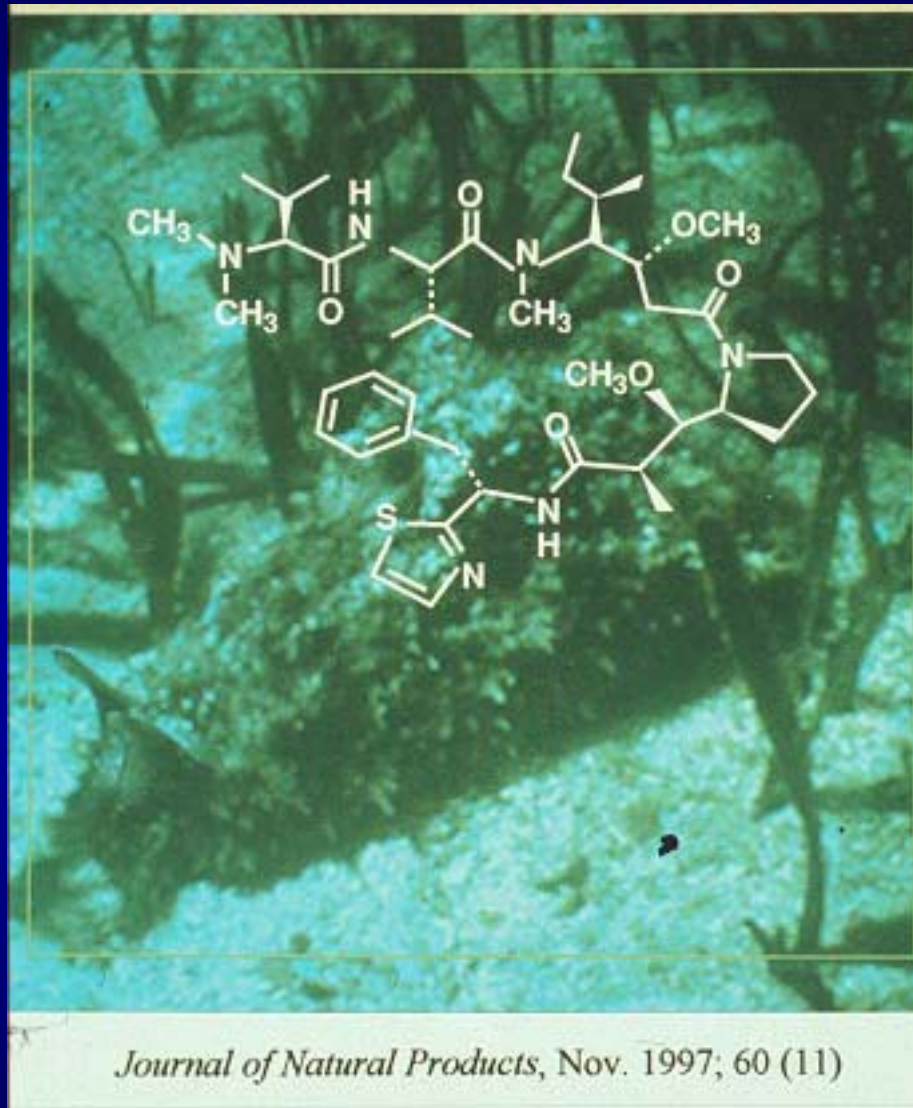
- \* Central Asian camels refused to eat a certain type of reed
- \* Characterization of gramine as the antifeedant principle led to the synthesis of isogramine
- \* Taste-test: numbness; therefore, lead for anesthetic agent development



# Natural Product Isolation Tree



# “You are what you eat”



*Dolabella auricularia*

Dolastatins come from a *Symploca* species that they graze on



# **“Non-culturable” versus “Cultured” microbes**

- \* The microbial World has only just been scratched.
  - Much less than 1% of the available organisms have even been seen, let alone identified.****
- \* In soil, there are estimates of > 1000 species per gram
  - very few can be cultured**
  - these may not be representative of the “Soil meta-Genome”****
- \* Over 1000 microbes per mL of seawater can be seen and only 1% can be cultured using current methods.**

# SOURCES OF DIVERSITY

- \* “Natural Products” = entities derived from plants, animals, bacteria, etc. May have “ethnopharmacognosy” to suggest use
  - “pure compound” collections
  - extracts: aqueous/organic
  - genetically altered producer organisms
- \* Target non-selected chemical compound libraries
  - peptide / protein
  - non-peptide
- \* Target-directed chemical compound libraries
  - “classical” medicinal chemistry / bona fide crystal structure - derived
  - “docked” lead structures into model

# TRIPEPTIDE COMBINATORIAL LIBRARY

X X X

Four amino acids in each position

$$4^3 = 64$$

A = Alanine

R = Arginine

T = Threonine

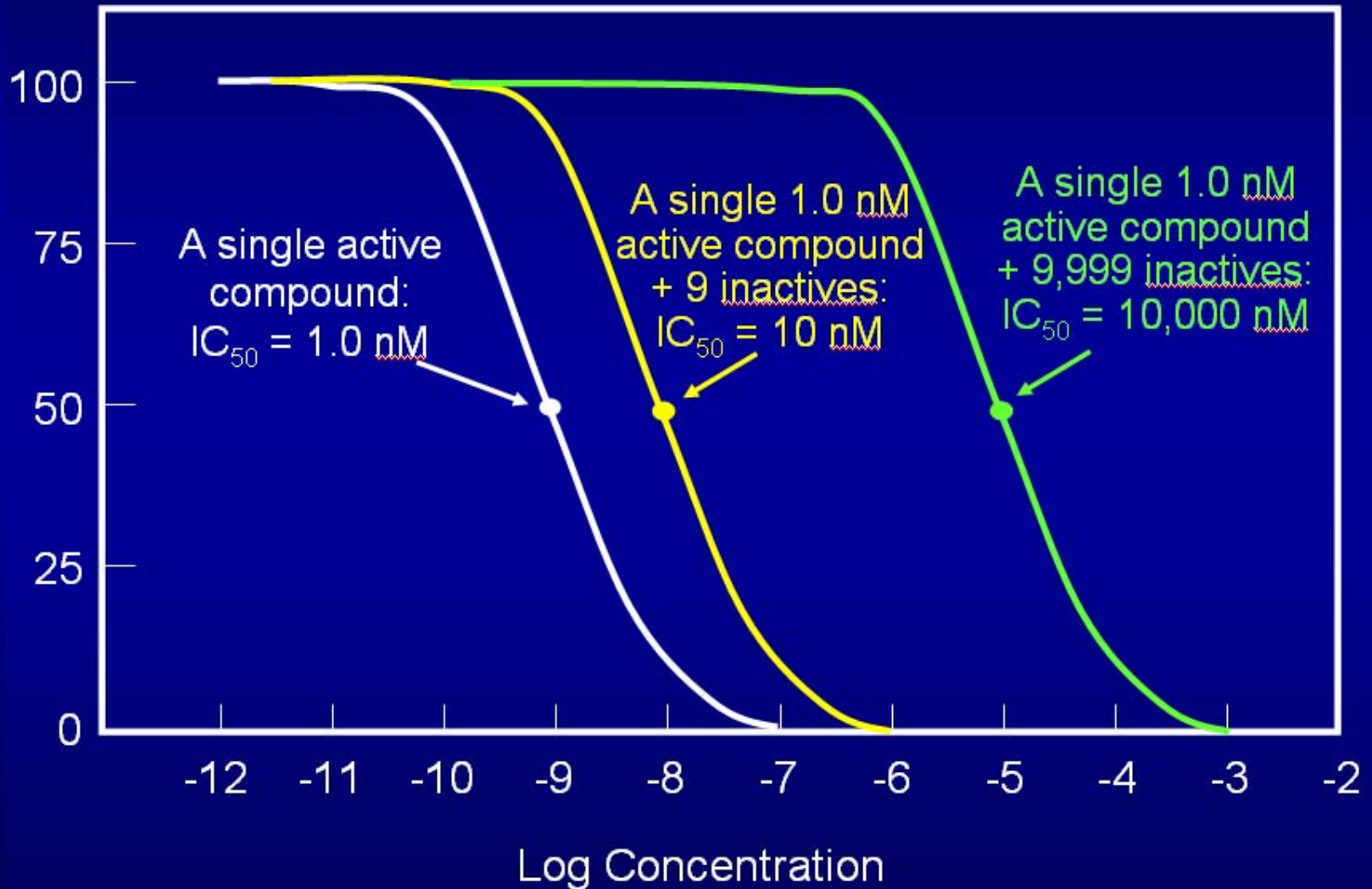
W = Tryptophan

# NUMBER OF PEPTIDES POSSIBLE WITH INCREASING LENGTH

Length	Peptide	Number
2	Ac – OO – NH <sub>2</sub>	400
3	Ac – OOO – NH <sub>2</sub>	8,000
4	Ac – OOOO – NH <sub>2</sub>	160,000
5	Ac – OOOOO – NH <sub>2</sub>	3,200,000
6	Ac – OOOOOO – NH <sub>2</sub>	64,000,000
7	Ac – OOOOOOO – NH <sub>2</sub>	1,280,000,000
8	Ac – OOOOOOOO – NH <sub>2</sub>	25,600,000,000

O = Individual Defined Amino Acid

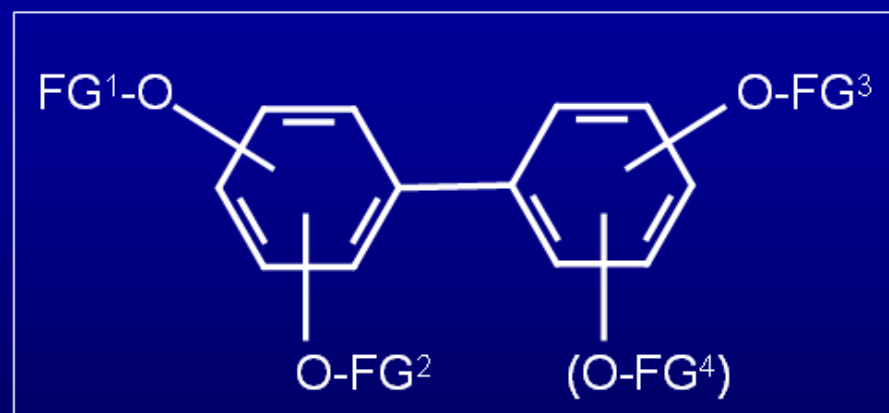
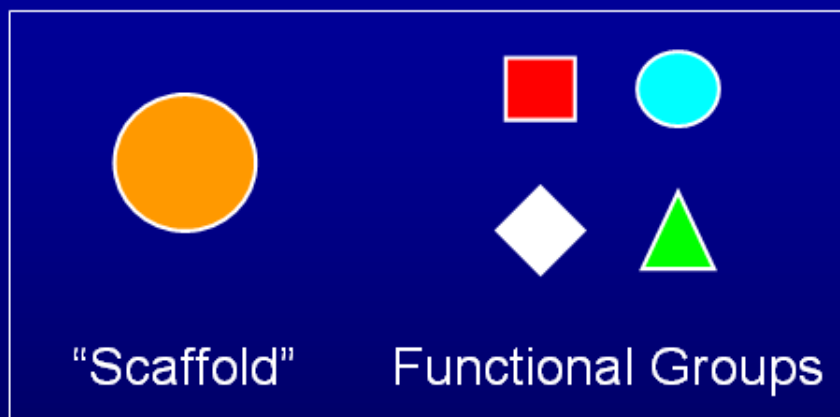
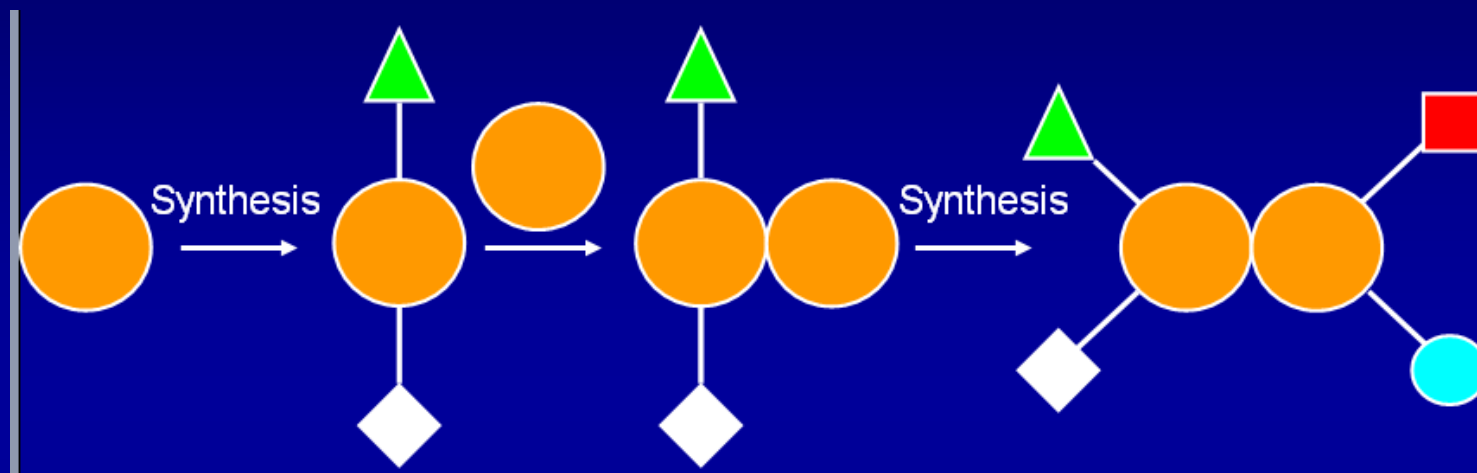
# IC<sub>50</sub> OF MIXTURES



# COMBINATORIAL LIBRARIES: THE MIXTURE QUESTION

	Natural Product Extracts	Synthetic Combinatorial Mixtures
Direct screening of compound mixtures	Yes	Yes
Discovery of highly active compounds	Yes	Yes
Equal concentrations of compounds	No	Yes
Chemical structures known	No	Yes
Synthetic pathway known	No	Yes
Structure – activity relationship known	No	Yes

# NON-PEPTIDE “COMBINATORIAL” STRATEGIES COMBINE “SCAFFOLDS” (OR “BACKBONES”) WITH “FUNCTIONAL GROUPS”



# THE RULE OF FIVE

An awareness tool for discovery chemists:

Compounds with two or more of the following characteristics are flagged as likely to have poor oral absorption

- \* More than 5 H-bond donors
- \* Molecular weight >500
- \*  $c \log P > 5$
- \* Sum of N's and O's (a rough measure of H-bond acceptors) > 10

Modern Drug Discovery

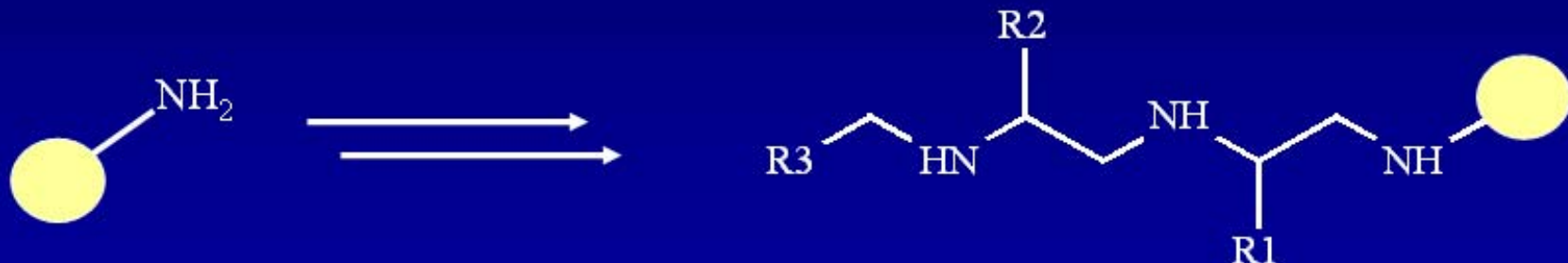
January/February 1999

*Modern Drug Discovery*, 1999, 2 (1), 55-60.

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# COMBINATORIAL LIBRARIES OF BICYCLIC GUANIDINES FROM REDUCED ACYLATED DIPEPTIDES



1.  $\text{CSIm}_2$
2.  $\text{HF/anisole}$



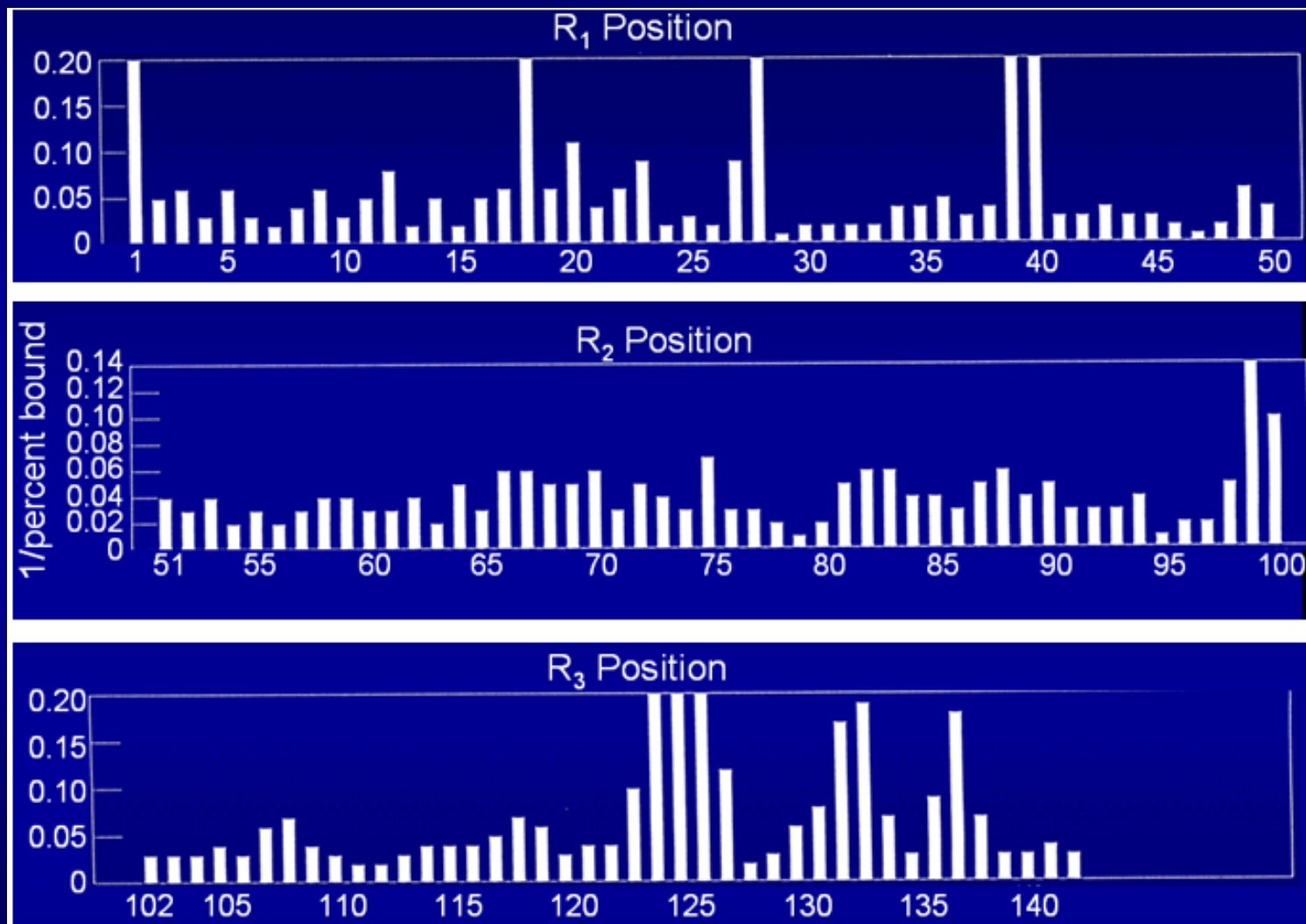
$$\text{R1} \times \text{R2} \times \text{R3} = 49 \times 51 \times 42 = 104,958 \text{ compounds}$$

# BIOASSAYS

## (READY APPLICATION OF SOLUBLE LIBRARIES)

- \* Soluble Acceptors
  - antibodies
  - enzymes
- \* Membrane-bound Receptors
  - tissue homogenate
  - functional cell based
- \* Microorganisms: Disruption of Function
  - bacteria
  - fungi
  - virus
- \* Differentiation
  - stem cells
- \* *In Vivo*

# POSITIONAL SCANNING BICYCLIC GUANIDINE LIBRARY ( $\kappa$ RECEPTOR)



after R. Houghten, 1999

# OUTLINE OF PRESENTATION

- ***Structure based design***

- Biochemical Screen

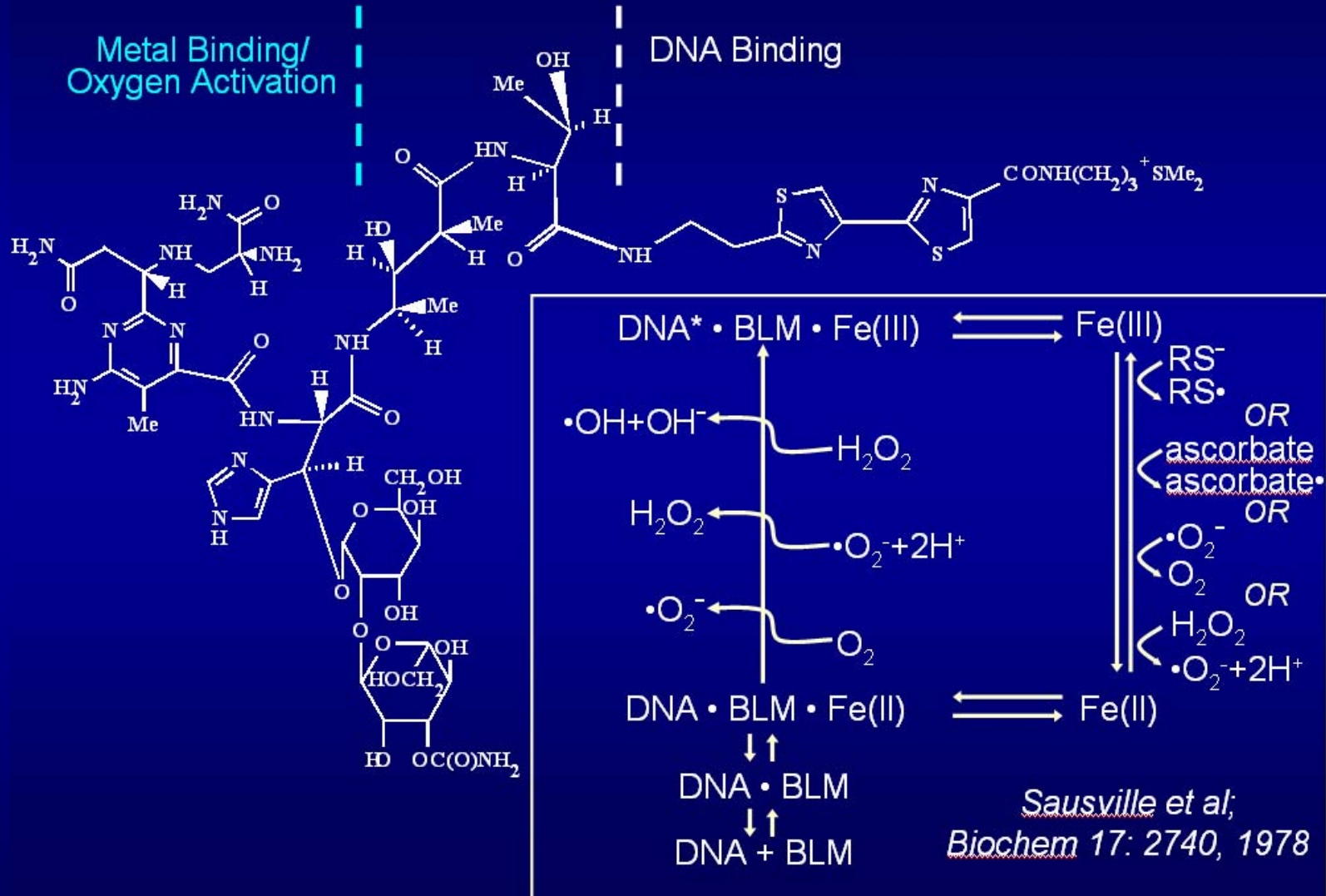
- Cell-based Screen

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# NMR-BASED SCREENING

1. Screen “fragment” like molecules with “leadlike” properties (MW <300; ClogP ~1.5)
2. Characterize **binding** and portion of molecule to which they bind
3. Ligands with weak affinities can be defined ( $\sim K_D = 5\text{mM}$ )
4. Lead to high affinity binders through iterative screening
5. Can label protein of interest with isotopes “sensitive” to ligand effects (e.g. N15) and utilize proton resonances of drug to simultaneously allow definition of ligand and receptor binding sites

# BLEOMYCIN METAL & DNA BINDING DOMAINS



*Sausville et al; Biochem 17: 2740, 1978*

# NMR AS MEANS OF DEFINING BINDING SITES

E.G., BLEOMYCIN BINDING TO DNA

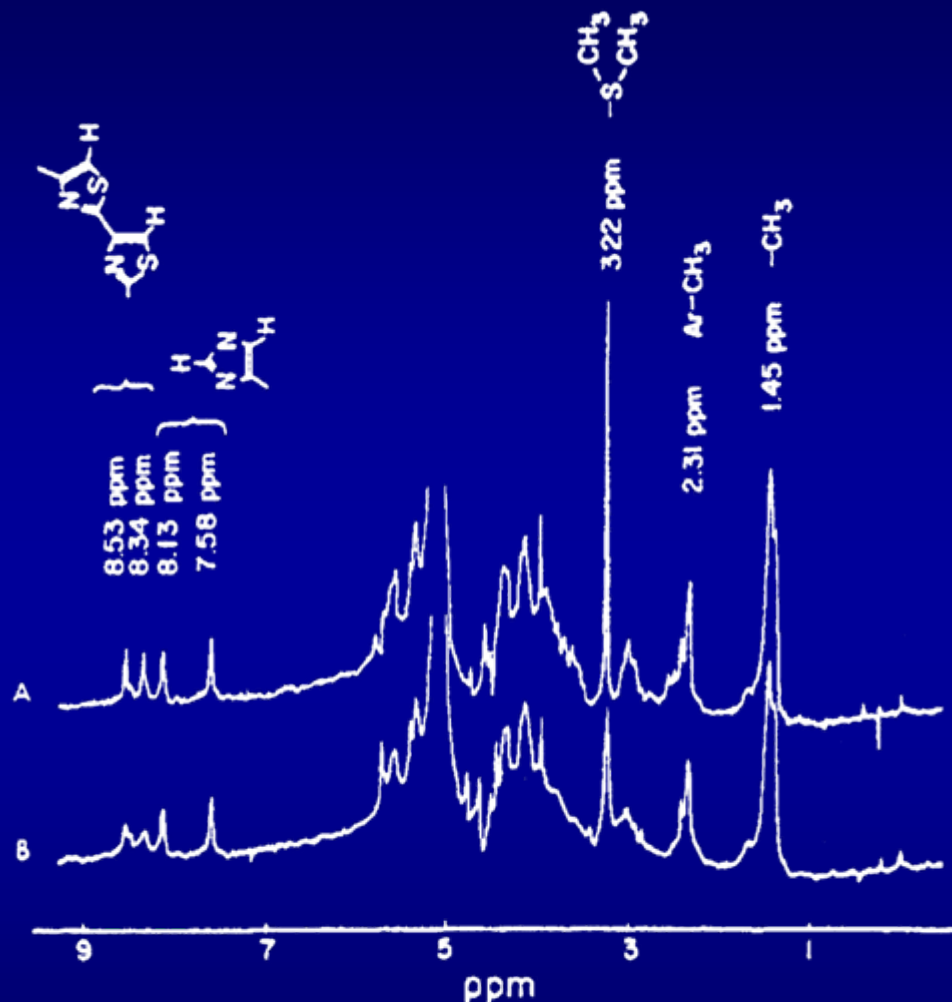
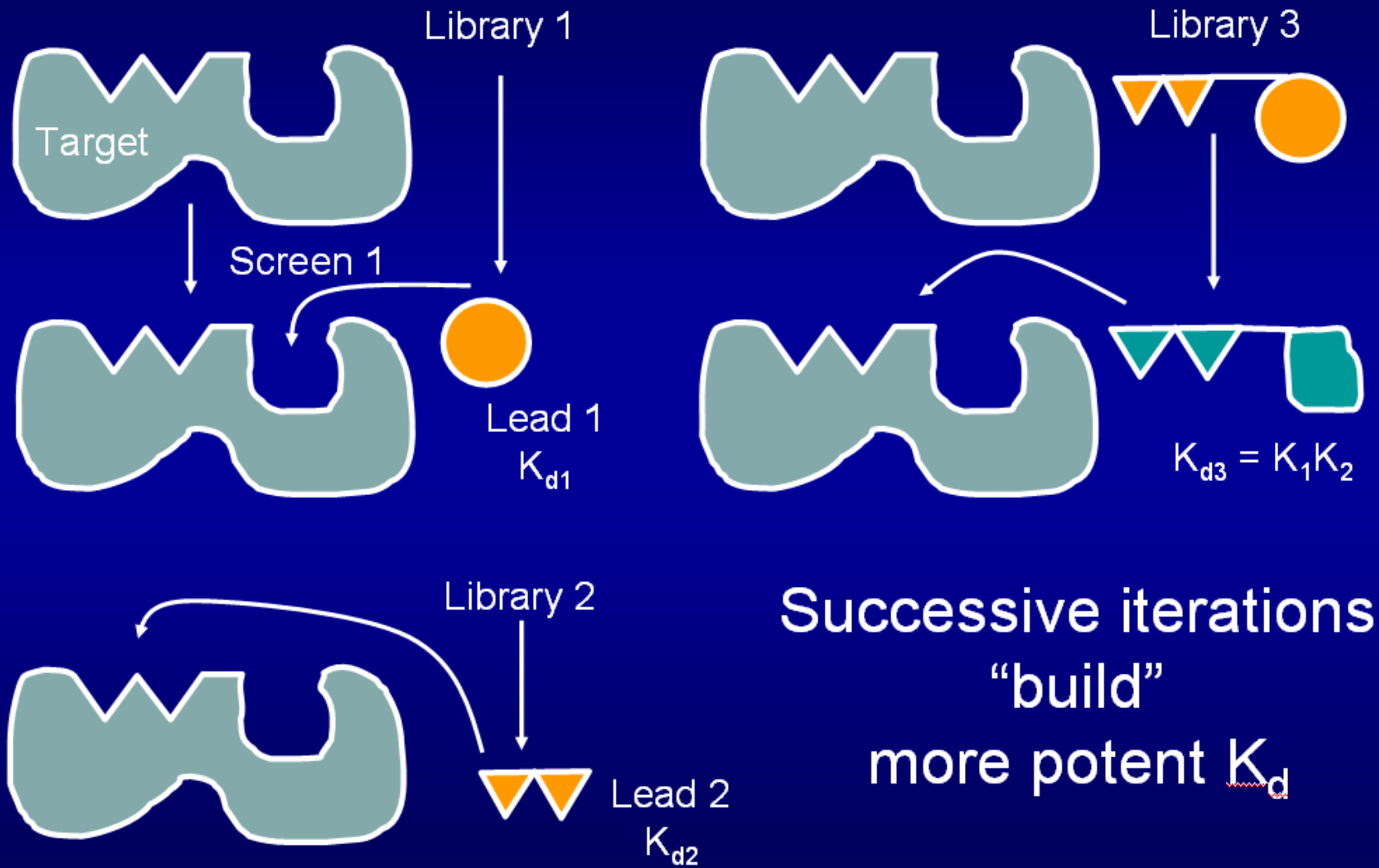




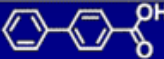
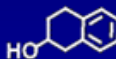
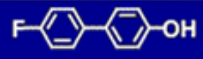
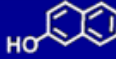
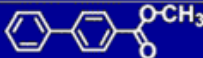

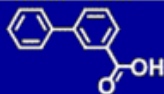
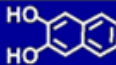
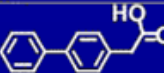
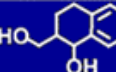
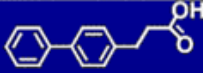
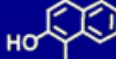
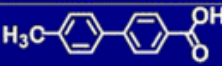

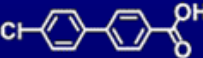
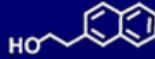
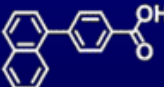
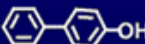
FIGURE 7: <sup>1</sup>H NMR spectra of bleomycin at 100-MHz resolution. Each spectrum is an average of 512 scans. (A) With 6 mM bleomycin in D<sub>2</sub>O at pD 8.4; (B) 6 mM bleomycin and 3.5 mM calf thymus DNA in D<sub>2</sub>O, pD 8.4.

# BUILDING A DRUG LEAD

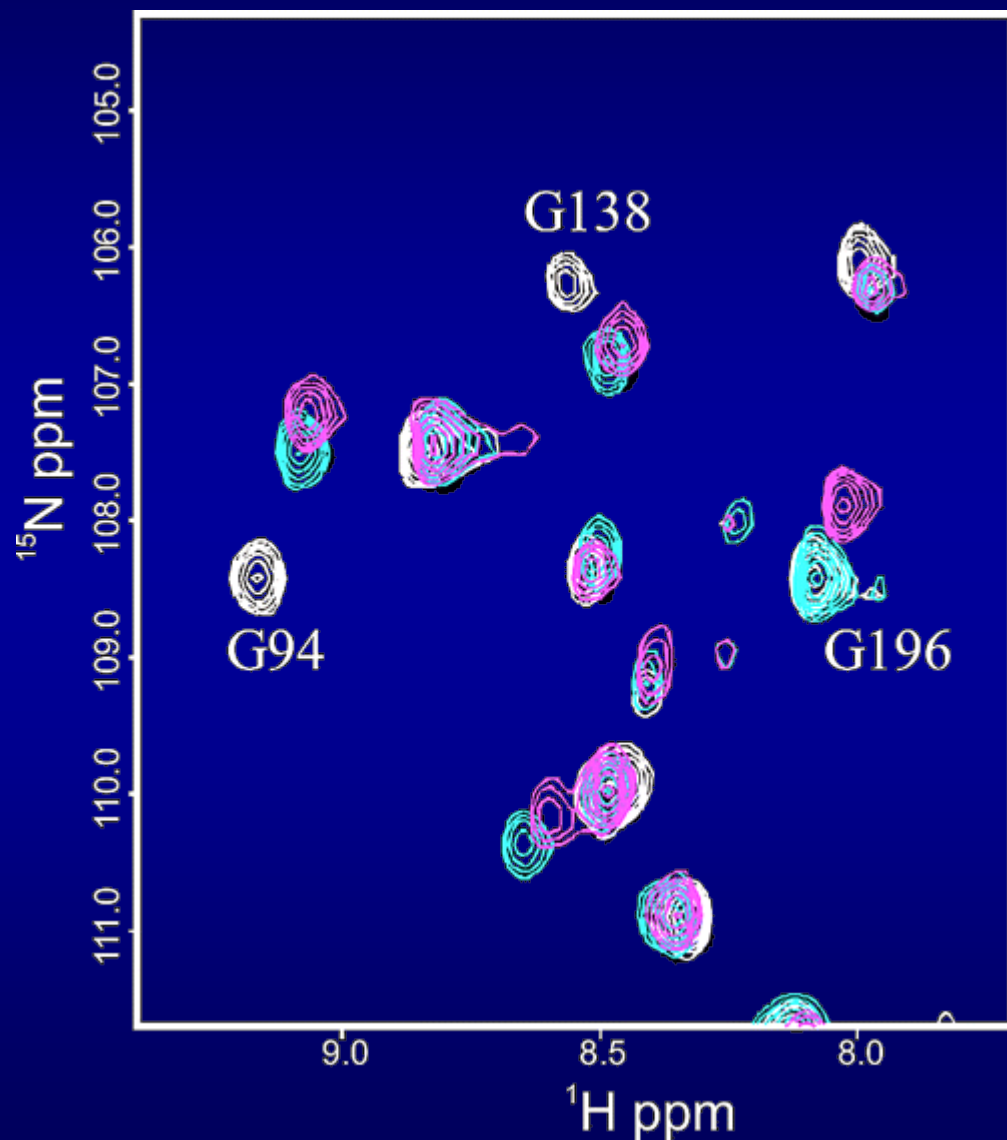




# AFFINITIES OF SELECTED BIARYL COMPOUNDS FOR BCL-XL

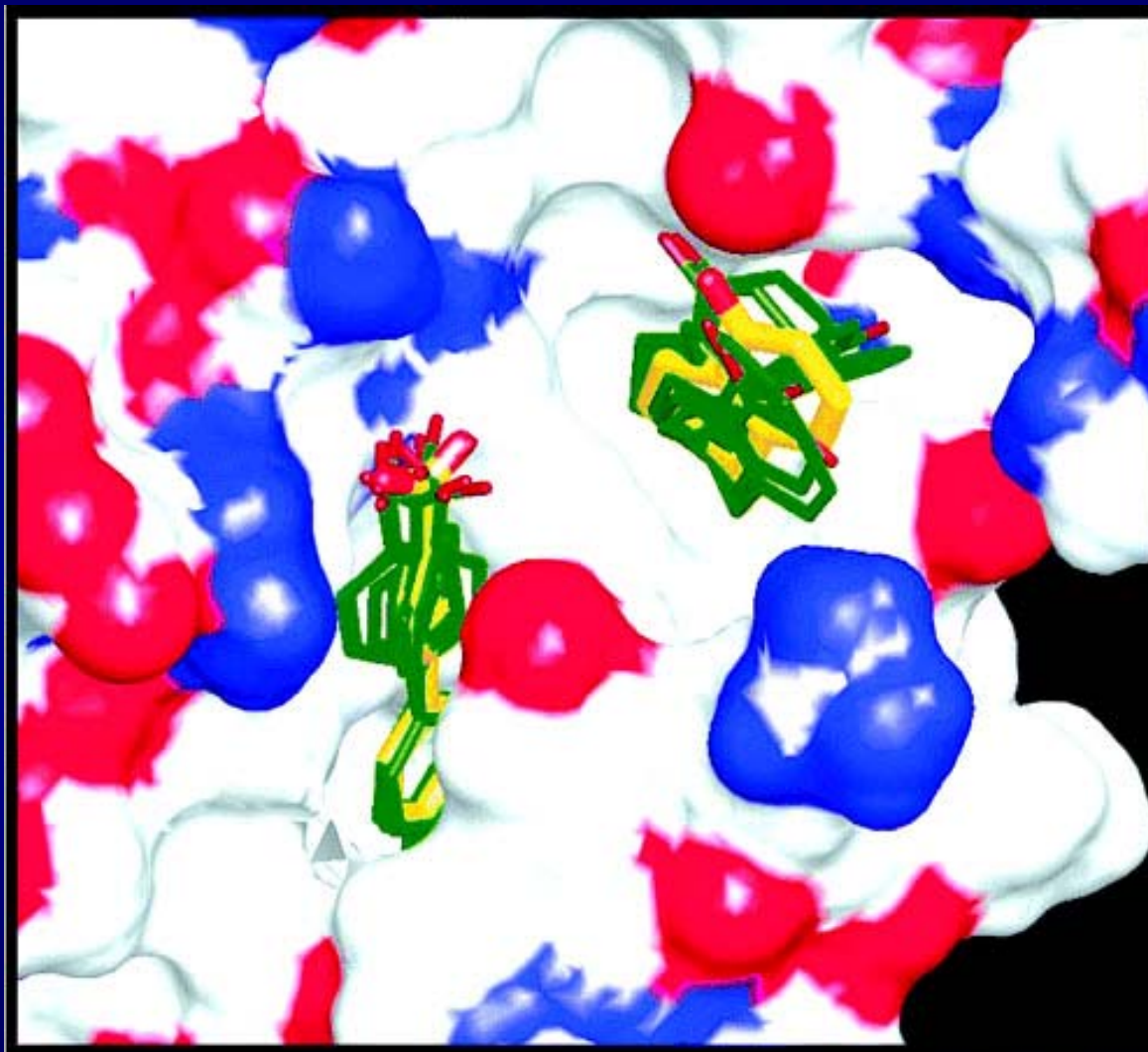
No.	Structure	NMR $K_d$ ( $\mu\text{M}$ )	No.	Structure	NMR $K_d$ ( $\mu\text{M}$ )
1		$300 \pm 30$	11		$4300 \pm 1600$
2		$1200 \pm 530$	12		$13000 \pm 7000$
3		$> 5000$	13		$5000 \pm 2000$
4		$> 5000$	14		$2000 \pm 440$
5		$> 5000$	15		$11000 \pm 4800$
6		$2000 \pm 1600$	16		$13000 \pm 4500$
7		$1990 \pm 990$	17		$9000 \pm 2000$
8		$383 \pm 117$	18		$4000 \pm 2050$
9		$238 \pm 110$	19		$6000 \pm 1970$
10		$250 \pm 139$	20		$6000 \pm 2000$

# SECTION FROM A $^{15}\text{N}$ HSQC SPECTRUM OF BCL-XL IN THE PRESENCE AND ABSENCE OF COMPOUND

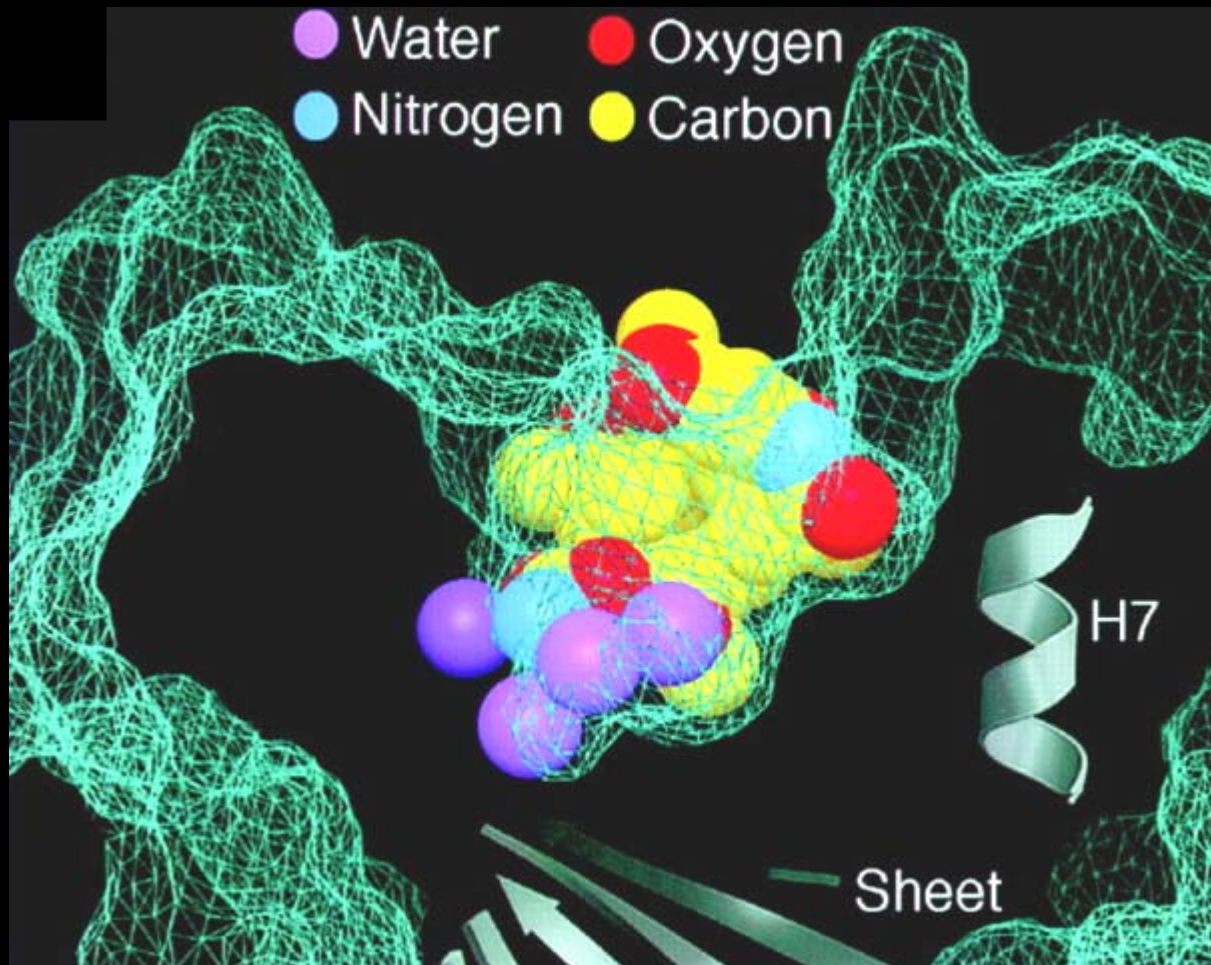


alone (white)  
2 mM biaryl acid **1**  
(cyan)  
2 mM biaryl acid **1** and  
5 mM naphthol  
derivative **11** (pink)

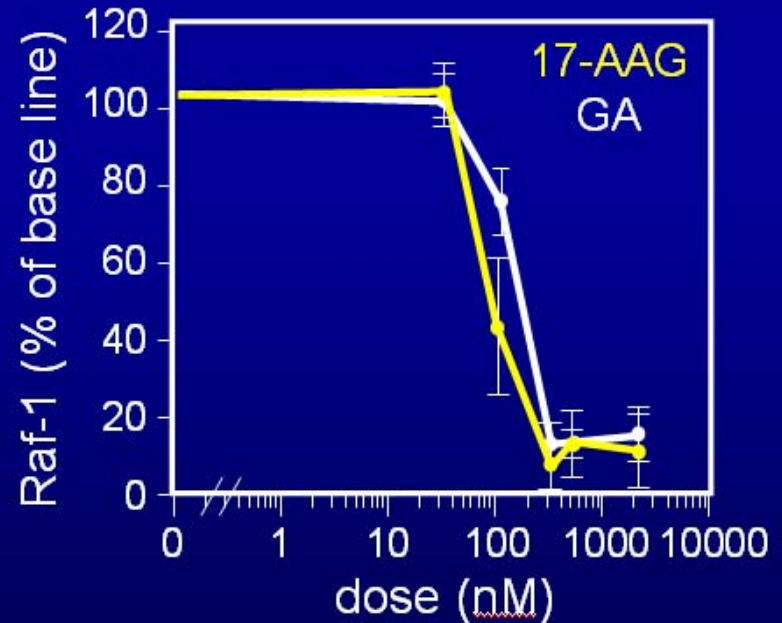
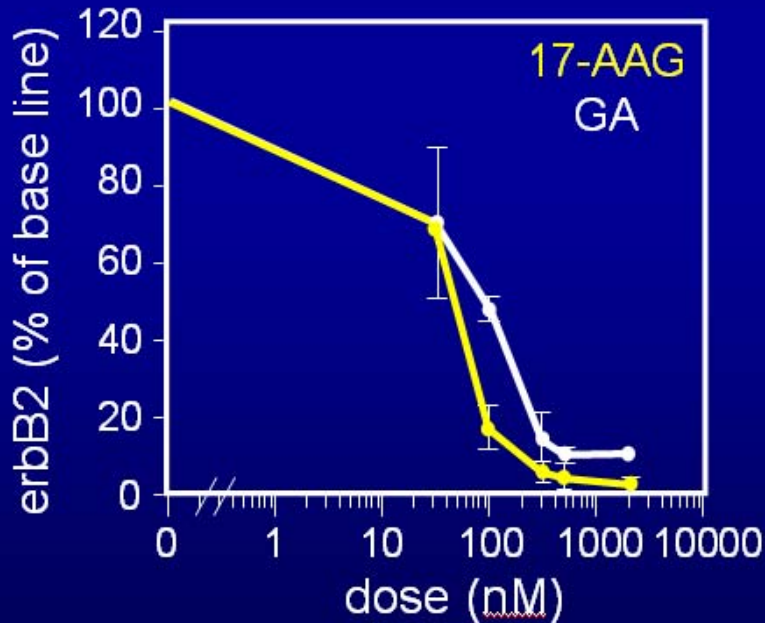
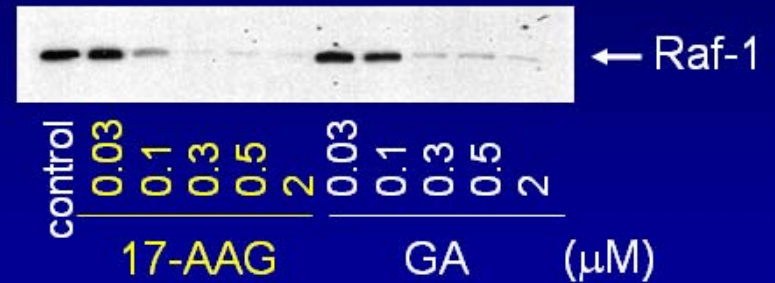
**SUPERPOSITION OF SEVEN LOW-ENERGY STRUCTURES CALCULATED FOR  
BCL-XL COMPLEXED TO 1 AND 11**



# THREE DIMENSIONAL VIEW OF GELDANAMYCIN BINDING POCKET IN AMINO TERMINUS OF HSP90



# 17-AAG BINDS TO HSP90 & SHARES IMPORTANT BIOLOGIC ACTIVITIES WITH GELDANAMYCIN



# OUTLINE OF PRESENTATION

-Structure based design

-**Biochemical Screen**

-Cell-based Screen

\* General Introduction

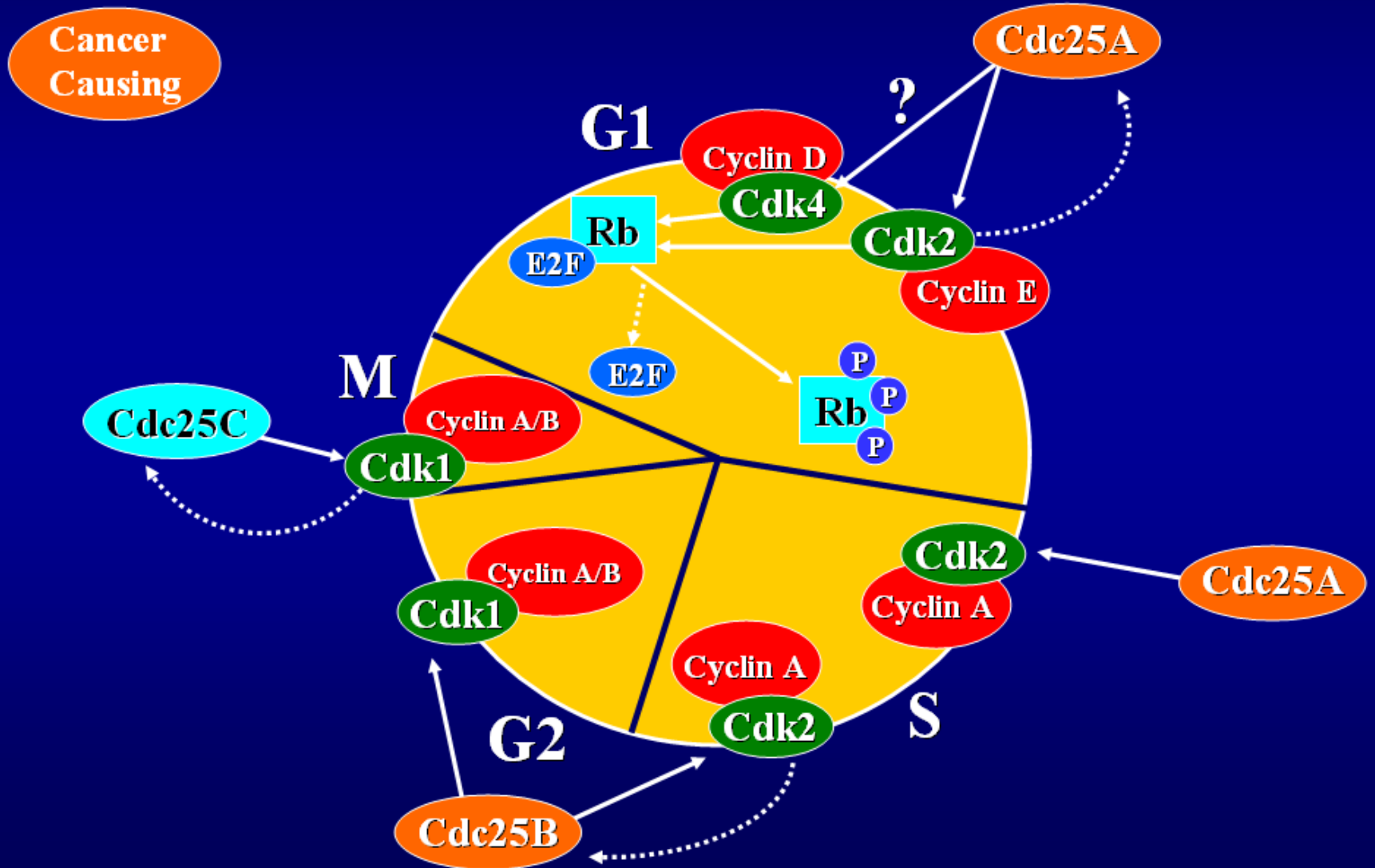
\* Definition of Drug Targets

\* Generating Diversity

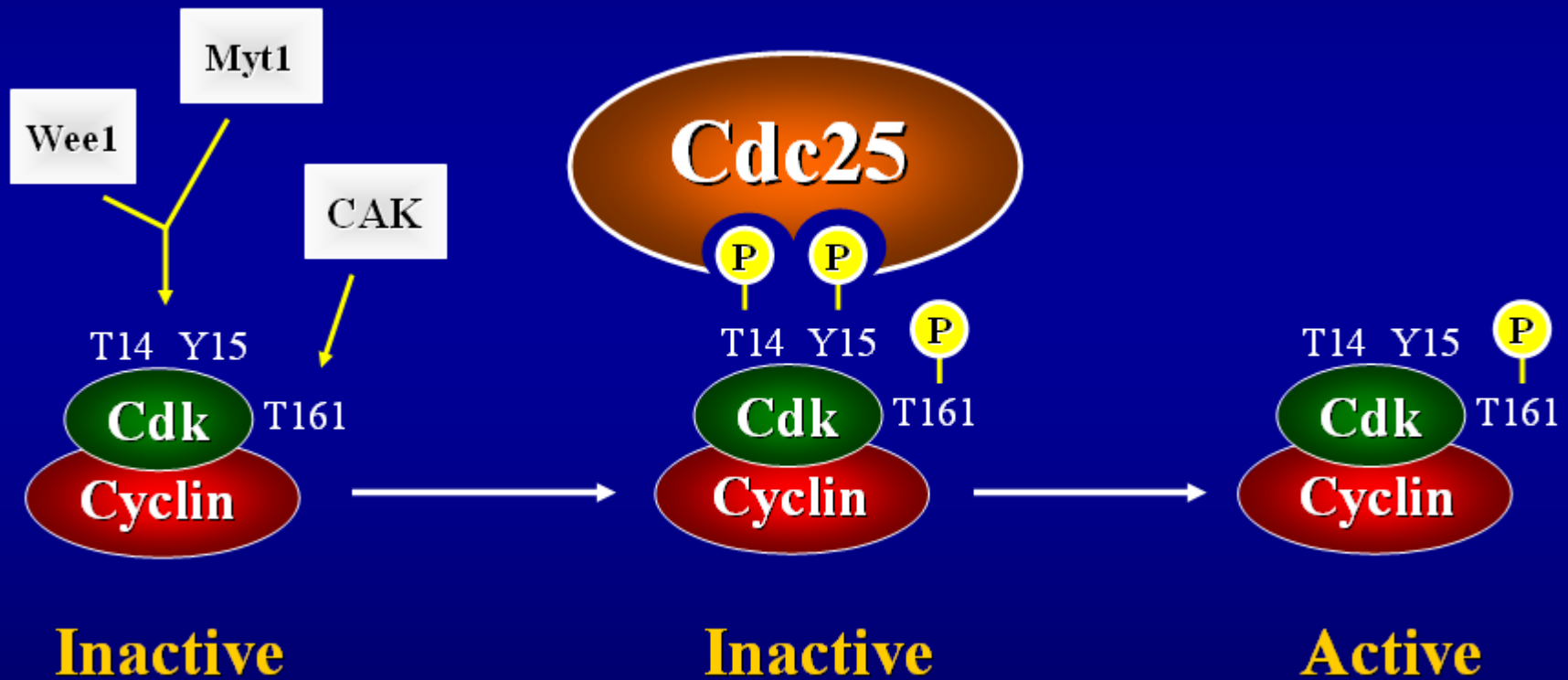
\* **Definition of Lead Structures**

\* Qualifying Lead for Transition to Early Trials

# Cell cycle regulation by Cdc25 phosphatases



# Regulation of Cell Cycle Progression by Cdc25: Cdk Activation





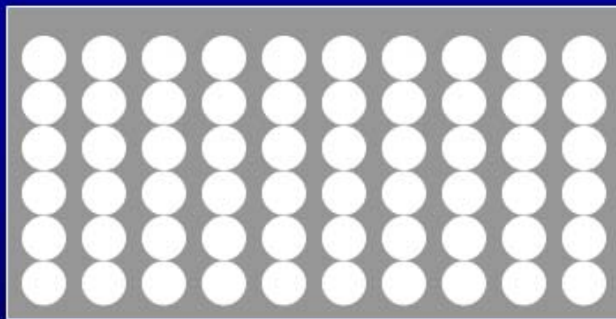
# CDC25 Phosphatases and Cancer

- \* CDC25A and B overexpressed in many cultured cancer cell lines.
- \* Cdc25A suppresses apoptosis.
- \* Overexpression of CDC25A or B has been detected in human breast, head and neck, cervical, skin, lymph, lung and gastric cancers.
- \* Human CDC25A & B cooperated with Ha-Ras<sup>G12V</sup> and CDC25A cooperated with Rb<sup>-/-</sup> in the oncogenic focus transformation of mouse embryonic fibroblasts and tumor formation in nude mice. Thus, Cdc25A & B may be human oncogenes.

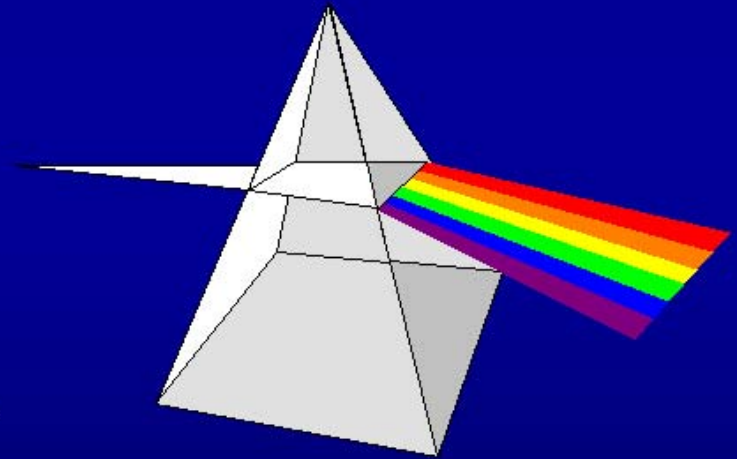
# Method for identifying Cdc25 phosphatase inhibitors

GST-Cdc25 in assay buffer

Fluorescein diphosphate



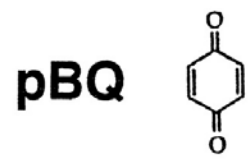
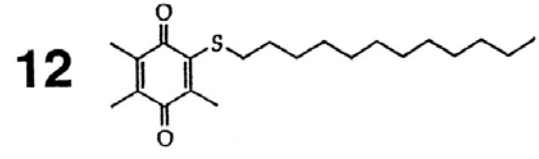
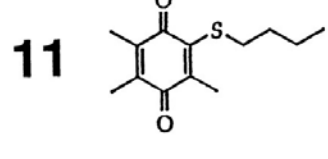
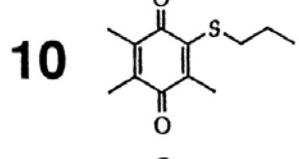
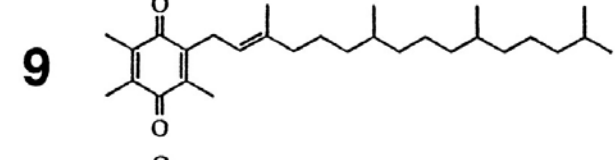
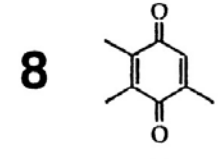
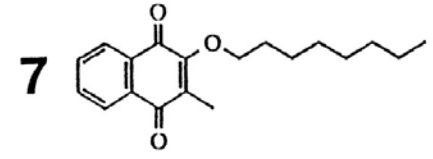
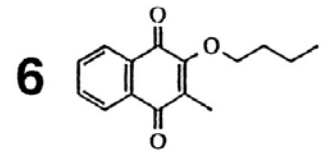
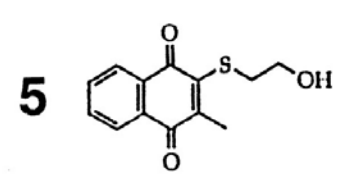
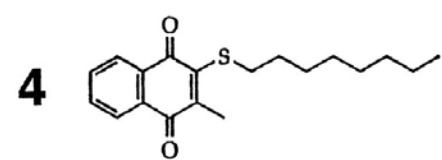
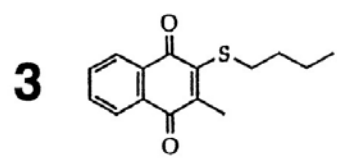
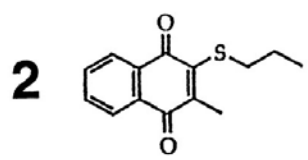
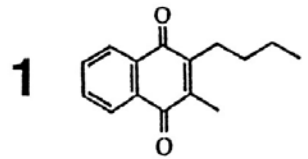
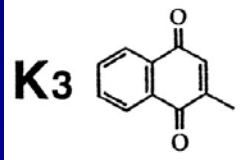
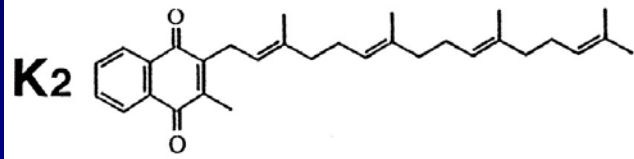
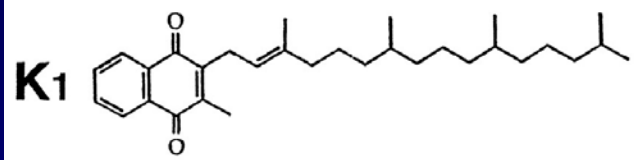
Incubate 1h  
RT



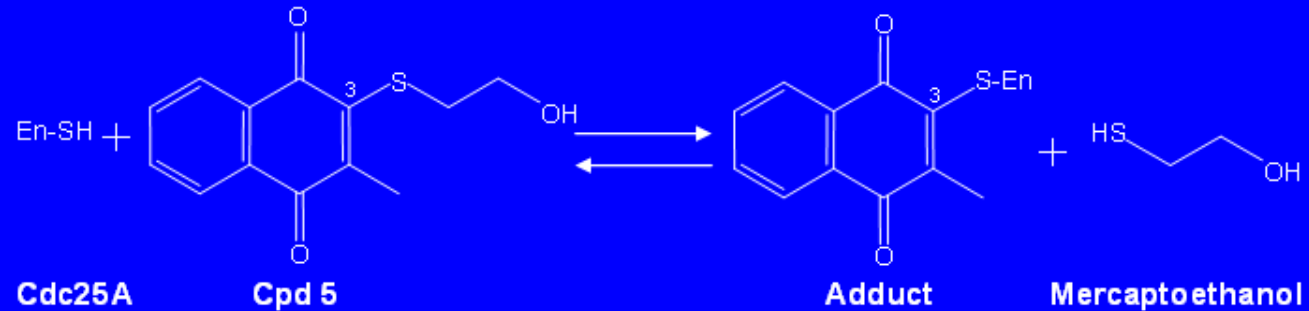
Read product  
(fluorescein monophosphate)  
on cytoflour II

# Chemical Screening Approach

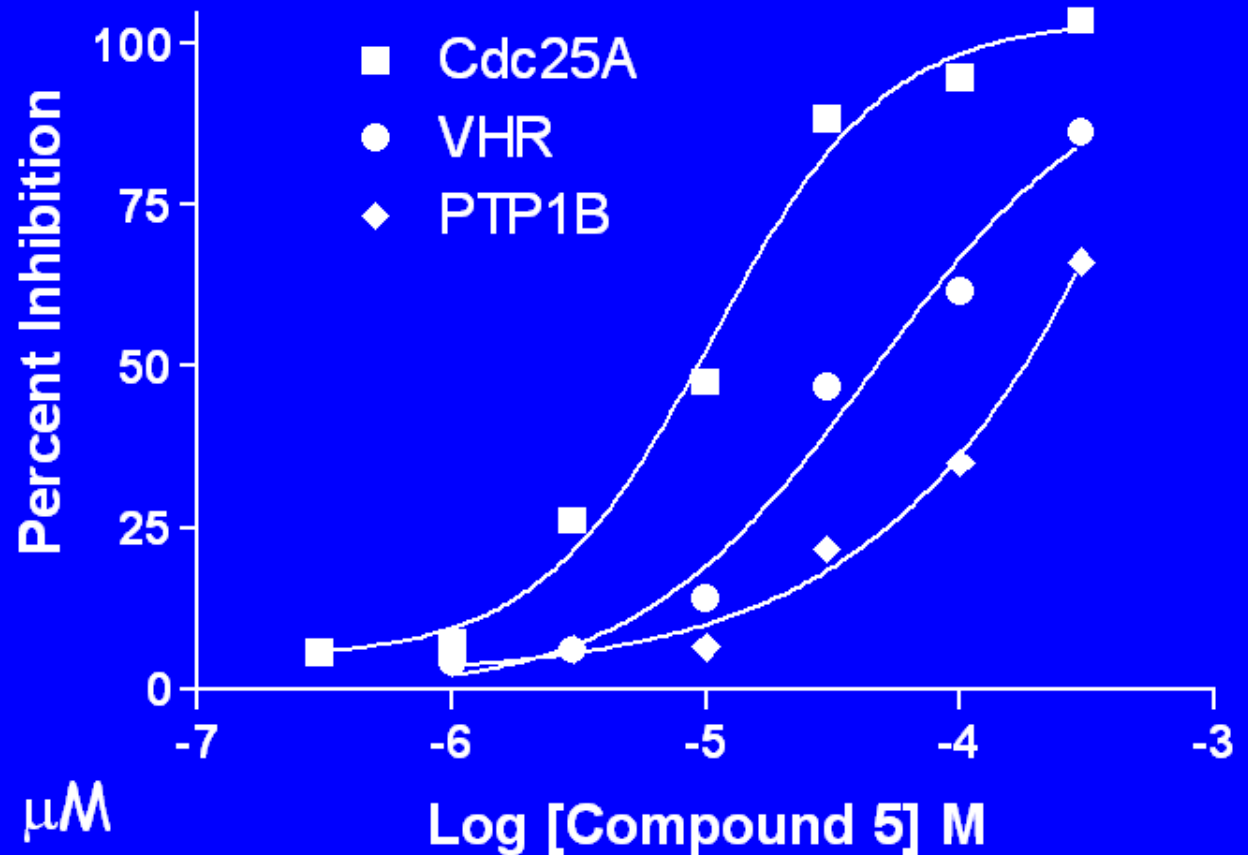
- \* Targeted Array Libraries
- \* Diverse Chemical Libraries



# Compound 5 inhibits Cdc25



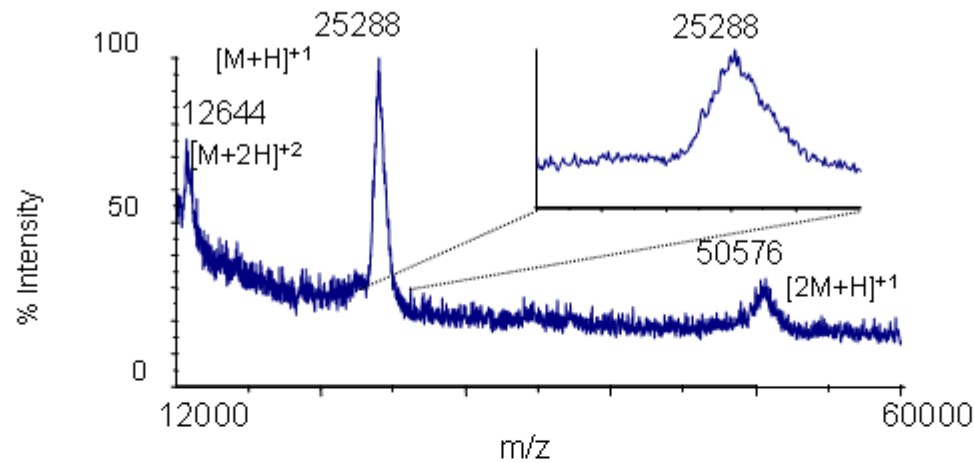
MW<sub>monoisotopic</sub> = 248.1 Da



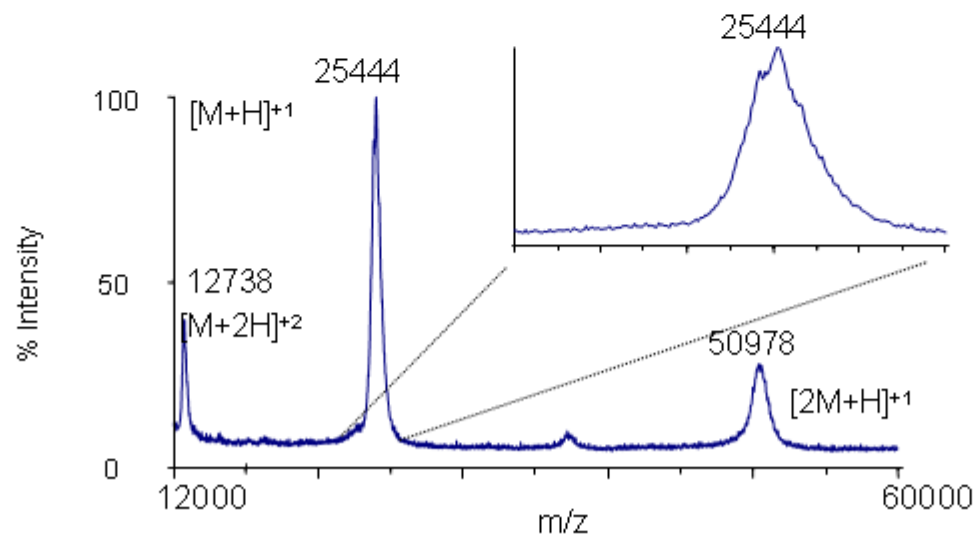
Cdc25B<sub>2</sub> K<sub>i</sub> ~ 2 μM

# MALDI-TOF ANALYSES

## Compound 5 binds tightly to the catalytic domain of Cdc25A



**DMSO**



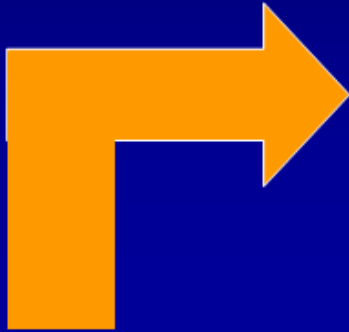
**Compound 5**

# Compound Validation

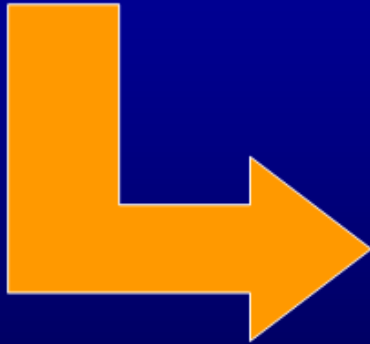
- \* **Cellular: Cell Cycle**
- \* **Biochemical: Substrate phosphorylation**
- \* **Genetic: Chemical complementation**

# tsFT210 Cell System

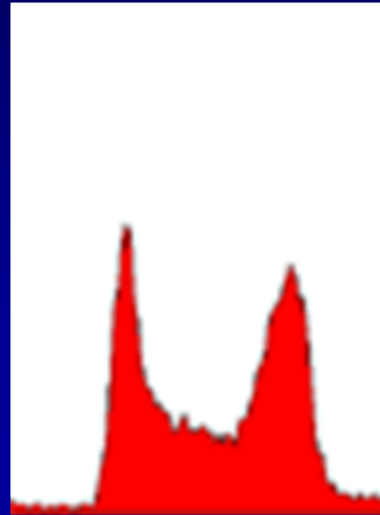
32° 17 h



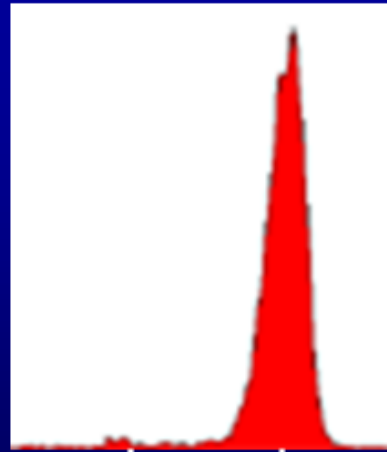
tsFT210 cells  
Cdk1 mutants



39.4° 17 h



Functional Cdk1

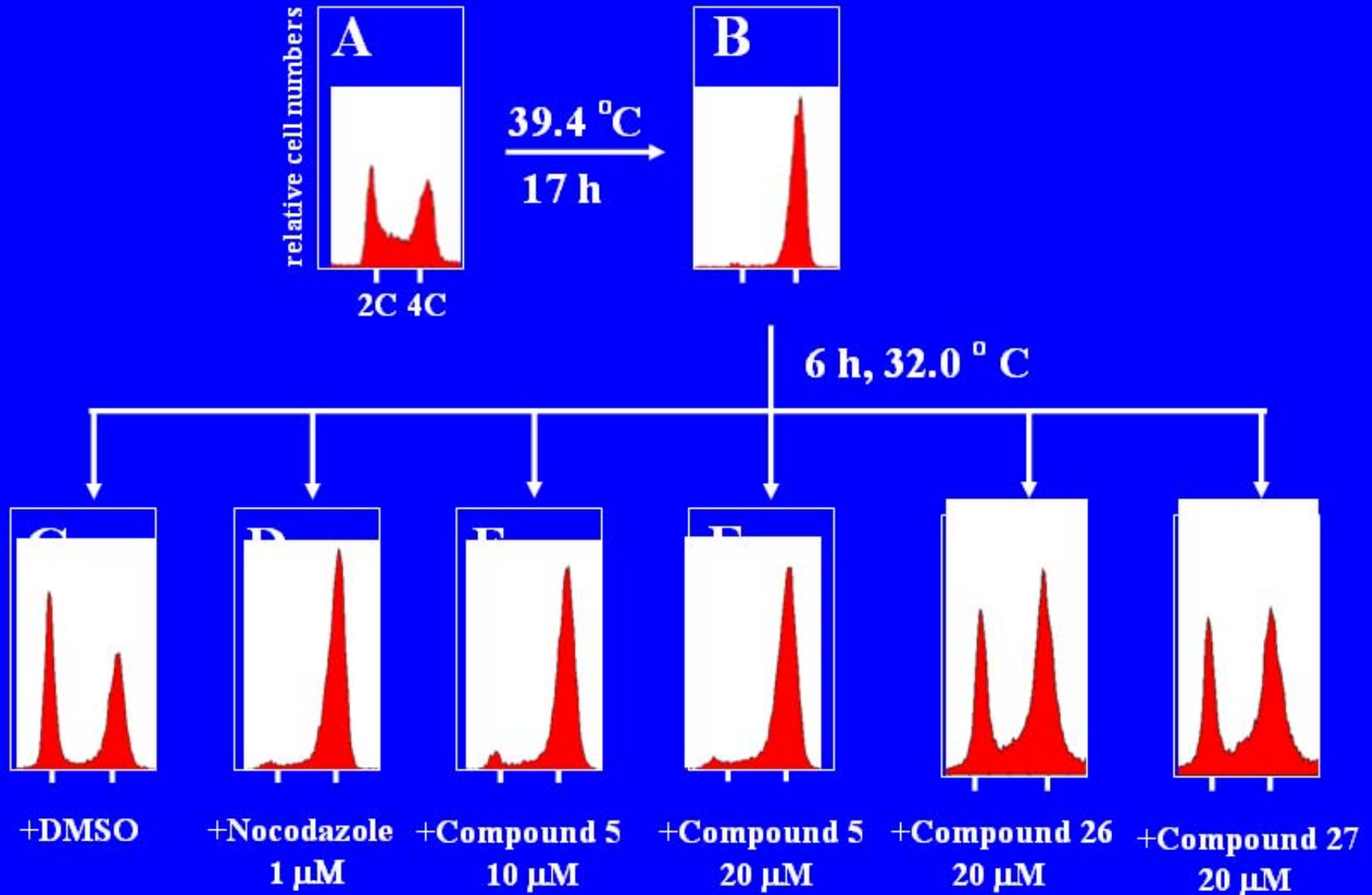


No functional Cdk1

G1 G2/M



# Compound 5 causes G2/M arrest



# OUTLINE OF PRESENTATION

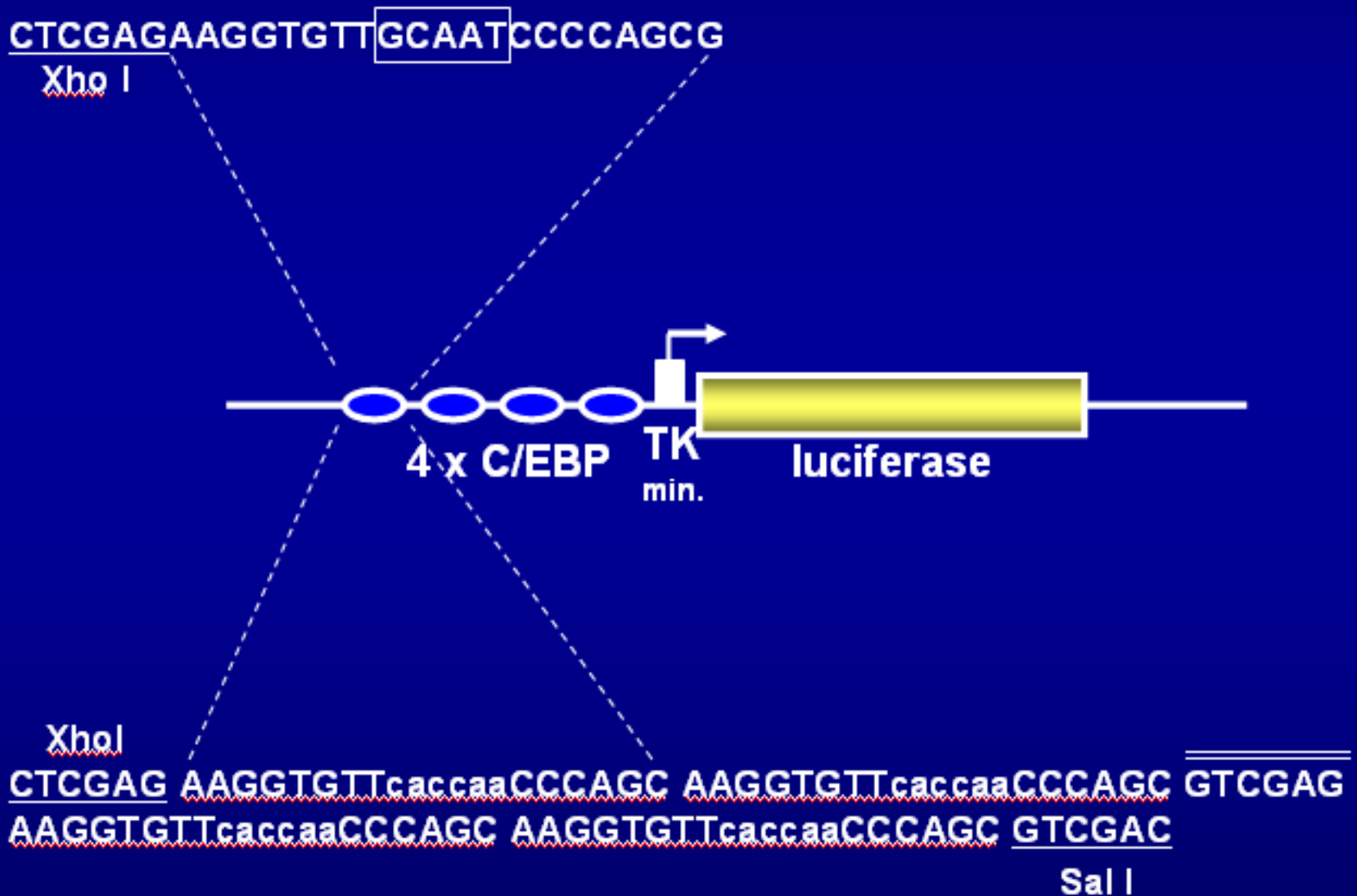
- Structure based design
- Biochemical Screen
- Cell-based Screen**

- \* General Introduction
- \* Definition of Drug Targets
- \* Generating Diversity
- \* **Definition of Lead Structures**
- \* Qualifying Lead for Transition to Early Trials

# **C/EBP *[alpha]* AS A TARGET FOR DEVELOPMENT OF NOVEL CANCER THERAPEUTICS**

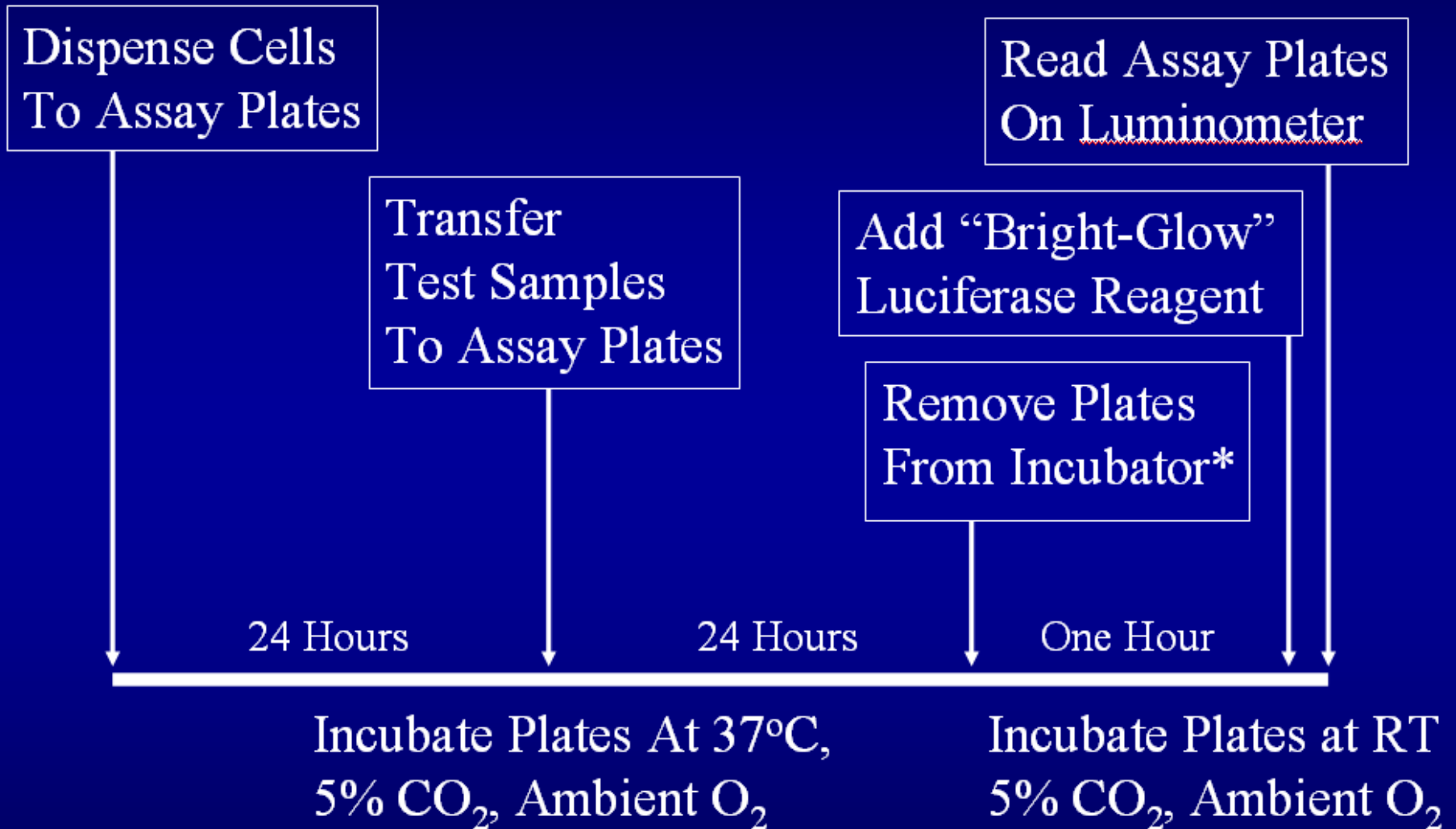
- \* The transcription factor C/EBP $\alpha$  plays key roles in regulation of differentiation of various cell lineages (adipocytes, keratinocytes, etc.)**
- \* Mutations in CEBPA (the gene coding for C/EBP $\alpha$ ) are associated with development of AML [t(8;21) - subtypes M1 and M2]**
- \* CEBPA knock-out mice show no mature neutrophils**
- \* Conditional expression of CEBPA is sufficient to trigger neutrophilic differentiation**
- \* Pharmacologic modulators of CEBPA could act as differentiation inducers and thus limit proliferation of AML cells**

# CEBP Reporter Construct\*



\*Host cell for this construct is U-937

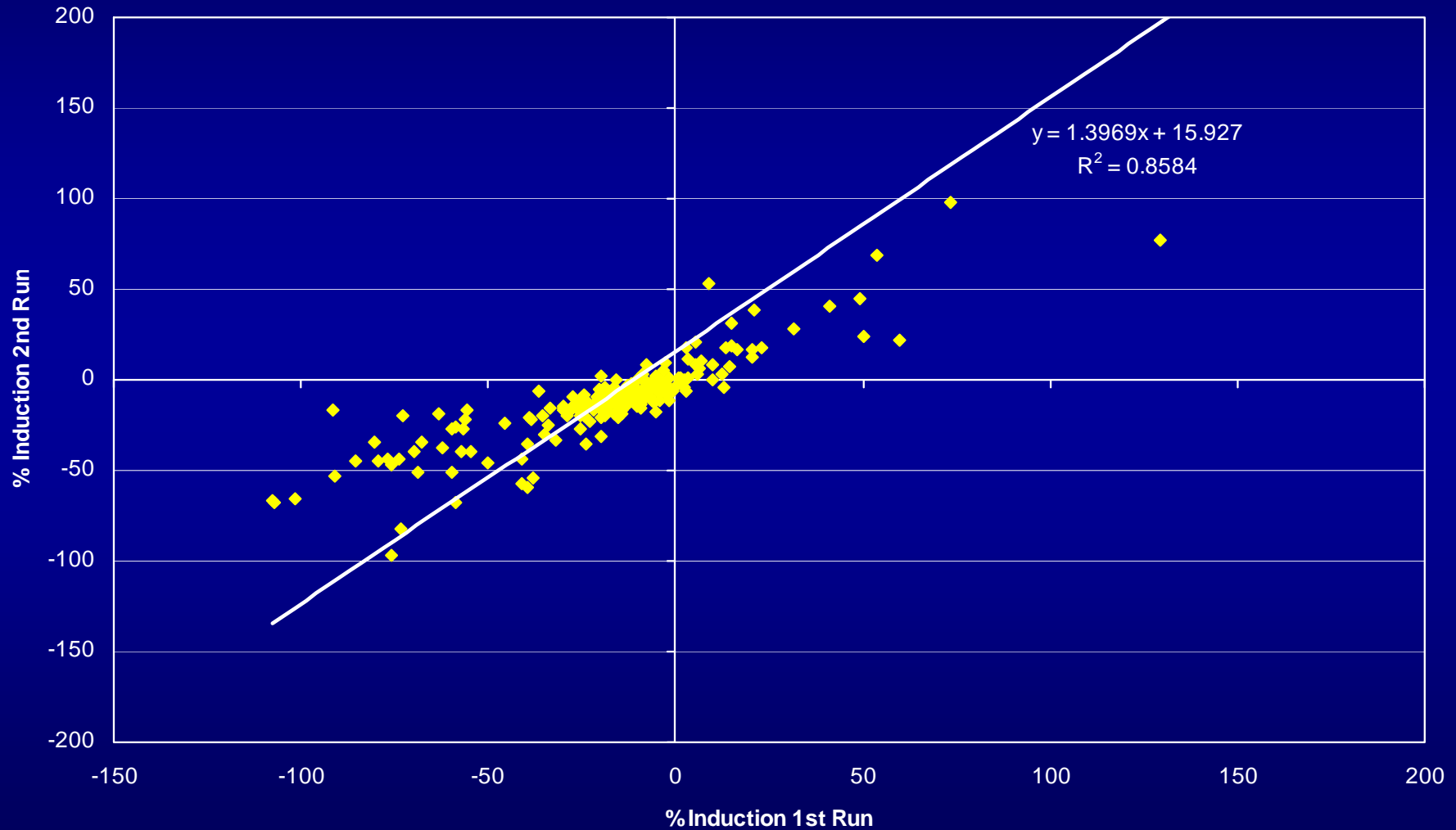
# CEBPA Assay Timeline



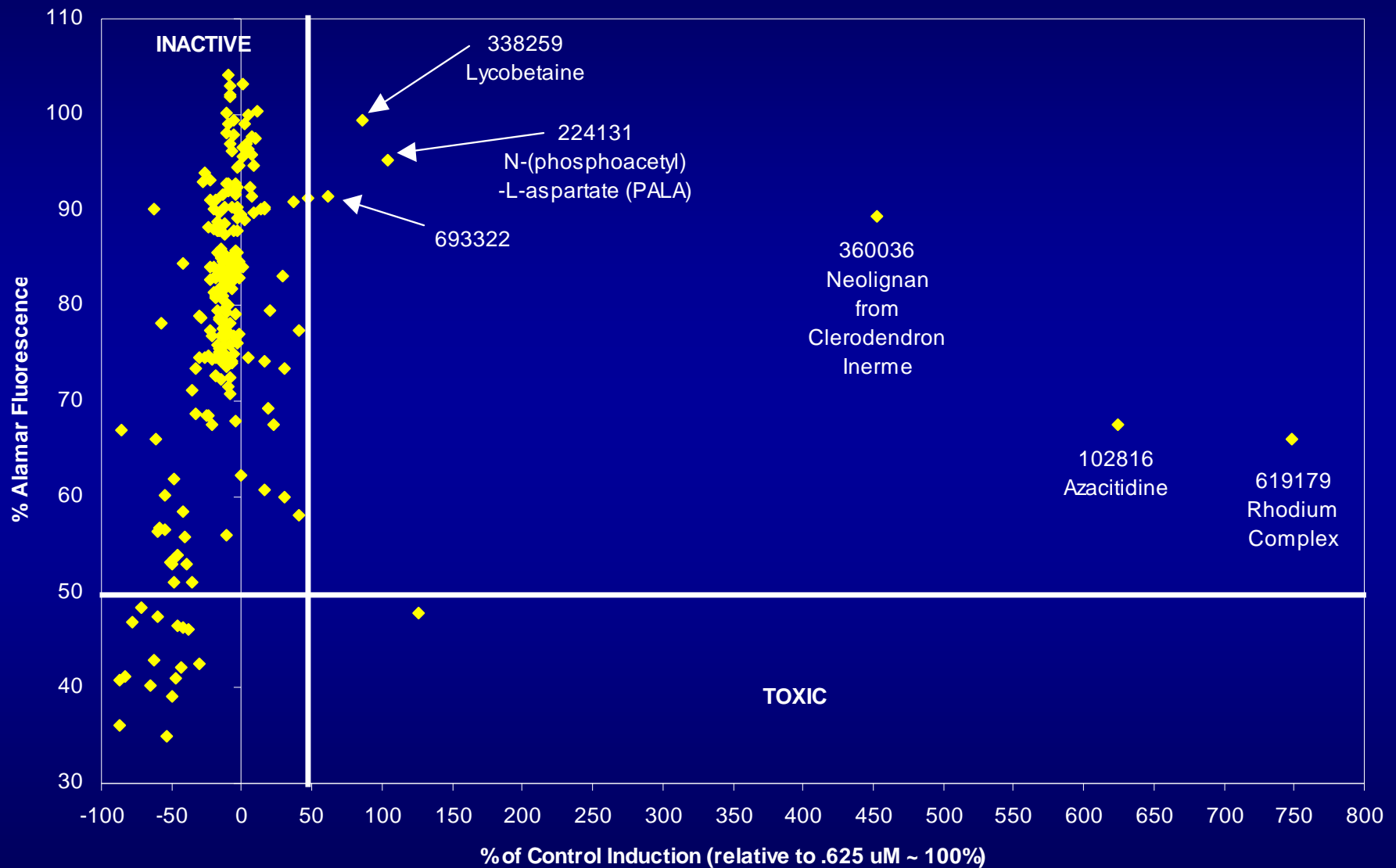
\*Sister plates processed for Alamar blue toxicity assay

# C/EBPa Training Set: 1st Run compared to 2nd Run % Induction

Correlation Coefficient = .9265

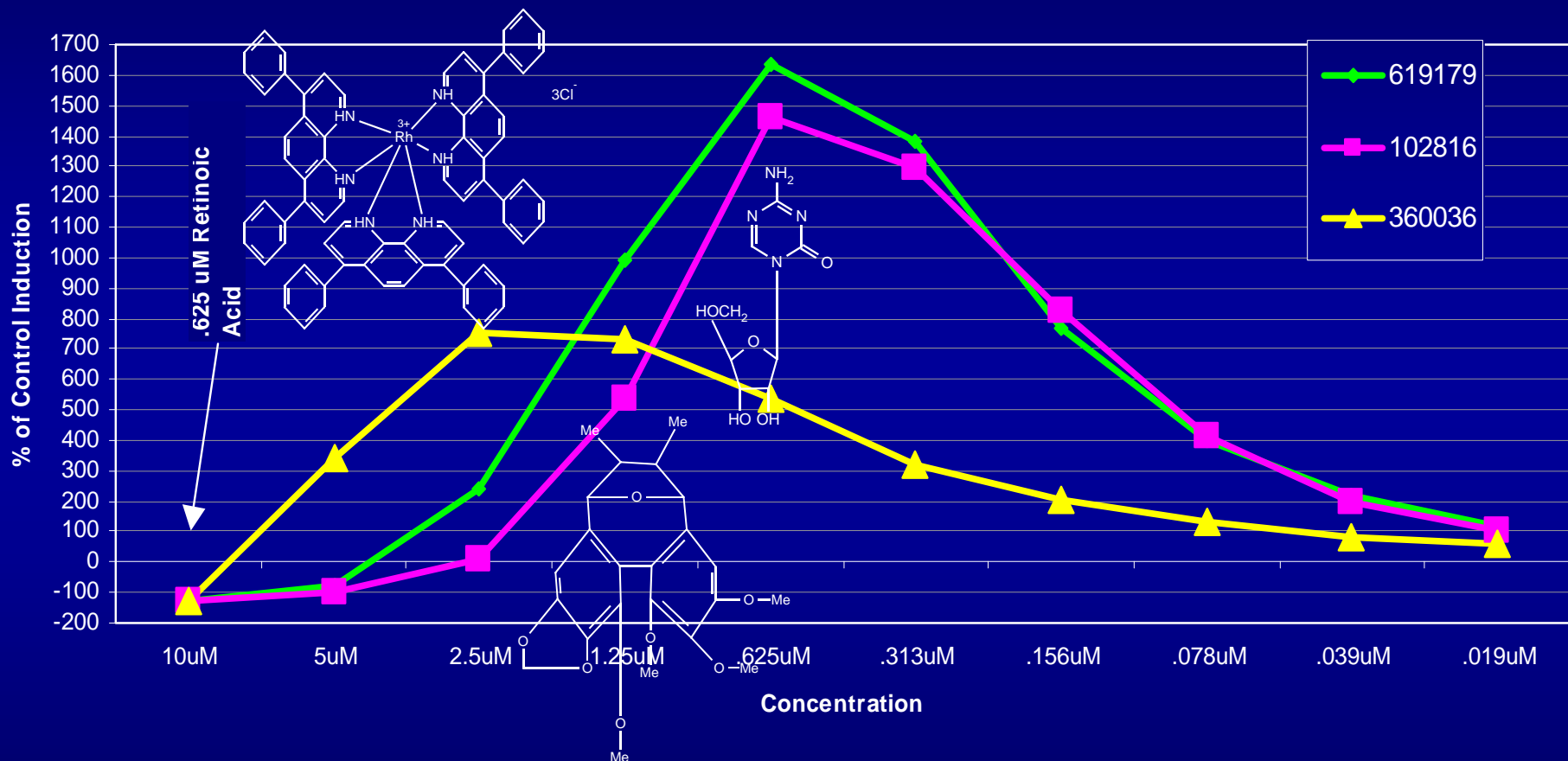


# C/EBP $\alpha$ Training Set 1 $\mu$ M Results \*



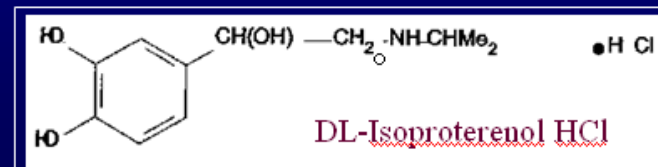
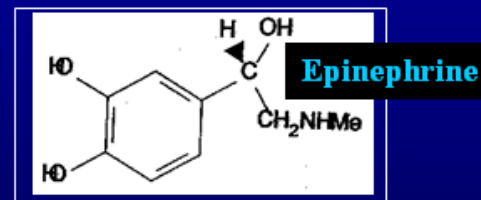
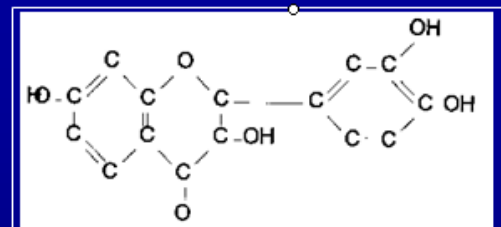
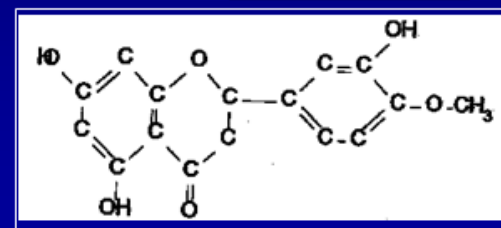
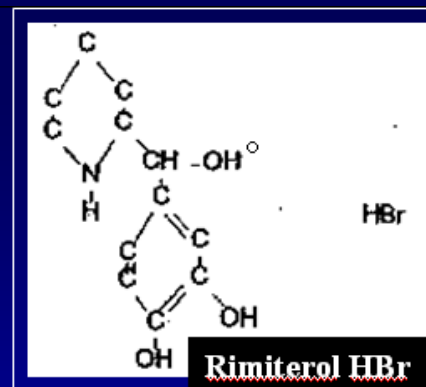
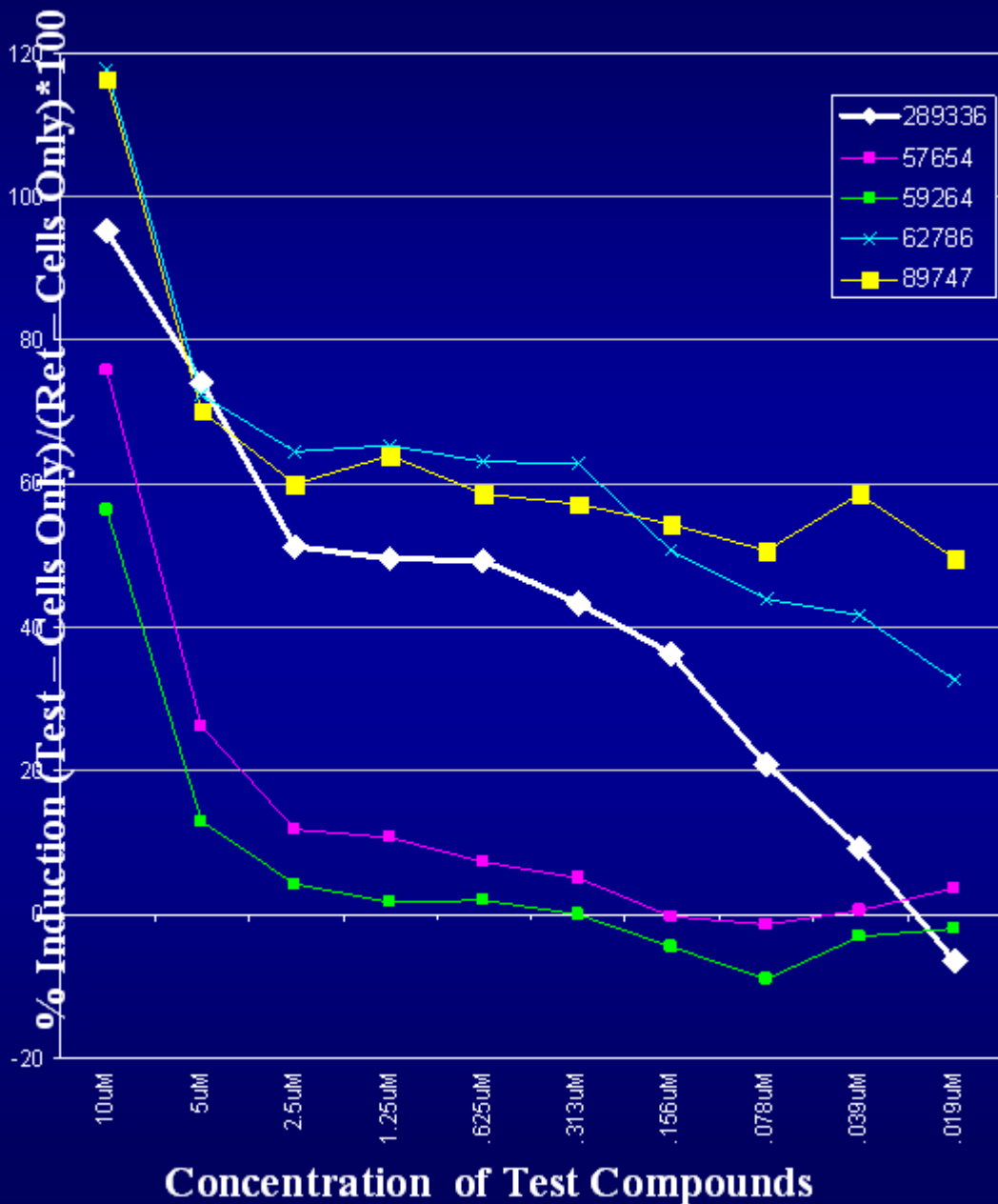
\*Data averaged from two independent assays

**C/EBPa Screen: % Concentration Response Graphs**  
**% Induction (relative to .625 uM retinoic acid induction) for seven select compounds**





# C/EBPa % Induction Dose Response Curves



# NCI IN VITRO DRUG SCREEN

## 1985 Hypothesis:

- \* Cell type specific agents
- \* Activity in solid tumors

## Emerging Realities:

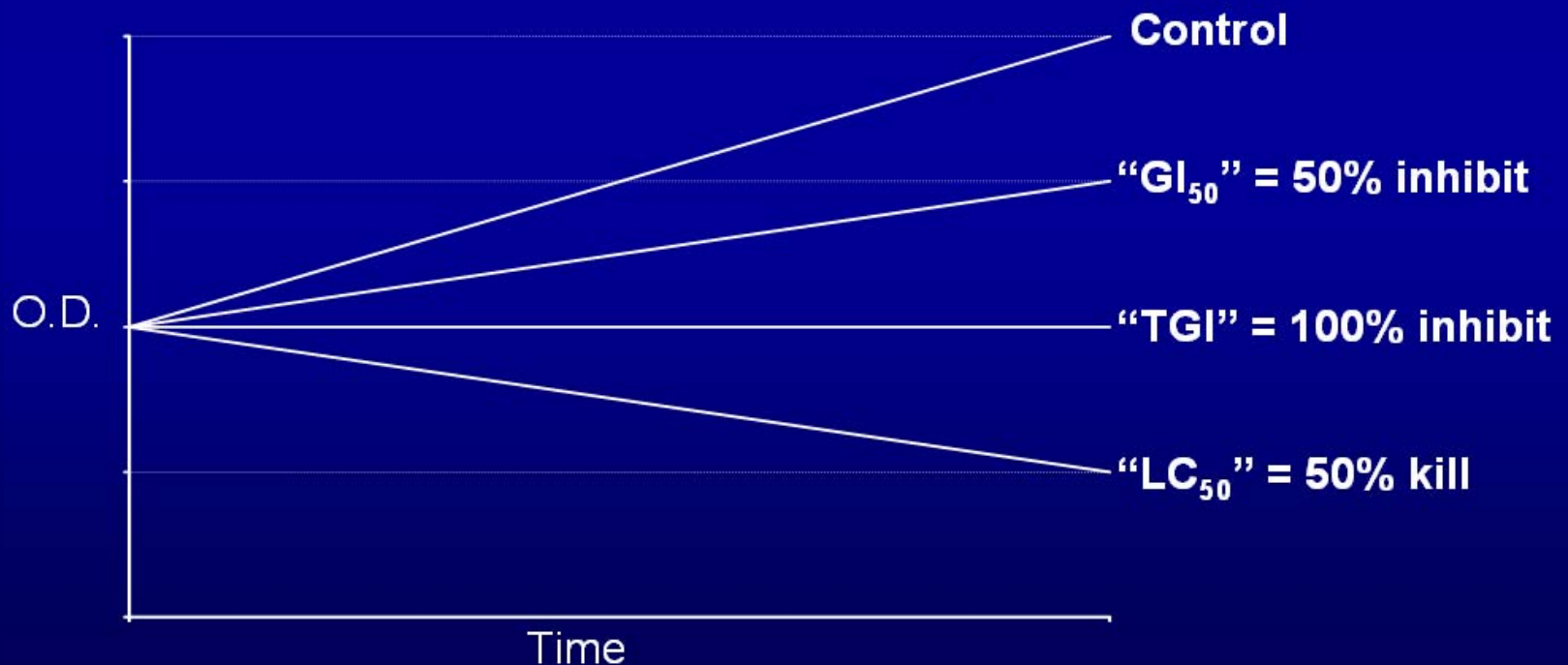
- \* Unique patterns of activity, cut across cell types

**AND**

- \* Cell type selective patterns found
- \* Correlations of compound activity
  - relate to molecular “target” expression
  - generate hypothesis re: molecular target

# NCI IN VITRO CANCER CELL LINE SCREEN

- 60 cell lines  
(8 breast, 2 prostate, 8 renal, 6 ovary, 7 colon,  
6 brain, 9 lung, 8 melanoma, 6 hematopoietic)
- 48 hr exposure; protein stain O.D.

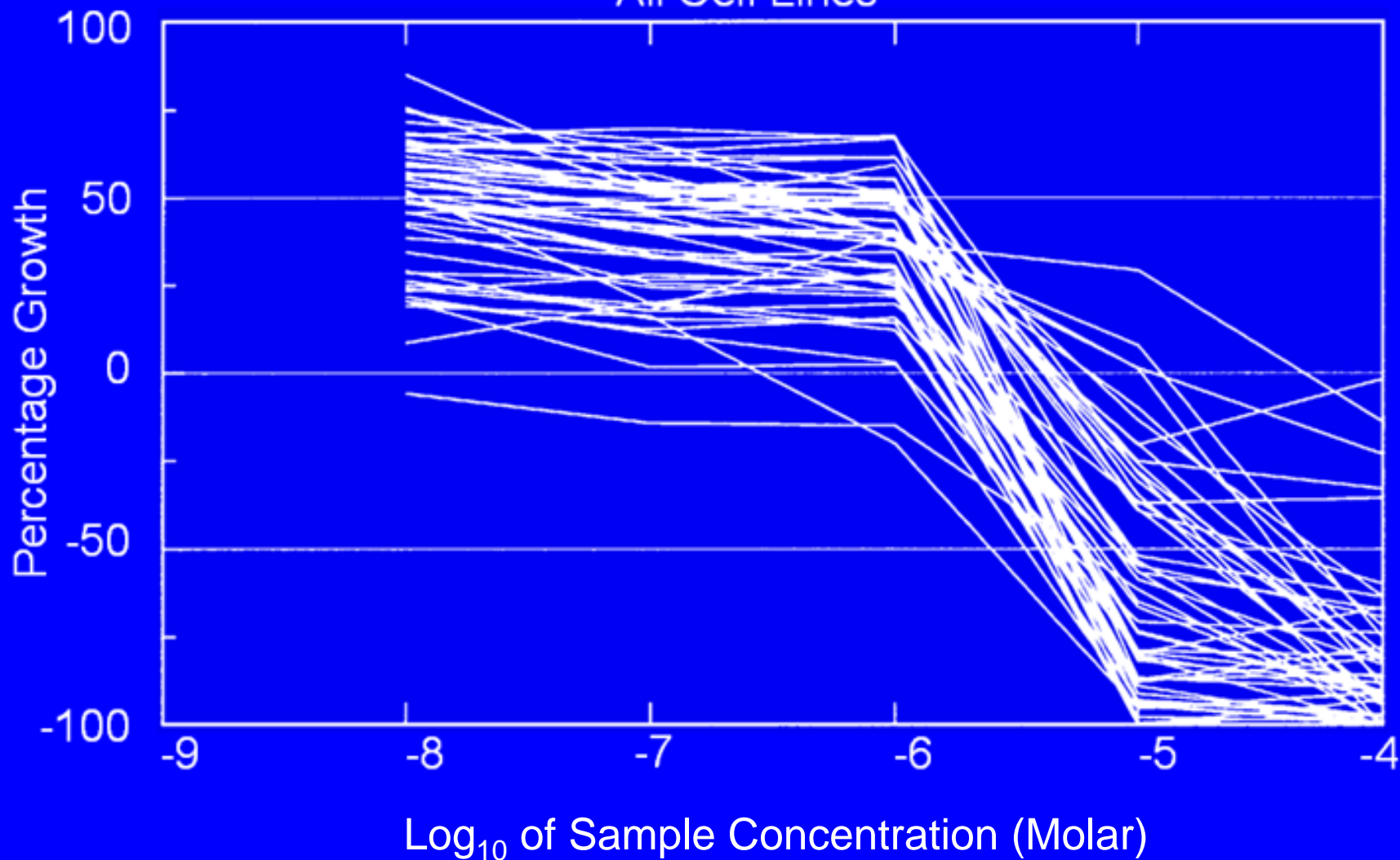


National Cancer Institute Developmental Therapeutics Program  
Dose Response Curves

**NSC:** 643248-Q/2 (*a rapamycin*)

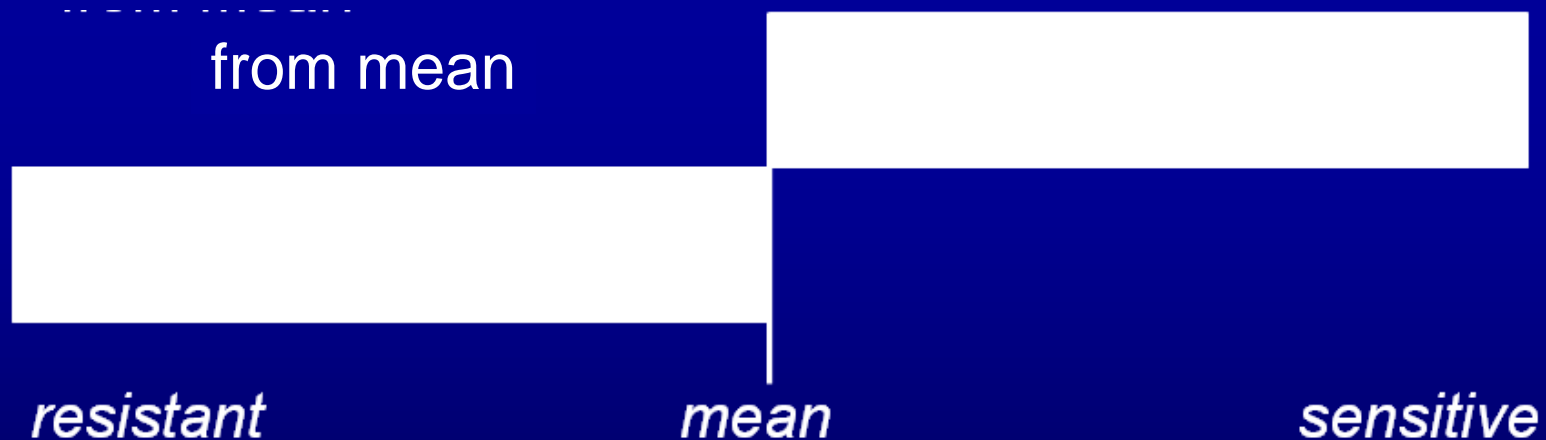
**Exp. ID:** 9503SC35-46

All Cell Lines



# PATTERN RECOGNITION ALGORITHM: COMPARE

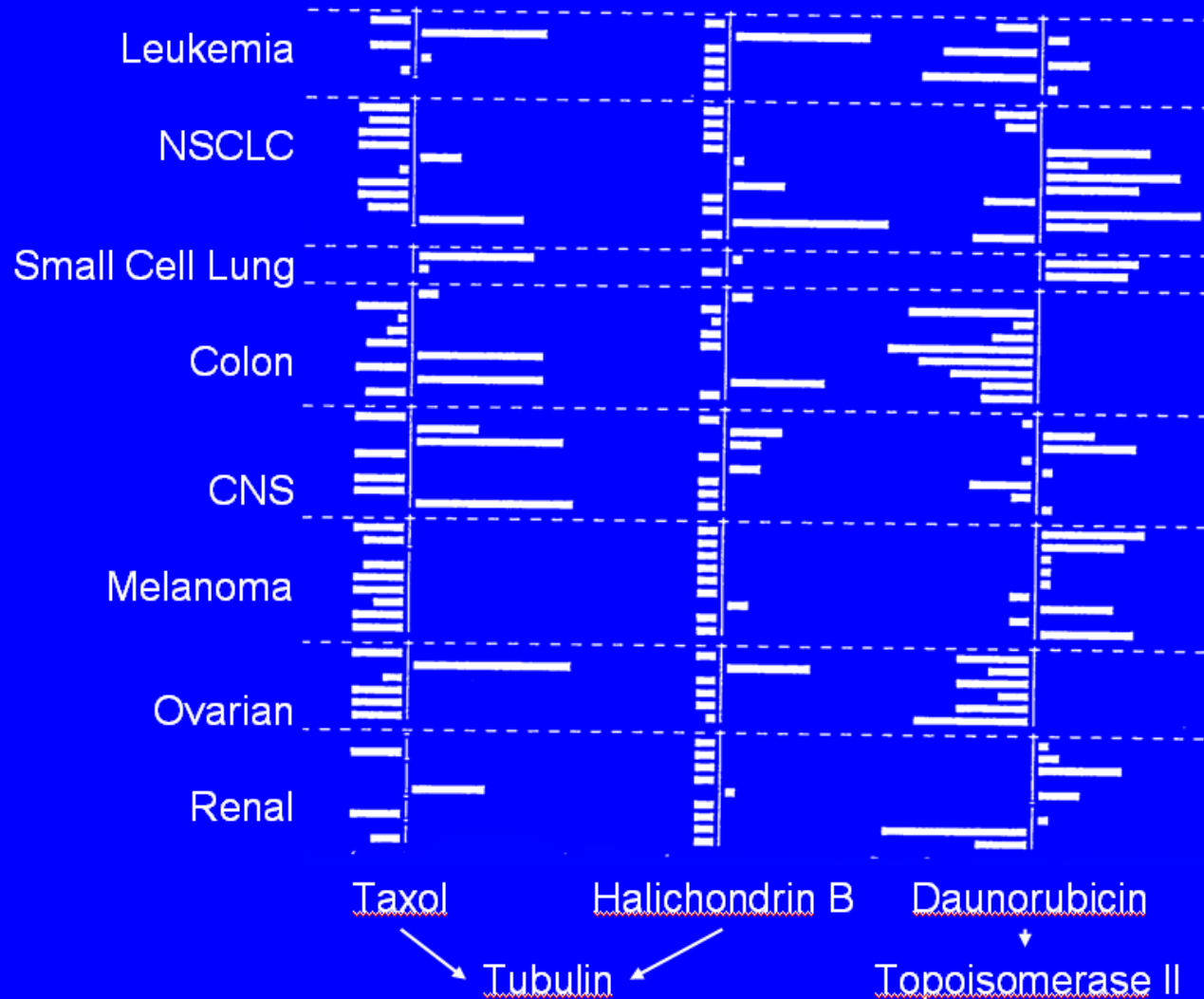
- \* Goal: COMPARE degree of similarity of a new
- \* Calculate mean  $GI_{50}$ , TGI or  $LC_{50}$
- \* Display behavior of particular cell line as deflection



- \* Calculate Pearson correlation coefficient:

**1 = identity; 0 = no correlation**

# AGENTS WITH SIMILAR MECHANISMS HAVE SIMILAR MEAN GRAPHS

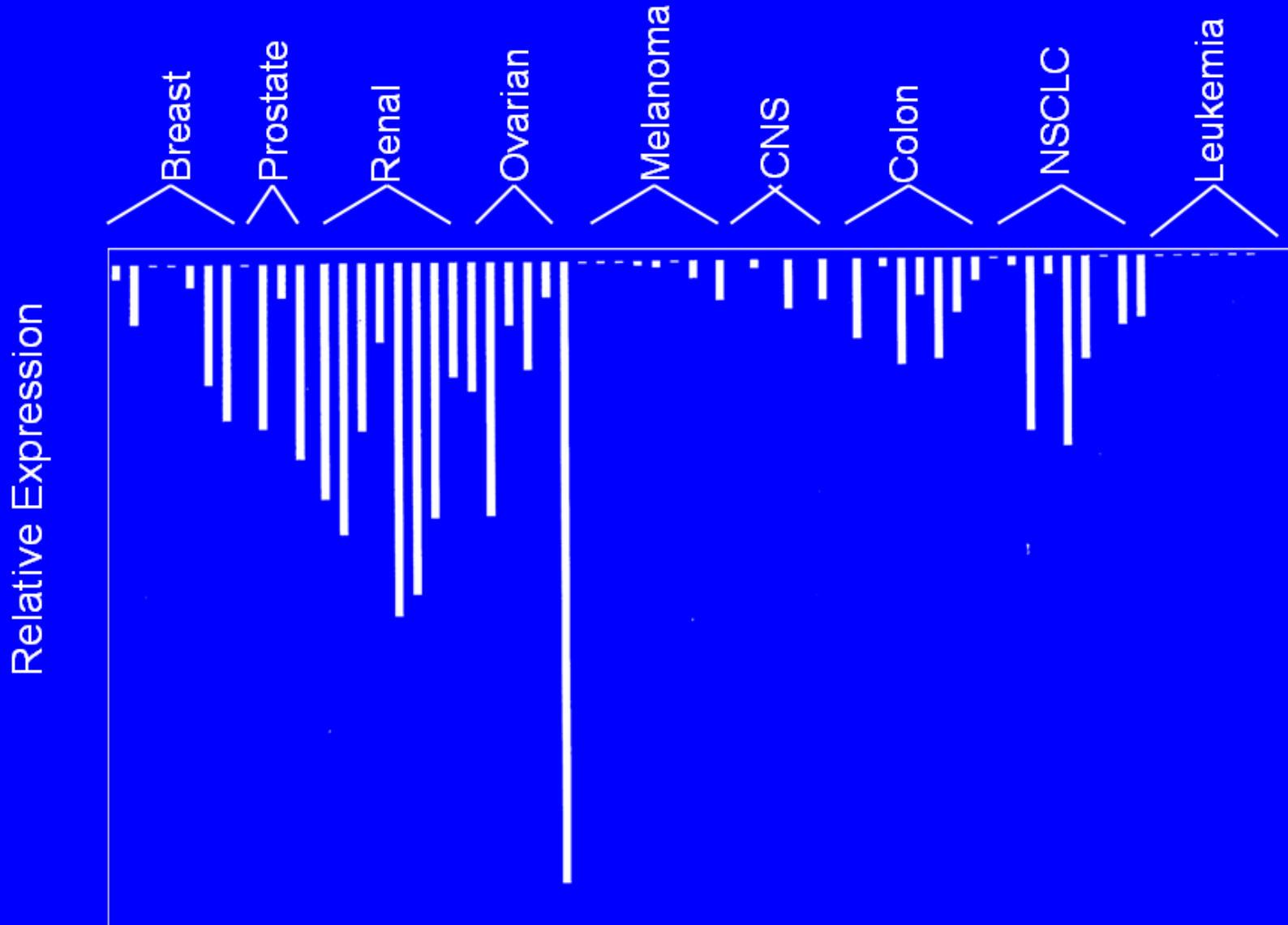


# THE COMPARE ALGORITHM

## Seed: Rubidazone

164011	1.000	Rubidazone
82151	0.921	Daunomycin
123127	0.915	Adriamycin
665934	0.891	Epipodophyllotoxin analogue
Discreet	0.880	Gyrase-To-TOPO analogue
Discreet	0.867	AMSA analogue
267469	0.865	Deoxydoxorubicin
305884	0.865	Acodazole HCL
665935	0.864	Epipodophyllotoxin analogue
668380	0.861	Azatoxin analogue
639659	0.854	Adriamycin analogue
644946	0.850	Epipodophyllotoxin analogue
254681	0.848	Daunomycin analogue
Discreet	0.847	Epipodophyllotoxin analogue
Discreet	0.843	Epipodophyllotoxin analogue
180510	0.842	Daunomycin analogue
Discreet	0.837	Epipodophyllotoxin analogue
Discreet	0.833	Gyrase-To-TOPO analogue

# RELATIVE EGF RECEPTOR mRNA EXPRESSION



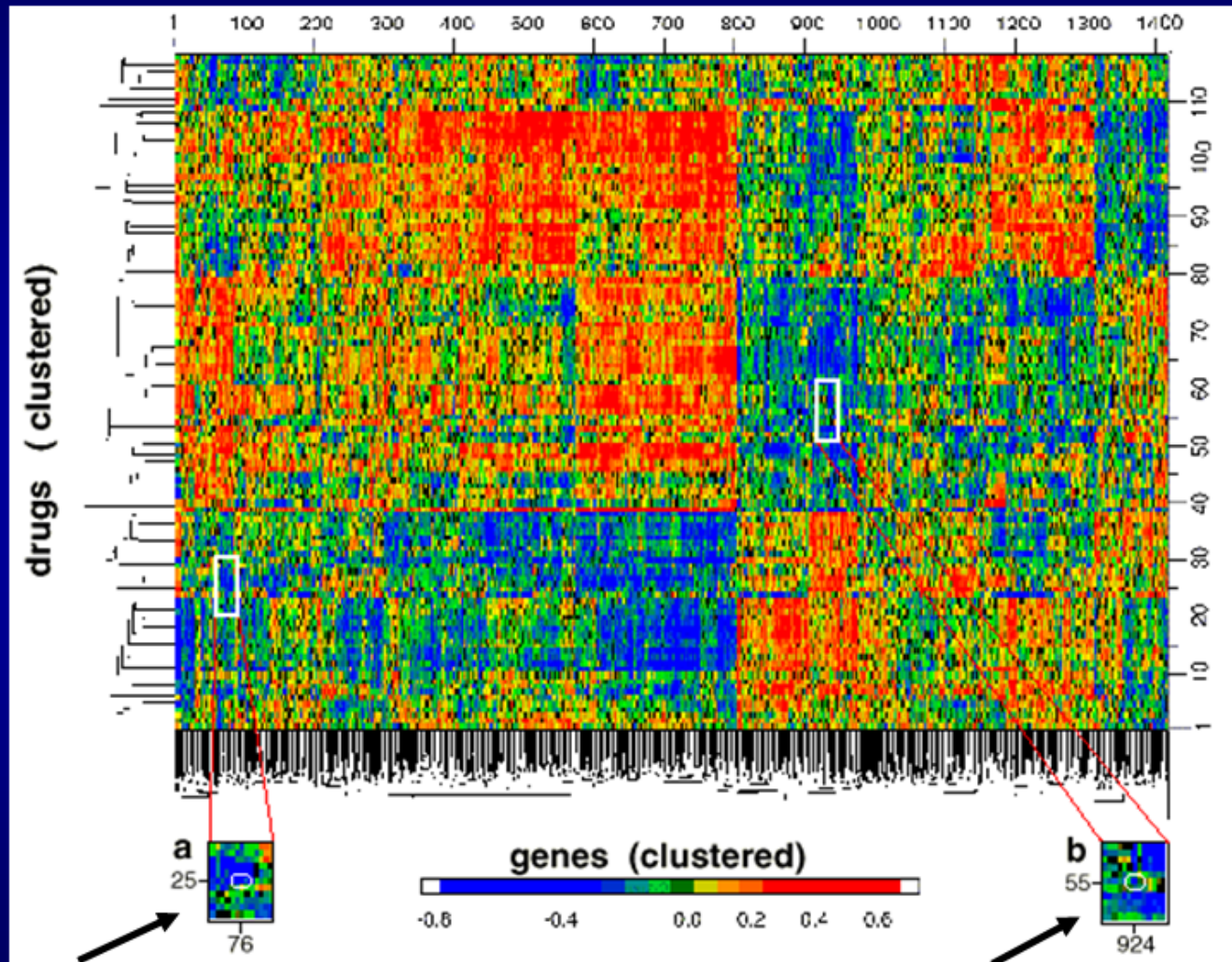


# COMPARE ANALYSIS: EGF RECEPTOR

RANK	CORRELATION	CHEMICAL NAME
1	0.71	TGF $\alpha$ -PE40
2	0.66	Toxin- $\Delta$ 53L, MW=43K
7	0.57	EGFR Tyrosine Kinase Inhibitor
88	0.43	EGFR Tyrosine Kinase Inhibitor

*40,421 COMPOUNDS IN THE NCI DATABASE*

# DRUG TARGET CLUSTERINGS REVEAL CLUES TO MECHANISM



**5FU/DPYD**

**L-Asparaginase/ASNS**

*Nature Genetics* 24: 236, 2000; <http://dtp.nci.nih.gov>

# WHAT TO DO AFTER THE LEAD COMPOUND IS IDENTIFIED?

- \* If “*empirical*” lead, OPTIMIZE: schedule; formulation vs. biological effect after identifying a “predictive” model; ideally bring series of close analogs through pharmacology and perhaps early toxicology
- \* If “*rational*” lead, capitalize on target-directed effects in optimizing process
- \* IN EITHER CASE, KEY TASKS ARE: ACTIVITY; PHARMACOLOGY; FORMULATION; SAFETY TESTING

# OUTLINE OF PRESENTATION

- \* General Introduction
- \* Definition of Drug Targets
- \* Generating Diversity
- \* Definition of Lead Structures
- \* ***Qualifying Lead for Transition to Early Trials***

# GOALS OF PRECLINICAL DRUG STUDIES

## *Regulatory framework*

- \* IND = “Investigational New Drug” application = approval by FDA to conduct human studies; main criterion : SAFETY AND LIKELY REVERSIBLE TOXICITY = allows *start* of Phase I trials
- \* NDA = “New Drug Application” = basis for sale to public; main criteria: SAFETY AND SOME MEASURE OF EFFICACY = *result* of Phase II/III trials

# COMPONENTS OF AN IND

*The goal of the pre-clinical process*

- \* “Form 1571”
- \* Table of Contents
- \* Intro Statement / Plan
- \* Investigator Brochure
- \* Clinical Protocol
- \* Chemistry,  
Manufacture, Control
- \* Pharmacology/  
Toxicology
- \* Prior Human  
Experience
- \* Additional Info - Data  
monitoring, Quality  
Assurance

# OBJECTIVES OF PRECLINICAL PHARMACOLOGY STUDIES FOR ANTI-NEOPLASTIC DRUGS

- \* Development of Sensitive Analytical Methods for Drugs in Biological Fluids & Tissues
- \* Determine *In Vitro* Stability and Protein Binding
- \* Determine Pharmacokinetics in Rodents (& Dogs)
- \* Identification and Analysis of Metabolites
- \* Define Optimal Dose Schedule and Blood Sampling Times
- \* Define  $C_p$  and/or AUC with Efficacy, Safety & Toxicity
- \* Analog Evaluation - Determine Optimal Development Candidate

# OBJECTIVES OF PRECLINICAL TOXICOLOGY STUDIES

## \* DETERMINE IN APPROPRIATE ANIMAL MODELS:

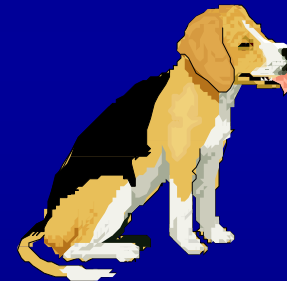
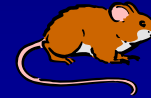
- The Maximum Tolerated Dose (MTD)
- Dose Limiting Toxicities (DLT)
- Schedule-Dependent Toxicity
- Reversibility of Adverse Effects
- A Safe Clinical Starting Dose



# FDA PRECLINICAL PHARMACOLOGY & TOXICOLOGY REQUIREMENTS: ONCOLOGY Rx

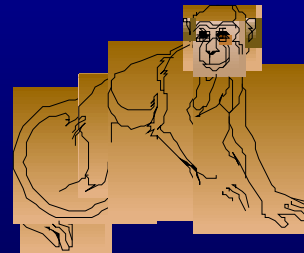
## \* DRUGS

- Two Species - Rodent & Non-rodent
- Clinical Route & Schedule
  - Follow NCI Guidelines
- Pharmacokinetics - Optional

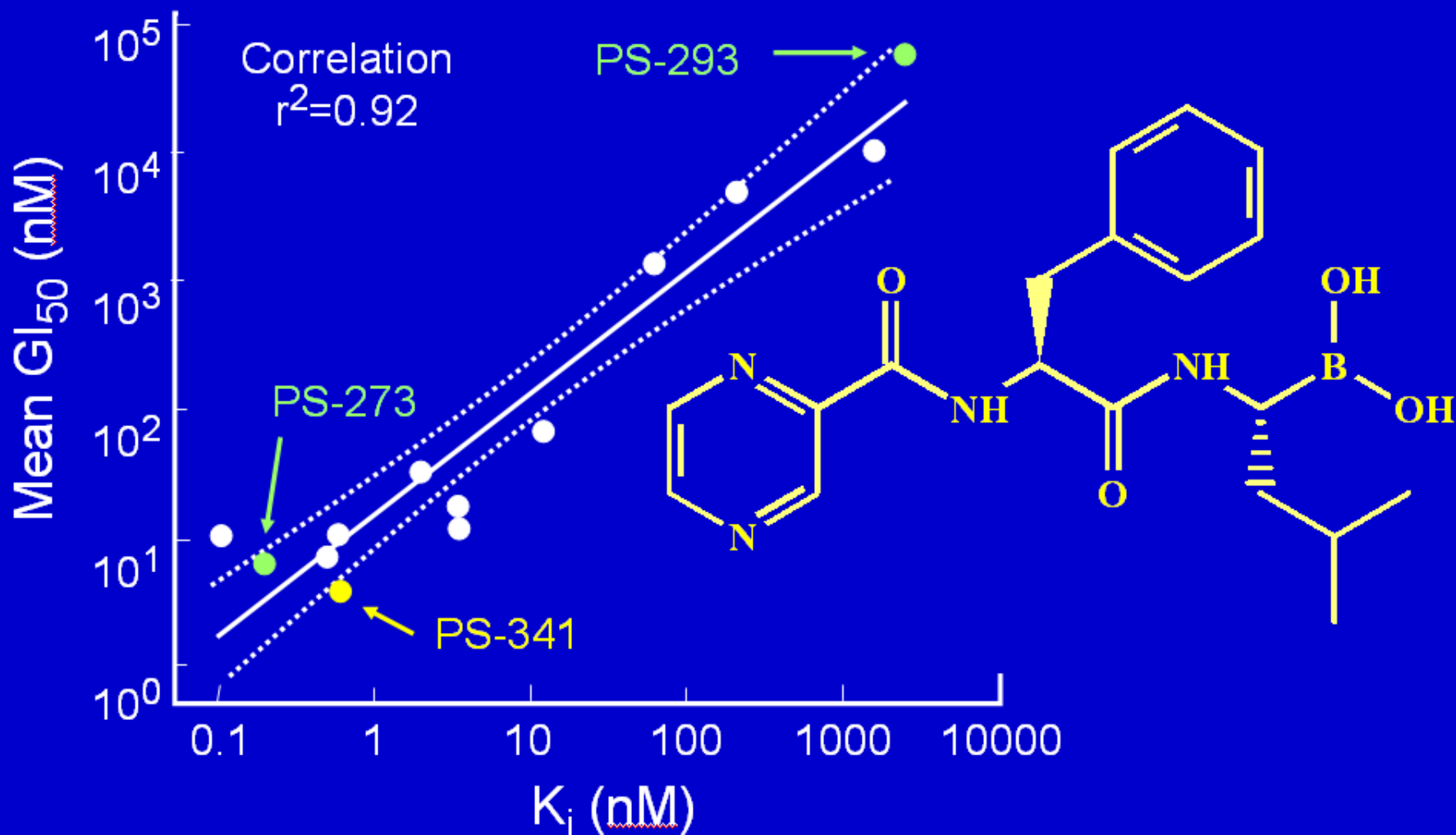


## \* BIOLOGICALS

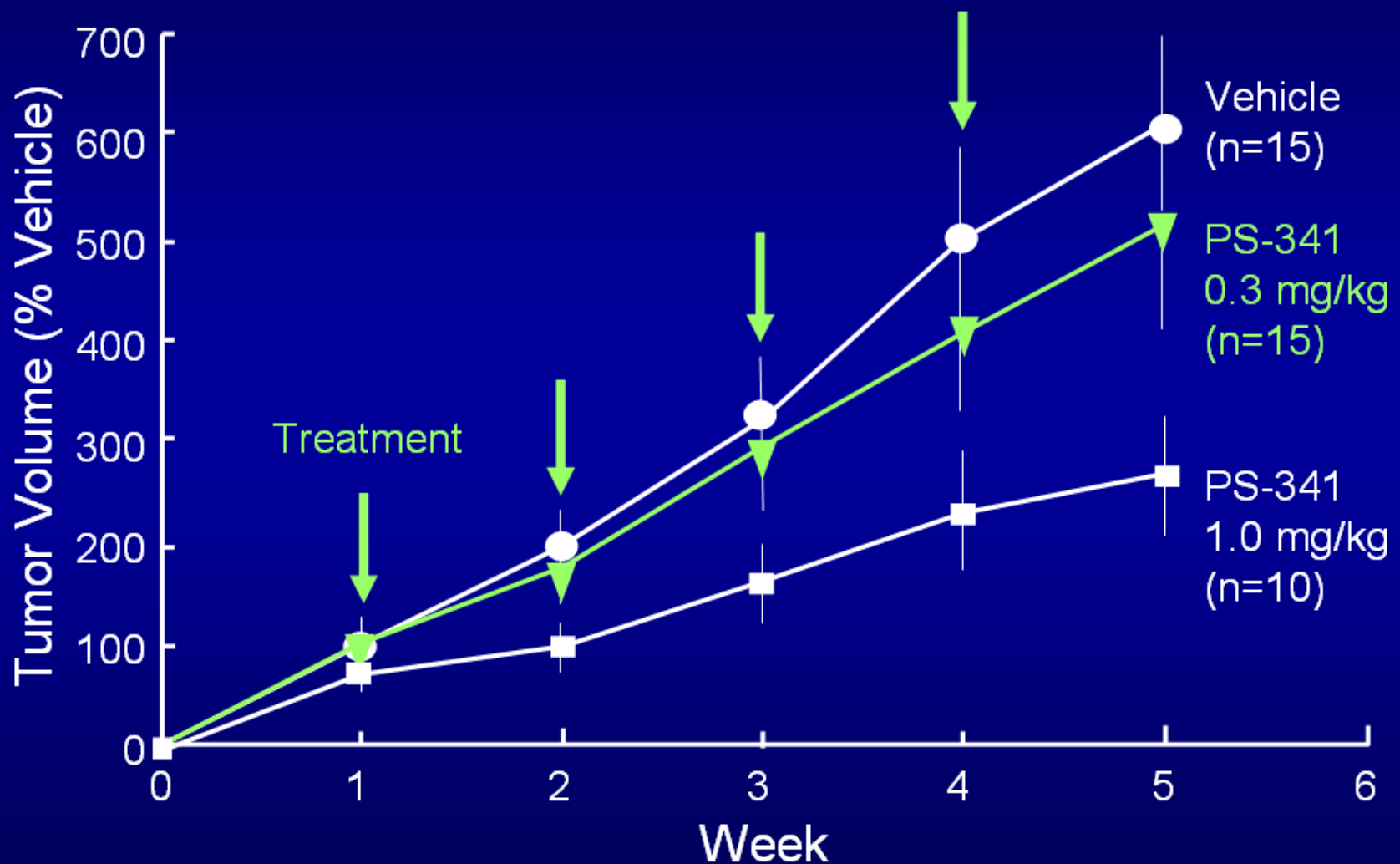
- Most Relevant Species
- Clinical Route & Schedule



# CORRELATION BETWEEN 20S PROTEASOME INHIBITORY POTENCY & GROWTH INHIBITION FOR 13 DIPEPTIDE BORONIC ACIDS

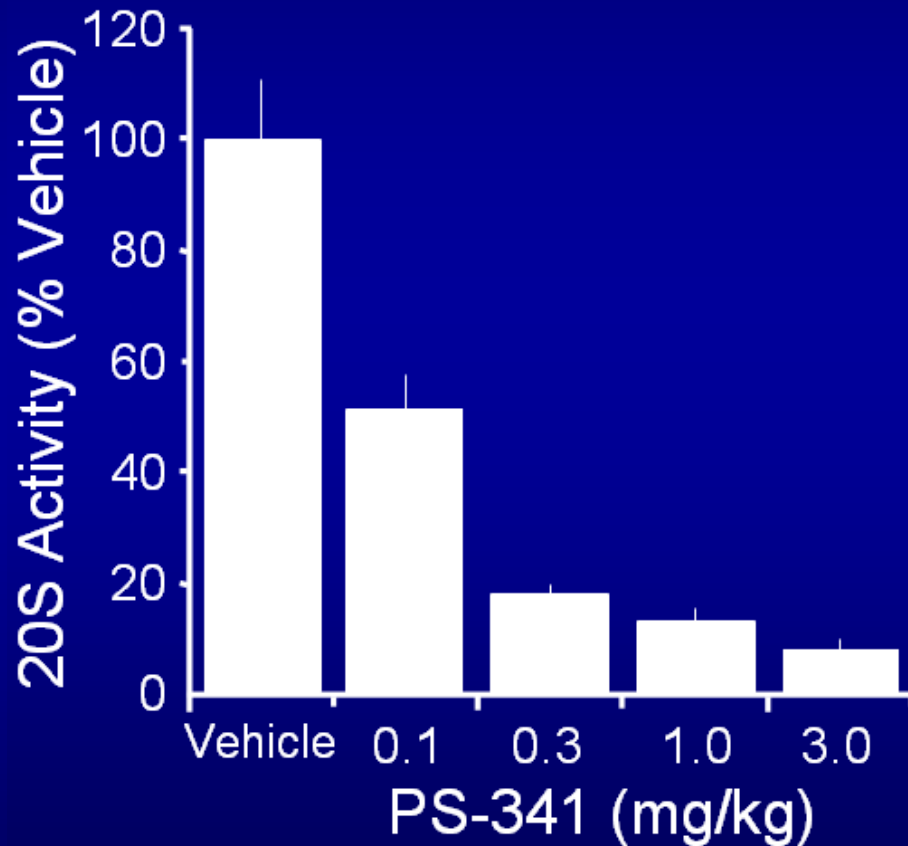


# EFFECT OF PS-341 ON PC-3 TUMOR GROWTH IN MICE

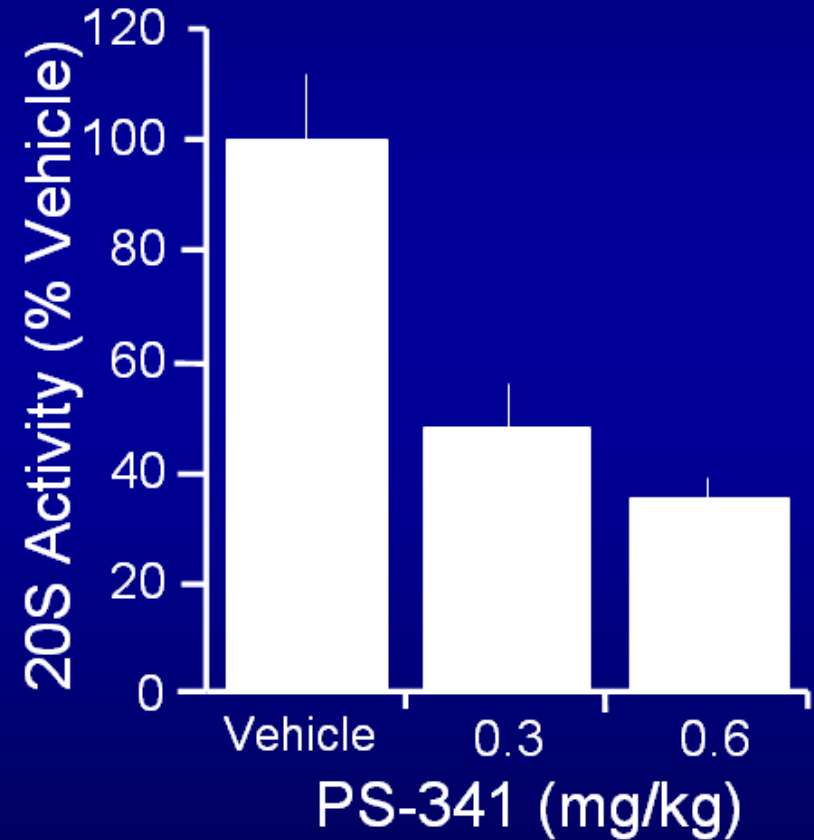


# EFFECT OF PS-341 ON 20S PROTEASOME ACTIVITY

## Mouse WBC



## PC-3



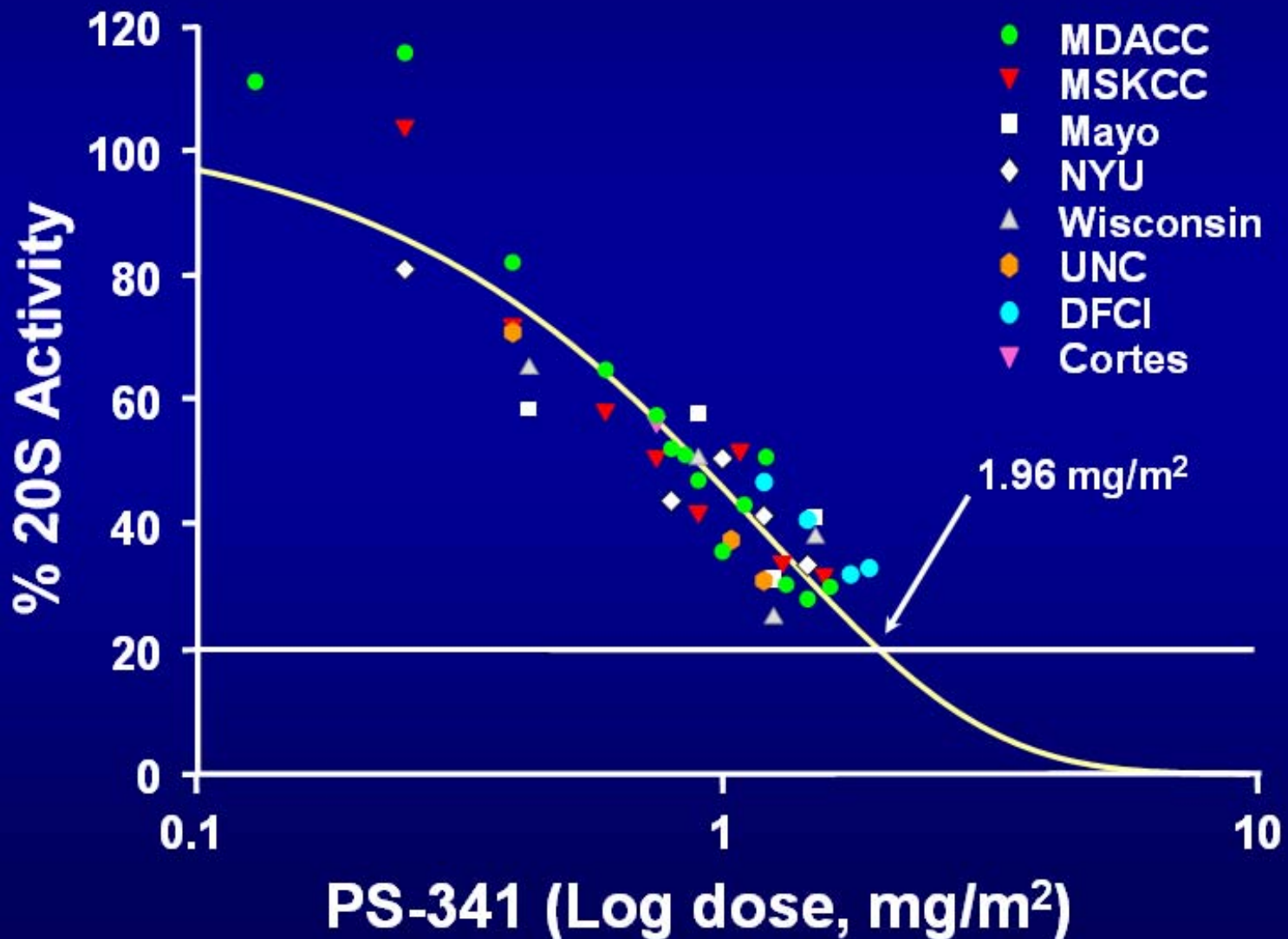
# PS-341: INTERSPECIES DOSE RELATIONSHIP

Q: Is the 'safe' dose in animals in the efficacy range for man?

Species	Dose (mg/kg)	Dose (mg/m <sup>2</sup> )	% 20S Proteasome Inhibition*
Mouse	1.0	3.0	80
Rat	0.25	1.5	80
NHP	0.067	0.8	70

\*In white blood cells at 1.0 h, post

# Ex Vivo Proteasome Activity: 1 Hour Post Treatment



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