

Review

Comprehensive Survey of Combinatorial Library Synthesis: 1998

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Reviews

Comprehensive Survey of Combinatorial Library Synthesis: 1998

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The art of solid-phase and solution-phase organic synthesis as applied to the assembly of chemical libraries is widely practiced in many academic and industrial laboratories throughout the world. Introduced in this decade, combinatorial chemistry, in its various formats, is now regarded as an important component of the drug discovery process. It is avidly employed by the biotechnology and pharmaceutical industry for this purpose. A previous comprehensive review provided a historical account of chemical libraries from which biologically active agents were obtained.¹ A total of 86 citations were compiled covering the years 1992 through 1997. In this 1998 annual update, there are 74 new citations,^{2–63} nearly equivalent to the cumulative total of published biologically active libraries for the preceding six years. This past year, more so than any other, was marked by the coapplication of library design and synthesis with molecular modeling and structure-based design. The first example of a compound, coming directly from an optimization library (solid-phase parallel synthesis), exhibiting biochemical efficacy and oral bioavailability was described.⁵⁸ Traditionally carried out on solid support, the use of solution-phase techniques for library generation is gaining momentum as ca. 30–40% of the 1998 libraries utilized solution-phase protocols. Because many more libraries are published annually without associated biological data and are of equal interest to the combinatorial and medicinal chemical communities, a compilation of these types of constructs is included in this review. In 1998, there were 247 libraries of this genus.^{64–257}

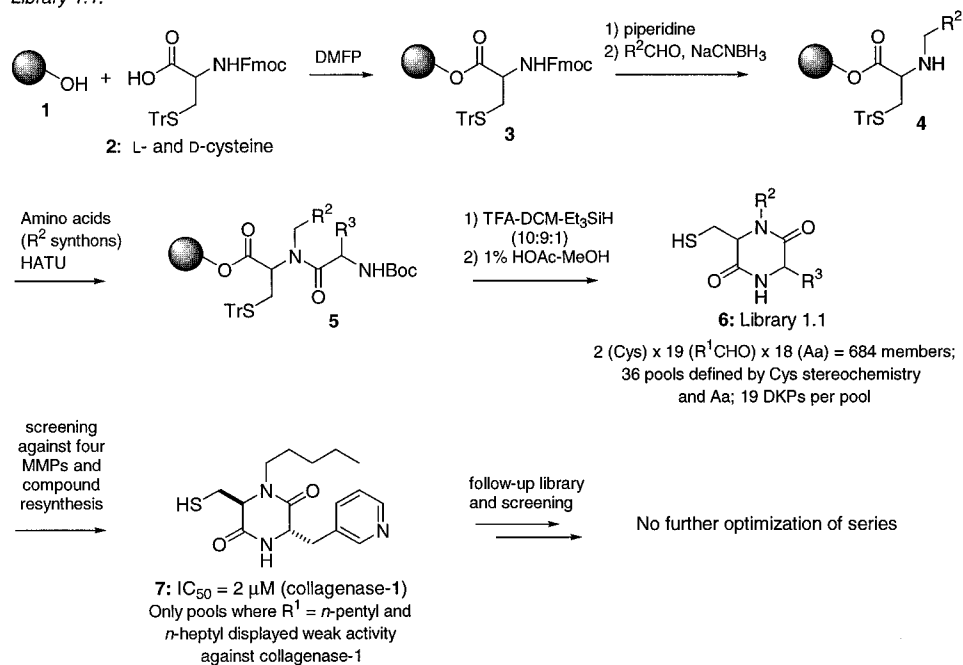
Library Descriptions

In keeping with the format of the previous review,¹ the biologically active libraries are segregated into five principal categories. Tables 1 and 2 list those libraries active against proteolytic and nonproteolytic enzymes, respectively. Table 3 lists libraries yielding agonists and antagonists of G-protein coupled receptors (GPCRs). Tables 4 and 5 delineate libraries active against non-GPCR targets (e.g., integrins, ion channels, domain interactions, nuclear receptors, and transcription factors) and whole-cell oncology and anti-infective targets. The name, generic structure, and affiliation is given for each library. The affiliation indicates whether the library was prepared in industry (company name), academia or another institution (senior author). The size of each library is also indicated, although it should be noted that the reported library size does not necessarily reflect confirmed library size. Each library is accompanied by the name of the molecular target against which it was evaluated and by the structure and potency of the most active library member. Each library is referenced with an entry code, e.g., library 4.11 refers to library entry 11 in Table 4.

In addition to the tabulations of biologically active libraries, an effort has been made to compile a list of libraries with undisclosed biological activity. These libraries, loosely defined as a multistep reaction sequence typically exemplified by >5 examples or members, are divided into five categories composing Tables 6–10. Table 6 entitled “Scaffold Derivatization” lists library constructs in which an existing scaffold or template is derivatized to provide a library. The addition of three nucleophiles to cyanuric chloride or Suzuki coupling of an aryl boronic acid to a resin-

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Library 1.1:



Library 1.2:

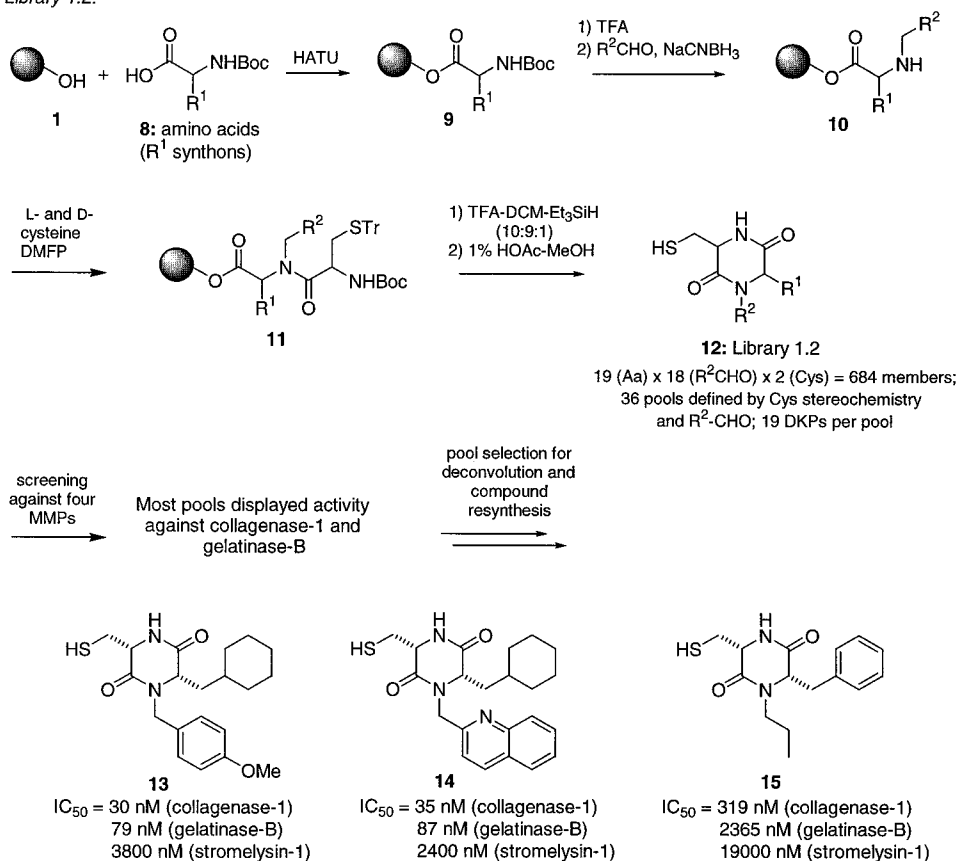


Figure 1. Affymax 3-thiomethyl-2,5-diketopiperazine libraries 1.1 and 1.2 as inhibitors of MMPs.⁴⁷

bound aryl iodide yielding a biaryl are examples of these types of constructs. Table 7 delineates the preparation of acyclic libraries, perhaps via a multicomponent condensation reaction (e.g., Ugi or Passerini reaction). Tables 8–10 include library constructs defined by monocyclic ring synthesis (e.g., Hantzsch thiazole synthesis), bicyclic and spirocyclic ring synthesis (e.g., indole synthesis, Knoevenagel condensation

yielding coumarins), and polycyclic (tetrahydro- β -carboline synthesis) and macrocyclic ring synthesis. Each table in turn is further subdivided into solid-phase and solution-phase synthesis. The affiliation, size (given by number of examples and corresponding yield or number of members if yield data was unavailable), and a brief descriptive note are indicated for each library. Single synthetic transformations, polypep-

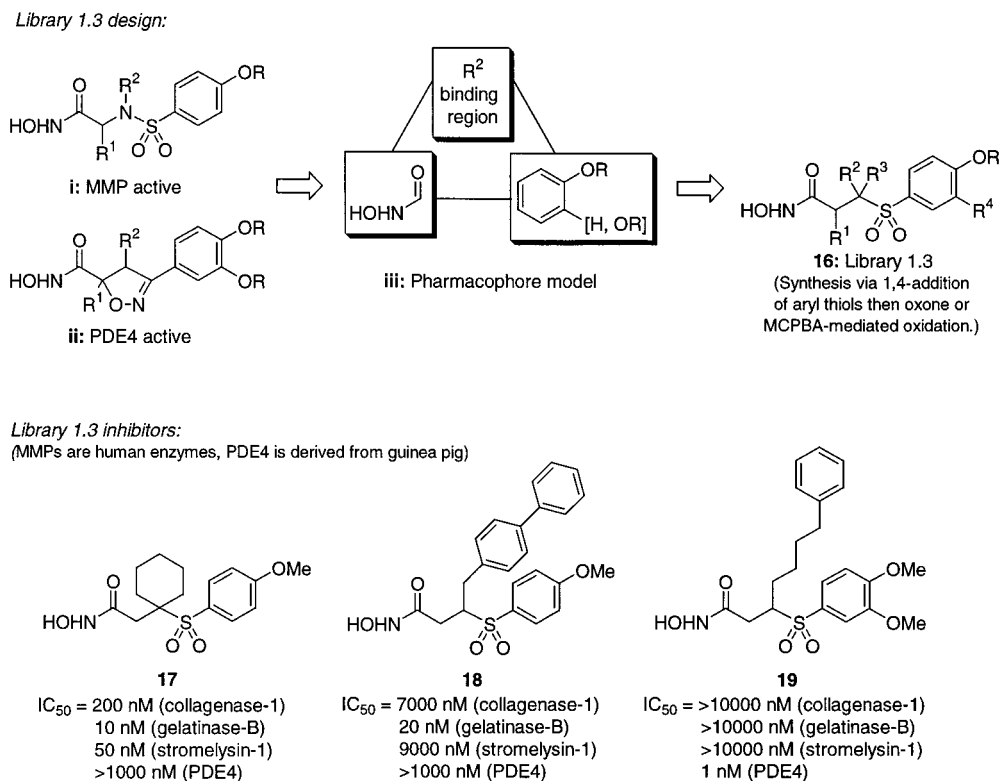


Figure 2. MMP and PDE4 selective inhibitors from the hydroxamate library 1.3.¹⁰

tide-, polysaccharide-, and oligonucleotide libraries, and libraries for nondrug discovery applications (e.g., catalysts) are generally not included in the tables.

Libraries Yielding Proteolytic Enzyme Inhibitors

Libraries directed toward the inhibition of proteolytic enzymes are listed in Table 1 (libraries 1.1–1.19). A common design strategy centers upon a mechanism-based approach to protease inhibition, i.e., the incorporation of a well-known pharmacophore into a suitable scaffold as a means to elicit potency and selectivity against a particular mechanistic class of protease. Pharmacophores utilized in library design include the following: thiols and hydroxamic acids for the metalloproteases (libraries 1.1–1.3); hydroxyethylamine- and statine-based transition-state isosteres for the aspartic acid proteases (libraries 1.4–1.6); arginine-, lysine-, and amidine-containing ligands and aminimides for the trypsin superfamily of serine proteases (libraries 1.8–1.17); and acyloxymethyl ketones and acylodides (irreversible inactivators) for cysteine proteases (libraries 1.18 and 1.19).

Affymax described two novel series of 3-thiomethyl-2,5-diketopiperazines (DKP) as inhibitors of the matrix metalloproteases (MMPs, libraries 1.1 and 1.2; Figure 1).⁴⁷ The selection of this heterocyclic scaffold was arrived at by comparative overlap of a number of heterocycles with a pharmacophore model derived from crystal structures of succinyl hydroxamate inhibitor-MMP complexes. The DKP scaffold was hypothesized to orient its thiomethyl group toward the catalytic zinc atom and direct the R¹ and R² appendages into the S₁' and S₂' binding subsites. There also existed the potential for hydrogen bond formation between the scaffold's heteroatoms and the active site of the enzyme, an essential feature of the tight-binding succinyl hydroxamate

inhibitors. Split-pool synthesis of the DKP inhibitor libraries (36 pools, 19 DKP inhibitors per pool) was straightforward, except that a rather unique coupling reagent, 1,3-dimethyl-2-fluoropyridinium 4-toluenesulfonate (DMFP), was used to minimize epimerization of the optically active cysteine amino acid synthons during the coupling steps.

Inhibition of collagenase-1 was observed in library 1.1 in only a few pools where R¹ = *n*-heptyl and *n*-pentyl, e.g., DKP **7** (IC₅₀ = 2 μM). A follow-up library was prepared (details not given) based on the limited structure–activity relationship (SAR) data obtained from the initial screening of the library; however, no further improvement in activity for this series of DKPs was obtained.

In contrast to library 1.1, the regioisomeric DKP library 1.2 displayed broad activity against collagenase-1 and gelatinase-B. The library was essentially devoid of inhibitory activity against stromelysin-1 or matrilysin. Deconvolution of one of the more active pools (library 1.2, R² = CH₂-(4-OMe-phenyl) and resynthesis of individual library members provided novel MMP inhibitors, **13–15**. Nascent SAR obtained from library screening results and resynthesized compounds indicated a very strict dependence of activity on the thiomethyl and R¹ stereochemistries, limited tolerance for variations at R¹, and rather broad tolerance for functionality at R².

Hydroxamic acid library 1.3 was designed and synthesized at Rhone-Poulenc Rorer following in-house observations that *N*-sulfonylamino hydroxamates **i** and dihydroisoxazole hydroxamates **ii** are inhibitors of MMPs and phosphodiesterase-4 (PDE4), respectively (Figure 2).¹⁰ The apparent SAR data suggested that the two mechanistically distinct enzymes may share common pharmacophore elements as depicted in **iii**. Library synthesis of single compounds (> 300

Library 1.4 synthesis:

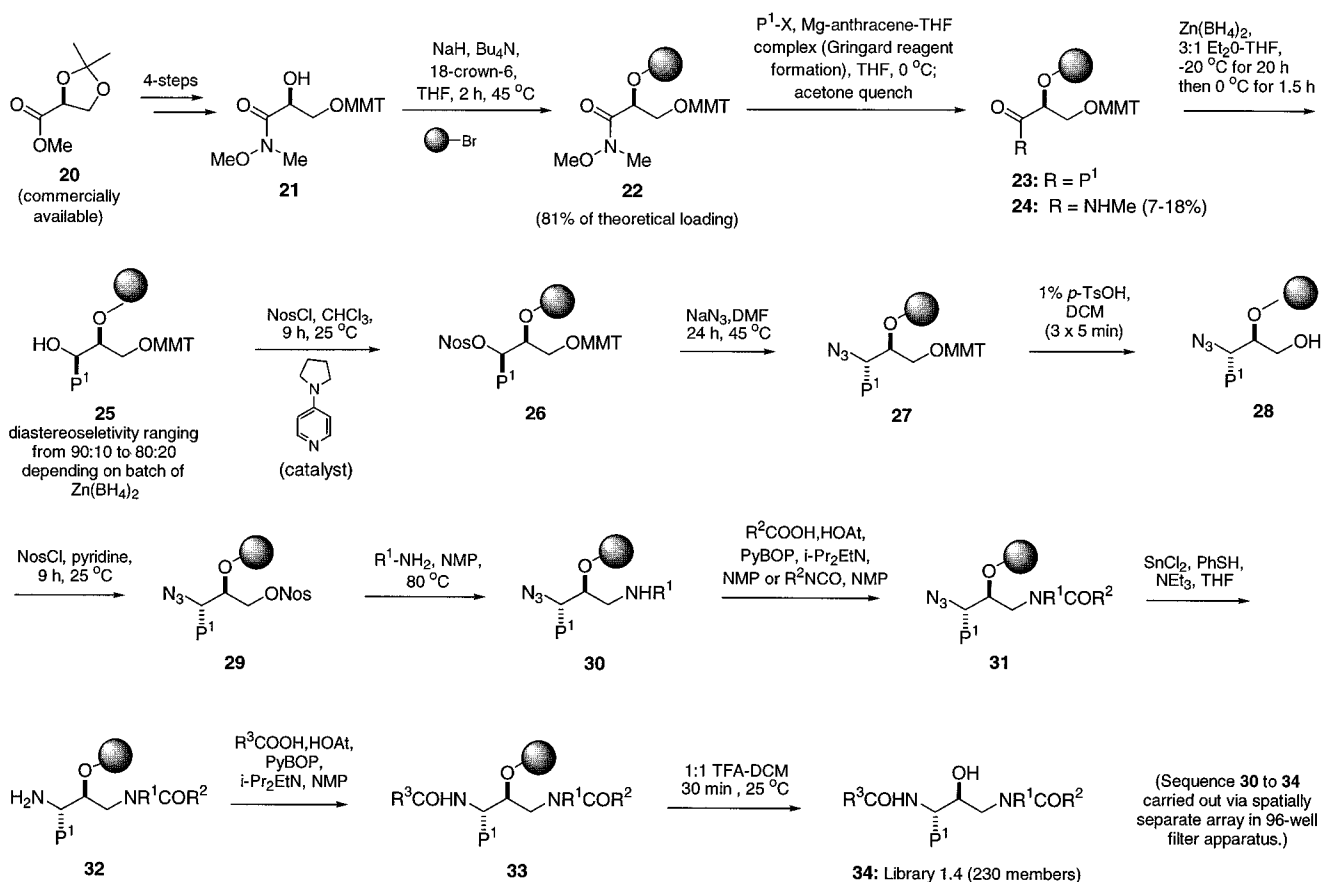


Figure 3. Ellman's library synthesis of mechanism-based inhibitors of aspartic acid proteases.²⁶

compounds) was conducted using both solution- and solid-phase methods. Potent and selective inhibitors of each enzyme class were obtained upon *in vitro* evaluation of the library. Remarkably, there was a striking dependence of target selectivity on the arylsulfonyl moiety; nanomolar potency for either the MMPs or PDE4 could be modulated by a single *m*-methoxy substituent (**17** and **18** versus **19**; hydrophobic R²R³ not withstanding). The MMP enzymes were of human origin, while the PDE4 enzyme was obtained from guinea pig. It would be of interest to determine whether a similar SAR trend would be observed among enzymes of the same species.

Ellman published a full paper on the design and synthesis of hydroxyethylamine-based aspartyl protease transition-state isosteres, concluding a multiyear research endeavor.²⁶ An elegant 12-step synthetic sequence was developed on solid phase which provided full access to diversity at the P¹ side chain (R¹), the terminal amino appendages, and chirality at the secondary hydroxyl and amino groups (Figure 3). This was achieved without the use of amino acids as a source of chirality. The generality of the sequence was demonstrated by the construction of a 230-member library (library 1.4). The library synthesis began with a four-step solution synthesis of Weinreb amide **21** derived from commercially available, optically active isopropylidene glyceric acid methyl ester **20**. The selection of the monomethoxytrityl group for primary hydroxyl group protection in **21** was based upon the ability to remove this protecting group under mild acidic conditions that would not cleave material from the acid-

sensitive linker, and its strong UV chromophoric property which made it convenient to monitor spectrophotometrically. Attachment of **21** to the resin was carried out by the reaction of a resin bromide (prepared from Wang resin, Ph₃P, CBr₄ in DCM) with the sodium anion of **21** in THF (**21** → **22**). Resin **22** was reacted with one of 17 Grignard reagents to provide the corresponding ketones **23**. The alkyl Grignard reagents were prepared in the standard way, while the more reactive benzylic-type Grignard reagents were prepared via the addition of the benzylic halide to a solution of magnesium-anthracene-THF complex in THF. A byproduct obtained during the Grignard addition was the *N*-methyl amide **24** (up to 18%), formed by competitive N–O bond cleavage. Chelation-controlled reduction employing Zn(BH₄)₂ converted ketone **23** to the alcohol **25** with diastereoselectivities ranging from 90:10 to 80:20, with the ratio apparently independent of the P¹ group but rather dependent upon the batch of freshly prepared Zn(BH₄)₂ used for the reduction. Considerable solid-phase reaction optimization was required to convert alcohol **25** to azide **27**. Standard Mitsunobu reactions employing (PhO)₂P(O)N₃, HN₃, or Zn(N₃)₂-bis pyridine complex were unsuccessful. Ultimately, alcohol **25** was activated as its 4-nitrobenzenesulfonyl ester **26** using 4-pyrrolidinopyridine as the catalyst in chloroform. The choice of catalyst and solvent were critical as the poor conversion was observed with mesyl or tosyl esters in solvents other than chloroform, and DMAP salts readily precipitated into reaction sites on the resin. Displacement of the nosyl group in **26** with NaN₃ (**26** → **27**) was without

complications, (<5% nosyl elimination products). The MMT protecting group in **27** was readily removed and the resulting primary alcohol **28** then converted to its nosyl derivative (**27** → **29**). All scaffolds were cleaved at this stage and characterized. Library synthesis was completed by reaction of **29** with a selection of R¹ amines (**29** → **30**), acylation with R² functionality (**30** → **31**), followed by reduction of the azido group, acylation with a series of R³ carboxylic acids, and TFA-mediated cleavage of the inhibitors from resin (**32** → **34**). The selection of the R¹–R³ derivatizing reagents was reviewed previously.

Library 1.4 was evaluated against human liver cathepsin D, and resynthesis of the more potent inhibitors was carried out. Several of the inhibitors had a K_i of <5 nM, with structure–activity tracking to the more hydrophobic (aryllkyl) P¹ side chains.

Pharmacopeia described two encoded aspartic acid inhibitor libraries 1.5 and 1.6 exploiting the statine pharmacophore in library design.^{11,12} The libraries were prepared and evaluated against plasmepsin II, one of two aspartyl proteolytic isozymes required for hemoglobin metabolism in the malarial parasite. An encoded mixture of 21 Boc-protected statine amides **40** (derived from 7(R¹) amines × 3(R²) Boc-statines) served as a common encoded intermediate for the libraries (Figure 4). For library 1.5,¹² encoded intermediate **40** was deprotected and apportioned into 31 lots, and then each lot was coupled with one of 31 Fmoc-protected amine amino acids (R³ synthons corresponding to the P² residue; **40** → **41**). The resin lots were encoded with molecular tags and combined. The combined resin was treated with piperidine to remove the Fmoc protecting group, and then the resin was divided into 20 lots. Each lot was reacted with one of 20 N-derivatizing reagents (R⁴ synthons), yielding **42** (library 1.5) as 20 sublibraries containing 651 compounds per sublibrary for a total of 13 020 members (**41** → **42**). Library 1.5 was evaluated (off-bead, solution screening (**43**) against plasmepsin II). The results of the assay revealed that 10 of the 20 sublibraries displayed inhibitory activity against the enzyme. A total of some 60 beads were decoded across the 10 sublibraries, revealing the preference for hydrophobic synthons at R¹ and R⁴ and for hydrophobic P¹ statines (leucine or phenylalanine statine) at R². The more basic R¹ amines and alanine statine were not observed in the decoded structures. Interestingly, *only two* amino acids, isoleucine and valine, out of the potential 31 amino acids were seen at R³. This result may argue for β-branched amino acids as P² specificity determinants for the enzyme. A counter screen was conducted against cathepsin D, a human lysosomal aspartyl protease. Similar R¹, R², and R⁴ preferences were observed for this enzyme in addition to a much broader frequency of R³ (P²) amino acid residues. A total of 18 compounds were resynthesized, and inhibition constants (K_i) were determined against each enzyme. Inhibition constants ranged from 50 nM to >30 μM, with inhibitors **44**–**47** representative of the more active and selective agents. Inhibitor **45** was also active in malaria cell culture at ca. 10 μM.

Library 1.6 employed cyclic diamino acids as R³ synthons in place of the R³ amino acids used in library 1.5 (Figure

4).¹¹ A selection of heterocyclic peptidomimetics were docked into the active site of plasmepsin, and it was determined that piperazine carboxylic acids **48** and **49** and, possibly, 4-aminoproline **50** were potential surrogates for the P² amino acid residue. Encoded intermediate **40** was deprotected and apportioned into three resin lots. Each lot was coupled to one of three orthogonally protected diamino carboxylic acids (**40** → **51**). After an encoding step, the resins were combined, the Boc group was removed, and the corresponding amino resin was divided into 15 lots. Each lot was either acylated with one of six carboxylic acids or reductively aminated with one of nine aldehydes (15 R⁴ synthons in total; **51** → **52**). Following a fourth encoding step, the resins were once again combined, the Alloc group was removed, and the resin was reapportioned into 20 lots. These lots were derivatized with one of 20 carboxylic acids yielding **53** (library 1.6) as 20 sublibraries with 945 compounds per sublibrary for a total of 18 900 members. Evaluation of library 1.6 (off-bead assay, **53** → **54**) against malarial plasmepsin II and the counter screen, human cathepsin D, followed by decoding of some 100 active beads, revealed preferences for hydrophobic R¹ and R² synthons analogous to library 1.5. Of the three diamino acid scaffolds (R³ synthon), there was a high frequency found for the piperazine carboxylic acids **48** and **49** in the decoded structures. Inhibition constants (K_i) for four resynthesized compounds were reported, with inhibitors **55** and **56** representative of the screening results.

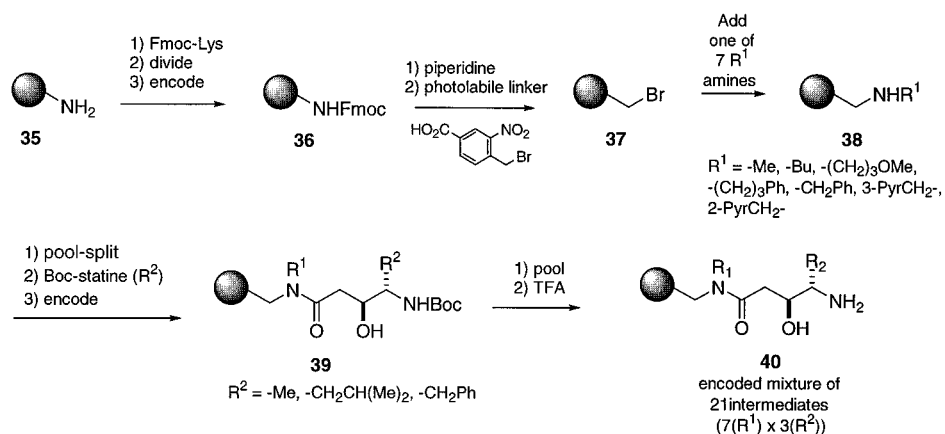
Three libraries 1.8–1.10 were reported to display activity against factor Xa.^{20,31,39} Two of the libraries utilized heterocyclic cores in their design: a triazine core (library 1.8)²⁰ and the 3,5-difluoro-4-trifluoromethylpyridine core (library 1.9).³¹ Each library was prepared from their respective halogenated templates. The third library 1.10 was a collection of L-octapeptides.³⁹

Library 1.9 is a focused library based on the previously known bisamidine **57** (K_i = 13 nM, Figure 5).³¹ Its purpose was to identify a replacement for one of the benzamidine groups in **57** so as to enhance the overall drug-like characteristics of the series. Library 1.9 was moderately successful in its task. Modest inhibitors **59** (K_i = 560 nM) and **60** (K_i = 495 nM) were obtained. Structurally related compounds **61** and **62** were inactive against the enzyme.

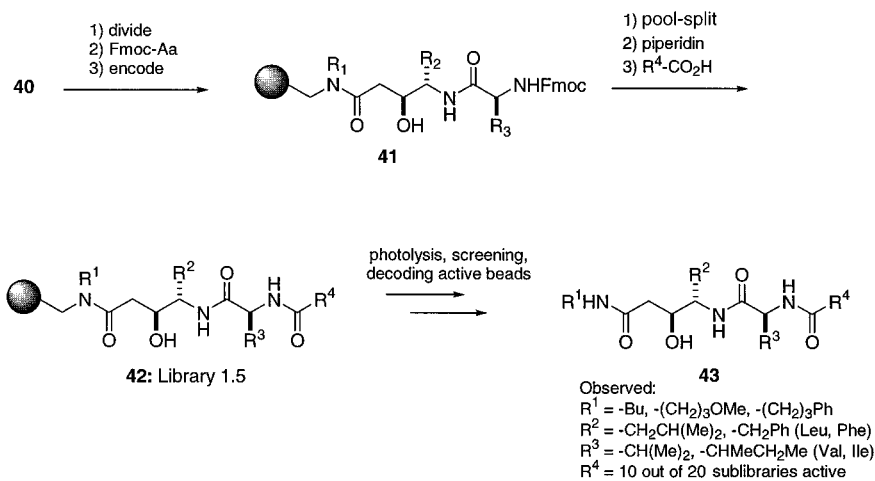
Selectide Corporation conducted an on-bead screening assay for factor Xa inhibition using a large L-octapeptide library (Figure 6).³⁹ Active beads (colored) were manually retrieved from the assay, and the structures of the associated peptides were determined via Edman degradation. Among the active beads, the sequence -L-Tyr-L-Ile-L-Arg- was highly conserved at or near the N-terminus. Interestingly, this same sequence is known as a minimal inhibitory sequence for factor Xa. Resynthesis of actives revealed a family of octapeptides with micromolar inhibitory activity against factor Xa (K_i = 4–15 μM, e.g., **63**). Further modification of the series led to the pentapeptide **64** (K_i = 3 nM) as a potent and selective inhibitor of factor Xa.

Serine proteases typically bind their pseudo-substrates and inhibitors as an extended antiparallel β-strand. By comparative analysis of enzyme inhibitor crystal structures, with

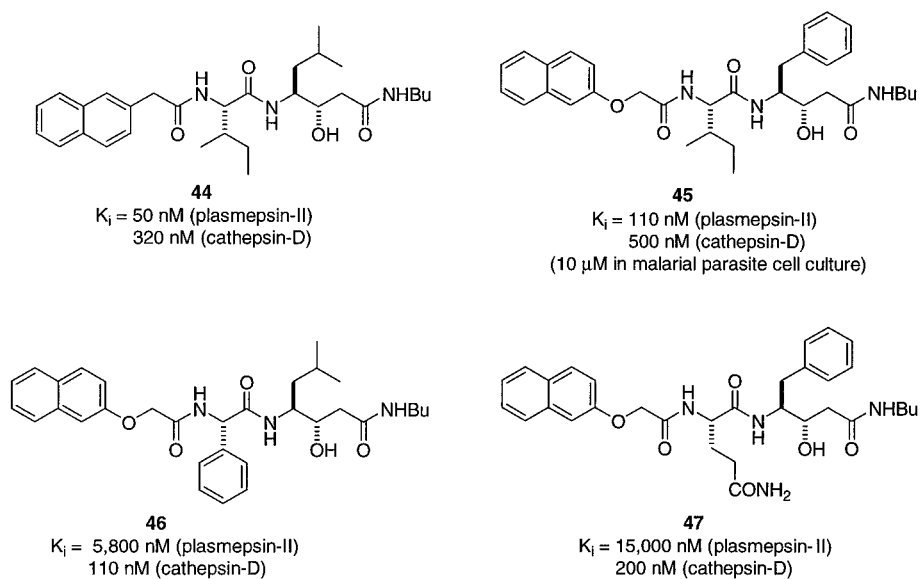
Synthesis of encoded intermediate **40** common to both libraries:

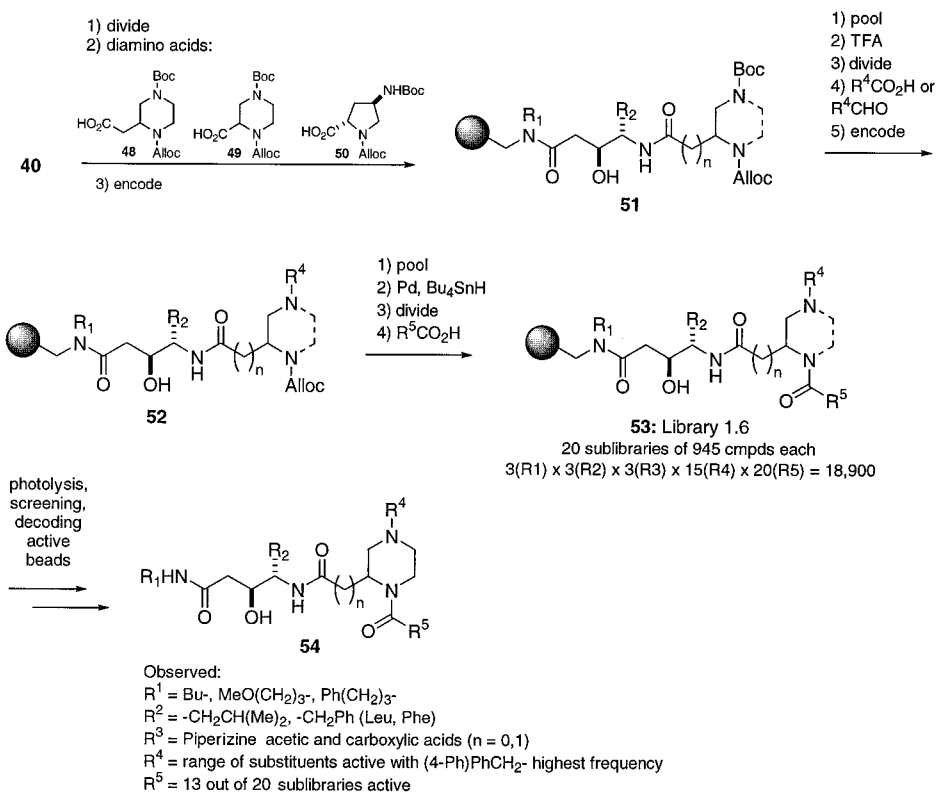


Library 1.5 synthesis:



Library 1.5 actives:



Library 1.6 synthesis:¹¹

Library 1.6 actives:

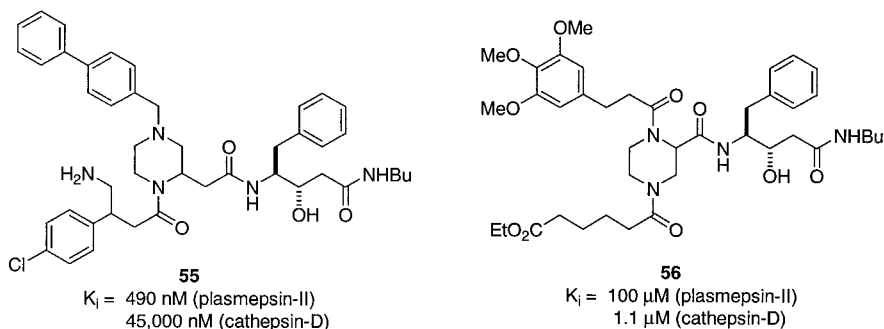


Figure 4. Pharmacoepia's encoded statine-based aspartyl protease inhibitor libraries 1.5 and 1.6.^{11,12}

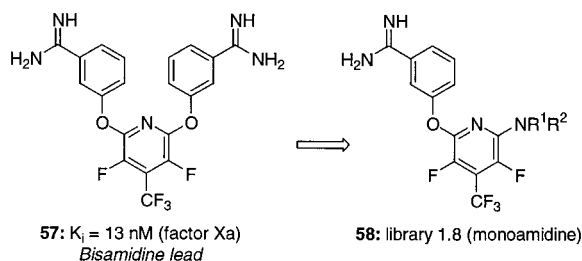
conformational searches carried out on potential β -strand mimetics, libraries 1.11 and 1.12 containing putative bicyclic β -strand mimetics were conceived.³⁸ The libraries were prepared via the Diels–Alder reaction between resin-bound diene **65** and dienophiles **66** and **70** followed by oxidation to install an α -keto amide function (**65** \rightarrow **67**; **65** \rightarrow **71**; Figure 7). The bicyclic template was thought to form three critical hydrogen bonds found at the active site of serine proteases, while the reactive carbonyl (α -keto amide) was designed to engage the active site serine hydroxyl group. Evaluation of the two libraries against thrombin revealed three subnanomolar inhibitors **68**, **72**, and **73**, and related inhibitor **69**.

The Merck proline amide libraries 1.14 and 1.15 represent interesting case studies for successful lead optimization through solid-phase synthesis (Figure 8). Inhibitors **74** and **75** were peptidomimetic leads identified in a thrombin inhibitor discovery program. Although potent and selective,

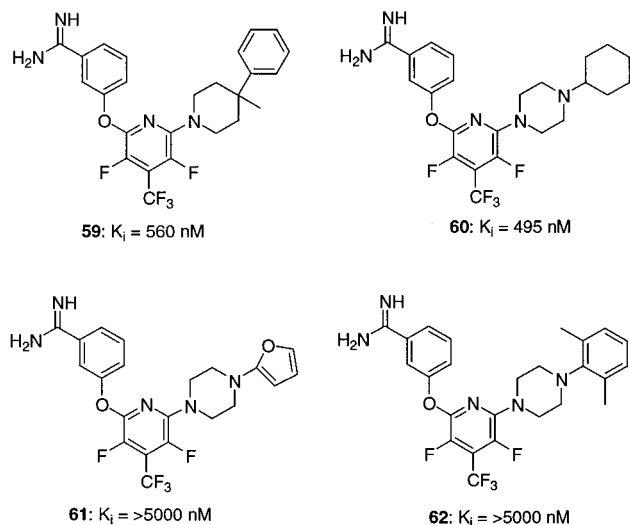
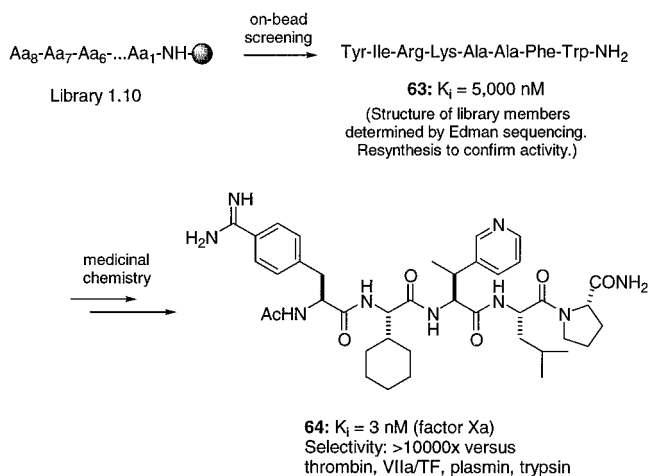
neither inhibitor displayed significant blood levels upon oral administration to rats and dogs. In an effort to identify analogues with improved pharmacokinetic properties, leads **74** and **75** were subjected to optimization via a parallel solid-phase synthesis. Library 1.15²⁸ was designed to identify less basic thrombin inhibitors. A small series of analogues (18 proline amides) were prepared in which the cyclohexylamine moiety in **75** was exchanged for neutral, lipophilic species. Evaluation of library 1.15 revealed inhibitors **77** ($K_i = 40$ nM) and **78** ($K_i = 3$ nM) possessing the lipophilic 2,5-dimethyl and 2,5-dichlorobenzyl amido groups.

Complementary to library 1.15, library 1.14 explored SAR in the region of the acylated proline nitrogen. In this optimization library, 200 new analogues of inhibitor **74** were synthesized. The N-acylating reagents were carefully selected from a combined commercial and in-house collection of over 2 200 carboxylic acids. Substructure features of particular interest included aromatic or hydrophobic moieties, con-

Library 1.9 design:



Library 1.9 actives:

Figure 5. Amidinopyridines as factor Xa inhibitors.³¹Figure 6. Selectide's factor Xa inhibitor library 1.10.³⁹

straints or conformational reinforcements affording directional diversity, heteroatoms to access potential H-bonding, and achirality to structurally simplify the lead. A number of structurally novel inhibitors were identified upon bioassay. Compound **76** proved to be a highly potent and selective inhibitor and fully efficacious in a rat model of FeCl₃-induced arterial thrombosis. The oral absorption of **76** was excellent in the dog (74% at 5 mg/kg, $C_{max} = 4.6$ μ M at 40 min, i.v. plasma half-life ca. 2 h) and cynomolgus monkey (39%, $C_{max} = 1.77$ μ M at 113 min, i.v. plasma half-life ca. 4 h). The unique, putative binding interactions of **76** with enzyme

were also determined via a molecular model of **76** created using the X-ray coordinates of thrombin-**74** complex. This is the first reported, successful example of improving a lead's pharmacokinetic parameters via analogue synthesis on solid support.

A solution-phase synthesis of aspartic acid-based acyl-oxymethyl ketones was reported by a Parke-Davis group (library 1.18; Figure 9).⁵² The two-step reaction sequence (**79** \rightarrow **82**) was optimized in 3–4 days via a nonlinear array where over 200 different reaction conditions were evaluated. Some 82 different reaction conditions alone were carried out to optimize the displacement of the bromide in *Z*-Asp(O-*t*-Bu)CH₂Br with naphthyl acetic acid. Excess bromomethyl ketone was removed from the reaction mixture using a thiourea scavenging resin. Optimal deprotection of the β -*tert*-butyl ester Asp side chain to provide the free β -carboxyl group was examined via 40 reaction conditions. Classical TFA-mediated deprotection in CH₂Cl₂ was found inferior to 1 M HCl in EtOAc. The optimized reaction conditions were then applied to library synthesis **83** \rightarrow **86**. Compounds of this class are known interleukin-1 β converting enzyme (ICE) inhibitors, and IC₅₀/ K_i values for five resynthesized compounds were reported.

Libraries Yielding Nonproteolytic Enzyme Inhibitors

Table 2 lists 13 libraries (2.1–2.13) targeted for nonproteolytic enzymes. These are subdivided into kinases (library 2.1 (tyrphostin analogues), library 2.2 (phosphonates), and library 2.3 (purines)) and phosphatases (library 2.4 (α , α -difluorophosphonates) and miscellaneous mammalian and nonmammalian enzymes. The mammalian enzyme entries include the following: cyclooxygenase-1 and -2 (COX-1/2; library 2.5), dihydroorotate dehydrogenase (library 2.5), and phosphodiesterase-4 (PDE4, library 2.7). The nonmammalian enzyme targets include the following: phosphomannose isomerase (PMI, libraries 2.8 and 2.9), glucosyltransferase-1 (GFT-1, library 2.10), β -galactosidase (library 2.11), HIV-1 reverse transcriptase (library 2.12), and flu A sialidase (library 2.13).

A novel class of 10-substituted phenothiazines as selective COX-2 inhibitors was identified through a combination of computational 3-D database searching and combinatorial library synthesis (Figure 10).⁴⁵ Tricyclic **87** (melitracene) was selected as a putative COX-1/2 inhibitor upon executing a DOCK search against the sheep COX-1 crystal structure. Although melitracene **87** was not available for biological evaluation, it was hypothesized that other tricyclic ring systems may adopt a binding orientation similar to that predicted for **87**. In this regard, *N*-substituted phenothiazines were tested and found to inhibit COX-1/2 with modest selectivity, e.g., **88**–**90**. A small parallel library **91** (library 2.5) of *N*-(3-amidopropyl)phenothiazines yielded **92** (IC₅₀ = 21 μ M, COX-2) and **93** (IC₅₀ = 1.3 μ M, COX-2) as selective COX-2 inhibitors (**92** and **93**: IC₅₀ > 50 μ M, COX-1).

Library 2.8 is a 1 296-member collection of acylated dipeptides with 2-aminoindane-2-carboxylic acid as a conserved central building block (**97**: Figure 11).⁶ The impetus for creating library 2.8 was the result of information obtained

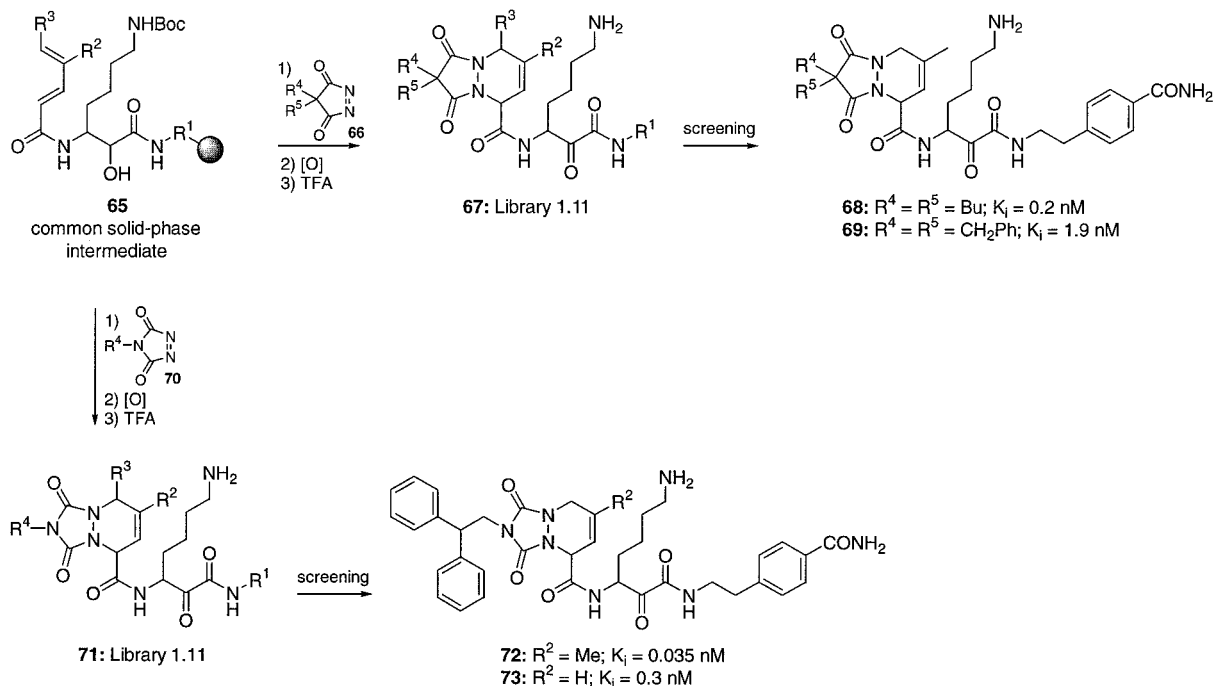


Figure 7. β -Strand mimetics as thrombin inhibitors (libraries 1.11 and 1.12).³⁸

from the screening of many combinatorial libraries (>300 000 total compounds). A single library of acylated dipeptides **94**, containing the 2-aminoindane-2-carboxylic acid, was the only library which possessed any appreciable activity against phosphomannose isomerase (PMI), an essential enzyme in fungal cell wall biosynthesis. Some 36 compounds from library 2.8 were selected for resynthesis following evaluation against PMI. There were two R^1 amino acid residues, 3-pyridylalanine and citrulline (e.g., **99–100**), that were associated with activity; however, the data was puzzling in that there was no direct correlation of activity with the synthons. An identical impurity, however, was observed in all of the HPLC traces of the crude resynthesized compounds. The structure of the impurity was deduced through mass spectrometry and shown to be N-acylated indane-2-carboxamide **101** ($K_i = 27 \mu\text{M}$). This material was a deletion adduct arising from incomplete coupling of the first amino acid to the photolabile amine resin. Library 2.8 was followed up with a series of optimization libraries (library 2.9) to furnish analogue **103** ($K_i = 4 \mu\text{M}$).

Libraries Yielding G-Protein Coupled Receptor Agonists and Antagonists

Table 3 delineates libraries active against GPCR targets including opioid receptors (libraries 3.1–3.4), somatostatin receptors (libraries 3.5–3.7), and the benzodiazepine receptor (library 3.8).

Dooley and co-workers, in their continuing interest in peptide libraries now spanning some five years, reported the synthesis of a 6 250 000-member tetrapeptide library (Table 3).¹⁷ Library 3.1 employed L-, and D-natural and unnatural amino acids as diversity elements. Using a mixture-based positional scanning format, library 3.1 was assayed against the μ , δ , and κ opiate receptors. Potent and selective agonists were identified for each receptor subtype. There was notable similarity between the peptides with μ and δ agonist activity.

Conservative changes in amino acids moderated μ and δ binding affinity. This result suggests that perhaps the two receptor subtypes may share a common topography with one another. This is reminiscent of topographies shared by other receptors, namely somatostatin with NK-1 receptors.²⁵⁸ The κ agonist series was structurally distinct from either of the μ or δ peptide series, favoring D-amino acids in all four positions. It should be noted too that the μ and δ binding assays were derived from the rat, while the κ receptors were obtained from the guinea pig. There may be species differences accounting for the distinct peptide motifs found for the κ versus μ/δ agonists.

A search of selective κ opioid receptor antagonists was initiated due to the potential of κ selective antagonists to be effective in treating substance abuse.⁴⁸ For a number of years, N-substituted derivatives of 3,4-dimethyl-(3-hydroxyphenyl)-piperidine were known for their pure opioid receptor antagonist activity but were lacking in subtype (μ , δ , κ) selectivity. A more recent finding that **104** possesses a measure of μ selectivity prompted the synthesis of library 3.2 in an effort to find κ receptor subtype selective agents (Figure 12). Library synthesis was carried out in solution starting with optically active **105**. Derivatization of **105** with 11 different Boc-protected amino acids followed by diborane reduction and TFA-mediated removal of the Boc protecting group gave diamines **106**. These in turn were acylated with substituted benzoic, phenylacetic, phenyl cinnamic, and 3-phenylpropionic acids to give a 288-member library (**107**). Screening the library at 100 nM against a κ selective ligand revealed **108–110** as potent and selective inhibitors. From the percent inhibition data it was observed that the stereochemistry of the *i*-Pr (R^1) group was critical for binding affinity as was the 3-(4-hydroxyphenyl)-propionyl group with $R^2 = \text{H}$. A purified sample of **108** possessed a $K_i = 7 \text{ nM}$ against the κ receptor. The μ/κ and δ/κ selectivity was 57 and >824, respectively. Examination of **108** in a functional

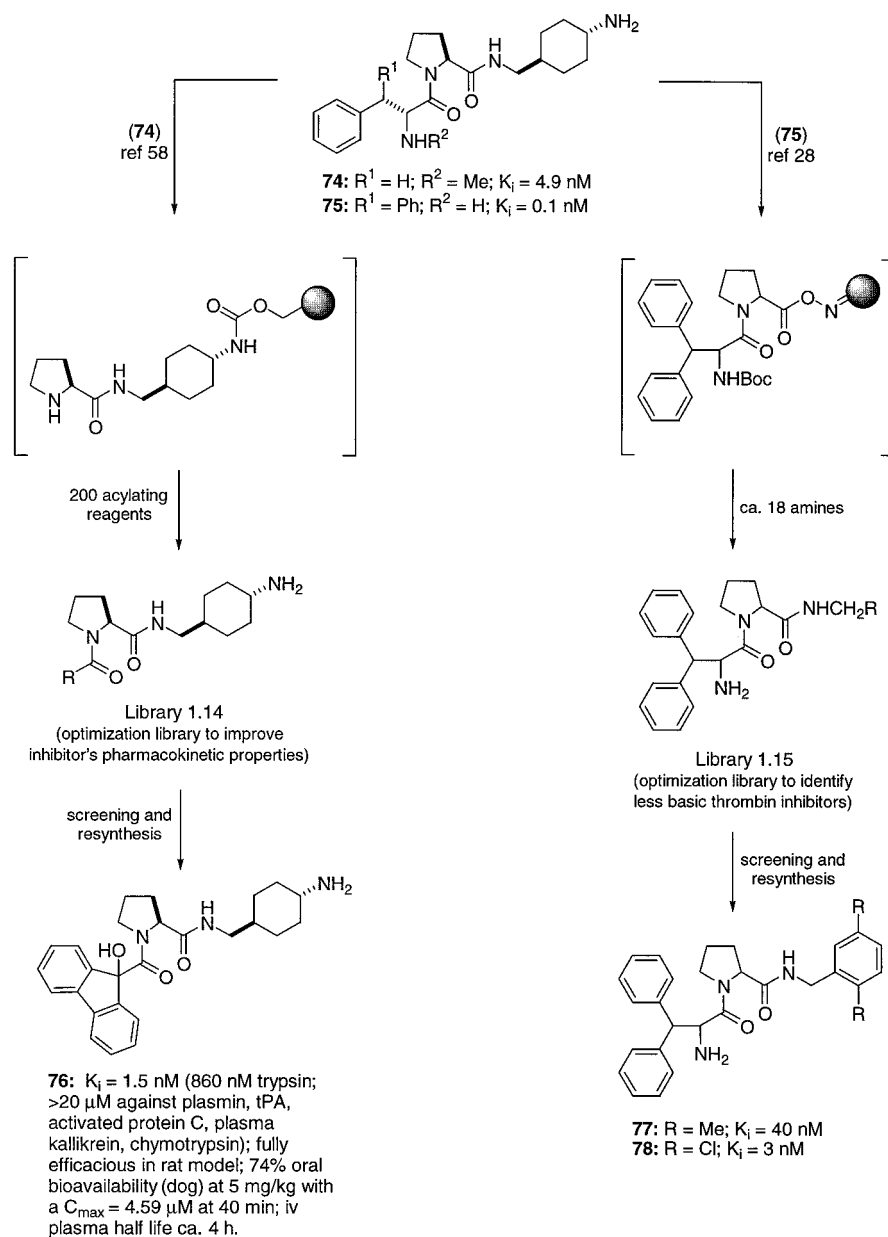


Figure 8. Merck's thrombin inhibitors (libraries 1.14 and 1.15).^{28,58}

assay revealed it to be an antagonist of the κ receptor, although the selectivity against μ and δ was not as great as observed in the radioligand binding assay.

Other non-peptide libraries active against the opiate receptors include Houghten's dialkylated hydantoin library 3.3 and bicyclic guanidine library 3.4.³³ The synthesis of library 3.3 is illustrated in Figure 13. The library of 38 000 hydantoin was examined in a σ opiate radio receptor binding assay. The IC₅₀ values of 12 resynthesized compounds ranged from 62 to 4615 nM. A basic residue (L- or D-Lys) at R³ and *N*-benzyl groups at R² and R⁴ and small hydrophobic groups at R¹ were found in the more potent δ binders, e.g., **117–119**. No selectivity data against μ , δ , or κ was given, nor any indication of whether **117** was a functional agonist or antagonist.

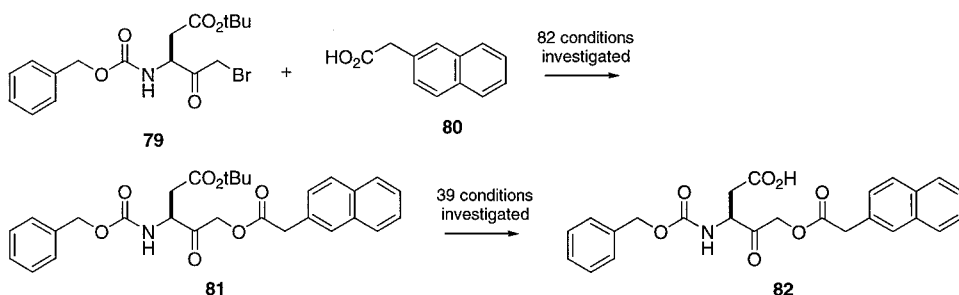
The bicyclic guanidine library 3.4 was derived from the condensation of resin-bound triamines with thiocarbonyldimidazole (TCDI). The triamines in turn were prepared via the borane-mediated reduction of a library of tripeptides.³³

Library 3.4 possessed selective κ opiate receptor activity. The most active compound had an IC₅₀ = 37 nM, although the actual structure was not disclosed.

Subtype selective agonists for each of the human somatostatin receptors (sstr1 through sstr5) were discovered at Merck via the synthesis and evaluation of libraries 3.5a–d based on lead **121** (Figure 14).⁴¹ The initial lead **121** (K_i = 100 nM, sstr2) was the most potent of 75 compounds extracted from an internal 200 000 member compound file collection, following a 3-D pharmacophore search using cyclic hexapeptide somatostatin agonist **120** as the probe.

Retro-combinatorial analysis dissects **121** into three fragments: 1,4-butylenediamine, tryptophan (Aa), and a spiroarylpiperidine unit. Further translation of this analysis into the design of lead optimization libraries suggested C-/N-terminal derivatized amino acids **122** as a generic library construct. This amino acid amide theme (**122**) served as the basis for the synthesis of libraries 3.5a–c; library 3.5d was an unrelated collection of arylindoles.

Reaction conditions for the synthesis **82** were optimized robotically:



Optimized reaction conditions then applied to the construction of a ca. 600 member library:

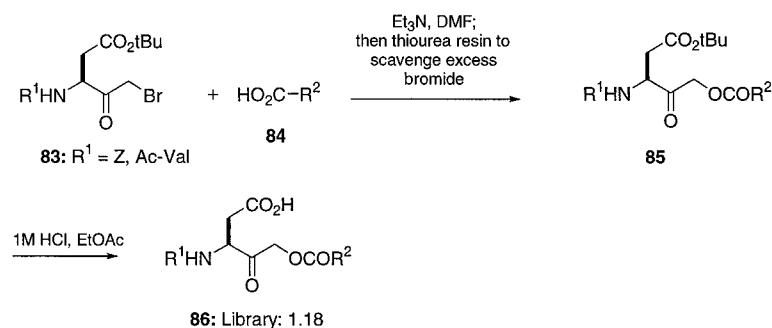


Figure 9. Solution-phase synthesis of ICE inhibitors (library 1.18).⁵²

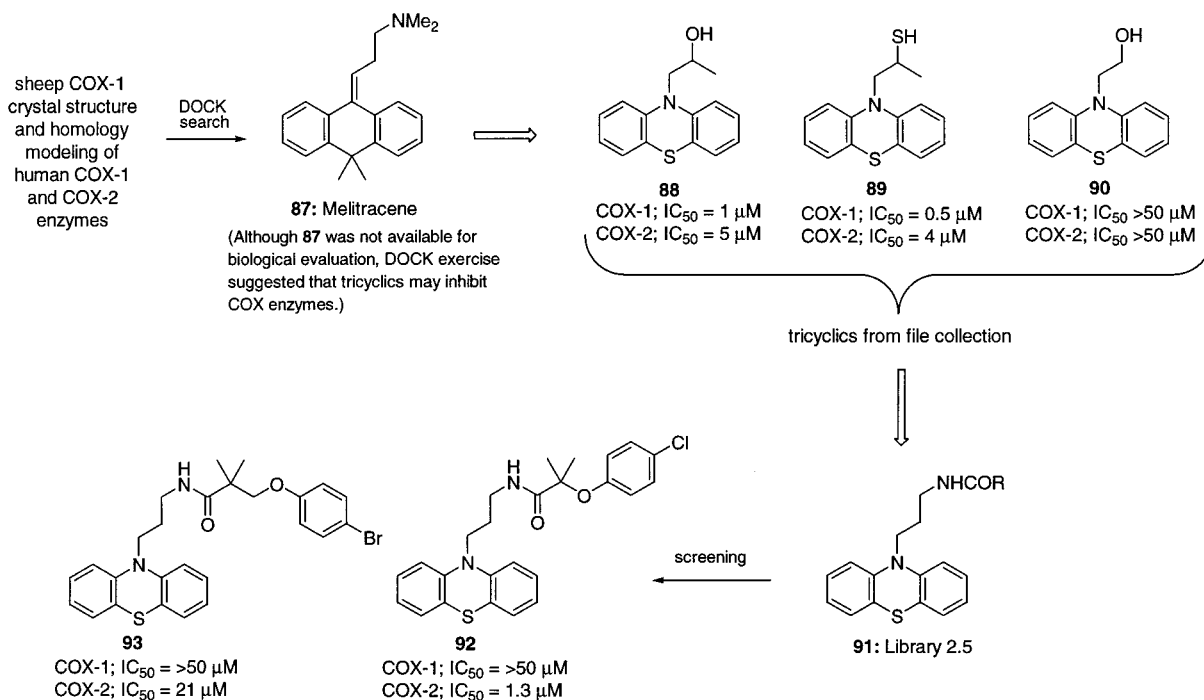


Figure 10. Phenothiazine-based COX-2 selective inhibitors (library 2.5).⁴⁵

Library 3.5a may be considered a “tryptophan amide library”, composed of 20 diamines (R¹), 20 tryptophan surrogates (Aa), and 79 spiroarylpiperidine replacements (R³). This gave a library of 20 × 20 × 79 = 31 600 compounds; however, taking into consideration that racemic synthons were used, the approximate library size was estimated to be 130 000 members. The details of the actual library synthesis were not given, but multiple pools of compound mixtures were prepared. The library was evaluated against all five sst receptors. Two pools active against sst were identified. The first pool of 1 330 spiroindane analogues

123, including lead **111**, was not deconvoluted as potent sstr2 agonists for this class were already known. The second active pool of 1 330 benzimidazolones **124** was of interest and subjected to further deconvolution. In a first round of deconvolution, where the R³ benzimidazolone moiety was kept constant, 20 pools of 20 compounds each were prepared. Each pool was defined by a single amino acid (Aa) and all possible combinations of the diamines (R¹). Screening indicated the pool with β-methyltryptophan **115** possessed the greatest activity (sstr2). Subjecting **125** to a second round of deconvolution (R³ and Aa constant, varying the 20 R¹

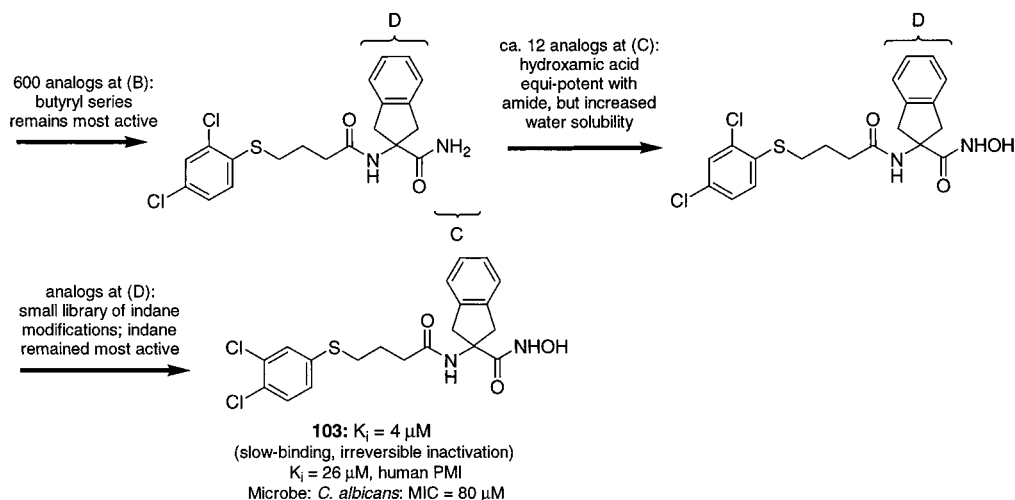


Figure 11. Deletion adduct from library 2.8 as an inhibitor of fungal phosphomannose isomerase (PMI).⁶

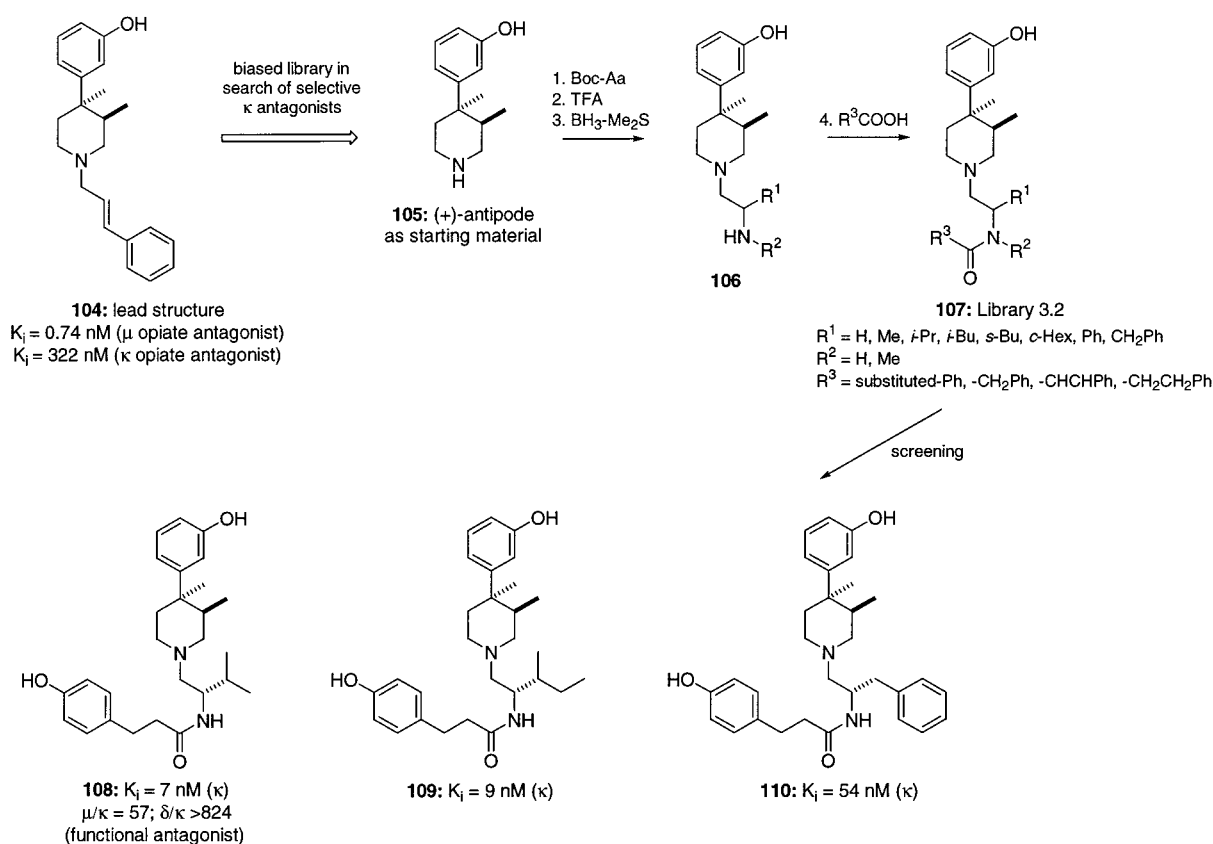


Figure 12. Solution-phase synthesis of biased library 3.2.⁴⁸

diamines) led to the identification of **126** as a potent sstr2 agonist (6000-fold selective versus sstr1,3–5).

Amino acid amide library 3.5b is an expanded version of library 3.5a and is composed ($21 (R^1) \times 22 (\text{Aa}) \times 147 (R^3)$) of approximately 350 000 compounds, again considering the use of racemic synthons. Two pools were selected for deconvolution (details not disclosed), resulting in the identification of **127** and **128** as potent, selective sstr1 and sstr3 agonists.

In a third extension of library 3.5a (details not disclosed), the sstr5 ligand **129** was obtained. Ligand **129** was highly selective (7100-fold) for the sstr2–4 receptor subtypes but possessed modest selectivity (8-fold) for the sstr1 receptor.

The fourth library, library 3.5d (**130**), is a library unrelated to the amino acid amide libraries 3.5a–c, but rather an “arylidole library of limited complexity” (details not disclosed). From library 3.5d, the highly potent and selective sstr4 ligand **131** ($K_i = 0.7 \text{ nM}$, sstr4) was obtained.

Functional activity for the selective ligands **126–129** and **131** was also investigated. The chart of Figure 14 summarizes the functional data for the ligands against cAMP accumulations (CHO K1), GH release, glucagon release, and insulin release. Clearly, compounds of this type are useful in unraveling the biological roles of the individual receptors. Fundamentally, the study represents a landmark prototypical model of how combinatorial chemistry may be used to

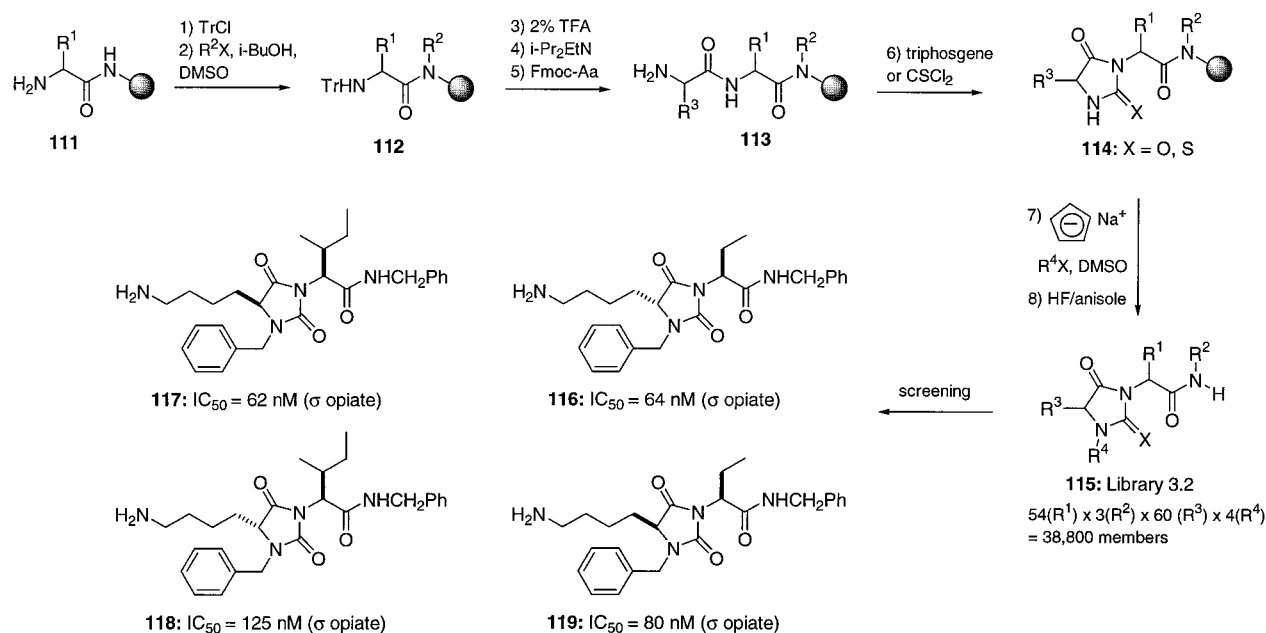


Figure 13. Hydantoin library 3.3 processing σ opiate binding affinity.³³

rapidly identify selective ligands to assess the functional significance of a given receptor. No doubt it is this type of exercise that will be repeated many times over in the future to unveil the roles of new proteins as they are characterized from genomic research.

In addition to Merck's libraries of subtype selective somatostatin agonists, Glaxo Wellcome described sstr5 selective agonists (library 3.6; Figure 15).⁴² The substituted thiazolidinone **132**, a potent and selective sstr5 agonist (pIC₅₀ = 5.85, human recombinant sstr5 receptors), discovered from an Affymax screening library, served as a lead compound. Because complex stereochemical mixtures are produced during thiazolidinone synthesis and the fact that a large library of compounds of this class had already been screened against the sst receptors, a heterocyclic surrogate for the thiazolidinone was sought. The hydantoin motif **133** was selected on the basis that substituents could be displayed analogous to the array found in **132** with stereochemical control and it was more amenable to solid-phase synthesis. The hydantoin library 3.6 was synthesized using Fukuyama–Mitsunobu chemistry to ensure diversity (alkyl and aralkyl) at the R² position. Library members were tested for their ability to inhibit [¹²⁵I] Thr¹¹-SRIF membrane binding (0.03 nM) in CHO K1 cells expressing human recombinant sstr2 and sstr5 receptors. None of the hydantoins exhibited appreciable activity against sstr2, but they were active against the sstr5. Preliminary SAR studies suggested that larger chain aralkyls (four-carbon tether, e.g., **134**) at R¹ and R² were preferred over short chain (<3 carbons) aralkyl substituents.

The discovery of a *somatostatin antagonist* was also described (library 3.7, Table 3).⁵⁶ The D-hexapeptide, Ac-his-phe-ile-arg-trp-phe-NH₂, identified from a 64-million-member library, was found to be active in vivo (i.v. administration). The D-hexapeptide bound to sstr2 with a K_i = 172 nM, blocked somatostatin inhibition of adenylate cyclase in vitro (IC₅₀ = 5.1), and induced growth hormone release when given alone to anesthetized rats with or without pretreatment with a long-active somatostatin agonist.

Libraries Targeted for Non-GPCRs

Table 4 delineates those libraries active in non-GPCR receptor targets: integrin receptors (libraries 4.1–4.5), selectins (libraries 4.6–4.7), ion channels and re-uptake mechanisms (libraries 4.8–4.10), domain interactions (libraries 4.11–4.14), nuclear receptors (library 4.15), transcription factors (library 4.16), and MHC-complex class I (library 4.16).

The -Arg-Gly-Asp- (RGD) is a well-known integrin binding motif for both the β_3 and β_1 classes of integrin families. Through the past decade, numerous peptidomimetic scaffolds have been described which display the salient positive and negative charged Arg and Asp side chains or their equivalents. These agents have been useful in the discovery of non-peptide integrin antagonists with potential application in treating thrombosis (β_3 class), unstable angina (β_3 class), restenosis (β_3 class), osteoporosis (β_3 class), tumor metastasis (β_3 class), and T-cell-mediated immune responses (β_1 class). Three new scaffolds displaying these charged side chains were incorporated into combinatorial libraries. These include the cyclic and acyclic oligocarbamates by Schultz¹³ (β_3 class; 20 000- to 530 000-member libraries, 4–13 nM antagonists), a biaryl scaffold reported by Schering-Plough³⁴ (β_3 class; 275 000 members, 34 μ M antagonist), and a cyclic turn mimetic scaffold synthesized in the Ellman laboratories⁴⁴ (β_1 class; 2304 members, 5 μ M antagonist).

Schreiber described selective binders of the Src SH3 and Hck SH3 domains.²¹ These were obtained from structure-based, encoded hexapeptide and nonapeptide libraries in which mono- and bicyclic peptidomimetics were attached to the N- or C-terminus, respectively (libraries 4.11 and 4.12). In this way non-peptide elements were thought to be directed toward the Leu-Pro specificity pockets of the SH3 domains. The libraries were useful in the identification of agents selective for one domain versus another and in further understanding of the domain–ligand binding interactions.

Troglitazone **135** is a marketed drug for the treatment of type 2 diabetes. Troglitazone **135** and structurally related thiazolidinediones act as agonists at the nuclear receptor peroxisome proliferator-activated receptor γ (PPAR γ), as demonstrated via the correlation between the PPAR γ binding affinity and the *in vivo* antihyperglycemic potency (Figure 16). During the course of an antidiabetic program at Glaxo Wellcome, a novel class of tyrosine-based nonthiazolidinedione PPAR γ agonists (**136**) were discovered.¹⁴ In an effort to improve binding affinity, functional activity, selectivity, and aqueous solubility for the series, an optimization program was initiated using a 2-fold strategy. Solution-phase synthesis (traditional medicinal analogue preparation) focused on modifying the oxazole moiety, introducing water-solubilizing groups in that region of the molecule. Complementary to this effort was the construction of library 4.15 (**138**: ca. 75 members), wherein a much broader exploration of the phenyl alkyl ether was undertaken. Although more potent oxazole surrogates were found through the solution-phase analogue synthesis, they were not significantly more soluble than **136**. Conversely, the more water soluble agents such as **137** (phenyl to pyridyl exchange) were not as potent as the original lead **136**. The solid-phase work did generate a number of potent and selective PPAR γ agonists (e.g., **139**), but again these agents did not possess binding affinity as high as **136**. Collectively, the SAR in conjunction with X-ray crystallographic studies have led to an detailed understanding of the binding interactions of these agents with PPAR γ (details to be published).

Nuclear factor- κ binding (NF- κ B) and activator protein-1 (AP-1) regulate the expression of a variety of proinflammatory cytokines and proteins. In chronic inflammatory disease states, where there is a continual overproduction of these proinflammatory cytokines, inhibition of NF- κ B and AP-1 transcriptional activation may lead to suppression of cytokine levels and subsequent modulation of the inflammatory response. Researchers at Signal Pharmaceuticals recently identified pyrimidine carboxamide **140** (IC₅₀ = 0.5 μ M) as an agent inhibiting both NF- κ B and AP-1 transcriptional activation in stably transfected human Jurkat T-cells (Figure 17).⁴⁶ Pyrimidine **140** displayed similar inhibitory action on the production of IL-2 and IL-8 levels in stimulated cells and was active in an animal model of inflammation. Through a traditional medicinal chemical approach, it was established that the 2-chloro group was important for activity (Cl \rightarrow H, OH, OR, NRR; inactive) as was the amino NH group (NH \rightarrow NMe, NBz; loss of activity). Consequently, the solution-phase parallel synthesis of library 4.16 (**141**) was carried out to discern an SAR for the carboxamide moiety of **140**. A library of some 160 compounds was synthesized by the reaction of the corresponding acid chloride of **140** with commercially available alkylamines, anilines, and heterocyclic amines. Operationally, this was performed by sonicating EtOAc solutions of a slight excess of the acid chloride and amine in the presence of Amberlyst A-21, quenching with water, and then further sonicating. The library of discrete compounds was tested, and 3,5-disubstituted arylamines were found to retain or enhance potency (**142**–**144**). In particular, pyrimidine carboxamide **144** showed a 10-fold improvement

over the original lead **140**. Pyrimidine **144** blocked the production of IL-2 and IL-8 in Jurkat T-cells (IC₅₀ = 30 nM). Curiously, this latter activity was specific to T-cells as the compound was inactive in monocytes, epithelial cells, fibroblasts, osteoblasts, or endothelial cells. Pyrimidine **144** was cell penetrant and active in several models of inflammation and immunosuppression.

Libraries Displaying Cytotoxic and Antimicrobial Activity

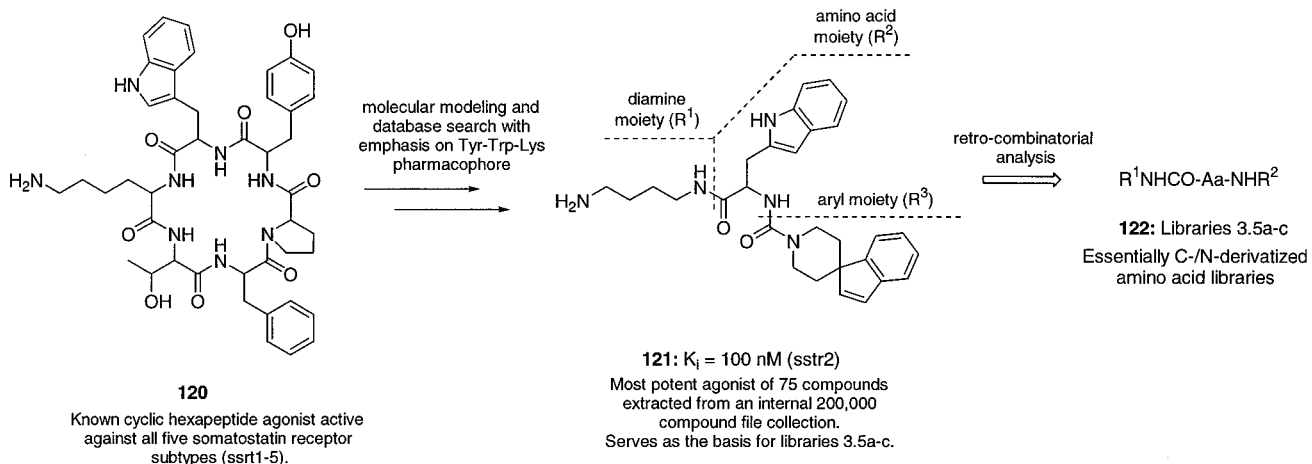
Chemical libraries of cytotoxic agents (libraries 5.1–5.3) and antiinfectives (libraries 5.4–5.15) are presented in Table 5.

Two contributions from the Scripps Research Institute describe the synthesis of libraries of cytotoxic agents (libraries 5.1 and 5.2). The first of these is from the Boger laboratories in which a vast number of polyamides were prepared using iminodiacetic acid **145** as a core template (Figure 18).⁸ The synthetic strategy utilized a solution-phase convergent approach to library synthesis allowing facile multiplication of diversity. This is in contrast to linear, divergent solid-phase synthesis (oligomer or template libraries) in which diversity elements are introduced sequentially. Using solution-phase methodology, libraries of dimers, trimers, and tetramers based on the template were synthesized. These are perhaps the largest collections of compounds yet to be prepared by solution-based methods. Polyamides of this type are thought to be useful in modulating protein–protein interactions, in particular as agonists or antagonists of receptor activation via dimerization. The specific biological activity of a 20 200 member library of iminodiacetic acid diamides **148** was disclosed with several agents displaying cytotoxic activity in L-1210 cells.

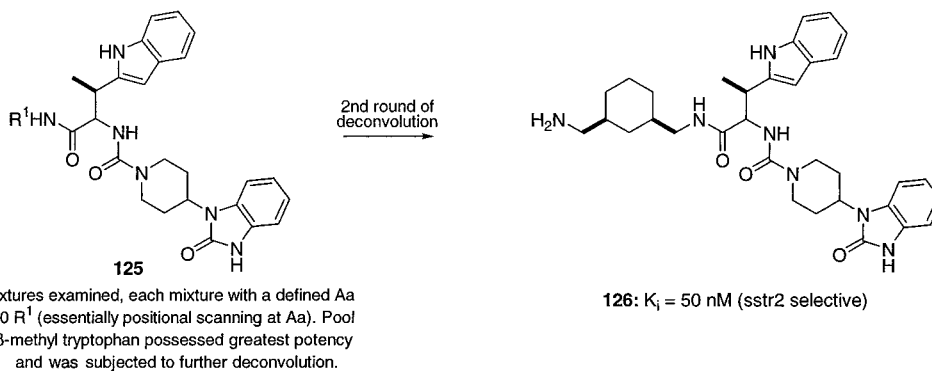
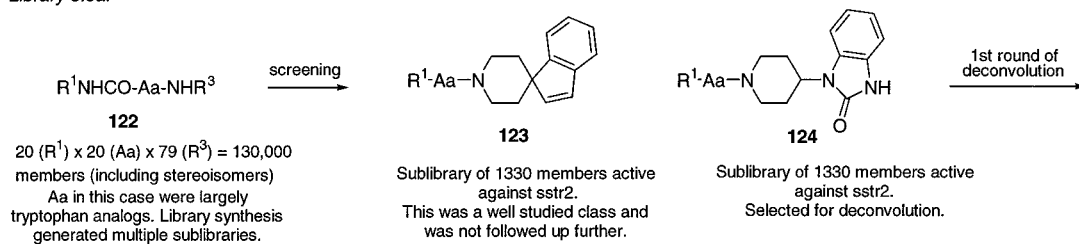
The second contribution from Scripps is from the laboratories of K. C. Nicolaou.³⁵ In recent years, Nicolaou has successfully tackled the total synthesis of several natural products with potent antitumor activity. These include Taxol, epothilone A and B, eleutherobin, **151**, eleuthosides A (**152**) and B (**153**), and the sarcodictyines A (**154**) and B (**155**; Figure 19). One of the distinguishing characteristics of his efforts is a potential paradigm shift toward the simultaneous development of solution- and solid-phase methodologies for natural product total synthesis and subsequent generation of analogue libraries. This is in contrast to the traditional approach to total synthesis in which the natural product construction is an end to itself. Case in point is the total synthesis of sarcodictyin A (**154**) and B (**155**) and the solid-phase synthesis of library 5.3 (Figure 19).

Intermediate **156**, generated during the total synthesis of sarcodictyins A (**154**) and B (**155**), was attached to solid support in a four-step sequence (**156** \rightarrow **158**), taking advantage of the facile transketalization chemistry of **156**. Resin-bound intermediate **158** was deacetylated (**158** \rightarrow **159**), reacted with a series of alcohol derivatizing agents (yielding esters and a carbamate), and subjected to desilylation to give resin-bound intermediates **160**. These intermediates in turn were subjected to a series of transformations which generated

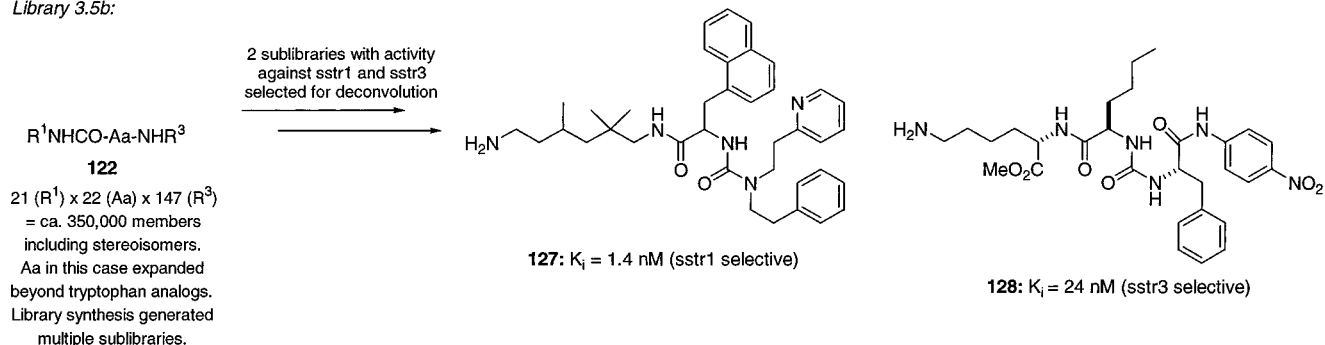
Overall library design:



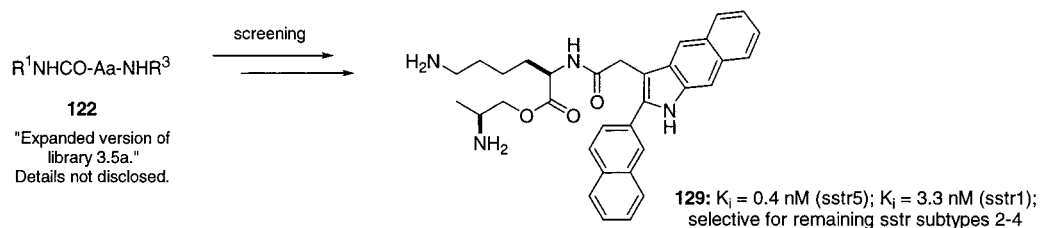
Library 3.5a:



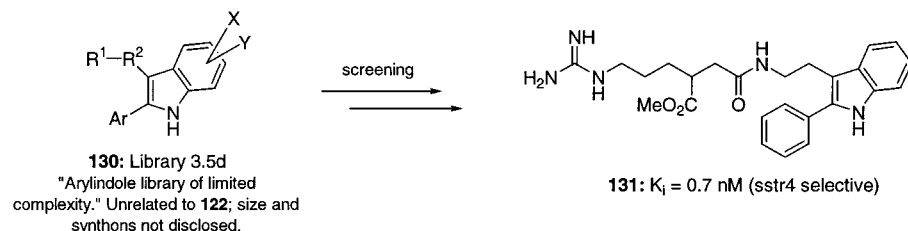
Library 3.5b:



Library 3.5c:



Library 3.5d:

Activity chart for selective sstr agonists obtained from libraries 3.5a-d.^a

Agonist	sstr1	sstr2	sstr3	sstr4	sstr5	cAMP accum. ^c	GH release assay	Glucagon release	Insulin release
ss-14^b	●	●	●	●	●	—	●	●	●
120	—	●	—	—	—	—	—	—	—
126	●	○	○	○	○	●	○	○	○
127	○	●	○	○	○	●	●	●	○
128	○	○	●	○	○	●	○	○	○
131	○	○	○	●	○	●	○	○	○
129	d	○	○	○	●	d	●	○	●

^aBlack dot indicates activity. White dot indicates inactivity. Dash indicates no data available.

^bss-14: naturally occurring somatostatin tetradecapeptide. ^ccAMP accumulation in CHO K1 or appropriate cell line. ^dWeak activity also seen against sstr1 and cAMP accumulation for **129** (sstr5/ssr1 8:1)

Figure 14. Subtype selective somatostatin receptor agonists as reported by Merck.⁴¹

three spurs **161–163** of library 5.3 and some 60 new sarcodictyin analogues (radio frequency encoding). In addition to the solid-phase synthesis, other analogues at R^1 were prepared in solution. Because of the structural resemblance of **161** and **162** to **151** and **153**, the combinatorial libraries may also be considered analogue libraries of eleutherobin and eleuthosides A and B. Evaluation of the library gave new agents with comparable or superior activity to the sarcodictyins and provided important SAR insights into this class of antitumor natural products.

With regard to antimicrobial agent discovery, Isis continued to publish on the synthesis and biological activities of their unique polyazapyridinocyclophanes,^{4a,5b} pyridinopolyamines,³ and the novel, structurally related polyazadipyridinocyclophanes,^{4b} oxytriamines,²⁴ and aminoethylpiperazine²⁵

classes of antibacterial agents (libraries 5.4–5.9). For several of the reported libraries, biological data is given for active sublibraries containing multiple compounds, without subsequent deconvolution to identify specific active compounds. In a few instances, certain sublibraries also acted to disrupt the HIV-1 tat/TAR protein-RNA binding.^{4,5}

Library Statistics and Summary

As compiled here, a total of 321 library constructs were reported in 1998. There were 74 biologically active libraries reported that year with approximately 60% of the contributions coming from industry. There were nearly twice the number of solid-phase versus solution-phase library syntheses from industry, while nearly equal numbers of solid- and solution-phase syntheses reported from academia. Of the 247 libraries with undisclosed biological activity, 66% of these

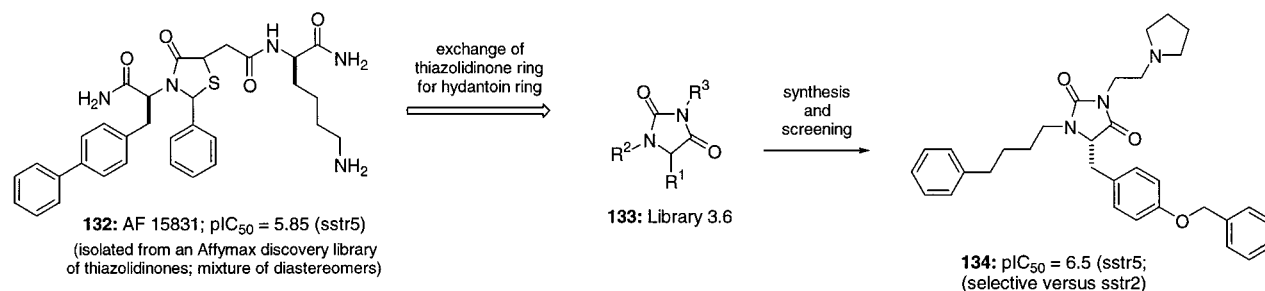


Figure 15. Glaxo Wellcome's hydantoin library 3.6 yielding selective sstr5 receptor agonists.⁴²

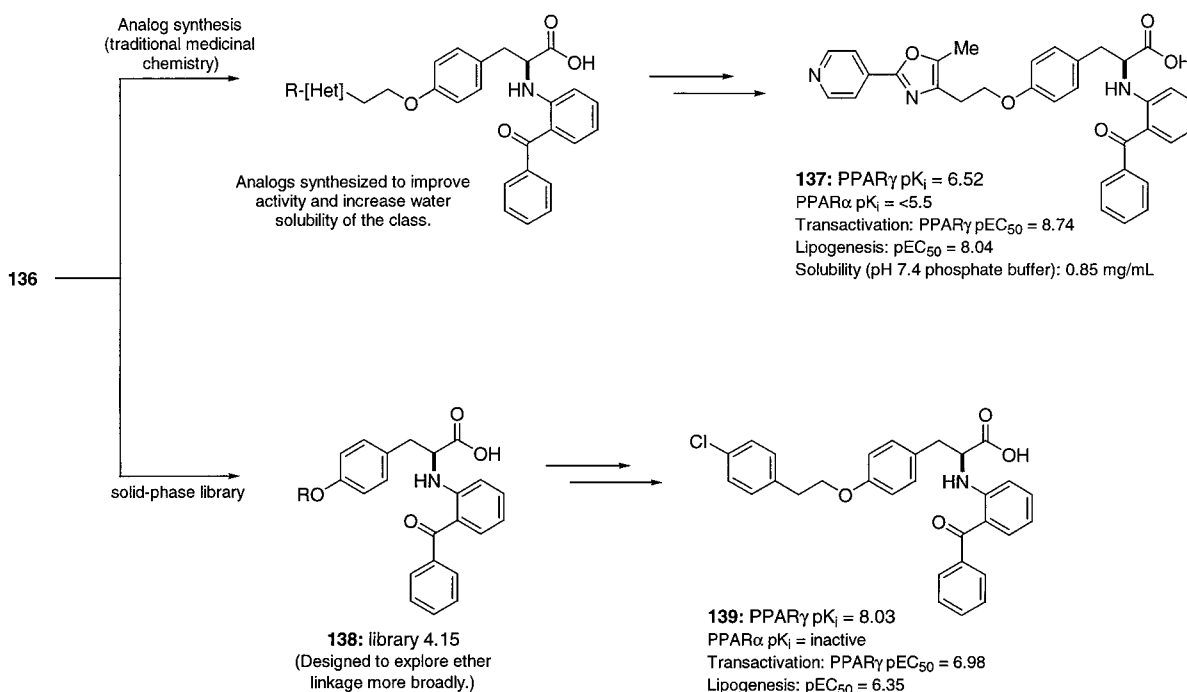
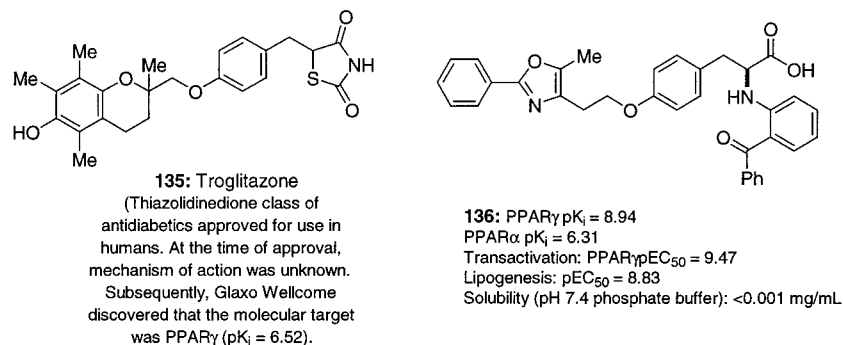


Figure 16. Optimization of nuclear receptor peroxisome proliferator-activated receptor γ (PPAR γ) agonists.¹⁴

came from industry and, again, with approximately a 2–3:1 ratio of library syntheses carried out on solid- versus solution-phase.

Considering the biologically active libraries of Tables 1–5, the entries across the target class are: 26% for proteolytic enzymes, ca. 15% for both nonproteolytic enzymes and GPCRs, 23% for non-GPCR targets, and 20% for the cytotoxics and antimicrobials. Solid-phase synthesis accounts for ca. 65% of the contributions, and with the exception of the cytotoxic and anti-infective category, solid-phase was the preferred method for library construction by a >2:1 margin. In the case of libraries without disclosed biological data

(Tables 6–10), there is a fairly equal distribution of constructs among the collections of scaffold derivatization, acyclic, monocyclic, bicyclic, and spirocyclic synthesis. These constructs account for 95% of the entries; only a few laboratories described polycyclic and macrocyclic libraries. Interestingly, about equal numbers of solution- and solid-phase synthesis of scaffold derivatization constructs were reported, while in all other categories, solid-phase was the method of choice. Up to 85% of the monocyclic ring syntheses were carried out on solid-phase.

Structure-based design and molecular modeling integrated with library design and synthesis proved quite effective as

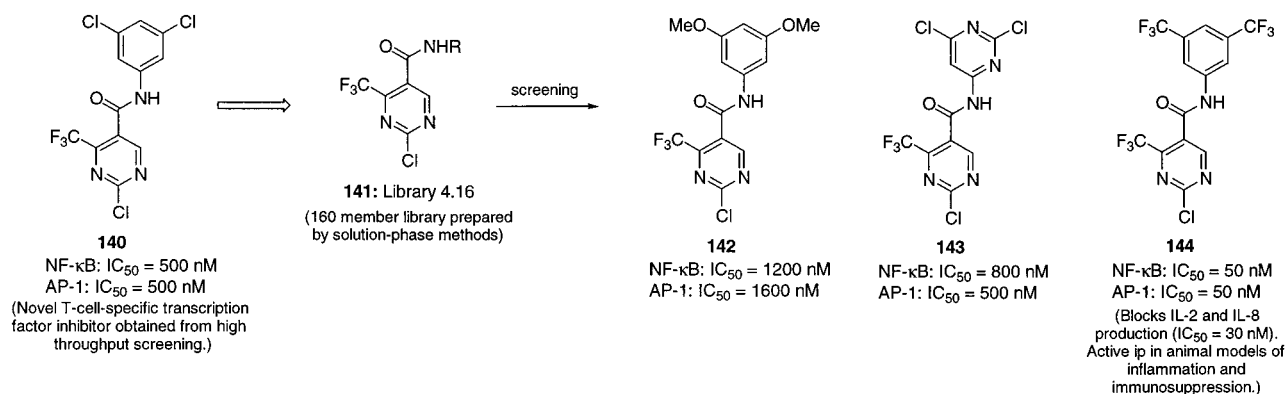


Figure 17. Inhibitors of NF- κ B and AP-1-mediated gene expression.⁴⁶

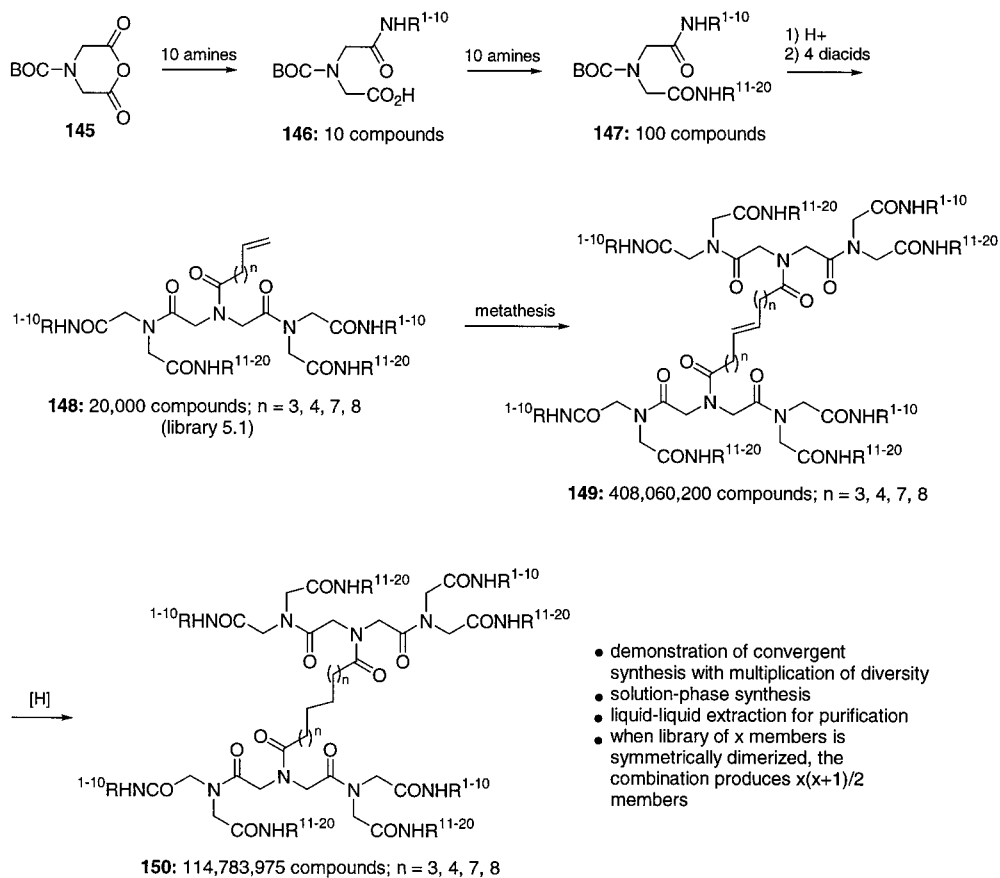


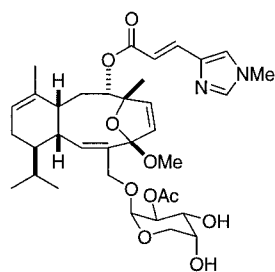
Figure 18. Boger's multistep convergent solution-phase synthesis of combinatorial libraries from iminodiacetic anhydride. Synthesis of library 5.1.⁸

applied to the discovery and optimization of lead structures. These computational techniques were essential components in the design of several libraries including: (1) Affymax's DKP-based metalloprotease inhibitor libraries (libraries 1.1 and 1.2),⁴⁷ (2) the selection of N-derivatizing reagents for Ellman's β -hydroxyethylamines (library 1.4),²⁶ (3) the selection of cyclic diamino acid P₂–P₄ surrogates in statine library 1.6,¹¹ (4) retrospective analysis of Vertex's new class for HIV inhibitors,⁵⁵ (5) the selection of the bicyclic template in libraries 1.11 and 1.12 of β -strand mimetics,³⁸ (6) the proline amide libraries 1.14 and 1.15 yielding thrombin inhibitors,^{28,58} (7) the phenothiazine library 2.5 leading to a new class of COX-2 inhibitors,⁴⁵ (8) analysis of the structural basis for the binding of substituted purines to human CDK2-cyclin A kinase complex,⁶⁰ (9) Merck's somatostatin receptor

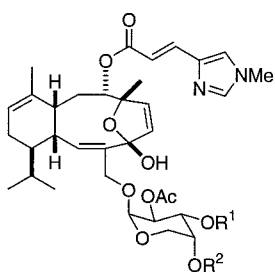
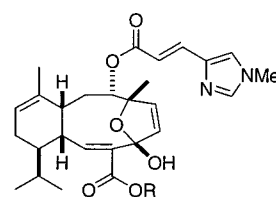
subtype selective agonists (libraries 3.5a–d),⁴¹ and (10) the work of Schreiber on the identification of selective Src and Hck domain binders (libraries 4.11 and 4.12).^{21,32}

The detailed descriptions of the SAR development of thrombin inhibitors from Merck (library 1.15)⁵⁸ and of PPAR γ agonists from Glaxo Wellcome (library 4.15)¹⁴ aptly demonstrate the synergy of combinatorial chemistry with traditional medicinal chemistry for lead optimization purposes, defining ligand affinity, selectivity, functional activity, aqueous solubility, and oral bioavailability. Specifically, the thrombin inhibitor case⁵⁸ represents the first example in which a lead compound, with a poor pharmacokinetic profile, was optimized on solid-phase to yield directly a potent, selective, efficacious, orally bioavailable agent. These are particularly timely accounts as there is appeal in establishing

Antitumor natural products:



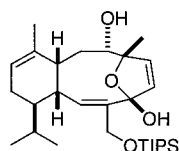
151: eleutherobin

152: R¹ = Ac; R² = H: eleuthoside A153: R¹ = H; R² = Ac: eleuthoside B

154: R = Me: sarcodictyin A

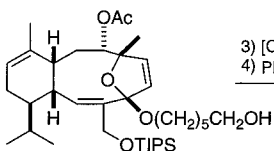
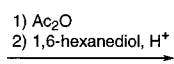
155: R = Et: sarcodictyin B

Resin attachment:

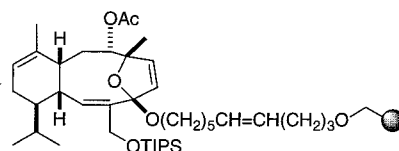
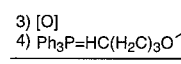


156

(intermediate from total synthesis)

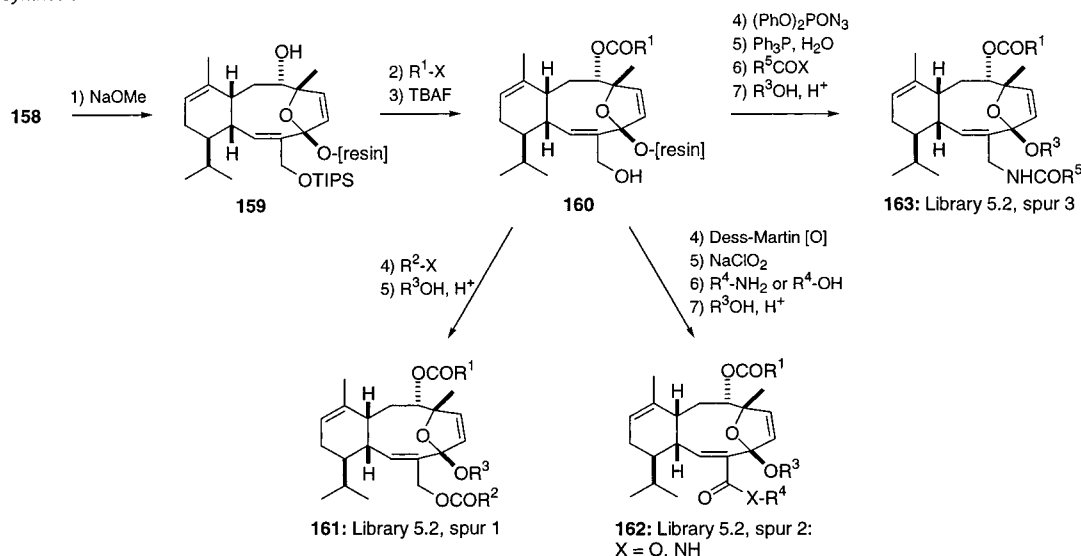


157



158

Library synthesis:



Derivatizing reagents:
 R¹-X = anhydrides, acid chloride, acid, PhNCO
 R²-X = Ac₂O, PhCOCl, MeOCOCI, PhNCO
 R³-OH = HOH, MeOH, EtOH, CF₃CH₂OH, *n*-PrOH
 R⁴-OH (-NH₂) = alkyl-, alkenyl-, haloalkyl-,
 aralkyl alcohols and MeNH₂, *n*-PrNH₂, PhCH₂NH₂,
 (4-Ome)PhCH₂NH₂
 R⁵COX = Ac₂O, PhCOCl

Figure 19. Nicolaou's sarcodictyin analogue library 5.2.³⁵

whether libraries may be of value in solving pharmacokinetic and toxicological problems associated with late stage discovery activities.

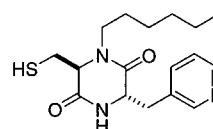
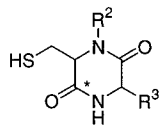
Last, the role of serendipity in drug discovery cannot be overlooked. Despite the heroic efforts on the part of the combinatorial chemist to define synthon compatibility and optimal reaction parameters for any given library, chemistry does not always proceed as planned. This was beautifully demonstrated in the discovery of the slow binding, irrevers-

ible phosphomannose isomerase inhibitor **101**, wherein a deletion adduct, formed through incomplete coupling of the first of three building blocks to solid support, was ultimately found as the enzyme inhibitor (library 2.8).⁶

Acknowledgment. The authors thank Ms. Karen Rivera for her expert assistance in the preparation of this manuscript, particularly for chemical structure drawing.

Table 1. Chemical Libraries Targeted for Proteases^a*Metalloproteases***Library: 1.1**

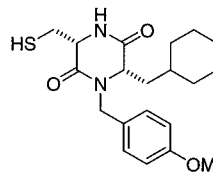
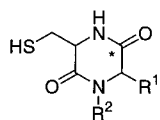
Name: Diketopiperazine
 Size: 684 members
 Affiliation: Affymax [47]
 Note: 36 pools of 19 DKPs per pool.
 Intracyclative cleavage
 from solid support.



Enzyme: Collagenase-1 (human)
 Activity: IC₅₀ = 2 μM

Library: 1.2

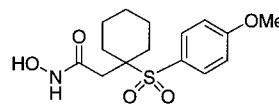
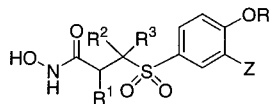
Name: Diketopiperazine
 Size: 684 members
 Affiliation: Affymax [47]
 Note: 36 pools of 19 DKPs per pool.
 Regioisomeric to library 1.1.
 Intracyclative cleavage
 from solid support.



Enzyme: Collagenase-1 (human)
 Activity: IC₅₀ = 30 nM (collagenase-1); 79 nM (gelatinase-B, human); 3800 nM (stromelysin-1, human)

Library: 1.3

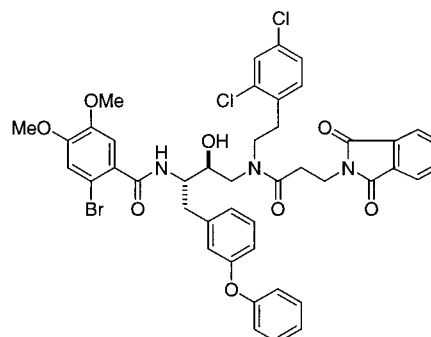
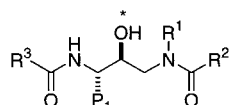
Name: Hydroxamic acid
 Size: >300 members
 Affiliation: Rhone-Poulenc Rorer [10]
 Note: Solution-phase synthesis of
 individual compounds.
 Cross reference: library 2.7



Enzyme: Gelatinase-A
 Activity: K_i = 10 nM (gelatinase-A, human); 50 nM (stromelysin-1, human); 200 nM (collagenase-1, human); >1,000 nM (phosphodiesterase (PDE4); guinea pig)

*Aspartic acid proteases***Library: 1.4**

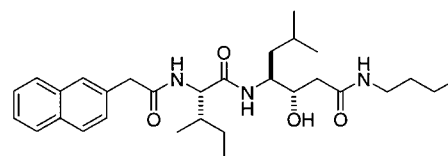
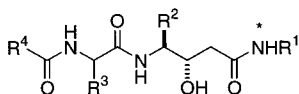
Name: β-Hydroxyethylamine
 Affiliation: Ellman, J. A.; *et al.* [26]
 Size: 204 members



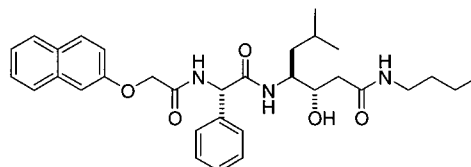
Enzyme: Cathepsin D (human liver)
 Activity: K_i = 0.7 nM

Library: 1.5

Name: Statine amide
 Size: 13,020
 Affiliation: Pharmacopeia, Inc. [12]
 Note: Encoded library
 using molecular tags.



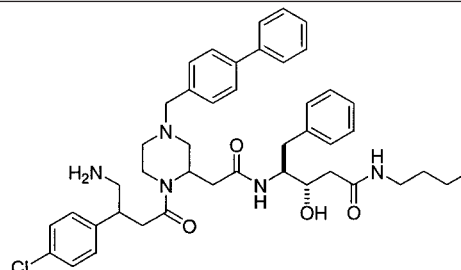
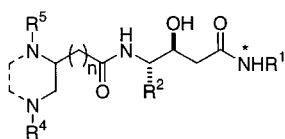
Enzyme: Plasmepsin-II (malaria; *Plasmodium falciparum*)
 Activity: K_i = 50 nM (K_i = 320 nM, human cathepsin D)



Enzyme: Cathepsin D (human liver)
 Activity: K_i = 110 nM (K_i = 5800 nM, malarial plasmepsin II)

Table 1. (Continued)**Library: 1.6**

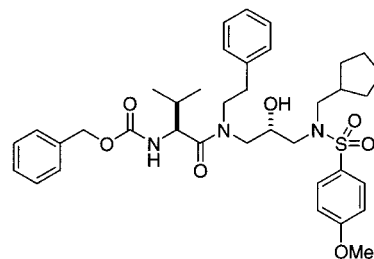
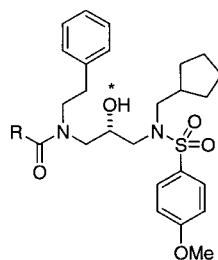
Name: Statine amide
Affiliation: Pharmacopeia, Inc. [11]
Size: 18,900 members



Enzyme: Plasmeprin-II (malaria; *Plasmodium falciparum*)
Activity: $K_i = 490$ nM (mixture of four diastereomers)

Library: 1.7

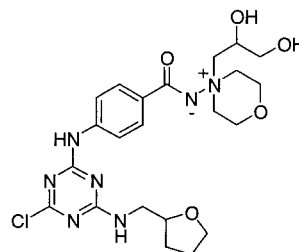
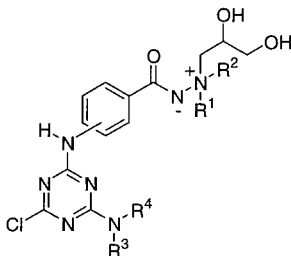
Name: β -Hydroxyethylamine
Affiliation: Vertex [55]
Size: 30 members
Note: Optimization library using THP linker.



Enzyme: HIV-1 protease
Activity: $K_i = 7$ nM

*Serine proteases***Library: 1.8**

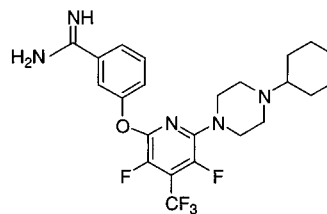
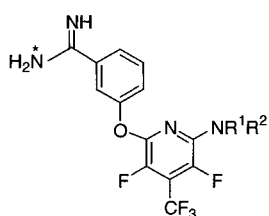
Name: Triazine
Size: 262 members
Affiliation: ArQule, Inc. [20]
Note: Solution-phase synthesis.



Enzyme: Factor Xa
Activity: $K_i = 700$ nm (mixture of diastereomers;
50% inhibition of plasmin @ 10 μ M)

Library: 1.9

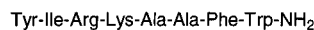
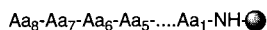
Name: Amidinophenoxypyrimidine
Affiliation: Berlex Biosciences [31]
Size: >400



Enzyme: Factor Xa
Activity: $K_i = 495$ nM

Library: 1.10

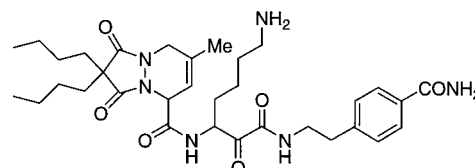
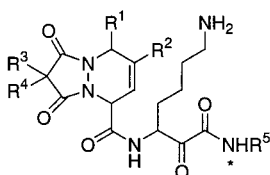
Name: Octapeptide
Size: Not defined (large)
Affiliation: Selectide Corp. [39]
Note: L-Amino acids only.
On-bead assay.



Enzyme: Factor Xa
Activity: $K_i = 5$ μ M

Library: 1.11

Name: β -Strand mimetic
Size: ca. 100 members
Affiliation: Molecumetics Ltd. [38]
Note: Diels-Alder reaction using resin-bound diene.

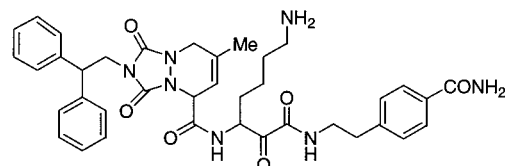
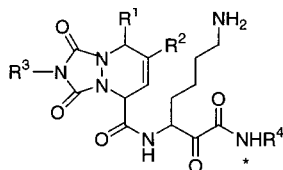


Enzyme: Thrombin
Activity: $K_i = 10$ nM

Table 1. (Continued)

Library: 1.12

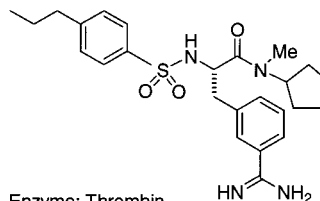
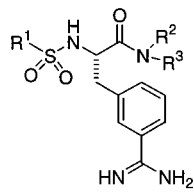
Name: β -Strand mimetic
 Size: ca. 1500 members
 Affiliation: Molecumetics Ltd. [38]
 Note: Diels-Alder reaction using resin-bound diene.



Enzyme: Thrombin
 Activity: $K_i = 0.035$ nM

Library: 1.13

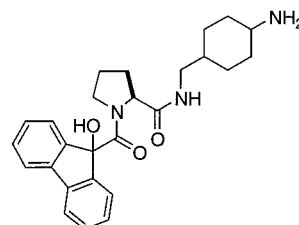
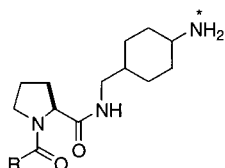
Name: Benzamidine sulfonamide
 Affiliation: LG Chemical Ltd. [22]
 Size: Not defined.



Enzyme: Thrombin
 Activity: $K_i = 10$ nM

Library: 1.14

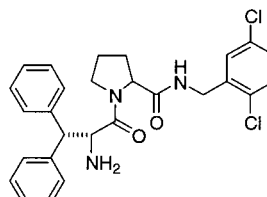
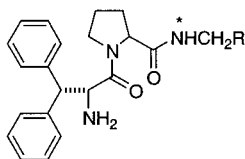
Name: Proline amide
 Size: ca. 200
 Affiliation: Merck [58]
 Note: Optimization library, coapplication with structure-based design.



Enzyme: Thrombin (human)
 Activity: $K_i = 1.5$ nM ($K_i = 860$ nM, trypsin)
 Orally bioavailable: 74% at 5 mg/kg (dog),
 $C_{max} = 4.6$ μ M at 40 min, iv plasma $t_{1/2} =$ ca. 4 h.

Library: 1.15

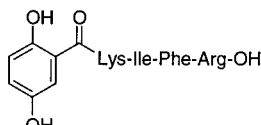
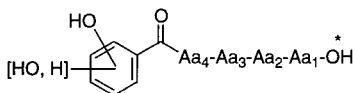
Name: Proline amide
 Size: ca. 18
 Affiliation: Merck [28]
 Note: Optimization library, coapplication with structure-based design.



Enzyme: Thrombin (human)
 Activity: $K_i = 3.0$ nM

Library: 1.16

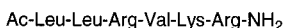
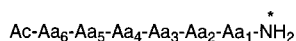
Name: Tetrapeptide
 Size: 390,625 members
 Ref: Kundu, B.; *et al.* [23]
 Note: Nazumamide analog library. Natural and unnatural amino acids used.



Enzyme: Thrombin
 Activity: $IC_{50} = 1.9$ μ M

Library: 1.17

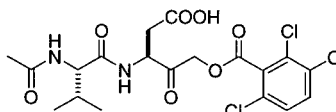
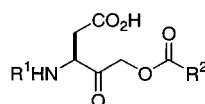
Name: Hexapeptide
 Size: 52,000,000 members
 Ref: Lindberg, I.; *et al.* [54]
 Note: Houghten library used in screening.



Enzyme: Prohormone convertase (mouse)
 Activity: $K_i = 3.2$ nM (PC-1); $K_i = 360$ nM (PC-2)
 $K_i = 1440$ nM (turin, human)

*Cysteine proteases***Library: 1.18**

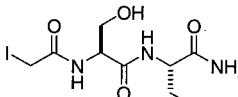
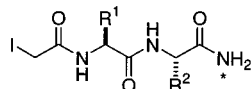
Name: Acyloxymethyl ketone
 Size: 590 members
 Affiliation: Parke-Davis [52]
 Note: Solution-phase synthesis.



Enzyme: Interleukin-1 β converting enzyme (ICE)
 Activity: $K_i = 113$ nM

Library: 1.19

Name: N-Iodo acetyldipeptide
 Size: ca. 100 members
 Ref: McKendrick, J.E.; *et al.* [30]
 Note: Optimal inactivators were identified from iodoacetate mixtures using ESI-MS.

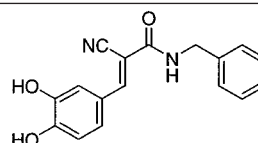
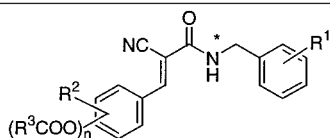


Enzyme: Hepatitis A virus 3C proteinase
 Activity: $k_2 = 840$ $M^{-1}s^{-1}$

^a The asterisk (*) represents the point of attachment to the solid support.

Table 2. Chemical Libraries Targeted for Nonproteolytic Enzymes^a**Library: 2.1**

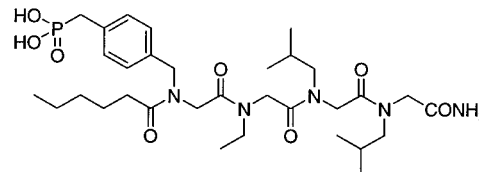
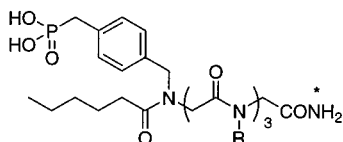
Name: Tyrphostin analog
 Size: 432 members
 Affiliation: IRORI [43]
 Note: Solid-phase synthesis using radio frequency tags.



Enzyme: Jak-2
 Activity: Blocks leukemia cell growth

Library: 2.2

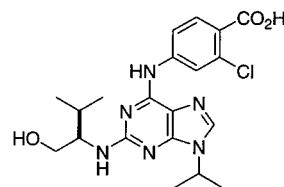
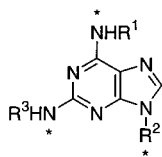
Name: Tetrapeptoid
 Size: 27 members
 Affiliation: Novartis [40]



Enzyme: ZAP-70
 Activity: IC₅₀ = 25 μM

Library: 2.3

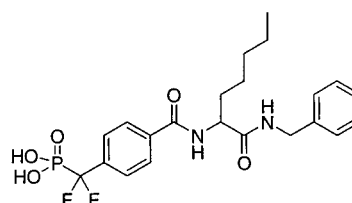
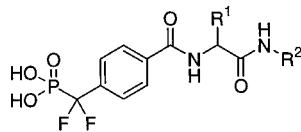
Name: Trisubstituted purine
 Size: not disclosed
 Affiliation: Schultz, P. G.; *et al.* [60]
 Note: First generation libraries carried out on solid-phase using multiple attachment strategies. Solution-phase synthesis employed for optimization. Details not disclosed.



Enzyme: CDK2-cyclin A (human)
 Activity: IC₅₀ = 6 nM (IC₅₀ = 9 nM, cdk2-cyclin E; IC₅₀ = 6 nM, cdc2-cyclin B)

Library: 2.4

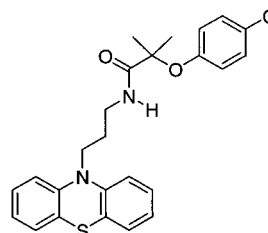
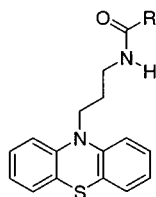
Name: α,α-Difluoromethylene-phosphoric acid
 Size: 108 members
 Affiliation: Li, Z.; *et al.* [27]
 Note: Ugi four-component condensation using RINK resin.



Enzyme = Protein tyrosine phosphatase (PTP_α, PTP_β, PTP_ε)
 Activity = >50% inhibition of PTP_ε @ 100 μM

*Other enzymes (mammalian)***Library: 2.5**

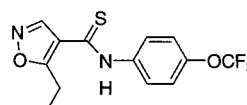
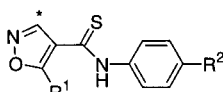
Name: Phenothiazine
 Size: 48 members
 Affiliation: Abbott Labs. [45]
 Note: Solution-phase synthesis. Structure-based design.



Enzyme: Cyclooxygenase-2 (COX-2; human)
 Activity: IC₅₀ = 1.3 μM (IC₅₀ >50 μM, COX-1)

Library: 2.6

Name: Isoxazolythioamide
 Size: ca. 25
 Affiliation: Novartis [2]
 Note: Derivatives of leflunomide.



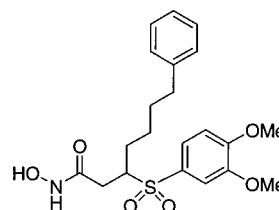
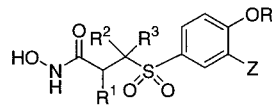
Enzyme: Dihydroorotate dehydrogenase (recombinant human)
 Activity: IC₅₀ = 700 nM

Table 2. (Continued)

Other enzymes (non-mammalian)

Library: 2.7

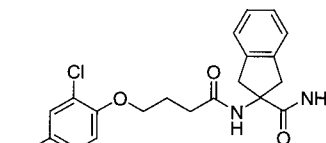
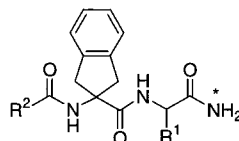
Name: Hydroxamic acid
 Size: >300 members
 Affiliation: Rhone-Poulenc Rorer [10]
 Note: Solution-phase synthesis.
 Cross-reference: library 1.3



Enzyme: Phosphodiesterase-4 (PDE-4)
 Activity: 1.0 nM (guinea pig macrophage homogenate)

Library: 2.8

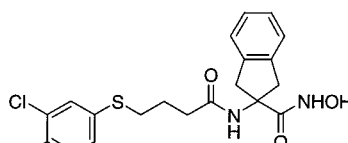
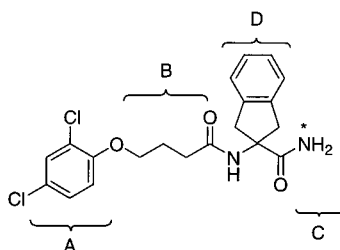
Name: N-acylated dipeptide
 Size: 1296 members
 Affiliation: Affymax [6]
 Note: Inhibitor found in the library was a deletion adduct formed through incomplete coupling of the first amino acid.



Enzyme: Phosphomannose isomerase (PMI; *C. albicans*)
 Activity: $K_i = 27 \mu\text{M}$ (slow-binding, irreversible inactivation)

Library: 2.9

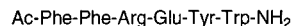
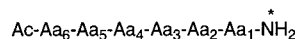
Name: Phenoxybutyric acid amide
 Size: ca. 700 members total
 Affiliation: Affymax [6]
 Note: Multiple optimization libraries prepared based on the 27 μM lead obtained in library 2.8.



Enzyme: Phosphomannose isomerase (PMI; *C. albicans*)
 Activity: $K_i = 4 \mu\text{M}$ (slow-binding, irreversible inactivation; $K_i = 26 \mu\text{M}$, human PMI)
 Microbe: *C. albicans*: MIC = 80 μM

Library: 2.10

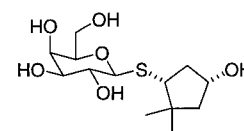
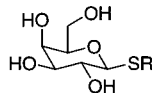
Name: L-Hexapeptide
 Affiliation: Mooser, G.; *et al.* [16]
 Size: >1,000,000 members



Enzyme: Glucosyltransferase-I (GFT-I; *Streptococcus sorinus*)
 Activity: $K_D = 1,400 \mu\text{M}$

Library: 2.11

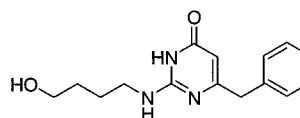
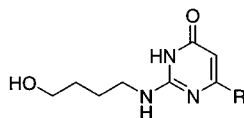
Name: 1-Thio- β -galactopyranoside
 Size: >3,000 members
 Affiliation: Hindsgaul, O.; *et al.* [36]
 Note: Solution-phase synthesis.



Enzyme: β -Galactosidase (*E. coli*)
 Activity: $K_i = 1.7 \mu\text{M}$

Library: 2.12

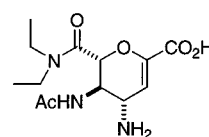
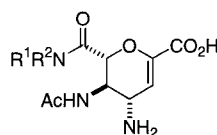
Name: 4(3H)-Pyrimidinone
 Size: 6 members
 Affiliation: Botta, M.; *et al.* [37]
 Note: Solution-phase synthesis.



Enzyme: HIV-1 reverse transcriptase
 Activity: $K_i = 75 \mu\text{M}$ (TIBO/nevirapine resistant mutant; $K_i = 410 \mu\text{M}$, wild type)

Library: 2.13

Name: Dihydropyranocarboxamides
 Size: 80 members
 Affiliation: Glaxo Wellcome [63]
 Note: Solution-phase synthesis.

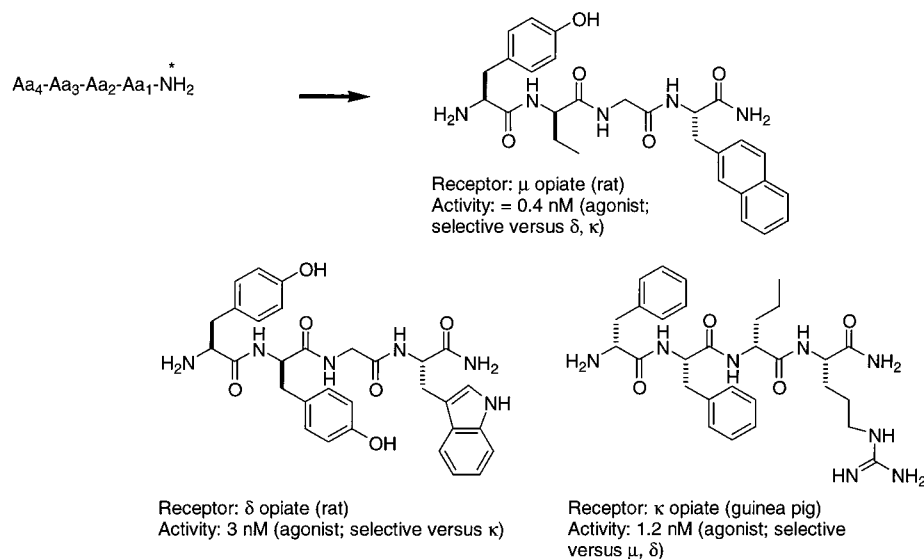


Enzyme: Influenza A virus sialidase
 Activity: $IC_{50} = 3 \text{ nM}$ (Flu A sialidase); $IC_{50} = 360 \text{ nM}$, Flu B sialidase)

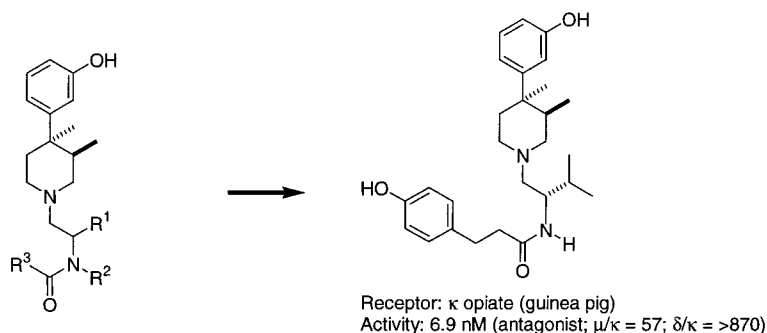
^a The asterisk (*) represents the point of attachment to the solid support.

Table 3. Chemical Libraries Targeted for G-Protein Coupled Receptors (GPCRs)^a*Opiate receptors***Library: 3.1**

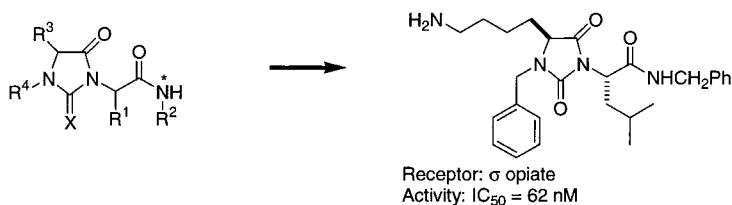
Name: Tetrapeptide
 Size: 6,250,000 members
 Ref: Dooley, C. T.; *et al.* [17]
 Note: Mixture-based positional scanning format. L-, D-natural and unnatural amino acids.

**Library: 3.2**

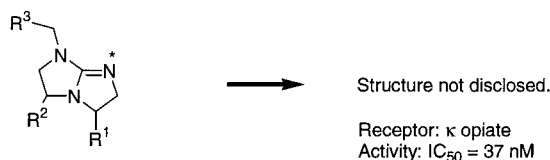
Name: 3-Hydroxyphenyl piperidine
 Size: 288 members
 Affiliation: Res. Triangle Inst. [48]
 Note: Solution-phase synthesis using optically active (+)-(3R,4R)-dimethyl-4-(3-hydroxyphenyl)piperidine.

**Library: 3.3**

Name: Hydantoin
 Size: 38,880 members
 Affiliation: Houghten, R. A.; *et al.* [33]

**Library: 3.4**

Name: Bicyclic guanidine
 Size: 102,459 members
 Affiliation: Houghten, R. A.; *et al.* [33]

*Somatostatin receptors***Libraries: 3.5a-d**

Name: Peptidomimetic
 Size: >100,000 members total
 Affiliation: Merck [41]
 Note: Multiple libraries based on amino acid amide theme. Original lead was a C-/N-derivatized tryptophan residue (see text). Split-pool synthesis and deconvolution methodology; not disclosed whether synthesis was carried out by solid- or solution-phase methods.

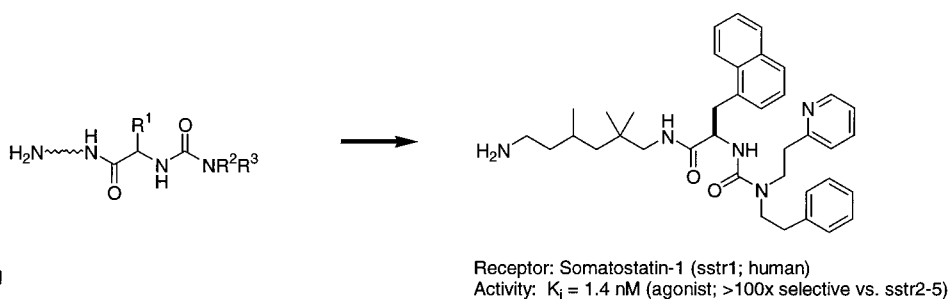
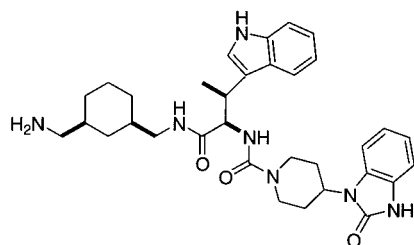
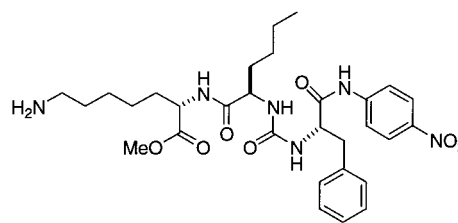


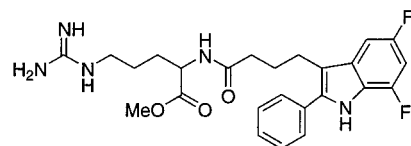
Table 3. (Continued)



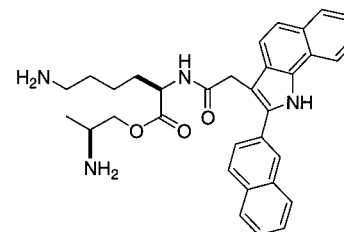
Receptor: Somatostatin-2 (sstr2; human)
Activity: $K_i = 0.5$ nM agonist; (>1000x selective vs. sstr1,3-5)



Receptor: Somatostatin-3 (sstr3; human)
Activity: $K_i = 24$ nM (agonist; >50x selective vs. sstr1,2,4,5)



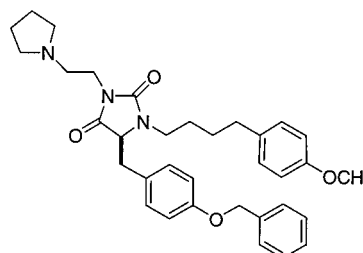
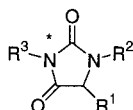
Receptor: Somatostatin-4 (sstr4; human)
Activity: $K_i = 0.7$ nM (agonist; >100x selective vs. sstr1-3,5)



Receptor: Somatostatin-5 (sstr5; human)
Activity: $K_i = 0.4$ nM (agonist; $K_i = 3.4$ nM, sstr1; >100x selective vs. sstr2-4)

Library: 3.6

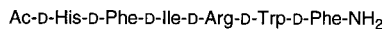
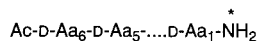
Name: Hydantoin
Size: >60 members
Affiliation: Glaxo Wellcome [42]
Note: Intracyclative cleavage.
Original lead was a thiazolidinone ($pIC_{50} = 5.85$: selective sstr5 agonist) obtained from an Affymax general screening library.



Receptor: Somatostatin-5 (sstr5; recombinant human)
Activity: $pIC_{50} = 6.5$ (agonist; selective against sstr2)

Library: 3.7

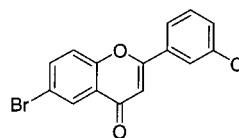
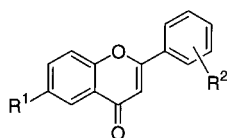
Name: D-Hexapeptide
Size: 64,000,000 members
Affiliation: American Cyanamid [56]
Note: Library synthesis via positional scanning protocol. Primary screening using SRIF-responsive yeast growth assay.



Receptor: Somatostatin-2 (sstr2; rat)
Activity: $K_i = 172$ nM (antagonist; sstr5: $K_i =$ ca. 230 nM)

*Benzodiazepine receptors***Library: 3.8**

Name: Flavone
Size: 36 members
Ref: Marder, M.; *et al.* [29]
Note: Solution-phase synthesis.

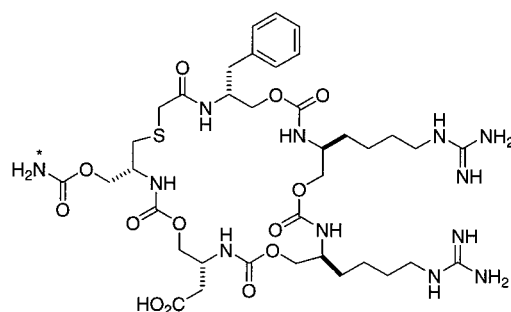
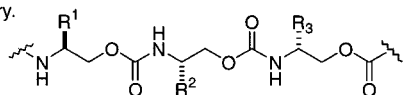


Receptor: Benzodiazepine (rat)
Activity: 17 nM

^a The asterisk (*) represents the point of attachment to the solid support.

Table 4. Chemical Libraries Targeted for Non-G-Protein Coupled Receptors (non-GPCRs)^a*Integrin receptors***Library: 4.1**

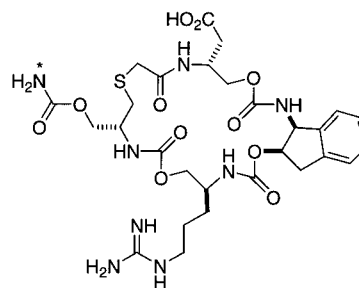
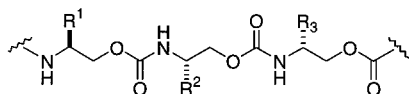
Name: Cyclic oligocarbamate
 Size: 530,000 members
 Affiliation: Schultz, P. G.; *et al.* [13]
 Note: Solid-phase synthesis.
 Sequencing performed using
 MALDI mass spectrometry.



Target: GPIIb/IIIa
 Activity: IC₅₀ = 4.9 nM

Library: 4.2

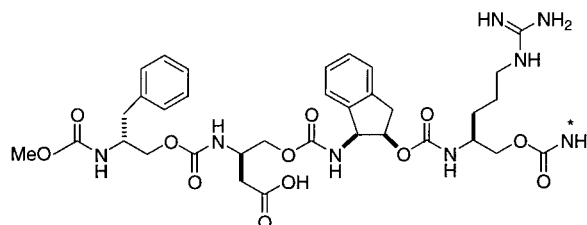
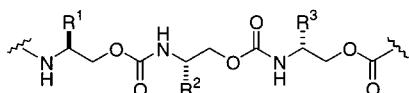
Name: Cyclic oligocarbamate
 Size: 20,000 members
 Affiliation: Schultz, P. G.; *et al.* [13]
 Note: See library 4.1.



Target: GPIIb/IIIa
 Activity: IC₅₀ = 3.9 nM

Library: 4.3

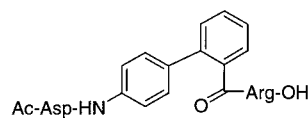
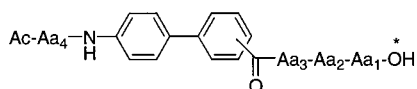
Name: Cyclic oligocarbamate
 Size: 20,000 members
 Affiliation: Schultz, P. G.; *et al.* [13]
 Note: See library 4.1.



Target: GPIIb/IIIa
 Activity: IC₅₀ = 13 nM

Library: 4.4

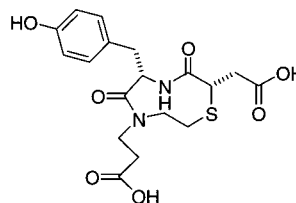
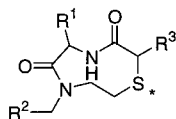
Name: Biaryl
 Size: ca. 275,000 members total
 Affiliation: Schering-Plough [34]
 Note: Multiple split-pool libraries.



Receptor: $\alpha_4\beta_3$ (human)
 Activity: IC₅₀ = 34 μ M

Library: 4.5

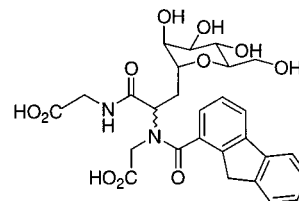
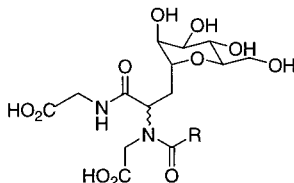
Name: Turn mimetic
 Size: 5,500 members
 Affiliation: Ellman, J. A.; *et al.* [44]
 Note: Reductive cleavage of
 disulfide and intramolecular
 cyclization. From the 5000+
 library, a subset of 2304
 members having an Asp residue
 was selected for screening.



Receptor: $\alpha_4\beta_1$ (integrin-CS1)
 Activity: IC₅₀ = 5.0 μ M

*Selectins***Library: 4.6**

Name: Sialyl Lewis X mimetic
 Size: 11 members
 Affiliation: Wong, C.-H.; *et al.* [50]
 Note: Ugi four-component reaction.

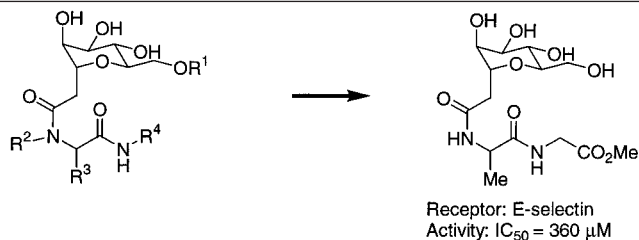


Receptor: E-selectin
 Activity: 48% inhibition @ 3 mM

Table 4. (Continued)

Library: 4.7

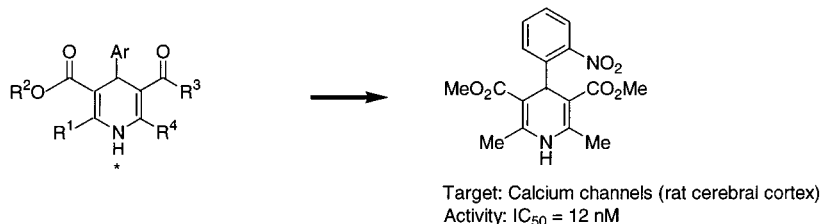
Name: Sialyl Lewis X mimetic
 Size: 15 members
 Affiliation: Wong, C.-H.; *et al.* [50]
 Note: Ugi four-component reaction.



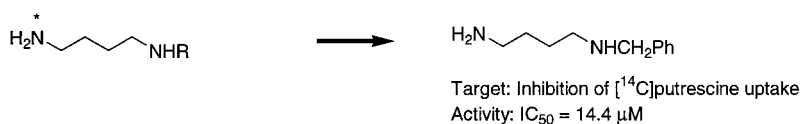
Ion channels and uptake mechanisms

Library: 4.8

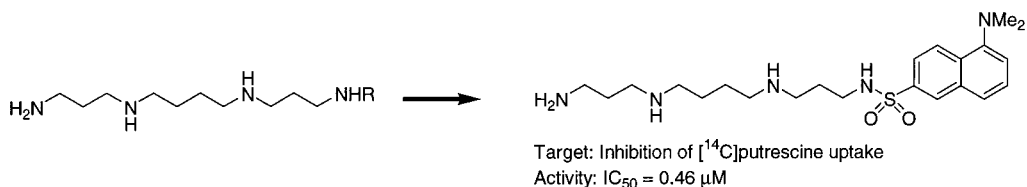
Name: 1,4-Dihydropyridine
 Size: 300 members
 Affiliation: Affymax [19]

**Library: 4.9**

Name: Polyamine
 Size: 6 members
 Affiliation: Uriac, P.; *et al.* [49]

**Library: 4.10**

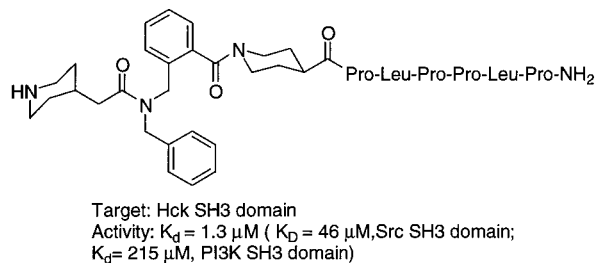
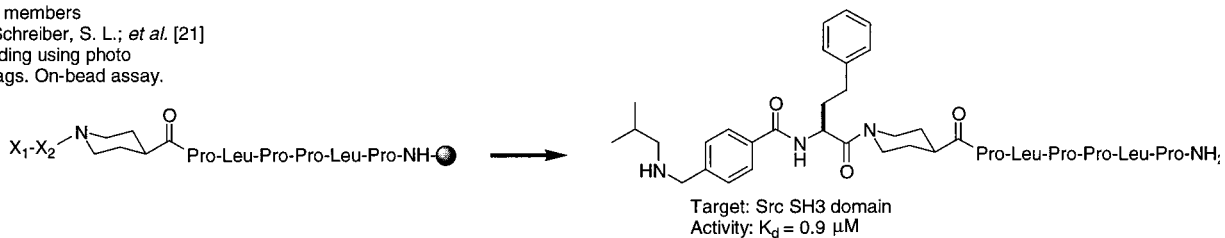
Name: Polyamine
 Size: 6 members
 Affiliation: Uriac, P.; *et al.* [49]



Domain interactions

Library: 4.11

Name: Peptidomimetic
 Size: 2,499 members
 Affiliation: Schreiber, S. L.; *et al.* [21]
 Note: Encoding using photo cleavable tags. On-bead assay.

**Library: 4.12**

Name: Peptidomimetic
 Size: 125,000 members
 Affiliation: Schreiber, S. L.; *et al.* [32]
 Note: Encoding using photo cleavable tags. On-bead assay.

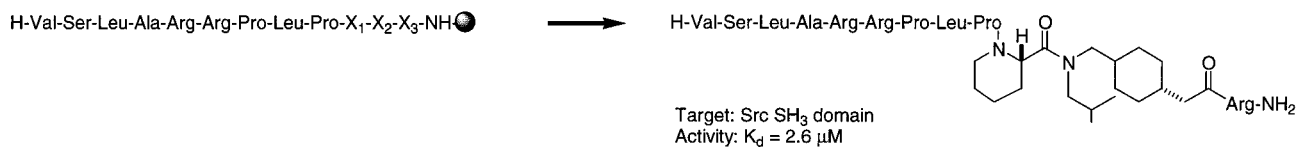
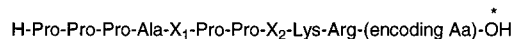


Table 4. (Continued)**Library: 4.13**

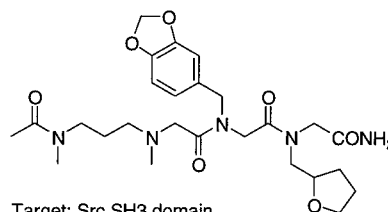
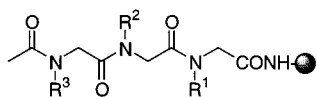
Name: Decapeptide
 Size: 14 members
 Affiliation: Muir, T. W.; *et al.* [59]
 Note: Encoded library using amino acid scanning.



Target: c-Crk SH3 domain
 Activity: $K_d = \text{ca } 0.5 \mu\text{M}$

Library: 4.14

Name: Peptoid
 Size: 1000 members
 Affiliation: Glaxo Wellcome [51]
 Note: On-bead assay. Encoded synthesis using stable isotopes.

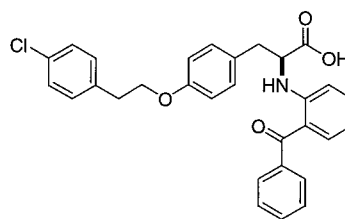
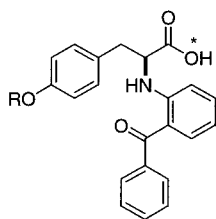


Target: Src SH3 domain
 Activity: not disclosed

Nuclear receptors, transcription factors, and other receptors

Library: 4.15

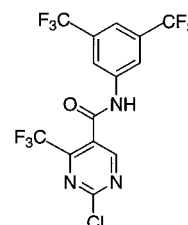
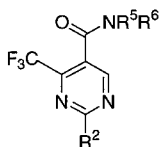
Name: N-(2-Benzoylphenyl)-L-tyrosine ether
 Size: ca. 75
 Affiliation: Glaxo Wellcome [14]
 Note: Solid- and solution-phase Mitsunobu etherification.



Receptor: Nuclear receptor peroxisome proliferator-activated receptor γ (PPAR γ)
 Activity: PPAR γ $pK_i = 8.03$ (PPAR α : inactive)

Library: 4.16

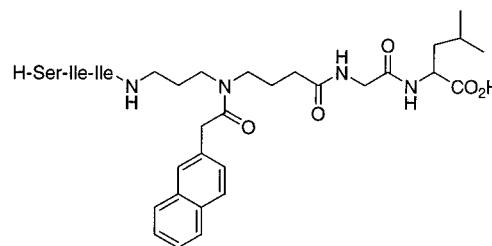
Name: Substituted pyrimidine
 Size: ca. 160 members
 Affiliation: Signal Pharm., Inc. [46]
 Note: Solution-phase parallel synthesis.



Transcription factors: NF- κ B and AP-1
 Activity: IC_{50} (NF- κ B) = 50 nM
 Activity: IC_{50} (AP-1) = 50 nM

Library: 4.17

Name: Peptidomimetic
 Size: 104 members
 Affiliation: Bianco, A.; *et al.* [57]
 Note: Four sub-libraries of 26 members each where Aa is defined by Leu, Ile, Val, and Met.

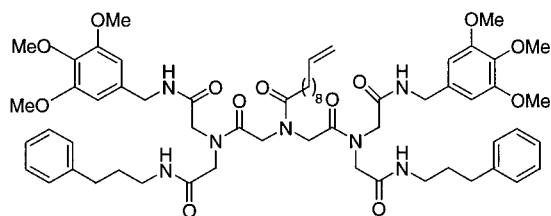
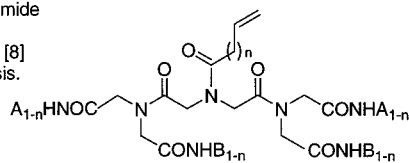


Target: MHC-I (mouse)
 Activity: H-2K^b stabilization (C_{stab50}) = ca. 5 μM

^a The asterisk (*) represents the point of attachment to the solid support.

Table 5. Chemical Libraries Displaying Cytotoxic and Antimicrobial Activity^a*Cytotoxic agents***Library: 5.1**

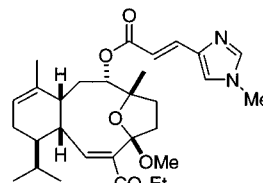
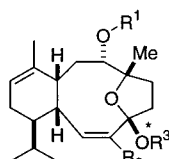
Name: Iminodiacetic acid diamide
 Size: 20,200 members
 Affiliation: Boger, D. L.; *et al.* [8]
 Note: Solution phase synthesis.



Target: L-1210 cells (in vitro cytotoxic assay)
 Activity: 0.6 $\mu\text{g/mL}$

Library: 5.2

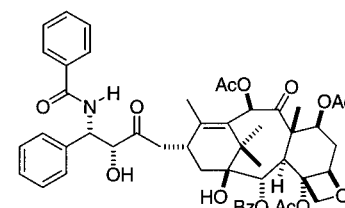
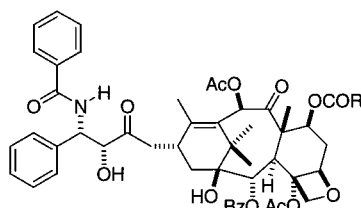
Name: Sarcodictyin analog
 Size: ca. 65 member
 Affiliation: Nicolaou, K. C.; *et al.* [35]
 Note: Combination of solution- and solid-phase methodology.



Target: Ovarian cancer cells (1A9)
 Activity: $\text{IC}_{50} = 2.0 \mu\text{M}$

Library: 5.3

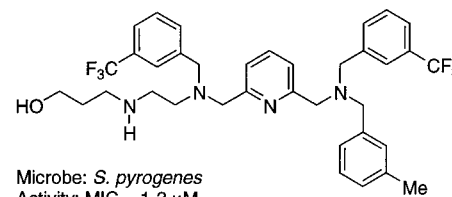
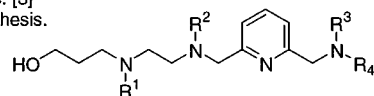
Name: Taxol analog
 Size: ca. 26 members
 Affiliation: Georg, G. I.; *et al.* [7]
 Note: Solution-phase synthesis.



Assay: Microtubule assembly
 Activity: $\text{ED}_{50}/\text{ED}_{50}$ (Paclitaxel) = 0.7

*Antimicrobial agents***Library: 5.4**

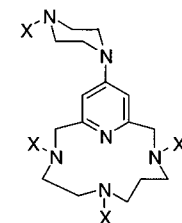
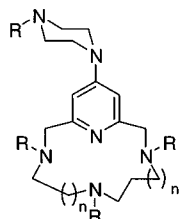
Name: Pyridinopolyamine
 Size: 1,638 members
 Affiliation: Isis Pharm., Inc. [3]
 Note: Solution-phase synthesis.



Microbe: *S. pyrogenes*
 Activity: $\text{MIC} = 1\text{-}3 \mu\text{M}$

Library: 5.5

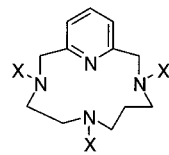
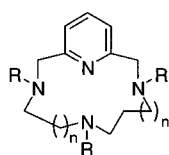
Name: Piperazinylpolyazacyclophane
 Size: 16,000 members total
 Affiliation: Isis Pharm., Inc. [5a]
 Note: Solution-phase synthesis of 26 libraries.



Microbe: *S. pyrogenes*
 Activity: $\text{MIC} = 2\text{-}10 \mu\text{M}$ (625 component mixture; deconvolution not performed)

Library: 5.6

Name: Polyazapyrimidinocyclophane
 Size: 4,275 members
 Affiliation: Isis Pharm., Inc. [4a]
 Note: Solution-phase synthesis of 40 libraries.

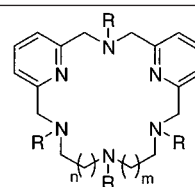
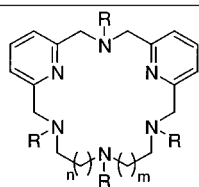


Microbe: *S. pyrogenes*
 Activity: $\text{MIC} = 1\text{-}5 \mu\text{M}$ (ca. 40 component mixture; deconvolution not performed)

Table 5. (Continued)

Library: 5.7

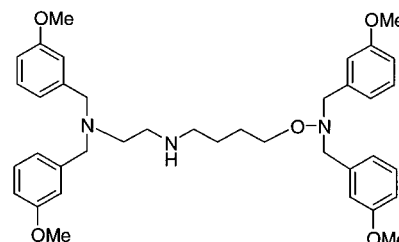
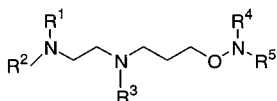
Name: Polyazadipyridinocyclophane
 Size: 24,875 members
 Affiliation: Isis Pharm., Inc. [4b]
 Note: Solution-phase synthesis of 29 libraries. Some mixtures active against the HIV-1 tat/TAR protein-RNA interaction.



Microbe: *S. pyogenes*
 Activity: MIC = 2-5 μM (625 component mixture; deconvolution not performed)

Library: 5.8

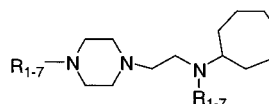
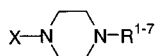
Name: Oxyamine
 Size: 15 members
 Affiliation: Isis Pharm., Inc. [24]
 Note: Solution-phase synthesis.



Microbe: *S. pyogenes*
 Activity: MIC = 1-5 μM

Library: 5.9

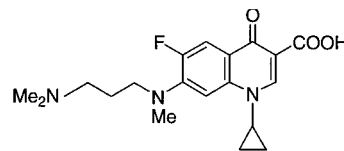
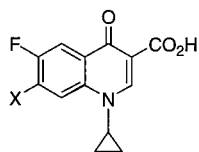
Name: Piperazine
 Size: ca. 100 members
 Affiliation: Isis Pharm., Inc. [25]
 Note: Solution-phase synthesis.



Microbe: *S. pyogenes*
 Activity: MIC = 25-50 μM (49 component mixture; deconvolution not performed)

Library: 5.10

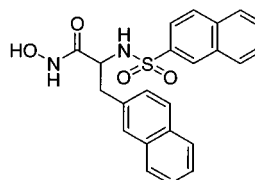
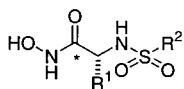
Name: Quinolone
 Size: 68 members
 Affiliation: Mitscher, L. A.; *et al.* [18]
 Note: Solution-phase synthesis.



Microbe: *S. aureus* ATCC 6538P
 Activity: MIC = 0.78 $\mu\text{g/mL}$

Library: 5.11

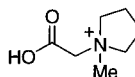
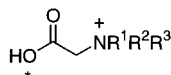
Name: Hydroxamic acid
 Size: 1,296 members
 Affiliation: ProtoGene Lab. [9]
 Note: 96 well parallel array synthesizer used. Resin bound carboxylic acid (Wang ester) cleaved with aq hydroxylamine.



Microbe: *E. coli*
 Activity: MIC = 0.7-1.5 μM

Library: 5.12

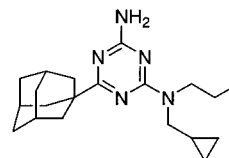
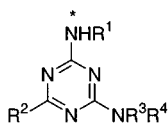
Name: Trialkylamino acetate
 Size: 7 members
 Affiliation: Pichereau, V.; *et al.* [15]



Microbe: *S. meliloti*
 Activity: D_{max} = 0.6

Library: 5.13

Name: Triazine
 Size: 46,000 members
 Affiliation: Affymax [62]
 Note: Encoded library (36 x 36 x 36) on photocleavable linker. Screening using a two-dimensional agar format.



Microbe: *S. aureus*
 Activity: MIC = 4 $\mu\text{g/mL}$

Table 5. (Continued)

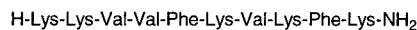
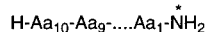
Library: 5.14

Name: Decapeptide

Size: 40,353,607 members

Affiliation: Mogam Biotech. Res. Inst. [61]

Note: Positional scanning using tea-bags.

Microbe: *C. albicans* ATCC 36232Activity: MIC = 0.78 $\mu\text{g/mL}$ (irreversible growth inhibition)**Library: 5.15**

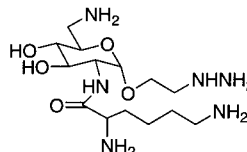
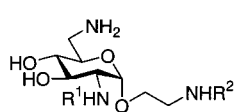
Name: Aminoglycoside mimetic

Size: 24 members

Affiliation: Wong, C.-H.; *et al.* [53]

Note: Solution-phase synthesis.

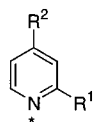
The 16S ribosome is the target for aminoglycoside antibiotics.



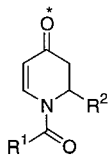
Target: A-site 16S ribosomal RNA

Activity: $K_d = 15 \mu\text{M}$ (wild-type RNA model)^a The asterisk (*) represents the point of attachment to the resin.Table 6. Scaffold Derivatization^a

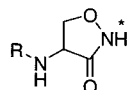
Solid-phase



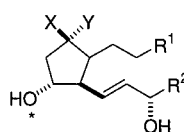
- SIBA Neurosci. [93]
- 5 ex; 65-75%
- up to 30% 1,2,5,6-tetrahydropyridine



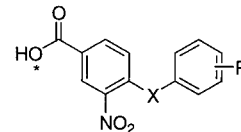
- SIBA; Neurosci. [92]
- 18 ex; 19-62%
- 1,4-addition to N-acylated-4-alkoxypyridine



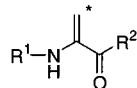
- Versicor [116]
- 80 members
- derivatization of resin-bound cycloserine



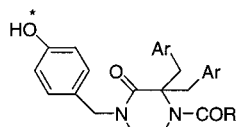
- Ellman, J. A. [209]
- 11 ex; 49-60%



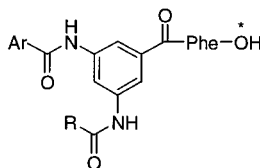
- Oxford Diversity [224]
- 17 ex; 40-58%
- biaryl ether formation; X = O, S



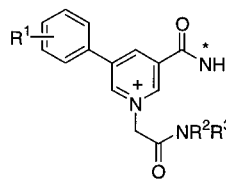
- Tanabe Seiyaku [229]
- 7 ex; 31-86%
- β -elimination of S-linked cysteine derivatives



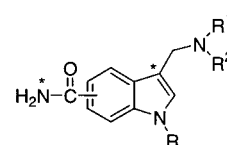
- Schering-Plough [232]
- 30 members
- C-alkylation of resin-bound 2-ketopiperazine



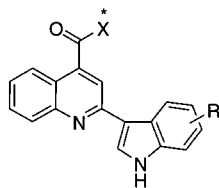
- Schering-Plough [171]
- 75 ex; 80-90%



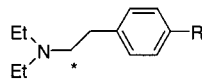
- SKB [150]
- 11 ex; 25-80%
- Suzuki biaryl coupling



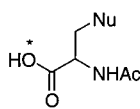
- R. W. Johnson [231]
- 10 ex; 90-100%
- Mannic reaction of resin-bound indoles



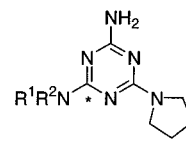
- Sepracor [123]
- 9 ex; 38-100%
- from resin-bound quinoline N-oxide; X = OH, NRR



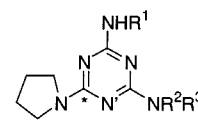
- R. W. Johnson [69]
- 14 ex; 45-95%
- Et₂NH-mediated cleavage of resin-bound sulfonate esters



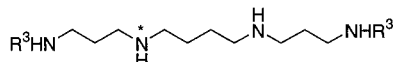
- Barbaste, M. [65]
- 2 members
- Michael addition of 1,2,4-triazole or pyrazole



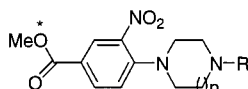
- Hoffmann-La Roche [161]
- 6 members
- from resin-bound thiouronium salt



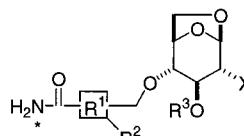
- Hoffmann-La Roche [161]
- 8 ex; 29-85%
- thiol resin and cyanuric chloride



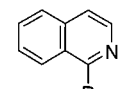
- Bradley, M. [177]
- 4 members



- Sun, C.-M. [178]
- 12 ex; >95%
- Nucleophilic aryl substitution (S_NAr)



- Novartis [84]
- 40 ex; 14-95%
- levoglucosan; X = OR; NRR; SR



- Miller, R. B. [155]
- 5 ex; ~ 50%
- alkylation of resin-bound Reissert complex

Table 6. (Continued)

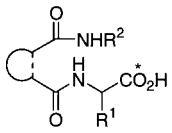
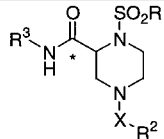

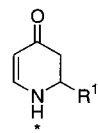
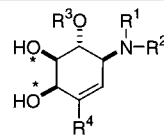
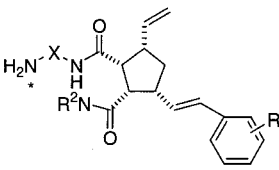
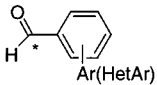
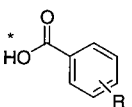
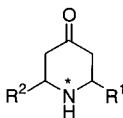
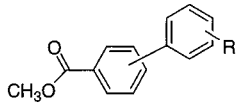
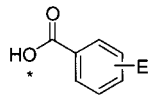

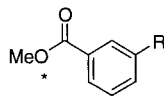

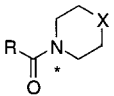
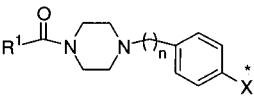

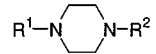
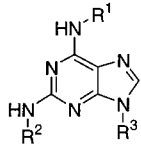
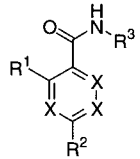
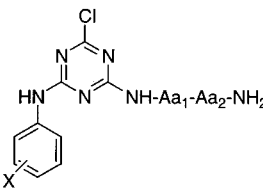
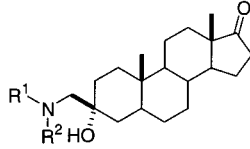
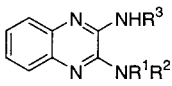
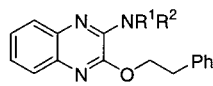
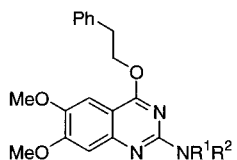
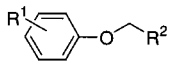
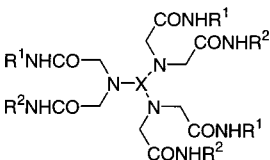
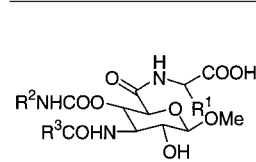
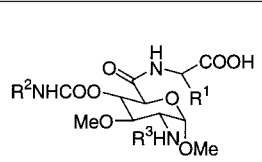
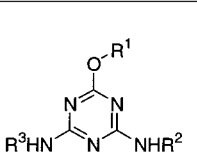
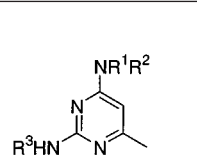
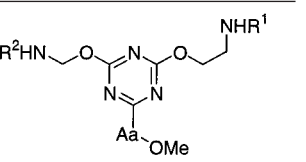
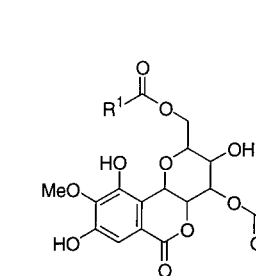
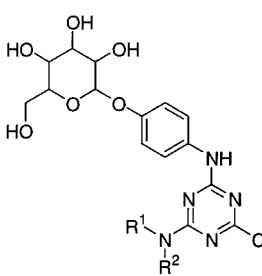
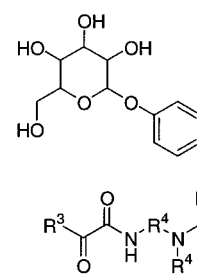
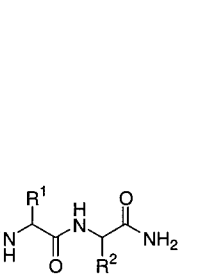
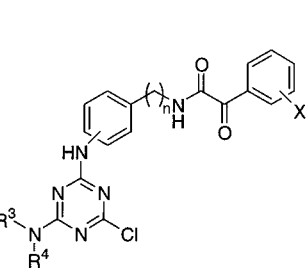
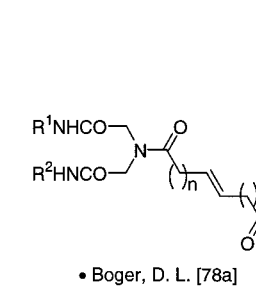
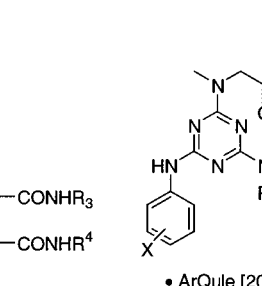
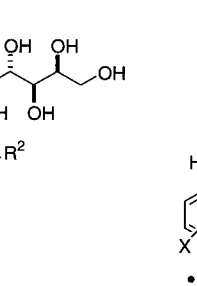
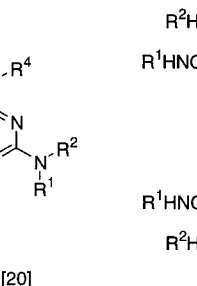
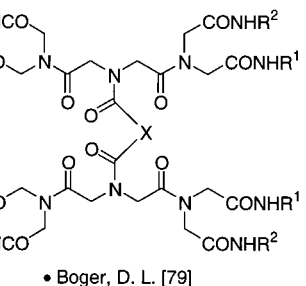
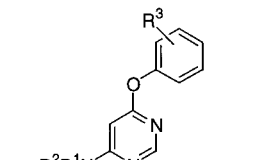
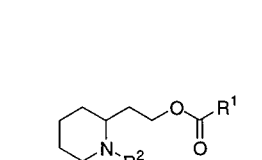
 <ul style="list-style-type: none"> • Scios [183] • 40 ex; 70-90% • ring opening and amidation of anhydrides 	 <ul style="list-style-type: none"> • Arris [82] • 2816 members • amine cleavage of ester linkage 	 <ul style="list-style-type: none"> • Nova Nordisk [190] • 12 ex; 34-78% • Curtius rearrangement 	 <ul style="list-style-type: none"> • SIBA Neurosci. [93] • 7 ex; 31-67% • C-2 alkylation of acyl pyridiniums 	 <ul style="list-style-type: none"> • Novartis [222] • 6 ex; 73-98% • Nu ring opening of epoxide; ketal linkage
 <ul style="list-style-type: none"> • Sepracor [88] • 4608 members • ring opening cross-metathesis on solid-phase 	 <ul style="list-style-type: none"> • Snieckus, V. [89] • 15 ex; 45-95% • acetal linker 	 <ul style="list-style-type: none"> • Snieckus, V. [90] • 22 ex; 71-75% • Stille cross-coupling 	 <ul style="list-style-type: none"> • SIBA Neurosci. [91] • 3 ex; 27-32% • 1,4-addition to dihydropyridone 	
 <ul style="list-style-type: none"> • Schotten, T. [235] • 18 ex; 52-98% • Suzuki coupling on soluble polymer support 	 <ul style="list-style-type: none"> • Knochel, P. [236] • 12 ex; > 90% • resin-bound Grignard reagent; heteroaryl also used. 	 <ul style="list-style-type: none"> • Park-Davis [245] • 12 ex; 0-85% • reductive cleavage of resin-bound arylsulfonates 	 <ul style="list-style-type: none"> • Kang, S.-K. [246] • 5 ex; 55-94% • CuI-catalyzed cross-coupling of resin-bound aryl iodide with organostannanes. 	 <ul style="list-style-type: none"> • Begtrup, M. [244] • 8 ex; 52-93% • ortho-lithiation
 <ul style="list-style-type: none"> • Schering-Plough [249] • 11 ex; 40-97% • N-dealkylation with acid chlorides; X = CH2, NBn 	 <ul style="list-style-type: none"> • Meiji Seika Kaisha [257] • 6 ex; 31-70% • asymmetric N,N-disubstituted piperazine; X = OH, COOH 	 <ul style="list-style-type: none"> • Pfizer [238] • 27 ex; 59-100% • use of indole linker 		
<i>Solution-phase</i>				
 <ul style="list-style-type: none"> • Neurocrine Biosci. [228] • 1086 members • N-alkylation and N-acylation using water soluble base 	 <ul style="list-style-type: none"> • Abell, C. [106] • ca. 19 ex; 54-98% • from 2,6-dichloropurine 	 <ul style="list-style-type: none"> • Signal Pharm. [207] • >4500 members • acylation reaction using ion-exchange resins 	 <ul style="list-style-type: none"> • ArQule [20] • 400 members 	 <ul style="list-style-type: none"> • Poirier, D. [158] • 20 ex; 40-70% • epoxide ring opening then N-acylation
 <ul style="list-style-type: none"> • Arris [130] • 384 members • from 2,3-dichloroquinoxaline; X = NRR, OR 	 <ul style="list-style-type: none"> • Arris [130] • 96 members • from 2-chloro-3-phenoxyethyl quinoxaline 	 <ul style="list-style-type: none"> • Arris [130] • 96 members • from 2-chloro-4-phenoxy-6,7-dimethoxy quinoxaline 	 <ul style="list-style-type: none"> • Higuchi Biosci. [213] • 15 ex; 59-94% • polymer-bound diaryl phosphine for Mitsunobu reaction 	 <ul style="list-style-type: none"> • Boger, D. L. [79] • 560 members • from iminodiacetic acid

Table 6. (Continued)

 <ul style="list-style-type: none"> • Transcell Tech. [202] • >48 members 	 <ul style="list-style-type: none"> • Transcell Tech. [202] • >48 members 	 <ul style="list-style-type: none"> • Arris [130] • 1920 members • from cyanuric acid 	 <ul style="list-style-type: none"> • Arris [130] • 384 members • from 2,4-dichloro-6-methylpyrimidine 	 <ul style="list-style-type: none"> • Falorni, M. [104] • 39 members
 <ul style="list-style-type: none"> • EnzyMed [167] • 167 ex; 60-90% • enzymatic acylation 	 <ul style="list-style-type: none"> • ArQule [20] • 320 members 	 <ul style="list-style-type: none"> • ArQule [20] • 320 members 	 <ul style="list-style-type: none"> • ArQule [20] • 2,500 members 	 <ul style="list-style-type: none"> • ArQule [20] • 2,500 members
 <ul style="list-style-type: none"> • Boger, D. L. [78a] • >100,00 members • multiple libraries • from iminodiacetic acid 	 <ul style="list-style-type: none"> • ArQule [20] • 6,400 members 	 <ul style="list-style-type: none"> • ArQule [20] • 12,800 members 	 <ul style="list-style-type: none"> • Boger, D. L. [79] • 1,260 members • from iminodiacetic acid 	 <ul style="list-style-type: none"> • Boger, D. L. [79] • 1,260 members • from iminodiacetic acid
 <ul style="list-style-type: none"> • Arris [130] • 768 members • from 4,6-dichloropyrimidine 	 <ul style="list-style-type: none"> • Searle [204] • 9 ex; 47-60% • Mitsunobu reaction with "tagged resin" capture method 			

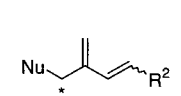
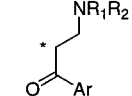
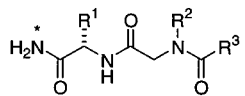
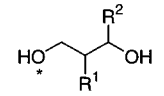
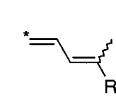
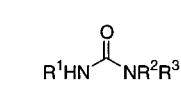
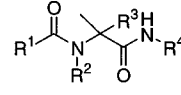
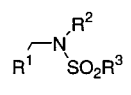
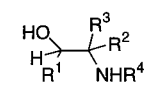
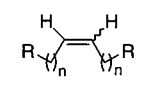
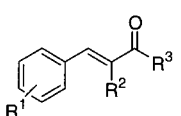
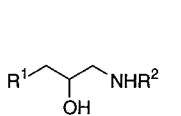
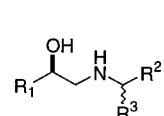
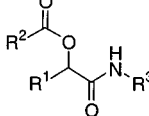
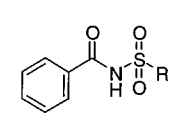
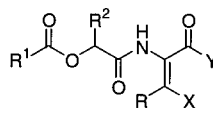
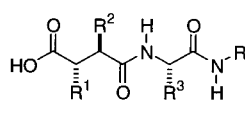
^a The asterisk (*) represents the point of attachment to the solid support.

Table 7. Acyclic Synthesis^a

Solid-phase

<ul style="list-style-type: none"> • BMS [99] • 13 ex; 0-100% • amine-mediated cleavage of resin-bound thiopseudoureas 	<ul style="list-style-type: none"> • Dominguez, E. [100] • 15 ex; 0-88% • Michael addition to benzophenone imine 	<ul style="list-style-type: none"> • Pfizer [101] • 7 ex; 22-44% 	<ul style="list-style-type: none"> • R. W. Johnson [103] • 13 ex; 70-89% • Sonogashira and Mannich reactions 	<ul style="list-style-type: none"> • Amgen [132] • 40 ex; 40-85% • novel thiourea linker
<ul style="list-style-type: none"> • Monsanto [119] • 4,096 members • successive Michael additions to acrylic amides 	<ul style="list-style-type: none"> • Amgen [132] • 40 members • novel thiourea linker; Y = OR, R 	<ul style="list-style-type: none"> • Monsanto [120] • 8 ex; 47-100% • Knoevenagel condensation; X = NH, O 	<ul style="list-style-type: none"> • Jung, G. [189] • 26 members • Baylis-Hillman reaction 	
<ul style="list-style-type: none"> • Cambridge Combin. [118] • 27 members • ozonolysis of resin-bound allylic amine 	<ul style="list-style-type: none"> • Lilly [102] • 9 members • amine-mediated cleavage of resin bound carbamates 	<ul style="list-style-type: none"> • BMS [186] • 24 ex; 30-73% • amines released from Knorr resin 	<ul style="list-style-type: none"> • Jung, G. [188] • 16 ex; 70-90% • three-component condensation 	
<ul style="list-style-type: none"> • Jung, G. [189] • 25 members • Baylis-Hillman followed by 1,4-amine addition 	<ul style="list-style-type: none"> • DuPont [184] • 10 ex; 77-99% • thermolytic cleavage of oxime-carbamates 	<ul style="list-style-type: none"> • Kobayashi, S. [146] • 6 members • condensation of resin-bound imine and silylenol ether with Yb(OTf)₃ 	<ul style="list-style-type: none"> • Ganesan, A. [155] • 12 ex; 53-93% 	<ul style="list-style-type: none"> • Amgen [175] • 14 ex; 10-70% • Hofmann elimination; >95% purity
<ul style="list-style-type: none"> • Organon [173] • >100; 70-100% • also performed in solution-phase 	<ul style="list-style-type: none"> • Houghten, R. A. [174] • >100,000 members • borane reduction of resin-bound N-acylated dipeptides 	<ul style="list-style-type: none"> • R. W. Johnson [164] • 3 ex; >80% • Mannich reaction with resin-bound amines or resin-bound aldehydes 	<ul style="list-style-type: none"> • Microside [152] • 10 ex; 37-71% • N-linked peptide synthesis 	<ul style="list-style-type: none"> • R. W. Johnson [164] • 21 ex; >80% • Mannich reaction with resin-bound amines or resin-bound aldehydes
<ul style="list-style-type: none"> • Armstrong, R. W. [137] • 96 members • Ugi four-component condensation on Rink resin 	<ul style="list-style-type: none"> • Molecumetics [76] • 6 ex; 60-80% • diene synthesis via Stille coupling or Wittig reaction 	<ul style="list-style-type: none"> • Tularik [134] • 10 ex; 65-95% 	<ul style="list-style-type: none"> • Ganesan, A. [198] • 7 ex; 30-50% • acylation of active methylene and decarboxylation 	<ul style="list-style-type: none"> • SKB [125] • 50 members • self-coded library facilitating MS analysis
<ul style="list-style-type: none"> • Houghten, R. A. [33] • 125,000 members • from amino acid amide 	<ul style="list-style-type: none"> • Gennari, C. [109] • 5-10 ex; 18-60% • Aldol reaction with resin-bound arylaldehydes 	<ul style="list-style-type: none"> • Anstyn, E. V. [192] • 9 ex; 5-84% • includes oligomeric guanidinium synthesis 	<ul style="list-style-type: none"> • Amgen [132] • 40 members • novel thiourea linker; R³ = alkyl, allyl, aryl 	<ul style="list-style-type: none"> • P&G [113] • 7 ex; 27-89% • TBSONH₂-mediated cleavage of Kaiser oximates

Table 7. (Continued)

 <ul style="list-style-type: none"> Blechert, S. [252] 13 ex; 32-86% Ru-catalyzed yne-ene cross metathesis and Pd-catalyzed cleavage 	 <ul style="list-style-type: none"> Novo Nordisk [242] 15 ex; 0-100% decarboxylation-based traceless linker 	 <ul style="list-style-type: none"> R. W. Johnson [243] 96 members use of visual encoding process 	 <ul style="list-style-type: none"> Tietze, L. F. [255] 7 ex; 40-60% Pd-catalyzed allylic substitution of beta-keto esters then reduction 	 <ul style="list-style-type: none"> Blechert, S. [253] 6 ex; ca. 60% Ru-catalyzed yne-ene cross metathesis
<i>Solution-phase</i>				
 <ul style="list-style-type: none"> Texas Biotech. [187] 14 ex; 46-100% from nitrophenyl carbamates 	 <ul style="list-style-type: none"> LG Chem. [139] 14 ex; 30-70% Ugi four-component condensation 	 <ul style="list-style-type: none"> Ley, S. V. [153] 96 ex; range of purity polymer-supported reagents 	 <ul style="list-style-type: none"> Ley, S. V. [80] 29 ex; 17-99% polymer-supported reagents 	 <ul style="list-style-type: none"> Ward, T. R. [81] ca. 10 members self-metathesis of internal olefins
 <ul style="list-style-type: none"> Ley, S. V. [121] 10 ex; 8-95% polymer supported reagents 	 <ul style="list-style-type: none"> Janda, K. D. [124] 20 members resin capture 	 <ul style="list-style-type: none"> Lilly [197] 96 ex; ~ 80% reductive amination of ethanalamines 	 <ul style="list-style-type: none"> Rhone-Poulenc [73] four-component Passerini reaction 	 <ul style="list-style-type: none"> Merck Frosst [205] 25 ex; 56-79% acylation using polymer carbodiimide
 <ul style="list-style-type: none"> Armstrong, R. W. [136] 21 ex; 0-90% three-component Passerini reaction 	 <ul style="list-style-type: none"> British Biotech Pharm. [251] 15 ex; 18-91% Ugi four-component condensation 			

^a The asterisk (*) represents the point of attachment to the solid support.

Table 8. Monocyclic Ring Synthesis^a*Solid-phase*

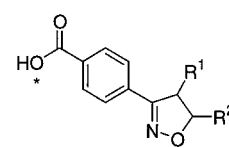
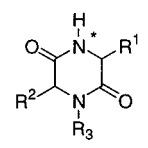
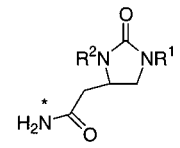
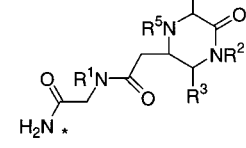
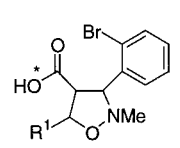
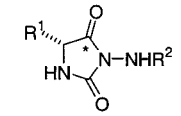
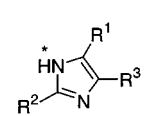
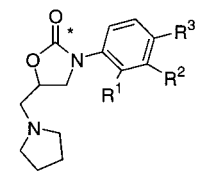
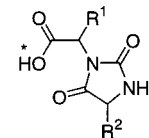
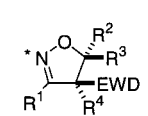
 <ul style="list-style-type: none"> Ontogen [94] 7 ex; 40-94% resin-bound aldoximes 	 <ul style="list-style-type: none"> Alberico, F. [98] 5 members 	 <ul style="list-style-type: none"> Chiron [112] 8 members tandem aminoacylation-Michael addition 	 <ul style="list-style-type: none"> Chiron [111] 11 ex; 36-93% intramolecular Michael addition 	 <ul style="list-style-type: none"> Jung, G. [117] 5 ex; 24-45% nitron addition to resin-bound acrylate
 <ul style="list-style-type: none"> Janda, K. D. [230] 10 ex; 62-80% intracyclative cleavage from soluble polymer 	 <ul style="list-style-type: none"> Merck [74] 12 ex; 53-99% Munchhoner [3+2] cycloaddition with a nitrile 	 <ul style="list-style-type: none"> Merck KGaA [85] 11 ex; 71-100% intracyclative cleavage 	 <ul style="list-style-type: none"> Jung, G. [68] 35 members intramolecular cyclization of N,N'-ureas 	 <ul style="list-style-type: none"> Kobayashi, S. [145] 13 ex; 47-89% 1,3-dipolar cycloaddition then DDQ-mediated reductive cleavage

Table 8. (Continued)

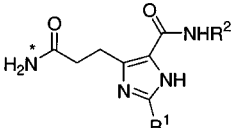
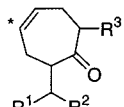
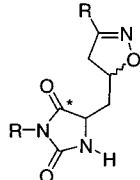
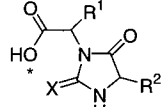
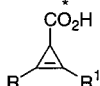
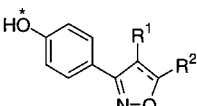
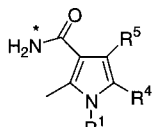
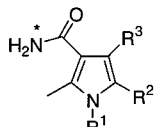
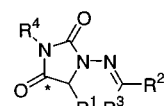
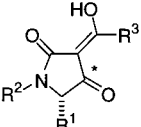
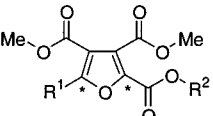
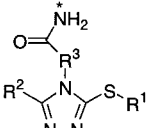
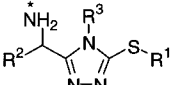
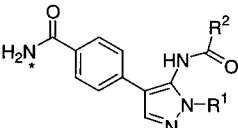
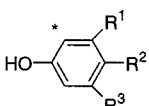
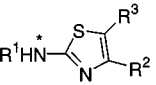
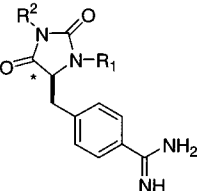
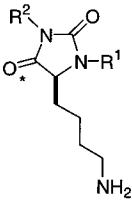
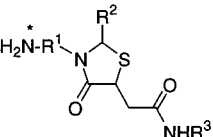
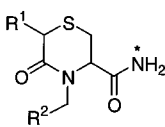
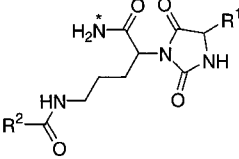
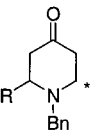
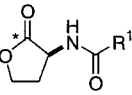
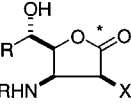
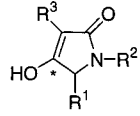
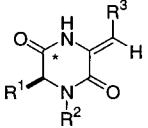
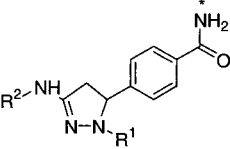
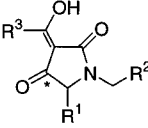
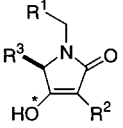
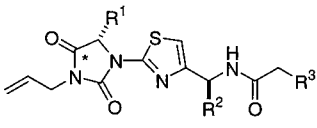
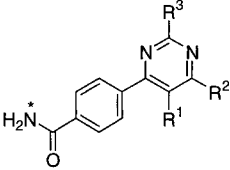
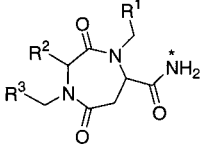
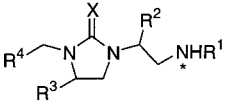
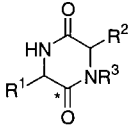
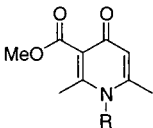
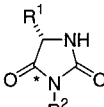
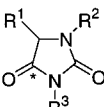
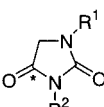
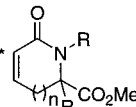
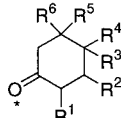
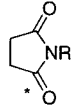
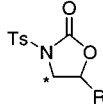
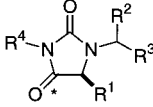
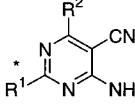
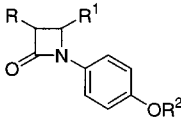
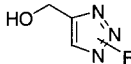
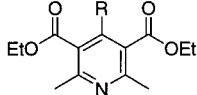
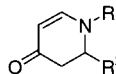
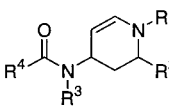
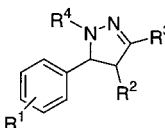
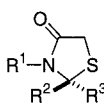
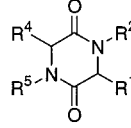
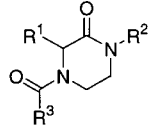
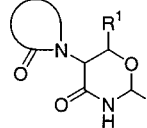
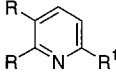
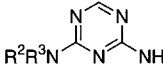
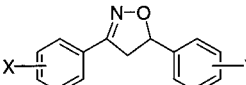
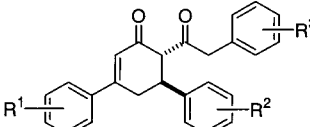
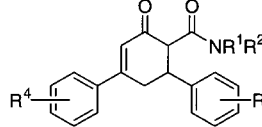
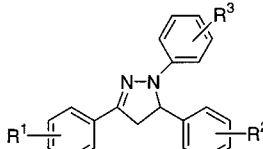
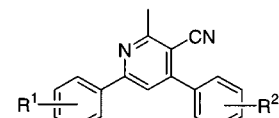
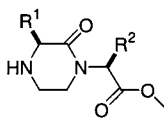
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 <ul style="list-style-type: none"> • Schering-Plough [195] • 10 ex; 60-80% • resin-bound nitrile oxide 	 <ul style="list-style-type: none"> • Jung, G. [210] • 22 ex; 46-90% • resin-bound enaminones and nitroalkenes 	 <ul style="list-style-type: none"> • Jung, G. [211] • 18 members • resin-bound enaminones and 2-bromoketones 	 <ul style="list-style-type: none"> • P&G [225] • 14 ex; 15-58% • intracyclic cleavage 	 <ul style="list-style-type: none"> • Affymax [191] • 21 ex; 51-92% • intracyclic cleavage
 <ul style="list-style-type: none"> • Austin, D. J. [223] • 18 members • cycloaddition-cycloreversion metathesis 	 <ul style="list-style-type: none"> • Parke-Davis [226] • 60 members 	 <ul style="list-style-type: none"> • Parke-Davis [226] • 60 members 	 <ul style="list-style-type: none"> • Glaxo Wellcome [227] • 8 members • 5-aminopyrazole synthesis then N-acylation 	 <ul style="list-style-type: none"> • Katritzky, A. R. [133] • 12 ex; 50-85% • simultaneous cyclization-cleavage reaction
 <ul style="list-style-type: none"> • Tularik [135] • 10 ex; 89-99% • Hantzsch thiazole synthesis 	 <ul style="list-style-type: none"> • LG Chem. [138] • 6 ex; 80-90% • intracyclic cleavage 	 <ul style="list-style-type: none"> • LG Chem. [138] • 5 ex; 80-90% • intracyclic cleavage 	 <ul style="list-style-type: none"> • Amgen [168] • 9 ex; 65-85% • 1000 members 	 <ul style="list-style-type: none"> • Houghten, R. A. [169, 33] • 10 ex; 15-95% • from cysteine and 2-bromo carboxylic acids
 <ul style="list-style-type: none"> • Houghten, R. A. [170] • 15 ex; 85-95% 	 <ul style="list-style-type: none"> • Barco, A. [66] • 5 members • tandem elimination and Michael addition 	 <ul style="list-style-type: none"> • CheilJedang [143] • 9 ex; 32-53% • intracyclic cleavage from methionine 	 <ul style="list-style-type: none"> • Kobayashi, S. [144] • 12 ex; 50-80% • Aldol reaction with resin-bound silyl enol ethers; X = H, Me, OBn 	 <ul style="list-style-type: none"> • Ganesan, A. [147] • 11 ex; 60-91% • intracyclic cleavage
 <ul style="list-style-type: none"> • Li, W.-R. [154] • 10 ex; 40-75% • intracyclic cleavage 	 <ul style="list-style-type: none"> • Nielsen, J. [157] • 24 ex; 70-95% 	 <ul style="list-style-type: none"> • Hoffmann-La Roche [220] • 12 ex; 11-61% • intracyclic cleavage 	 <ul style="list-style-type: none"> • R. W. Johnson [162] • 13 ex; 67-100% • intracyclic cleavage 	 <ul style="list-style-type: none"> • Hoffmann-La Roche [203] • 18 members • intracyclic cleavage

Table 8. (Continued)

 <ul style="list-style-type: none"> • Novartis [159] • 9 ex; 38-98% • condensation of imidates with resin-bound unsaturated ketones 	 <ul style="list-style-type: none"> • Houghten, R. A. [33] • 40 members • intramolecular lactam formation 	 <ul style="list-style-type: none"> • Houghten, R. A. [33] • size not defined • resin-bound triamine from reduction of acylated dipeptide; X = O, S 	 <ul style="list-style-type: none"> • Bayer [205] • >600 mem; 25-50% • intracyclative cleavage 	 <ul style="list-style-type: none"> • Tidwell, T. T. [239] • 4 ex; 91-90% • acetylketene cycloaddition with soluble polymer-bound enamines
 <ul style="list-style-type: none"> • Liskamp, R. M. J. [77] • 42 ex; 40-100% • intracyclative cleavage 	 <ul style="list-style-type: none"> • Liskamp, R. M. J. [77] • 6 ex; 85-100% • intracyclative cleavage 	 <ul style="list-style-type: none"> • Liskamp, R. M. J. [77] • 6 ex; 88-99% • intracyclative cleavage 	 <ul style="list-style-type: none"> • Ruties, P. J. T. [256] • 8 ex; 0-97% • ring-closing metathesis 	 <ul style="list-style-type: none"> • Barrett, A. G. M. [233] • 5 members • Tebbe olefination of resin-bound unsaturated ester, Diels-Alder and hydrolysis
 <ul style="list-style-type: none"> • Tidwell, T. T. [239] • 6 ex; 51-96% • soluble polymer-supported ketenyl esters 	 <ul style="list-style-type: none"> • Zwanenburg, B. [254] • 3 ex; ca. 70% • intracyclative cleavage 	 <ul style="list-style-type: none"> • Lee, Y.-S. [247] • 20 ex; 12-98% • transimination to yield resin-bound ketimines; reduction; intracyclative cleavage 	 <ul style="list-style-type: none"> • Hoffmann-La Roche [248] • 20 ex; 30-80% • ketene dithioacetal and thiuronium salt; R¹ = H SR, NRR; R² = SR, NRR 	 <ul style="list-style-type: none"> • Cozzi, F. [251] • 9 ex; 30-56% • [2+2] cycloaddition; imine generated on soluble support
<i>Solution-phase</i>				
 <ul style="list-style-type: none"> • Norris, P. [165] • 3 ex; 80% • azide dipolar cycloaddition using soluble polymer support 	 <ul style="list-style-type: none"> • EnzyMed [95] • 96 members • Hantzsch synthesis 	 <ul style="list-style-type: none"> • Park-Davis [97] • 40 members • hetero Diels-Alder 	 <ul style="list-style-type: none"> • Park-Davis [97] • 88 members • hetero Diels-Alder, L-Selectide, reductive amination, acylation 	 <ul style="list-style-type: none"> • Ley, S.V. [121] • 7ex; 92-95% • polymer-supported reagents
 <ul style="list-style-type: none"> • Park-Davis [64] • 22 members • use of scavenger resins 	 <ul style="list-style-type: none"> • RPR [126, 128] • >96 ex; 20-95% • Ugi four-component condensation 	 <ul style="list-style-type: none"> • RPR [127, 128] • 12 ex; 70-85% • Ugi four-component condensation using mono-Boc diamines 	 <ul style="list-style-type: none"> • Seneci, P. [179] • 24 ex; 10-80% • hetero Diels-Alder 	 <ul style="list-style-type: none"> • Sauer, J. [176] • 10 ex; 45-94% • oligopyridines from Diels-Alder reaction of 1,2,4-triazines and dienophile
 <ul style="list-style-type: none"> • Hoffmann-La Roche [160] • 6 ex; 80-95% • from thiuronium salts 	 <ul style="list-style-type: none"> • ArQule [185] • 1,280 members • chalcone and hydroxylamine 	 <ul style="list-style-type: none"> • ArQule [185] • 7680 members • chalcone and acetoacetanilides 	 <ul style="list-style-type: none"> • ArQule [185] • 12,800 members • chalcone and acetoacetanilides 	
 <ul style="list-style-type: none"> • ArQule [185] • 7,680 members • chalcone and phenylhydrazines 	 <ul style="list-style-type: none"> • ArQule [185] • 1,280 members • chalcone and 3-aminocrotonitrile 	 <ul style="list-style-type: none"> • Just, G. [250] • 6 ex; > 80% • intramolecular Fukuyama alkylation; one ex. on solid-phase 		

^a The asterisk (*) represents the point of attachment to the solid support.

Table 9. Bicyclic and Spirocyclic Ring Synthesis^a

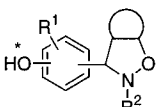
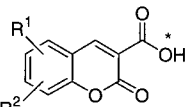
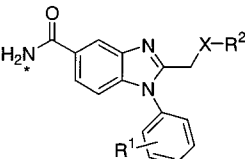
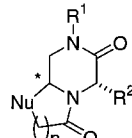
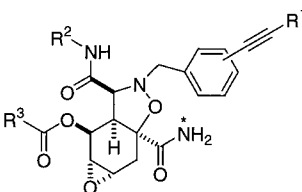
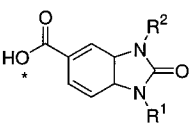
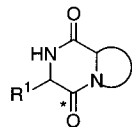
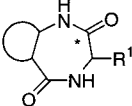
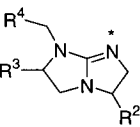
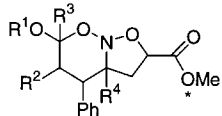
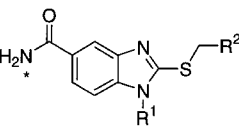
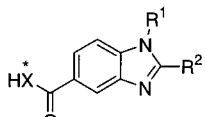
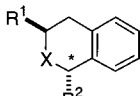
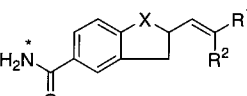
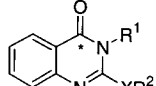
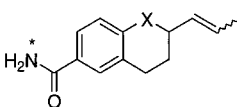
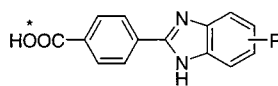
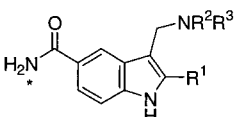
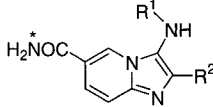
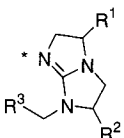
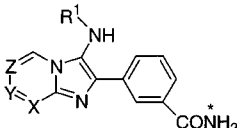
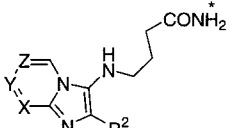
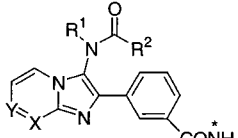
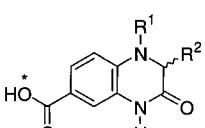
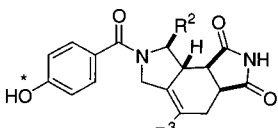
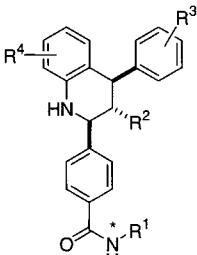
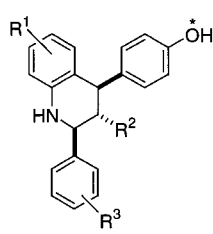
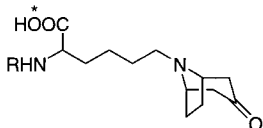
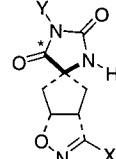
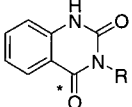
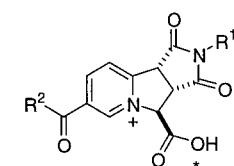
Solid-phase				
 <ul style="list-style-type: none"> • Jung, G. [117] • 12 ex; 0-87% • 1,3-dipolar cycloaddition 	 <ul style="list-style-type: none"> • Nova Nordisk [218] • 8 ex; 16-40% • Knoevenagel condensation 	 <ul style="list-style-type: none"> • Affymax [212] • 24 ex; 55-95% • X = NH, NR³ or S 	 <ul style="list-style-type: none"> • Selectide [216] • 8 ex; 18-87% • intracyclic cleavage via N-acyliminium ion cyclization 	 <ul style="list-style-type: none"> • Schreiber, S. L. [208] • 2.18 million members • derived from shikimic acid
 <ul style="list-style-type: none"> • Berlex Biosci. [221] • 13 ex; 90-100% • from 4-fluoro-3-nitrobenzoic acid 	 <ul style="list-style-type: none"> • Bayer [201] • >600 mem; 25-50% • intracyclic cleavage 	 <ul style="list-style-type: none"> • Bayer [201] • >600 mem; 25-50% • intracyclic cleavage 	 <ul style="list-style-type: none"> • Houghten, R. A. [33] • 102,459 members • from triamine generated from reduction of acylated dipeptide 	 <ul style="list-style-type: none"> • Scheeren, H. W. [149] • 6 ex; 33-52% • tandem [4+2]/[3+2] cycloaddition of enol ethers with nitrostyrenes and resin-bound acrylate
 <ul style="list-style-type: none"> • R. W. Johnson [151] • 16 ex; 74-99% • resin-bound phenylenediamines and TCDI 	 <ul style="list-style-type: none"> • Amgen [163] • 160 members • from 4-fluoro-3-nitrobenzoic acid; X = NH, O 	 <ul style="list-style-type: none"> • Craig, D. [96] • 10 ex; 10-47% • tandem hetero Diels-Alder and Lewis-acid mediated cleavage; X = O, NTs 	 <ul style="list-style-type: none"> • Hoffmann-La Roche [217] • 12 ex; 91-76% • from <i>o</i>-iodoanilines and <i>o</i>-iodo-phenols; X = O, NSO₂R, NCO₂R 	 <ul style="list-style-type: none"> • Hoffmann-La Roche [215] • 12 ex; 42-85% • from <i>o</i>-azidobenzoic acids and intracyclic cleavage; X = S, NR³
 <ul style="list-style-type: none"> • Hoffmann-La Roche [217] • 3 ex; 84-93% • from <i>o</i>-iodoanilines or <i>o</i>-iodophenols; X = O, NTs 	 <ul style="list-style-type: none"> • Novartis [206] • 5 members • condensation of phenylenediamines with resin-bound aldehyde 	 <ul style="list-style-type: none"> • R. W. Johnson [231] • 10 ex; 81-95% • from <i>o</i>-iodosulfonamide via tandem Pd-catalyzed heteroannulation of alkyne and Mannich condensation 	 <ul style="list-style-type: none"> • Millennium [75] • 3 ex; 30-80% • three-component condensation 	 <ul style="list-style-type: none"> • Houghten, R. A. [174] • >200 members • cyclization of reduced N-acylated dipeptides
 <ul style="list-style-type: none"> • Millennium [75] • 5 ex; 0-78% • three-component condensation 	 <ul style="list-style-type: none"> • Millennium [75] • 7 ex; 5-50% • three-component condensation 	 <ul style="list-style-type: none"> • Millennium [75] • 6 ex; 20-80% • three-component condensation 	 <ul style="list-style-type: none"> • DuPont Merck [166] • 7 ex; ~50% • from 4-fluoro-3-nitrobenzoic acid 	 <ul style="list-style-type: none"> • SKB [122] • 1800 members • olefin-alkyne metathesis tandem Diels-Alder
 <ul style="list-style-type: none"> • Amgen [140] • 50 members, 60-87% • three-component condensation 	 <ul style="list-style-type: none"> • Amgen [140] • 32 ex; 61-85% • three-component condensation 	 <ul style="list-style-type: none"> • Uden, A. [131] • 1 ex; 93% • Robinson's tropone synthesis on resin-bound lysine 	 <ul style="list-style-type: none"> • Kurth, M. J. [181] • 6 ex; 20-30% • intracyclic cleavage 	 <ul style="list-style-type: none"> • Cadus Pharm. [196] • 12 ex; 72-81% • intracyclic cleavage

Table 9. (Continued)

<ul style="list-style-type: none"> • Ganesan, A. [199] • 15 ex; 22-95% • intracyclic cleavage 	<ul style="list-style-type: none"> • Merck [200] • 6 ex; 53-97% • THP-linked iodoaniline 	<ul style="list-style-type: none"> • Versicor [115] • 13 ex; members • from amino acid and carbamate-linked anthranilic acid 	<ul style="list-style-type: none"> • Axys Pharm. [83] • 8,800 members • titanium-mediated reductive amination (X = CO, CONH, CSNH) 	<ul style="list-style-type: none"> • Nova Nordisk [219] • 7 ex; 60-99% • intramolecular Knoevenagel condensation
<ul style="list-style-type: none"> • Affymax [193] • >18 ex; 56-90% 	<ul style="list-style-type: none"> • Amgen [142] • 40 ex; 62-92% • three-component condensation 	<ul style="list-style-type: none"> • Armstrong, R. W. [237] • 6 ex; 5-45% • SmI₂-mediated radical cyclization/anionic capture 		
<i>Solution-phase</i>				
<ul style="list-style-type: none"> • ArQule [107] • 25,600 members • azomethine ylide and chalcone 	<ul style="list-style-type: none"> • Searle [182] • 35 ex; 30-99% 	<ul style="list-style-type: none"> • Cerep [67] • 1,920 members • three-component cycloaddition 	<ul style="list-style-type: none"> • ArQule [185] • 25,600 members • chalcone, isatins and L-proline 	<ul style="list-style-type: none"> • RPR [128, 129] • ca. 12 ex; 50-70% • Ugi four-component condensation using N-Boc anthranilic acids
<ul style="list-style-type: none"> • Berlex Biosci. [86] • 13 ex; 73-93% • resin-bound carbodiimide 	<ul style="list-style-type: none"> • RPR [72] • 31 ex; 40-98% • multi-component reaction 	<ul style="list-style-type: none"> • Ganesan, A. [148] • 10 ex; 78-96% • intramolecular Claisen-type condensation 	<ul style="list-style-type: none"> • RPR [128] • 1 ex; 50% • Ugi condensation 	<ul style="list-style-type: none"> • Mitscher, L. A. [108] • 107 members
<ul style="list-style-type: none"> • ArQule [185] • 7,680 members • chalcone and 3-amino-5,5-dimethylcyclohexenone 	<ul style="list-style-type: none"> • ArQule [185] • 1,280 members • chalcone and 6-amino-1,3-dimethyluracil 	<ul style="list-style-type: none"> • Millennium Pharm. [234] • 60 members • three-component condensation 		
<ul style="list-style-type: none"> • Millennium Pharm. [234] • 60 members • three-component condensation then acylation 				

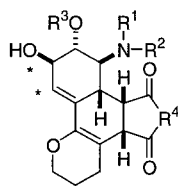
^a The asterisk (*) represents the point of attachment to the solid support.

Table 10. Polycyclic Ring Synthesis^a*Solid-phase*

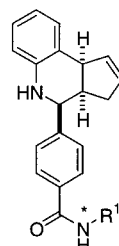
- SKB [71]
- 96 members
- multi-component Tsuge reaction with resin-bound pyridinium methylides



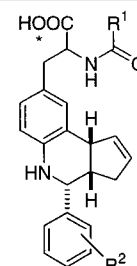
- Novartis [222]
- 3 ex; 81-96%
- dehydration of resin-bound 1,2-diols; ketal linkage



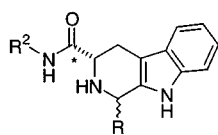
- Novartis [222]
- 3 ex; 61-71%
- dehydration of resin-bound 1,2-diols; ketal linkage



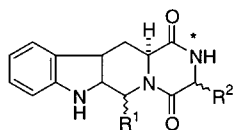
- Amgen [140]
- 10 ex; 69-86%
- three-component condensation



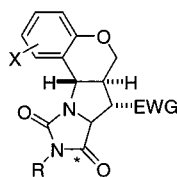
- Amgen [142]
- 10 ex; 61-92%
- three-component condensation



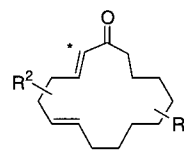
- Arris [105]
- 345 members
- Pictet-Spengler reaction



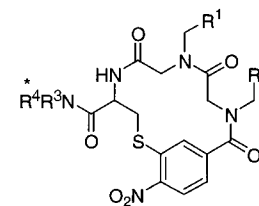
- van Loevezijn, A. [214]
- 42 ex; 50-99%
- Pictet-Spengler reaction and intracyclative cleavage



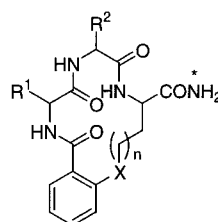
- Kurth, M. J. [114]
- 6 ex; 6-15%
- use of azomethine ylide; intracyclative cleavage



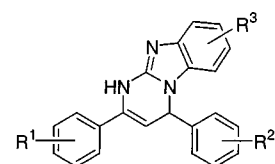
- Nicolaou, K. C. [172]
- 12 ex; ~ 65%
- intramolecular ketophosphonate condensation



- Amgen [141]
- 12 ex; 55-70%
- S_NAr cyclization



- Burgess, K. [240]
- 12 members
- S_NAr cyclization; X = O, S, NR

Solution-phase

- ArQule [185]
- 7,680 members
- chalcone and aminobenzimidazoles

^a The asterisk (*) represents the point of attachment to the solid support.

References and Notes

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