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(71) Demandeur/Applicant:
THE SCRIPPS RESEARCH INSTITUTE, US

(72) Inventeurs/Inventors:
SMITH, PETER A., US;
ROBERTS, TUCKER C., US;
ROMESBERG, FLOYD E., US

(74) Agent: GOUDREAU GAGE DUBUC

(54) Titre : ANALOGUES D'ARYLOMYCINE ANTIBIOTIQUES A LARGE SPECTRE
(54) Title: BROAD SPECTRUM ANTIBIOTIC ARYLOMYCIN ANALOGS

(57) **Abrégé/Abstract:**

Arylomycin analogs are provided, wherein the analogs can have broad spectrum bioactivity. Resistance to the antibiotic bioactivity of natural product arylomycin in a range of pathogenic bacterial species has been found to depend upon single amino acid mutations at defined positions of bacterial Signal Peptidases (SPases), wherein the presence of a proline residue confers arylomycin resistance. Arylomycin analogs are provided herein that can overcome that resistance and provide for a broader spectrum of antibiotic bioactivity than can natural product arylomycins such as arylomycin A2. Methods for determining if a bacterial strain is susceptible to narrow spectrum arylomycin antibiotics, or if a broad spectrum analog is required for treatment, is provided. Pharmaceutical compositions and methods of treatment of bacterial infections, and methods of synthesis of arylomycin analogs, are provided.



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(72) Inventors; and

(71) Applicants : ROMESBERG, Floyd E. [US/US]; 8109 Camino Del Sol, La Jolla, California 92037-3152 (US). SMITH, Peter A. [US/US]; 3127 Myrtle Avenue, San Diego, California 92104-4217 (US). ROBERTS, Tucker C. [US/US]; 5701 Stresemann Street, San Diego, California 92122-3138 (US).

(74) Agents: PERDOK SHONKA, Monique M. et al.; Schwegman, Lundberg & Woessner, P.A., P. O. Box 2938, Minneapolis, Minnesota 55402 (US).

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(54) Title: BROAD SPECTRUM ANTIBIOTIC ARYLOMYCIN ANALOGS

(57) Abstract: Arylomycin analogs are provided, wherein the analogs can have broad spectrum bioactivity. Resistance to the antibiotic bioactivity of natural product arylomycin in a range of pathogenic bacterial species has been found to depend upon single amino acid mutations at defined positions of bacterial Signal Peptidases (SPases), wherein the presence of a proline residue confers arylomycin resistance. Arylomycin analogs are provided herein that can overcome that resistance and provide for a broader spectrum of antibiotic bioactivity than can natural product arylomycins such as arylomycin A2. Methods for determining if a bacterial strain is susceptible to narrow spectrum arylomycin antibiotics, or if a broad spectrum analog is required for treatment, is provided. Pharmaceutical compositions and methods of treatment of bacterial infections, and methods of synthesis of arylomycin analogs, are provided.



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BROAD SPECTRUM ANTIBIOTIC ARYLOMYCIN ANALOGS

STATEMENT OF GOVERNMENT SUPPORT

This invention was made with government support under Grant No. N00014-08-
5 0478, awarded by the Office of Naval Research. The U.S. government has certain rights
in the invention.

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of priority of U.S. Patent Application Serial
10 No. 61/382,988, entitled "BROAD SPECTRUM ANTIBIOTIC ARYLOMYCIN
ANALOGS," filed September 15, 2010, which is incorporated herein by reference in its
entirety.

BACKGROUND

15 The arylomycin class of natural product, which includes the arylomycin A and B
series, was initially discovered by the group of Hans-Peter Frielder, and described in a
2002 publication in the Journal of Antibiotics (J. Schimana, et al., J. Antibiotics (2002),
55(6), 565-570 and 571-577). The arylomycins, as characterized in this publication,
comprise a unique structural class of natural product composed of a hexapeptide with a
20 unique biaryl bridge between N-methyl-4-hydroxyphenylglycine⁵ (MeHpg⁵) and
tyrosine⁷, and N-terminal acyl tails of various lengths. See FIG. 1 showing the
structures of natural products of the arylomycin A and B classes as determined by the
Frielder group.

The initial report describing the arylomycins provided data describing the
25 antibiotic activity of these compounds against the soil bacteria, *Arthrobacter globiformis*
DSM20124, *Arthrobacter oxygens* DSM 6612, *Arthrobacter pascens* DSM 20545,
Rhodococcus erythropolis DSM 1069 (currently characterized *Rhodococcus opacus*),
Streptomyces viridochromogenes Tu 57, and *Brevibacillus brevis* DSM 30, and against
the fungus *Mucor hiemalis* Tu 179/180. The data appear to suggest and the authors
30 conclude that the arylomycins have limited to no activity against the examined bacteria
with the exception of *Rhodococcus opacus* and *Brevibacillus brevis*. Furthermore while
no data is provided, the authors state that no the arylomycin lack activity against the
Gram-negative bacteria *Escherichia coli* K12, *Proteus mirabilis* ATCC 35501,
Pseudomonas fluorescens DSM 50090 and against the eukaryotic organisms

Saccharomyces cerevisiae ATCC 9080, *Botrytis cinerea* Tu 157 and against the green algae *Chlorella fusca* and against the duckweed *Lemna minor*.

In 2004 Kulanthaivel, et al., independently discovered a subclass of the arylomycins, the lipoglycopeptides, which differ from the arylomycin A and B series via glycosylation and aromatic hydroxylation of the hydroxyphenylglycine residue as well as in the length of the N-terminal acyl tail. Kinetic evidence was provided to support the conclusion that the lipoglycopeptides inhibit the essential bacterial enzyme type I signal peptidase *in vitro*. However, most active members of the lipoglycopeptides displayed only moderate whole cell activity against the human pathogen *Streptococcus pneumoniae* R6, and extremely little to no activity against the human pathogens *Staphylococcus aureus* ATCC13709, *Haemophilus influenzae* ATCC49247, and *Escherichia coli* K12. Furthermore the intrinsic resistance of *E. coli* K12 to the lipoglycopeptide subclass of arylomycins was attributed to outer membrane penetrance of drug efflux based on genetic data, suggesting that the arylomycins are not suitable as antimicrobial agents against Gram-negative bacteria. See U.S. Pat. No. 6,951,840, issued Oct. 4, 2005; see also P. Kulanthaivel, et al., *J. Biol. Chem.* (2004), 279(35), 36250-36258.

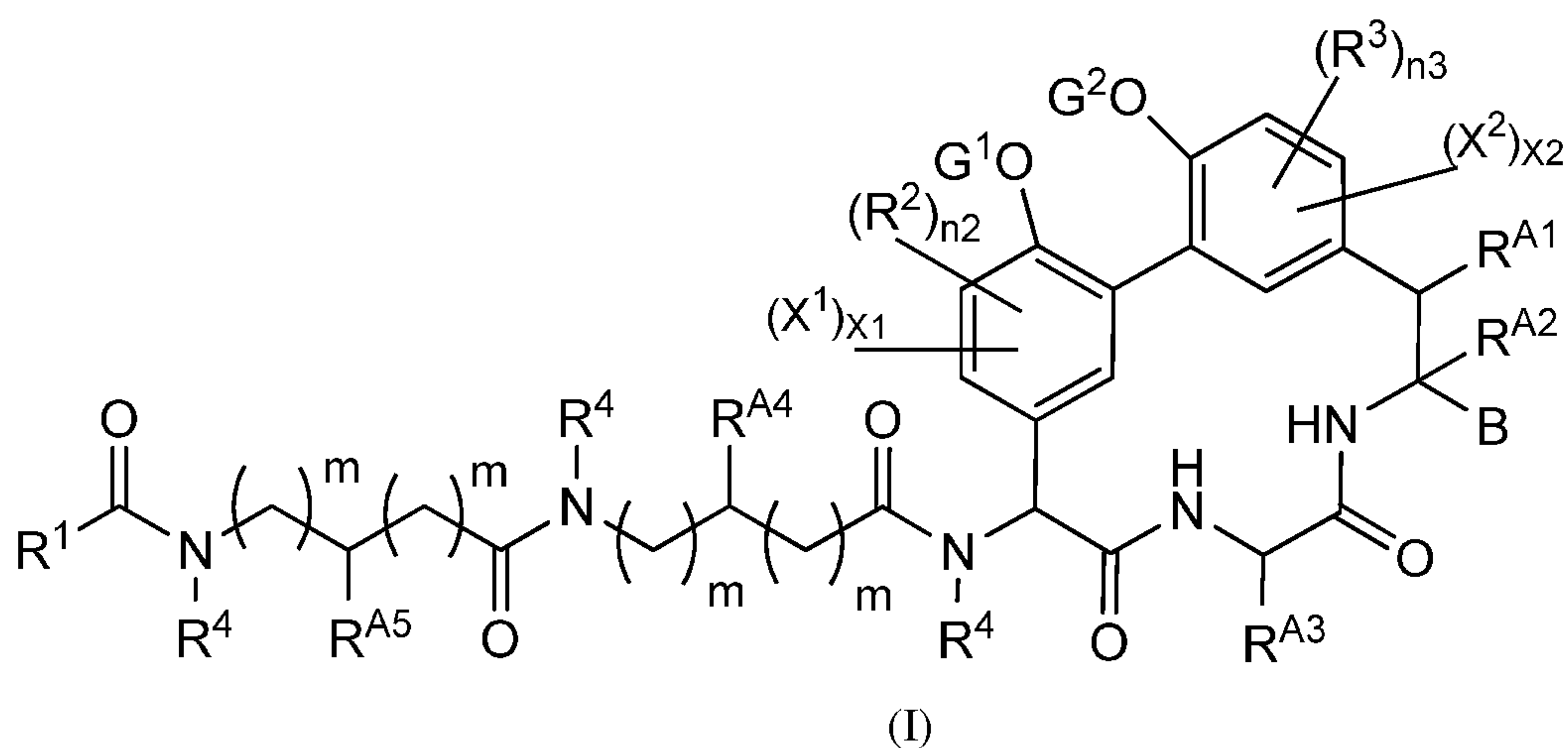
The natural products as described by Frielder and Kulanthaivel are as shown in FIG. 1; the compounds termed “arylomycins” by Frielder’s group, and the compounds termed “lipoglycopeptides” by the Lilly workers including Kulanthaivel.

A total synthesis of arylomycin A2 has been reported by the inventors herein, see T. Roberts, et al. (2007), *J. Am. Chem. Soc.* 129, 15830-15838.

SUMMARY

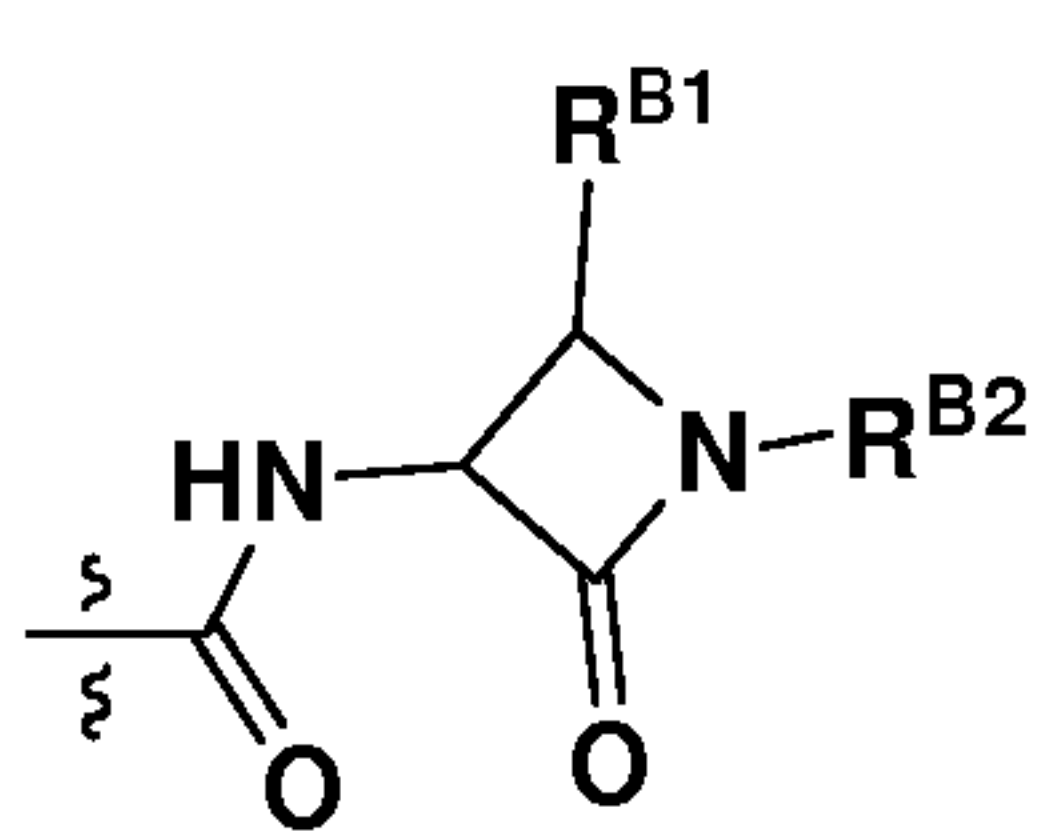
The present invention is directed to the use of analogs of the natural product arylomycin for the treatment of microbial infections, such as for the treatment of bacterial infections. In various embodiments, the invention provides classes and subclasses of chemical compounds structurally related to arylomycin for the treatment of bacterial infections. In various embodiments, the bacterial infections are resistant to treatment with the natural product arylomycin, but are susceptible to treatment with an arylomycin analog of the invention.

In various embodiments, the invention provides a compound of formula (I)

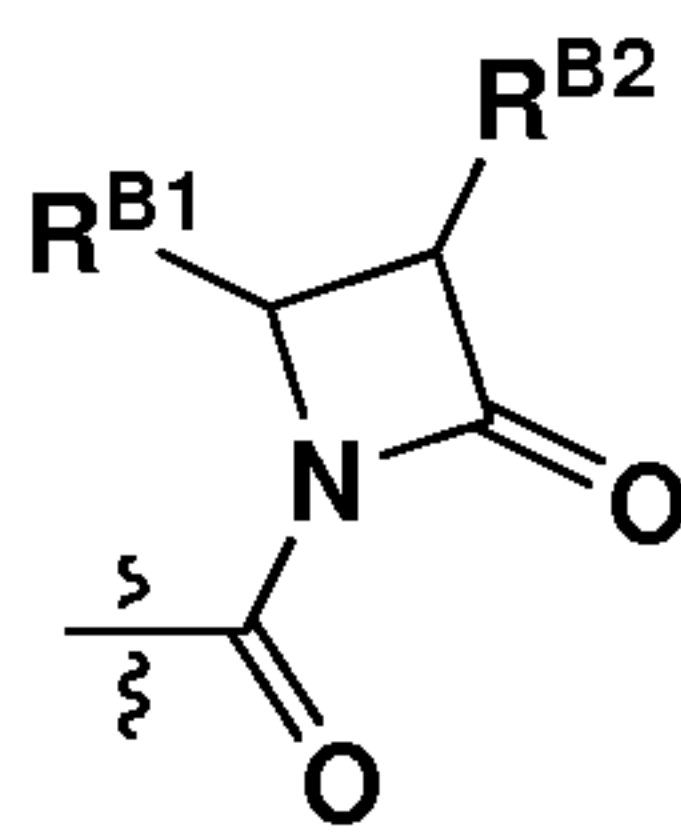


wherein

- B is CO_2H , $\text{CH}_2\text{CO}_2\text{H}$, $\text{C}(=\text{O})\text{NHCH}_2\text{C}(=\text{O})\text{H}$, $\text{CH}_2\text{C}(=\text{O})\text{H}$,
 5 $\text{C}(=\text{O})\text{NHCH}_2\text{B}(\text{OR}^{\text{B}})_2$ or $\text{C}(=\text{O})\text{NHCH}_2\text{P}(=\text{O})(\text{OR}^{\text{B}})_2$ wherein R^{B} is H or $(\text{C}_1\text{-C}_6)\text{alkyl}$,
 or B is a group of formula



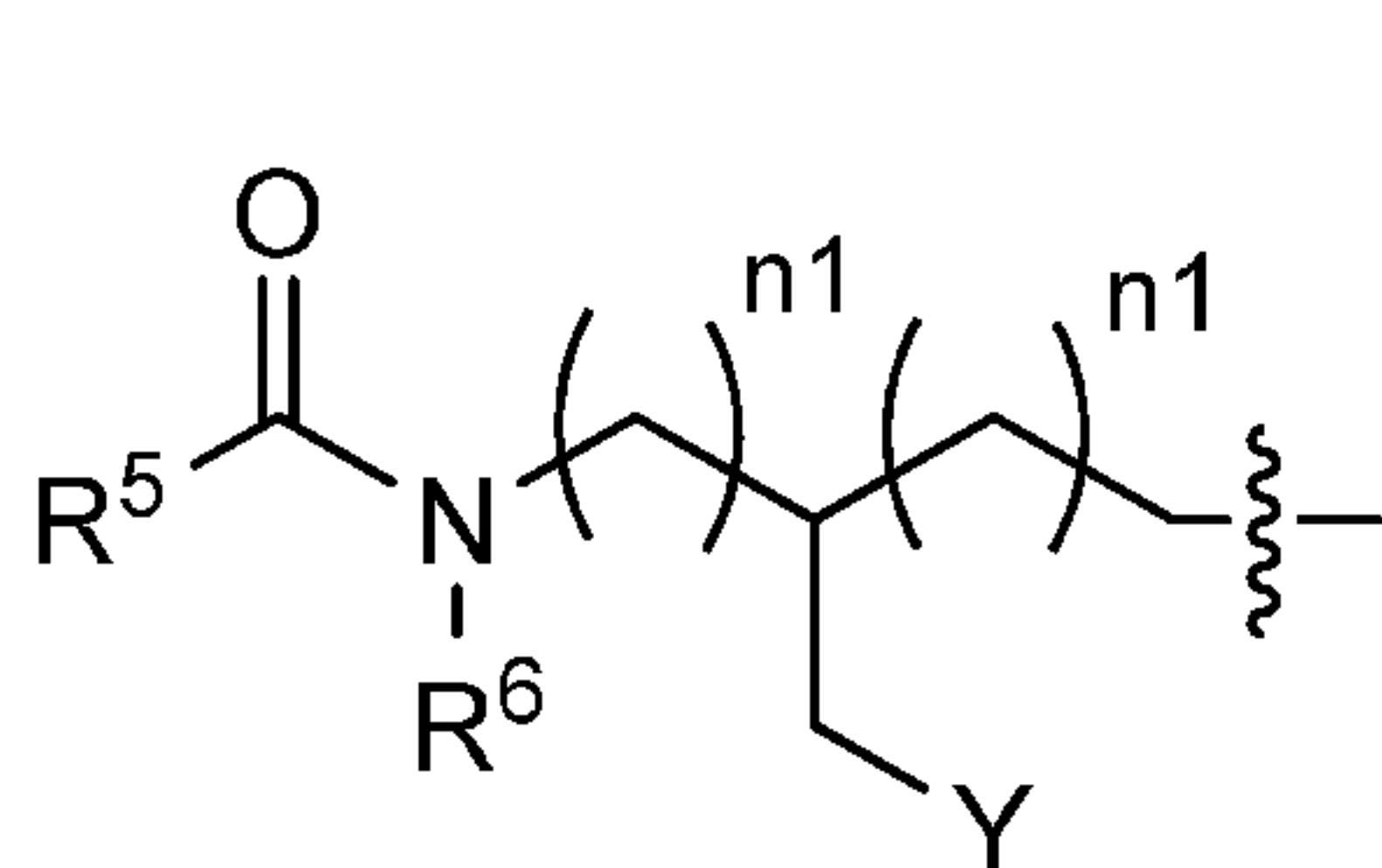
or



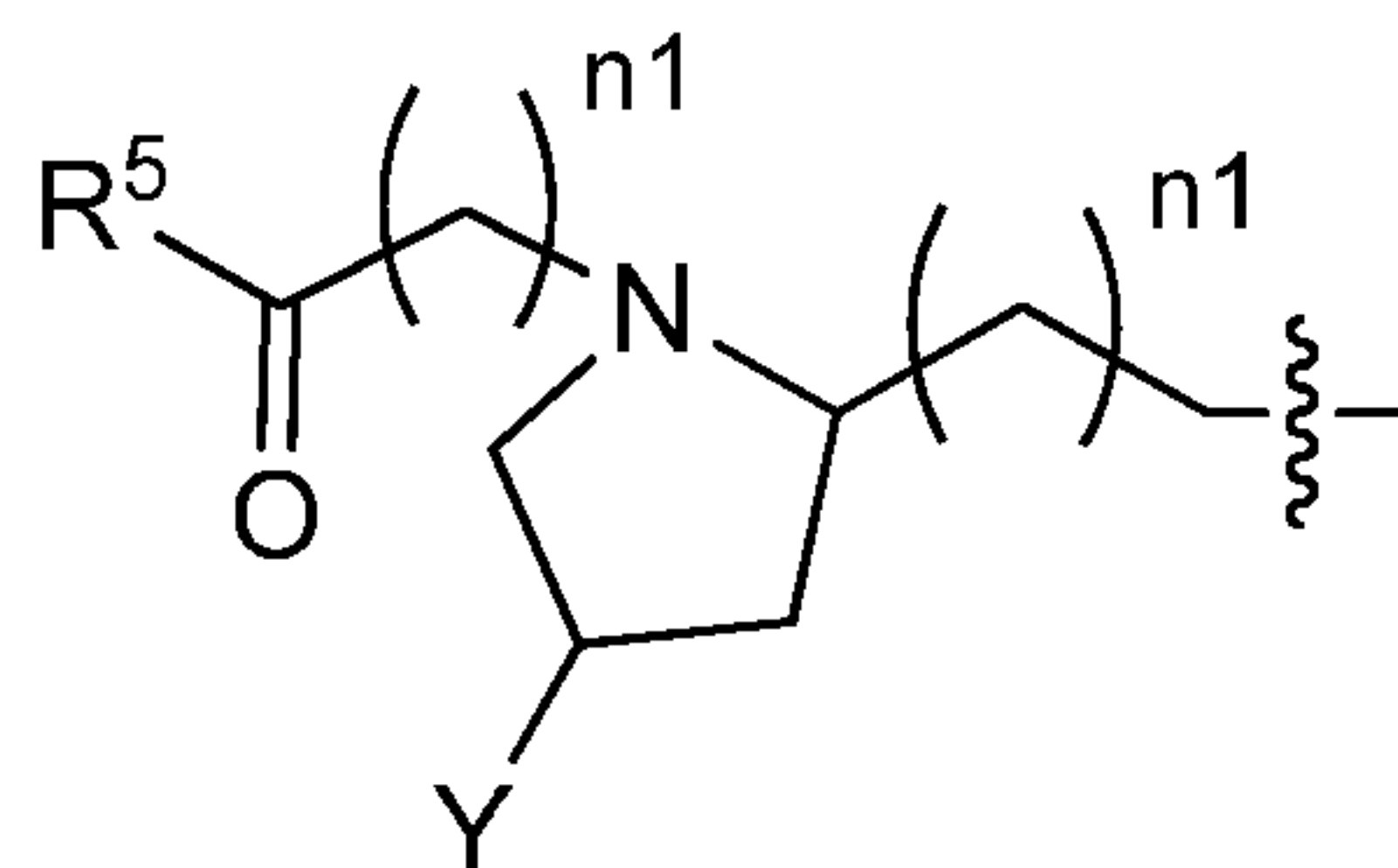
, wherein R^{B1} and R^{B2} are each

- independently H, $(\text{C}_1\text{-C}_6)$ alkyl, $(\text{C}_3\text{-C}_6)$ cycloalkyl, OR^{C} , $\text{C}(=\text{O})\text{NR}^{\text{C}}_2$, $\text{O C}(=\text{O})\text{NR}^{\text{C}}_2$,
 $\text{C}(=\text{O})\text{OR}^{\text{C}}$, $\text{OC}(=\text{O})\text{OR}^{\text{C}}$, nitro, trifluoromethyl, trifluoromethoxy, $(\text{C}_1\text{-C}_6)\text{alkoxy}$, $(\text{C}_1\text{-C}_6)\text{thioalkoxy}$, NR^{C}_2 , 5-7 membered heterocyclyl or 5-7 membered heteroaryl, or $(\text{C}_6\text{-C}_{10})$ aryl;
 10 R^{C} is independently at each occurrence H or $(\text{C}_1\text{-C}_6)$ alkyl, and a wavy line indicates a point of attachment of B to a carbon of formula (I) bearing B;

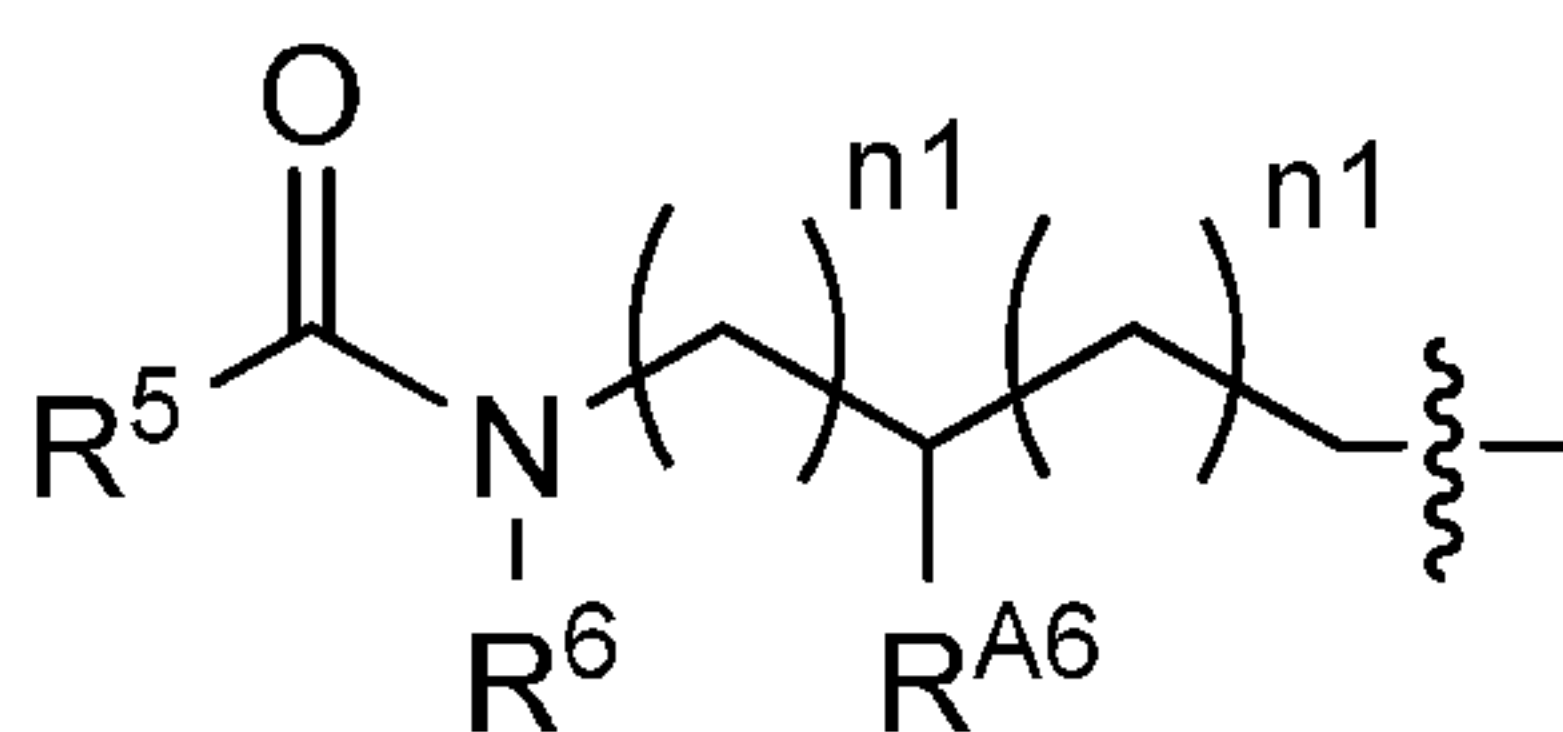
R^1 comprises a group of formula (IIA) or (IIB) or (IIC)



(IIA)



(IIB)



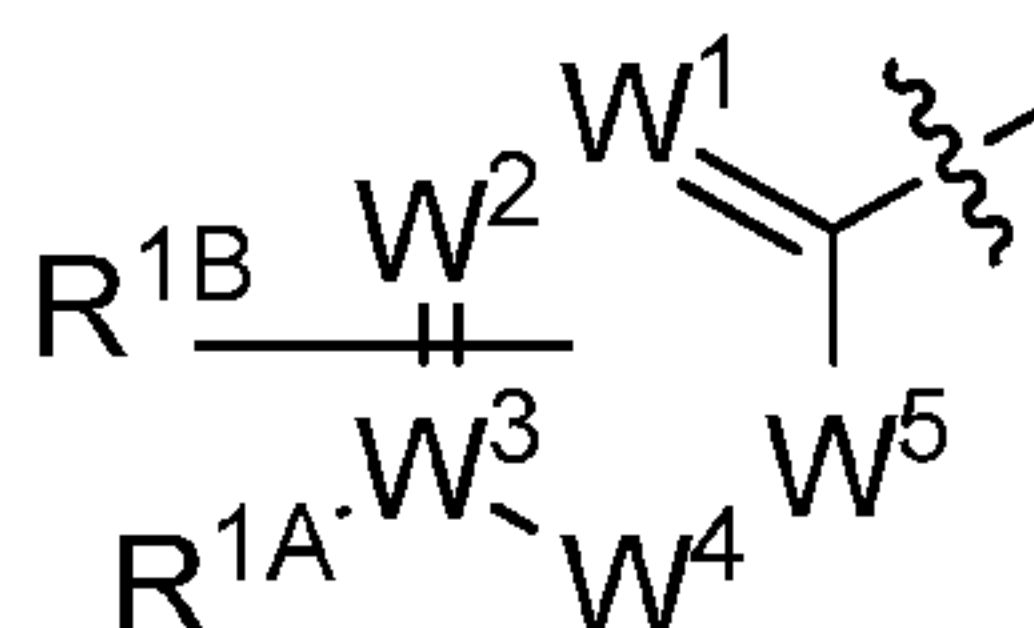
(IIC)

15

wherein each m is independently 0, 1, or 2, n1 is independently at each occurrence 0, 1, or 2; Y is (CH₂)₀₋₂H, (CH₂)₀₋₂OH, or (CH₂)₀₋₂OC(=O)(C₁-C₆)alkyl; R^{A6} is hydrogen, (C₁-C₆)alkyl, (C₃-C₇)cycloalkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl, wherein any alkyl, cycloalkyl, heterocyclyl, aryl or heteroaryl may be substituted with 1 to 3 substituents, wherein each substituent is independently selected from the group consisting of halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, cyano, trifluoromethyl, trifluoromethoxy, 5- to 7- membered heterocyclyl, (C₁-C₆)alkoxy, (C₁-C₆)alkyl, (C₃-C₇)cycloalkyl, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)alkoxycarbonyl, (C₁-C₆)alkylhydroxycarbonyl, (C₁-C₆)alkylaminocarbonyl, (C₁-C₆)alkylsulfonylamino, and (C₆-C₁₀)-arylsulfonylamino; and a wavy line indicates a point of attachment of R¹ to an atom of formula (I) bearing R¹; and

R⁵ is a linear or branched alkyl chain of about 1-22 carbon atoms, bonded to the carbonyl carbon to which it is attached directly or by an O or NR, to provide an amide, carbamate, or urea linkage respectively; optionally comprising within the chain or at a chain terminus, any of the following groups:

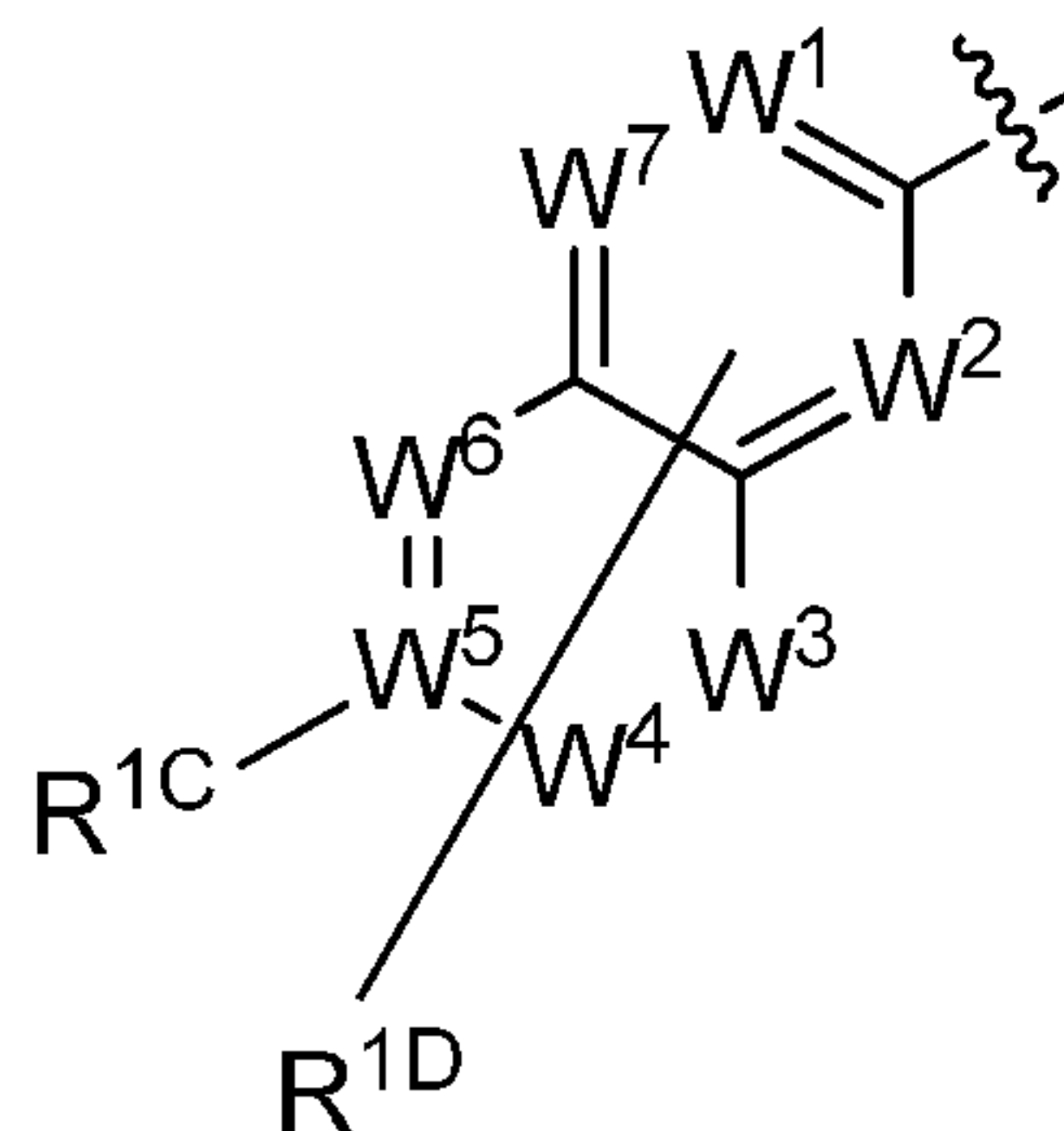
(A)



wherein W¹, W², W³, W⁴ and W⁵ are each independently C or N, provided that no more than two of W¹, W², W³, W⁴ and W⁵ are N; provided that when R^{1A} or R^{1B} is non-hydrogen, any W atom to which the R^{1A} or R^{1B} is respectively bonded is C, wherein there can be one or more R^{1B} bonded to the ring bearing the W atoms; R^{1A} is hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, cyano, (C₁-C₆)-thioether, fluoroalkoxy, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1B} is hydrogen, alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1A} or R^{1B} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-

alkoxy, (C₁-C₆)-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl groups; wherein a wavy line indicates a point of attachment;

(B)



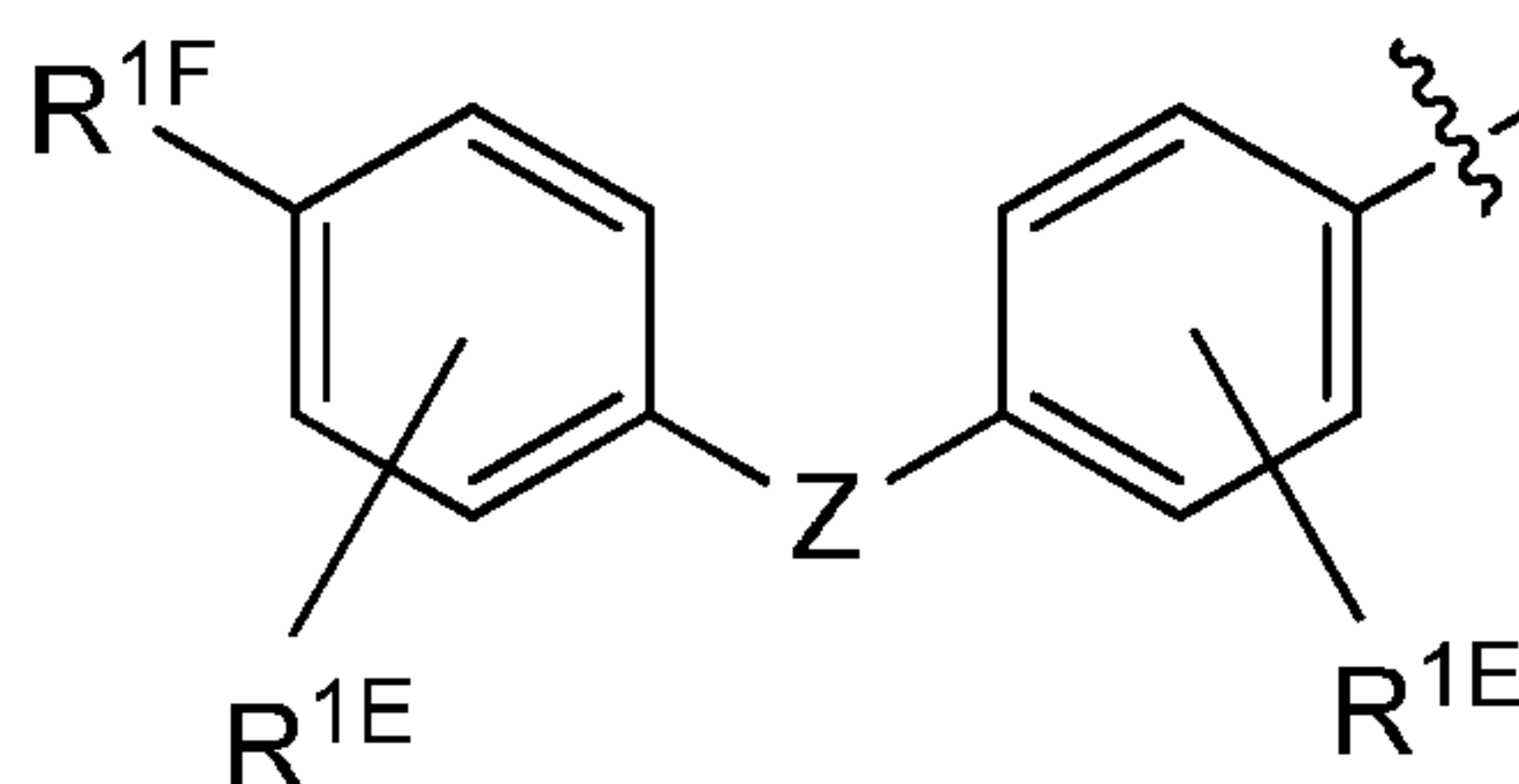
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wherein W¹, W², W³, W⁴, W⁵, W⁶, and W⁷ are each independently C or N, provided that no more than three of W¹, W², W³, W⁴, W⁵, W⁶, and W⁷ are N; provided that when R^{1C} or R^{1D} is non-hydrogen, any W atom to which the R^{1C} or R^{1D} is respectively bonded is C, wherein either ring can bear one or more R^{1D}; R^{1C} is hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1D} is hydrogen, alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1C} or R^{1D} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment;

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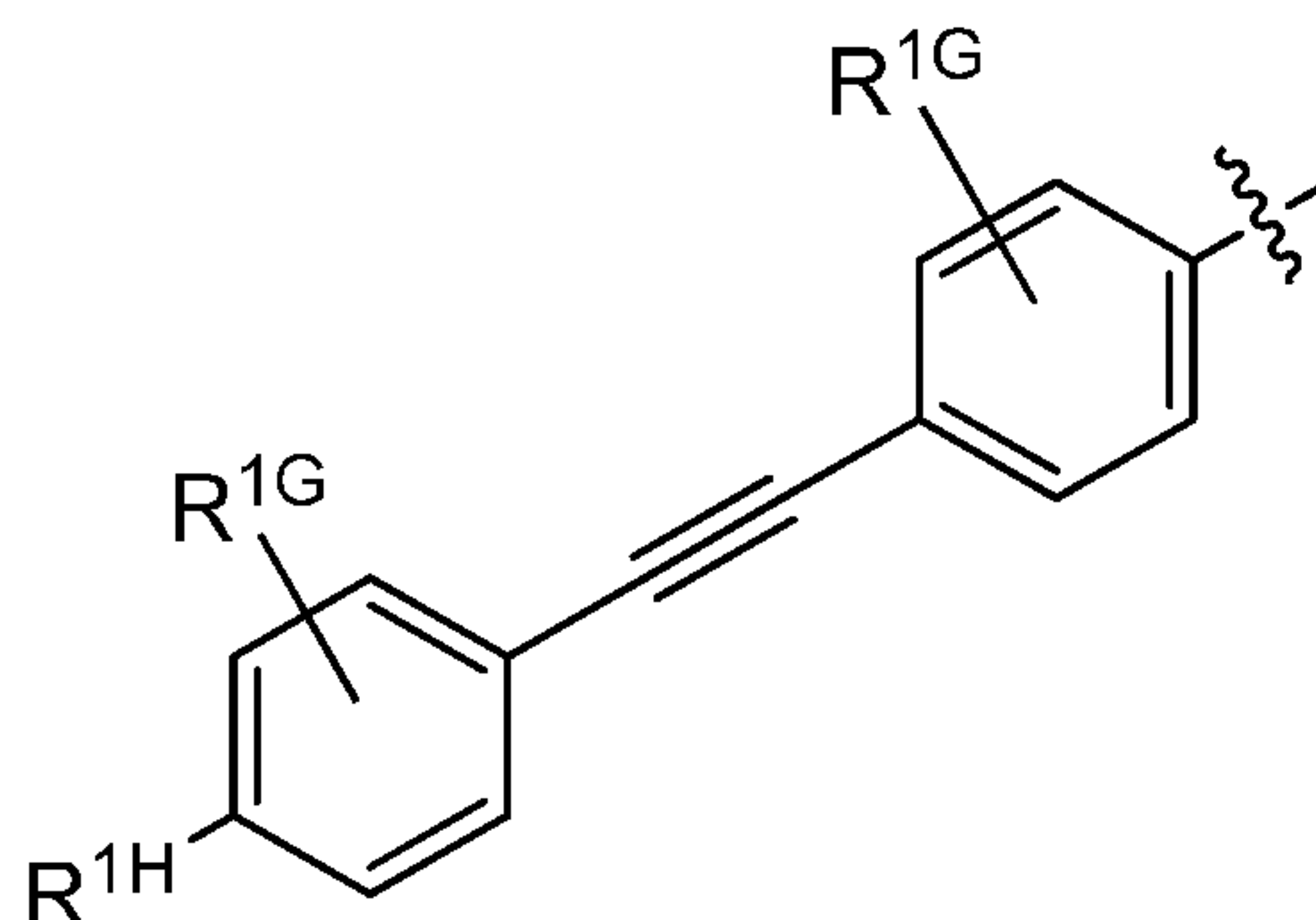
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(C)



wherein Z is O, S, NH or CH₂; R^{1E} at each occurrence is independently hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁- C₆)-alkyl, (C₁- C₆)-alkoxy, (C₁- C₆)-mono- or di-alkylamino, (C₁- C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1F} is hydrogen or alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁- C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁- C₆)-alkoxy, (C₁- C₆)-mono- or di-alkylamino, (C₁- C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1E} or R^{1F} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)thioalkyl, fluoroalkoxy, cyano, (C₁- C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment; or

(D)



wherein R^{1G} at each occurrence is independently hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁- C₆)-alkyl, (C₁- C₆)-alkoxy, (C₁- C₆)-mono- or di-alkylamino, (C₁- C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1H} is hydrogen or alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁- C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁- C₆)-alkoxy, (C₁- C₆)-mono- or di-alkylamino, (C₁- C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1G} or R^{1H} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)thioalkyl, fluoroalkoxy, cyano, (C₁- C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7-

membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment;

R² and R³ are each independently nitro, halo, cyano, hydroxy, glycosyloxy, amino, (C₁-C₄)alkoxy, (C₁-C₄)acyloxy, or (C₁-C₄)alkyl, wherein any carbon atom can be unsubstituted or substituted with J, wherein n² and n³ are independently 0, 1, 2, or 3; or wherein two R² groups taken together, and/or two R³ groups taken together, can comprise fused cycloalkyl, aryl, heterocyclyl, or heteroaryl ring or rings, any of which is substituted with 0-3 J;

R⁴ and R⁶ are each independently at every occurrence hydrogen, (C₁-C₆)alkyl, (C₃-C₇)cycloalkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl, wherein any alkyl, cycloalkyl, heterocyclyl, aryl or heteroaryl can be substituted with 1 to 3 J;

R^{A1}, R^{A2}, R^{A3}, R^{A4}, R^{A5} are independently at each occurrence hydrogen, (C₁-C₆)alkyl, (C₃-C₇)cycloalkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl, wherein any alkyl, cycloalkyl, heterocyclyl, aryl or heteroaryl can be substituted with 1 to 3 J;

J is halogen, R', OR', CN, CF₃, OCF₃, O, S, C(O), S(O), methylenedioxy, ethylenedioxy, (CH₂)_{0-p}N(R')₂, (CH₂)_{0-p}SR', (CH₂)_{0-p}S(O)R', (CH₂)_{0-p}S(O)₂R', (CH₂)_{0-p}S(O)₂N(R')₂, (CH₂)_{0-p}SO₃R', (CH₂)_{0-p}C(O)R', (CH₂)_{0-p}C(O)CH₂C(O)R', (CH₂)_{0-p}C(S)R', (CH₂)_{0-p}C(O)OR', (CH₂)_{0-p}OC(O)R', (CH₂)_{0-p}C(O)N(R')₂, (CH₂)_{0-p}OC(O)N(R')₂, (CH₂)_{0-p}C(S)N(R')₂, (CH₂)_{0-p}NH-C(O)R', (CH₂)_{0-p}N(R')N(R')C(O)R', (CH₂)_{0-p}N(R')N(R')C(O)OR', (CH₂)_{0-p}N(R')N(R')CON(R')₂, (CH₂)_{0-p}N(R')SO₂R', (CH₂)_{0-p}N(R')SO₂N(R')₂, (CH₂)_{0-p}N(R')C(O)OR', (CH₂)_{0-p}N(R')C(O)R', (CH₂)_{0-p}N(R')C(S)R', (CH₂)_{0-p}N(R')C(O)N(R')₂, (CH₂)_{0-p}N(R')C(S)N(R')₂, (CH₂)_{0-p}N(COR')COR', (CH₂)_{0-p}N(OR')R', (CH₂)_{0-p}C(=NH)N(R')₂, (CH₂)_{0-p}C(O)N(OR')R', or (CH₂)_{0-p}C(=NOR')R'; wherein p is about 4,

each R' is independently at each occurrence hydrogen, (C₁-C₁₂)-alkyl, (C₂-C₁₂)-alkenyl, (C₂-C₁₂)-alkynyl, (C₃-C₁₀)-cycloalkyl, (C₃-C₁₀)-cycloalkenyl, [(C₃-C₁₀)cycloalkyl or (C₃-C₁₀)-cycloalkenyl]-[(C₁-C₁₂)-alkyl or (C₂-C₁₂)-alkenyl or (C₂-C₁₂)-alkynyl], (C₆-C₁₀)-aryl, (C₆-C₁₀)-aryl-[(C₁-C₁₂)-alkyl or (C₂-C₁₂)-alkenyl or (C₂-C₁₂)-alkynyl], mono- or bicyclic 3-10 membered heterocyclyl, mono- or bicyclic 3-10 membered heterocyclyl-[(C₁-C₁₂)-alkyl or (C₂-C₁₂)-alkenyl or (C₂-C₁₂)-alkynyl], mono- or bicyclic 5-10 membered heteroaryl, or mono- or bicyclic 5-10 membered heteroaryl-

[(C₁-C₁₂)-alkyl or (C₂-C₁₂)-alkenyl or (C₂-C₁₂)-alkynyl], wherein R' is substituted with 0-3 substituents selected independently from J;

or, when two R' are bound to a nitrogen atom or to two adjacent nitrogen atoms, the two R' groups together with the nitrogen atom or atoms to which they are bound can form a 3- to 8-membered monocyclic heterocyclic ring, or an 8- to 20-membered, bicyclic or tricyclic, heterocyclic ring system, wherein any ring or ring system can further contain 1-3 additional heteroatoms selected from the group consisting of N, NR', O, S, S(O) and S(O)₂, wherein each ring is substituted with 0-3 substituents selected independently from J;

wherein, in any bicyclic or tricyclic ring system, each ring is linearly fused, bridged, or spirocyclic, wherein each ring is either aromatic or nonaromatic, wherein each ring can be fused to a (C₆-C₁₀)aryl, mono- or bicyclic 5-10 membered heteroaryl, (C₃-C₁₀)cycloalkyl or mono- or bicyclic 3-10 membered heterocyclyl;

G¹ and G² are each independently a hydrogen or a glycosyl residue, or a group cleavable under physiological conditions to provide a compound of formula (I) wherein G¹ or G² respectively is hydrogen;

(X¹)_{X1} and (X²)_{X2} each signify that 0, 1, or 2 ring atoms of each respective ring can be nitrogen, provided that where a non-hydrogen substituent is bonded, X¹ or X², respectively, is C;

provided that when G¹ is a 6-deoxyhexopyranosyl residue, G² is H, R¹ is of formula (IIA), R² is hydrogen or hydroxy, R³ is hydrogen, R^{A1} and R^{A2} and R^{A4} are H, R^{A3} and R^{A5} are methyl, and B is CO₂H, or when G¹ and G² are H, R¹ is of formula (IIA), R² is hydrogen, R³ is hydrogen or nitro, R^{A1} and R^{A2} and R^{A4} are H, R^{A3} and R^{A5} are methyl, and B is CO₂H, then R⁵ is not unsubstituted (C₁₀-C₁₆)-alkyl;

or a salt thereof.

In various embodiments, the present invention relates to the use of arylomycins to treat a microbial or bacterial infection caused by a microbe (e.g., a bacterium) that encodes a type I signal peptidase bearing a specific amino acid sequence signature. In addition, in various embodiments, the present invention relates to the use of arylomycin to treat indications known to be caused predominantly by bacteria that encoded type I signal peptidases bearing a specific amino acid sequence signature.

In various embodiments, the invention is direct to the use of genetically modified organisms harboring mutations in the type I bacterial signal peptidase enzyme to screen for or to characterize the activity of type I signal peptidase inhibitors such as arylomycin

analogues of the invention. In various embodiments, the invention provides methods for the use of genetically altered recombinant forms of bacterial signal peptidase protein, in which specific residues have been mutated, to screen for or characterize the activity of type I signal peptidase inhibitors, such as arylomycin analogues of the invention.

5

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1 shows the structures of arylomycins A and B, natural products, as characterized in J. Schimana, et al., *J. Antibiotics* (2002), 55(6), 565-570). R¹ refers to a substituent on the tyrosine residue, and R² refers to an acyl group of the indicated number of carbon atoms bonded to the N-methylserine nitrogen atom.

FIG. 2 graphically correlates the doubling time and the minimum inhibitory concentrations (MICs) of arylomycin C16 observed for *E. coli* strains harboring the indicated amino acid at SPase residue 84. Horizontal bars indicate standard deviation of doubling times from three independent experiments. MIC values varied less than 2-fold between experiments. The His (MIC 4 µg/ml) and Phe or His (MIC 2 µg/ml) variants have a temperature sensitive phenotype and therefore not shown. For Pro29, the MIC exceeded the detection limit of 256 µg/ml.

FIG. 3 shows some of the physical and biochemical evidence for a mechanism of arylomycin resistance. FIG. 3A shows the structure of crystalline *E. coli* SPase in complex with arylomycin A2 (PDB ID 1T7D) (see, Paetzel et al., *J. Biol. Chem.* 279, 30781-30790 (2004)). Hydrogen-bonds observed in the crystal structure are shown in green, while the potential hydrogen bond prevented by Pro84 is shown in red. FIG. 3B-3C show the equilibrium binding affinities of arylomycin for Pro- and Ser- variants of *E. coli* (FIG. 3B) and *S. aureus* (FIG. 3C) SPases. Data points and bars represent average values and standard deviations within a single experiment. KD values shown are the average of three independent experiments. FIG. 3D shows the affinity of arylomycin C16 for the soluble N-terminally truncated *E. coli* SPase. The steady state binding affinities of arylomycin C16 for WT (open diamonds) and P84S (open square) variants of the soluble N-terminally truncated *E. coli* SPase are shown as a function of Arylomycin C concentration.

FIG. 4 shows a phylogenetic reconstruction of the evolution of Pro29 within Staphylococcaceae SPases. The left side shows the phylogeny of Staphylococcaceae based on 16S RNA sequences. For each species, color bars indicate the number of SPases and presence or absence of Pro at residue 29; the amino acid(s) at residue(s) 29

is/are parenthetically noted in single letter code following the species name. The right side shows the phylogenetic relationship of SPase sequences from the indicated species. For each gene, the amino acid at residue 29 is parenthetically noted in single letter code following the name of the species in which the gene is found. Red and Blue branches
 5 represent the evolution of two distinct SPase lineages present in the common ancestor of sequenced Staphylococcaceae. Branches with an alternative likelihood ratio test support of less than 50% are collapsed.

FIG. 5 is a list of organisms that lack a proline residue at positions -5 and/or -7 (N-terminal) to the active site serine of the SPase encoded in their genome.

10

DETAILED DESCRIPTION

Definitions

As used in the specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the context clearly dictates otherwise.

15 The term "about" as used herein, when referring to a numerical value or range, allows for a degree of variability in the value or range, for example, within 10%, or within 5% of a stated value or of a stated limit of a range.

All percent compositions are given as weight-percentages, unless otherwise stated.

20 All average molecular weights of polymers are weight-average molecular weights, unless otherwise specified.

As used herein, "individual" (as in the subject of the treatment) means both mammals and non-mammals. Mammals include, for example, humans; non-human primates, e.g. apes and monkeys; and non-primates, e.g. dogs, cats, cattle, horses, sheep,
 25 and goats. Non-mammals include, for example, fish and birds.

The term "disease" or "disorder" or "malcondition" are used interchangeably, and are used to refer to diseases or conditions wherein a bacterial SPase plays a role in the biochemical mechanisms involved in the disease or malcondition such that a therapeutically beneficial effect can be achieved by acting on the enzyme. "Acting on"
 30 SPase can include binding to SPase and/or inhibiting the bioactivity of an SPase.

The expression "effective amount", when used to describe therapy to an individual suffering from a disorder, refers to the amount of a compound of the invention that is effective to inhibit or otherwise act on SPase in the individual's tissues wherein

SPase involved in the disorder is active, wherein such inhibition or other action occurs to an extent sufficient to produce a beneficial therapeutic effect.

"Substantially" as the term is used herein means completely or almost completely; for example, a composition that is "substantially free" of a component either
5 has none of the component or contains such a trace amount that any relevant functional property of the composition is unaffected by the presence of the trace amount, or a compound is "substantially pure" if there are only negligible traces of impurities present.

"Treating" or "treatment" within the meaning herein refers to an alleviation of symptoms associated with a disorder or disease, or inhibition of further progression or
10 worsening of those symptoms, or prevention or prophylaxis of the disease or disorder, or curing the disease or disorder. Similarly, as used herein, an "effective amount" or a "therapeutically effective amount" of a compound of the invention refers to an amount of the compound that alleviates, in whole or in part, symptoms associated with the disorder or condition, or halts or slows further progression or worsening of those symptoms, or
15 prevents or provides prophylaxis for the disorder or condition. In particular, a "therapeutically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic result. A therapeutically effective amount is also one in which any toxic or detrimental effects of compounds of the invention are outweighed by the therapeutically beneficial effects.

20 By "chemically feasible" is meant a bonding arrangement or a compound where the generally understood rules of organic structure are not violated; for example a structure within a definition of a claim that would contain in certain situations a pentavalent carbon atom that would not exist in nature would be understood to not be within the claim. The structures disclosed herein, in all of their embodiments are
25 intended to include only "chemically feasible" structures, and any recited structures that are not chemically feasible, for example in a structure shown with variable atoms or groups, are not intended to be disclosed or claimed herein.

When a substituent is specified to be an atom or atoms of specified identity, "or a bond", a configuration is referred to when the substituent is "a bond" that the groups that
30 are immediately adjacent to the specified substituent are directly connected to each other in a chemically feasible bonding configuration.

All chiral, diastereomeric, racemic forms of a structure are intended, unless a particular stereochemistry or isomeric form is specifically indicated. Compounds used in the present invention can include enriched or resolved optical isomers at any or all

asymmetric atoms as are apparent from the depictions, at any degree of enrichment.

Both racemic and diastereomeric mixtures, as well as the individual optical isomers can be isolated or synthesized so as to be substantially free of their enantiomeric or diastereomeric partners, and these are all within the scope of the invention.

5 The inclusion of an isotopic form of one or more atoms in a molecule that is different from the naturally occurring isotopic distribution of the atom in nature is referred to as an "isotopically labeled form" of the molecule. All isotopic forms of atoms are included as options in the composition of any molecule, unless a specific isotopic form of an atom is indicated. For example, any hydrogen atom or set thereof in a
10 molecule can be any of the isotopic forms of hydrogen, i.e., protium (^1H), deuterium (^2H), or tritium (^3H) in any combination. Similarly, any carbon atom or set thereof in a molecule can be any of the isotopic form of carbons, such as ^{11}C , ^{12}C , ^{13}C , or ^{14}C , or any nitrogen atom or set thereof in a molecule can be any of the isotopic forms of nitrogen, such as ^{13}N , ^{14}N , or ^{15}N . A molecule can include any combination of isotopic forms in
15 the component atoms making up the molecule, the isotopic form of every atom forming the molecule being independently selected. In a multi-molecular sample of a compound, not every individual molecule necessarily has the same isotopic composition. For example, a sample of a compound can include molecules containing various different isotopic compositions, such as in a tritium or ^{14}C radiolabeled sample where only some
20 fraction of the set of molecules making up the macroscopic sample contains a radioactive atom. It is also understood that many elements that are not artificially isotopically enriched themselves are mixtures of naturally occurring isotopic forms, such as ^{14}N and ^{15}N , ^{32}S and ^{34}S , and so forth. A molecule as recited herein is defined as including isotopic forms of all its constituent elements at each position in the molecule. As is well
25 known in the art, isotopically labeled compounds can be prepared by the usual methods of chemical synthesis, except substituting an isotopically labeled precursor molecule. The isotopes, radiolabeled or stable, can be obtained by any method known in the art, such as generation by neutron absorption of a precursor nuclide in a nuclear reactor, by cyclotron reactions, or by isotopic separation such as by mass spectrometry. The
30 isotopic forms are incorporated into precursors as required for use in any particular synthetic route. For example, ^{14}C and ^3H can be prepared using neutrons generated in a nuclear reactor. Following nuclear transformation, ^{14}C and ^3H are incorporated into precursor molecules, followed by further elaboration as needed.

The term "amino protecting group" or "N-protected" as used herein refers to those groups intended to protect an amino group against undesirable reactions during synthetic procedures and which can later be removed to reveal the amine. Commonly used amino protecting groups are disclosed in Protective Groups in Organic Synthesis, Greene, T.W.; Wuts, P. G. M., John Wiley & Sons, New York, NY, (3rd Edition, 1999). Amino protecting groups include acyl groups such as formyl, acetyl, propionyl, pivaloyl, t-butylacetyl, 2-chloroacetyl, 2-bromoacetyl, trifluoroacetyl, trichloroacetyl, o-nitrophenoxyacetyl, α -chlorobutyryl, benzoyl, 4-chlorobenzoyl, 4-bromobenzoyl, 4-nitrobenzoyl, and the like; sulfonyl groups such as benzenesulfonyl, p-toluenesulfonyl and the like; alkoxy- or aryloxy-carbonyl groups (which form urethanes with the protected amine) such as benzyloxycarbonyl (Cbz), p-chlorobenzyloxycarbonyl, p-methoxybenzyloxycarbonyl, p-nitrobenzyloxycarbonyl, 2-nitrobenzyloxycarbonyl, p-bromobenzyloxycarbonyl, 3,4-dimethoxybenzyloxycarbonyl, 3,5-dimethoxybenzyloxycarbonyl, 2,4-dimethoxybenzyloxycarbonyl, 4-methoxybenzyloxycarbonyl, 2-nitro-4,5-dimethoxybenzyloxycarbonyl, 3,4,5-trimethoxybenzyloxycarbonyl, 1-(p-biphenyl)-1-methylethoxycarbonyl, α,α -dimethyl-3,5-dimethoxybenzyloxycarbonyl, benzhydryloxycarbonyl, t-butyloxycarbonyl (Boc), diisopropylmethoxycarbonyl, isopropylloxycarbonyl, ethoxycarbonyl, methoxycarbonyl, allyloxycarbonyl (Alloc), 2,2,2-trichloroethoxycarbonyl, 2-trimethylsilylethylloxycarbonyl (Teoc), phenoxycarbonyl, 4-nitrophenoxy carbonyl, fluorenyl-9-methoxycarbonyl (Fmoc), cyclopentylloxycarbonyl, adamantylloxycarbonyl, cyclohexylloxycarbonyl, phenylthiocarbonyl and the like; aralkyl groups such as benzyl, triphenylmethyl, benzyloxymethyl and the like; and silyl groups such as trimethylsilyl and the like. Amine protecting groups also include cyclic amino protecting groups such as phthaloyl and dithiosuccinimidyl, which incorporate the amino nitrogen into a heterocycle. Typically, amino protecting groups include formyl, acetyl, benzoyl, pivaloyl, t-butylacetyl, phenylsulfonyl, Alloc, Teoc, benzyl, Fmoc, Boc and Cbz. It is well within the skill of the ordinary artisan to select and use the appropriate amino protecting group for the synthetic task at hand.

The term "hydroxyl protecting group" or "O-protected" as used herein refers to those groups intended to protect an OH group against undesirable reactions during synthetic procedures and which can later be removed to reveal the amine. Commonly used hydroxyl protecting groups are disclosed in Protective Groups in Organic Synthesis, Greene, T.W.; Wuts, P. G. M., John Wiley & Sons, New York, NY, (3rd Edition, 1999).

Hydroxyl protecting groups include acyl groups such as formyl, acetyl, propionyl, pivaloyl, t-butylacetyl, 2-chloroacetyl, 2-bromoacetyl, trifluoroacetyl, trichloroacetyl, o-nitrophenoxyacetyl, α -chlorobutyryl, benzoyl, 4-chlorobenzoyl, 4-bromobenzoyl, 4-nitrobenzoyl, and the like; sulfonyl groups such as benzenesulfonyl, p-toluenesulfonyl and the like; acyloxy groups (which form urethanes with the protected amine) such as benzyloxycarbonyl (Cbz), p-chlorobenzyloxycarbonyl, p-methoxybenzyloxycarbonyl, p-nitrobenzyloxycarbonyl, 2-nitrobenzyloxycarbonyl, p-bromobenzyloxycarbonyl, 3,4-dimethoxybenzyloxycarbonyl, 3,5-dimethoxybenzyloxycarbonyl, 2,4-dimethoxybenzyloxycarbonyl, 4-methoxybenzyloxycarbonyl, 2-nitro-4,5-dimethoxybenzyloxycarbonyl, 3,4,5-trimethoxybenzyloxycarbonyl, 1-(p-biphenyl)-1-methylethoxycarbonyl, α,α -dimethyl-3,5-dimethoxybenzyloxycarbonyl, benzhydryloxycarbonyl, t-butyloxycarbonyl (Boc), diisopropylmethoxycarbonyl, isopropyloxycarbonyl, ethoxycarbonyl, methoxycarbonyl, allyloxycarbonyl (Alloc), 2,2,2-trichloroethoxycarbonyl, 2-trimethylsilylethoxycarbonyl (Teoc), phenoxycarbonyl, 4-nitrophenoxy carbonyl, fluorenyl-9-methoxycarbonyl (Fmoc), cyclopentyloxycarbonyl, adamantyloxycarbonyl, cyclohexyloxycarbonyl, phenylthiocarbonyl and the like; aralkyl groups such as benzyl, triphenylmethyl, benzyloxymethyl and the like; and silyl groups such as trimethylsilyl and the like. It is well within the skill of the ordinary artisan to select and use the appropriate hydroxyl protecting group for the synthetic task at hand.

In general, "substituted" refers to an organic group as defined herein in which one or more bonds to a hydrogen atom contained therein are replaced by one or more bonds to a non-hydrogen atom such as, but not limited to, a halogen (i.e., F, Cl, Br, and I); an oxygen atom in groups such as hydroxyl groups, alkoxy groups, aryloxy groups, aralkyloxy groups, oxo(carbonyl) groups, carboxyl groups including carboxylic acids, carboxylates, and carboxylate esters; a sulfur atom in groups such as thiol groups, alkyl and aryl sulfide groups, sulfoxide groups, sulfone groups, sulfonyl groups, and sulfonamide groups; a nitrogen atom in groups such as amines, hydroxylamines, nitriles, nitro groups, N-oxides, hydrazides, azides, and enamines; and other heteroatoms in various other groups. Non-limiting examples of substituents that can be bonded to a substituted carbon (or other) atom include F, Cl, Br, I, OR', OC(O)N(R')₂, CN, NO, NO₂, ONO₂, azido, CF₃, OCF₃, R', O (oxo), S (thiono), C(O), S(O), methylenedioxy, ethylenedioxy, N(R')₂, SR', SOR', SO₂R', SO₂N(R')₂, SO₃R', C(O)R', C(O)C(O)R', C(O)CH₂C(O)R', C(S)R', C(O)OR', OC(O)R', C(O)N(R')₂, OC(O)N(R')₂, C(S)N(R')₂,

(CH₂)₀₋₂N(R')C(O)R', (CH₂)₀₋₂N(R')N(R')₂, N(R')N(R')C(O)R', N(R')N(R')C(O)OR',
 N(R')N(R')CON(R')₂, N(R')SO₂R', N(R')SO₂N(R')₂, N(R')C(O)OR', N(R')C(O)R',
 N(R')C(S)R', N(R')C(O)N(R')₂, N(R')C(S)N(R')₂, N(COR')COR', N(OR')R',
 C(=NH)N(R')₂, C(O)N(OR')R', or C(=NOR')R' wherein R' can be hydrogen or a carbon-
 5 based moiety, and wherein the carbon-based moiety can itself be further substituted.

When a substituent is monovalent, such as, for example, F or Cl, it is bonded to the atom it is substituting by a single bond. When a substituent is more than monovalent, such as O, which is divalent, it can be bonded to the atom it is substituting by more than one bond, i.e., a divalent substituent is bonded by a double bond; for example, a C
 10 substituted with O forms a carbonyl group, C=O, which can also be written as "CO", "C(O)", or "C(=O)", wherein the C and the O are double bonded. When a carbon atom is substituted with a double-bonded oxygen (=O) group, the oxygen substituent is termed an "oxo" group. When a divalent substituent such as NR is double-bonded to a carbon atom, the resulting C(=NR) group is termed an "imino" group. When a divalent
 15 substituent such as S is double-bonded to a carbon atom, the results C(=S) group is termed a "thiocarbonyl" group.

Alternatively, a divalent substituent such as O, S, C(O), S(O), or S(O)₂ can be connected by two single bonds to two different carbon atoms. For example, O, a
 20 divalent substituent, can be bonded to each of two adjacent carbon atoms to provide an epoxide group, or the O can form a bridging ether group, termed an "oxy" group, between adjacent or non-adjacent carbon atoms, for example bridging the 1,4-carbons of a cyclohexyl group to form a [2.2.1]-oxabicyclo system. Further, any substituent can be bonded to a carbon or other atom by a linker, such as (CH₂)_n or (CR'₂)_n wherein n is 1, 2, 3, or more, and each R' is independently selected.

25 C(O) and S(O)₂ groups can be bound to one or two heteroatoms, such as nitrogen, rather than to a carbon atom. For example, when a C(O) group is bound to one carbon and one nitrogen atom, the resulting group is called an "amide" or "carboxamide." When a C(O) group is bound to two nitrogen atoms, the functional group is termed a urea. When a S(O)₂ group is bound to one carbon and one nitrogen atom, the resulting
 30 unit is termed a "sulfonamide." When a S(O)₂ group is bound to two nitrogen atoms, the resulting unit is termed a "sulfamate."

Substituted alkyl, alkenyl, alkynyl, cycloalkyl, and cycloalkenyl groups as well as other substituted groups also include groups in which one or more bonds to a hydrogen atom are replaced by one or more bonds, including double or triple bonds, to a carbon

atom, or to a heteroatom such as, but not limited to, oxygen in carbonyl (oxo), carboxyl, ester, amide, imide, urethane, and urea groups; and nitrogen in imines, hydroxyimines, oximes, hydrazones, amidines, guanidines, and nitriles.

Substituted ring groups such as substituted cycloalkyl, aryl, heterocyclyl and
5 heteroaryl groups also include rings and fused ring systems in which a bond to a hydrogen atom is replaced with a bond to a carbon atom. Therefore, substituted cycloalkyl, aryl, heterocyclyl and heteroaryl groups can also be substituted with alkyl, alkenyl, and alkynyl groups as defined herein.

By a "ring system" as the term is used herein is meant a moiety comprising one,
10 two, three or more rings, which can be substituted with non-ring groups or with other ring systems, or both, which can be fully saturated, partially unsaturated, fully unsaturated, or aromatic, and when the ring system includes more than a single ring, the rings can be fused, bridging, or spirocyclic. By "spirocyclic" is meant the class of structures wherein two rings are fused at a single tetrahedral carbon atom, as is well
15 known in the art.

As to any of the groups described herein, which contain one or more substituents, it is understood, of course, that such groups do not contain any substitution or substitution patterns which are sterically impractical and/or synthetically non-feasible. In addition, the compounds of this disclosed subject matter include all stereochemical
20 isomers arising from the substitution of these compounds.

Selected substituents within the compounds described herein are present to a recursive degree. In this context, "recursive substituent" means that a substituent may recite another instance of itself or of another substituent that itself recites the first substituent. Because of the recursive nature of such substituents, theoretically, a large
25 number may be present in any given claim. One of ordinary skill in the art of medicinal chemistry and organic chemistry understands that the total number of such substituents is reasonably limited by the desired properties of the compound intended. Such properties include, by of example and not limitation, physical properties such as molecular weight, solubility or log P, application properties such as activity against the intended target, and
30 practical properties such as ease of synthesis.

Recursive substituents are an intended aspect of the disclosed subject matter. One of ordinary skill in the art of medicinal and organic chemistry understands the versatility of such substituents. To the degree that recursive substituents are present in a

claim of the disclosed subject matter, the total number should be determined as set forth above.

Alkyl groups include straight chain and branched alkyl groups and cycloalkyl groups having from 1 to about 20 carbon atoms, and typically from 1 to 12 carbons or, in some embodiments, from 1 to 8 carbon atoms. Examples of straight chain alkyl groups include those with from 1 to 8 carbon atoms such as methyl, ethyl, n-propyl, n-butyl, n-pentyl, n-hexyl, n-heptyl, and n-octyl groups. Examples of branched alkyl groups include, but are not limited to, isopropyl, iso-butyl, sec-butyl, t-butyl, neopentyl, isopentyl, and 2,2-dimethylpropyl groups. As used herein, the term “alkyl” encompasses n-alkyl, isoalkyl, and anteisoalkyl groups as well as other branched chain forms of alkyl. Representative substituted alkyl groups can be substituted one or more times with any of the groups listed above, for example, amino, hydroxy, cyano, carboxy, nitro, thio, alkoxy, and halogen groups. A description herein that a group is alkyl chain “optionally comprising within the chain or at a chain terminus” a moiety, the term signifies that the moiety can be disposed between two subunits of the alkyl chain, or can be disposed at an unsubstituted end of the chain, or can be disposed between the chain and a point of attachment of the chain, for example to a carbonyl, NR, or O group. For example, an alkylbenzoyl group is an alkyl chain with a phenyl group disposed between the alkyl and a carbonyl, fitting the above description; an N-alkylphenylcarboxamido is an alkyl chain with a phenyl group disposed between the alkyl and the aminocarbonyl group, fitting within the above description.

Cycloalkyl groups are cyclic alkyl groups such as, but not limited to, cyclopropyl, cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl, and cyclooctyl groups. In some embodiments, the cycloalkyl group can have 3 to about 8-12 ring members, whereas in other embodiments the number of ring carbon atoms range from 3 to 4, 5, 6, or 7. Cycloalkyl groups further include polycyclic cycloalkyl groups such as, but not limited to, norbornyl, adamantyl, bornyl, camphenyl, isocamphenyl, and carenyl groups, and fused rings such as, but not limited to, decalanyl, and the like. Cycloalkyl groups also include rings that are substituted with straight or branched chain alkyl groups as defined above. Representative substituted cycloalkyl groups can be mono-substituted or substituted more than once, such as, but not limited to, 2,2-, 2,3-, 2,4- 2,5- or 2,6-disubstituted cyclohexyl groups or mono-, di- or tri-substituted norbornyl or cycloheptyl groups, which can be substituted with, for example, amino, hydroxy, cyano, carboxy,

nitro, thio, alkoxy, and halogen groups. The term "cycloalkenyl" alone or in combination denotes a cyclic alkenyl group.

The terms "carbocyclic," "carbocyclyl," and "carbocycle" denote a ring structure wherein the atoms of the ring are carbon, such as a cycloalkyl group or an aryl group. In
5 some embodiments, the carbocycle has 3 to 8 ring members, whereas in other embodiments the number of ring carbon atoms is 4, 5, 6, or 7. Unless specifically indicated to the contrary, the carbocyclic ring can be substituted with as many as N-1 substituents wherein N is the size of the carbocyclic ring with, for example, alkyl, alkenyl, alkynyl, amino, aryl, hydroxy, cyano, carboxy, heteroaryl, heterocyclyl, nitro,
10 thio, alkoxy, and halogen groups, or other groups as are listed above. A carbocyclyl ring can be a cycloalkyl ring, a cycloalkenyl ring, or an aryl ring. A carbocyclyl can be monocyclic or polycyclic, and if polycyclic each ring can be independently be a cycloalkyl ring, a cycloalkenyl ring, or an aryl ring.

(Cycloalkyl)alkyl groups, also denoted cycloalkylalkyl, are alkyl groups as
15 defined above in which a hydrogen or carbon bond of the alkyl group is replaced with a bond to a cycloalkyl group as defined above.

Alkenyl groups include straight and branched chain and cyclic alkyl groups as defined above, except that at least one double bond exists between two carbon atoms. Thus, alkenyl groups have from 2 to about 20 carbon atoms, and typically from 2 to 12
20 carbons or, in some embodiments, from 2 to 8 carbon atoms. Examples include, but are not limited to vinyl, $-\text{CH}=\text{CH}(\text{CH}_3)$, $-\text{CH}=\text{C}(\text{CH}_3)_2$, $-\text{C}(\text{CH}_3)=\text{CH}_2$, $-\text{C}(\text{CH}_3)=\text{CH}(\text{CH}_3)$, $-\text{C}(\text{CH}_2\text{CH}_3)=\text{CH}_2$, cyclohexenyl, cyclopentenyl, cyclohexadienyl, butadienyl, pentadienyl, and hexadienyl among others.

Cycloalkenyl groups include cycloalkyl groups having at least one double bond
25 between 2 carbons. Thus for example, cycloalkenyl groups include but are not limited to cyclohexenyl, cyclopentenyl, and cyclohexadienyl groups. Cycloalkenyl groups can have from 3 to about 8-12 ring members, whereas in other embodiments the number of ring carbon atoms range from 3 to 5, 6, or 7. Cycloalkyl groups further include polycyclic cycloalkyl groups such as, but not limited to, norbornyl, adamantyl, bornyl,
30 camphenyl, isocamphenyl, and carenyl groups, and fused rings such as, but not limited to, decalinyl, and the like, provided they include at least one double bond within a ring. Cycloalkenyl groups also include rings that are substituted with straight or branched chain alkyl groups as defined above.

(Cycloalkenyl)alkyl groups are alkyl groups as defined above in which a hydrogen or carbon bond of the alkyl group is replaced with a bond to a cycloalkenyl group as defined above.

Alkynyl groups include straight and branched chain alkyl groups, except that at least one triple bond exists between two carbon atoms. Thus, alkynyl groups have from 2 to about 20 carbon atoms, and typically from 2 to 12 carbons or, in some embodiments, from 2 to 8 carbon atoms. Examples include, but are not limited to $-\text{C}\equiv\text{CH}$, $-\text{C}\equiv\text{C}(\text{CH}_3)$, $-\text{C}\equiv\text{C}(\text{CH}_2\text{CH}_3)$, $-\text{CH}_2\text{C}\equiv\text{CH}$, $-\text{CH}_2\text{C}\equiv\text{C}(\text{CH}_3)$, and $-\text{CH}_2\text{C}\equiv\text{C}(\text{CH}_2\text{CH}_3)$ among others.

The term "heteroalkyl" by itself or in combination with another term means, unless otherwise stated, a stable straight or branched chain alkyl group consisting of the stated number of carbon atoms and one or two heteroatoms selected from the group consisting of O, N, and S, and wherein the nitrogen and sulfur atoms may be optionally oxidized and the nitrogen heteroatom may be optionally quaternized. The heteroatom(s) may be placed at any position of the heteroalkyl group, including between the rest of the heteroalkyl group and the fragment to which it is attached, as well as attached to the most distal carbon atom in the heteroalkyl group. Examples include: $-\text{O}-\text{CH}_2-\text{CH}_2-\text{CH}_3$, $-\text{CH}_2-\text{CH}_2\text{CH}_2-\text{OH}$, $-\text{CH}_2-\text{CH}_2-\text{NH}-\text{CH}_3$, $-\text{CH}_2-\text{S}-\text{CH}_2-\text{CH}_3$, $-\text{CH}_2\text{CH}_2-\text{S}(=\text{O})-\text{CH}_3$, and $-\text{CH}_2\text{CH}_2-\text{O}-\text{CH}_2\text{CH}_2-\text{O}-\text{CH}_3$. Up to two heteroatoms may be consecutive, such as, for example, $-\text{CH}_2-\text{NH}-\text{OCH}_3$, or $-\text{CH}_2-\text{CH}_2-\text{S}-\text{S}-\text{CH}_3$.

A "cycloheteroalkyl" ring is a cycloalkyl ring containing at least one heteroatom. A cycloheteroalkyl ring can also be termed a "heterocyclyl," described below.

The term "heteroalkenyl" by itself or in combination with another term means, unless otherwise stated, a stable straight or branched chain monounsaturated or di-unsaturated hydrocarbon group consisting of the stated number of carbon atoms and one or two heteroatoms selected from the group consisting of O, N, and S, and wherein the nitrogen and sulfur atoms may optionally be oxidized and the nitrogen heteroatom may optionally be quaternized. Up to two heteroatoms may be placed consecutively. Examples include $-\text{CH}=\text{CH}-\text{O}-\text{CH}_3$, $-\text{CH}=\text{CH}-\text{CH}_2-\text{OH}$, $-\text{CH}_2-\text{CH}=\text{N}-\text{OCH}_3$, $-\text{CH}=\text{CH}-\text{N}(\text{CH}_3)-\text{CH}_3$, $-\text{CH}_2-\text{CH}=\text{CH}-\text{CH}_2-\text{SH}$, and $-\text{CH}=\text{CH}-\text{O}-\text{CH}_2\text{CH}_2-\text{O}-\text{CH}_3$.

Aryl groups are cyclic aromatic hydrocarbons that do not contain heteroatoms in the ring. Thus aryl groups include, but are not limited to, phenyl, azulenyl, heptalenyl, biphenyl, indacenyl, fluorenyl, phenanthrenyl, triphenylenyl, pyrenyl, naphthacenyl, chrysenyl, biphenylenyl, anthracenyl, and naphthyl groups. In some embodiments, aryl groups contain about 6 to about 14 carbons in the ring portions of the groups. Aryl

groups can be unsubstituted or substituted, as defined above. Representative substituted aryl groups can be mono-substituted or substituted more than once, such as, but not limited to, 2-, 3-, 4-, 5-, or 6-substituted phenyl or 2-8 substituted naphthyl groups, which can be substituted with carbon or non-carbon groups such as those listed above.

5 Aralkyl groups are alkyl groups as defined above in which a hydrogen or carbon bond of an alkyl group is replaced with a bond to an aryl group as defined above. Representative aralkyl groups include benzyl and phenylethyl groups and fused (cycloalkylaryl)alkyl groups such as 4-ethyl-indanyl. Aralkenyl group are alkenyl groups as defined above in which a hydrogen or carbon bond of an alkyl group is
10 replaced with a bond to an aryl group as defined above.

Heterocyclyl groups or the term "heterocyclyl" includes aromatic and non-aromatic ring compounds containing 3 or more ring members, of which, one or more is a heteroatom such as, but not limited to, N, O, and S. Thus a heterocyclyl can be a cycloheteroalkyl, or a heteroaryl, or if polycyclic, any combination thereof. In some
15 embodiments, heterocyclyl groups include 3 to about 20 ring members, whereas other such groups have 3 to about 15 ring members. A heterocyclyl group designated as a C₂-heterocyclyl can be a 5-ring with two carbon atoms and three heteroatoms, a 6-ring with two carbon atoms and four heteroatoms and so forth. Likewise a C₄-heterocyclyl can be a 5-ring with one heteroatom, a 6-ring with two heteroatoms, and so forth. The number
20 of carbon atoms plus the number of heteroatoms sums up to equal the total number of ring atoms. A heterocyclyl ring can also include one or more double bonds. A heteroaryl ring is an embodiment of a heterocyclyl group. The phrase "heterocyclyl group" includes fused ring species including those comprising fused aromatic and non-aromatic groups. For example, a dioxolanyl ring and a benzdioxolanyl ring system
25 (methylenedioxyphenyl ring system) are both heterocyclyl groups within the meaning herein. The phrase also includes polycyclic ring systems containing a heteroatom such as, but not limited to, quinuclidyl. Heterocyclyl groups can be unsubstituted, or can be substituted as discussed above. Heterocyclyl groups include, but are not limited to, pyrrolidinyl, piperidinyl, piperazinyl, morpholinyl, pyrrolyl, pyrazolyl, triazolyl,
30 tetrazolyl, oxazolyl, isoxazolyl, thiazolyl, pyridinyl, thiophenyl, benzothiophenyl, benzofuranyl, dihydrobenzofuranyl, indolyl, dihydroindolyl, azaindolyl, indazolyl, benzimidazolyl, azabenzimidazolyl, benzoxazolyl, benzothiazolyl, benzothiadiazolyl, imidazopyridinyl, isoxazolopyridinyl, thianaphthalenyl, purinyl, xanthinyl, adeninyl, guaninyl, quinolinyl, isoquinolinyl, tetrahydroquinolinyl, quinoxalinyl, and quinazolinyl

groups. Representative substituted heterocyclyl groups can be mono-substituted or substituted more than once, such as, but not limited to, piperidinyl or quinolinyl groups, which are 2-, 3-, 4-, 5-, or 6-substituted, or disubstituted with groups such as those listed above.

5 Heteroaryl groups are aromatic ring compounds containing 5 or more ring members, of which, one or more is a heteroatom such as, but not limited to, N, O, and S; for instance, heteroaryl rings can have 5 to about 8-12 ring members. A heteroaryl group is a variety of a heterocyclyl group that possesses an aromatic electronic structure. A heteroaryl group designated as a C₂-heteroaryl can be a 5-ring with two carbon atoms
 10 and three heteroatoms, a 6-ring with two carbon atoms and four heteroatoms and so forth. Likewise a C₄-heteroaryl can be a 5-ring with one heteroatom, a 6-ring with two heteroatoms, and so forth. The number of carbon atoms plus the number of heteroatoms sums up to equal the total number of ring atoms. Heteroaryl groups include, but are not limited to, groups such as pyrrolyl, pyrazolyl, triazolyl, tetrazolyl, oxazolyl, isoxazolyl,
 15 thiazolyl, pyridinyl, thiophenyl, benzothiophenyl, benzofuranyl, indolyl, azaindolyl, indazolyl, benzimidazolyl, azabenzimidazolyl, benzoxazolyl, benzothiazolyl, benzothiadiazolyl, imidazopyridinyl, isoxazolopyridinyl, thianaphthalenyl, purinyl, xanthinyl, adeninyl, guaninyl, quinolinyl, isoquinolinyl, tetrahydroquinolinyl, quinoxalinyl, and quinazolinyl groups. Heteroaryl groups can be unsubstituted, or can be
 20 substituted with groups as is discussed above. Representative substituted heteroaryl groups can be substituted one or more times with groups such as those listed above.

Additional examples of aryl and heteroaryl groups include but are not limited to phenyl, biphenyl, indenyl, naphthyl (1-naphthyl, 2-naphthyl), N-hydroxytetrazolyl, N-hydroxytriazolyl, N-hydroxyimidazolyl, anthracenyl (1-anthracenyl, 2-anthracenyl, 3-
 25 anthracenyl), thiophenyl (2-thienyl, 3-thienyl), furyl (2-furyl, 3-furyl), indolyl, oxadiazolyl, isoxazolyl, quinazolinyl, fluorenyl, xanthenyl, isoindanyl, benzhydryl, acridinyl, thiazolyl, pyrrolyl (2-pyrrolyl), pyrazolyl (3-pyrazolyl), imidazolyl (1-imidazolyl, 2-imidazolyl, 4-imidazolyl, 5-imidazolyl), triazolyl (1,2,3-triazol-1-yl, 1,2,3-triazol-2-yl, 1,2,3-triazol-4-yl, 1,2,4-triazol-3-yl), oxazolyl (2-oxazolyl, 4-oxazolyl, 5-
 30 oxazolyl), thiazolyl (2-thiazolyl, 4-thiazolyl, 5-thiazolyl), pyridyl (2-pyridyl, 3-pyridyl, 4-pyridyl), pyrimidinyl (2-pyrimidinyl, 4-pyrimidinyl, 5-pyrimidinyl, 6-pyrimidinyl), pyrazinyl, pyridazinyl (3-pyridazinyl, 4-pyridazinyl, 5-pyridazinyl), quinolyl (2-quinolyl, 3-quinolyl, 4-quinolyl, 5-quinolyl, 6-quinolyl, 7-quinolyl, 8-quinolyl), isoquinolyl (1-isoquinolyl, 3-isoquinolyl, 4-isoquinolyl, 5-isoquinolyl, 6-isoquinolyl, 7-

isoquinolyl, 8-isoquinolyl), benzo[b]furanyl (2-benzo[b]furanyl, 3-benzo[b]furanyl, 4-benzo[b]furanyl, 5-benzo[b]furanyl, 6-benzo[b]furanyl, 7-benzo[b]furanyl), 2,3-dihydro-benzo[b]furanyl (2-(2,3-dihydro-benzo[b]furanyl), 3-(2,3-dihydro-benzo[b]furanyl), 4-(2,3-dihydro-benzo[b]furanyl), 5-(2,3-dihydro-benzo[b]furanyl), 6-(2,3-dihydro-benzo[b]furanyl), 7-(2,3-dihydro-benzo[b]furanyl), benzo[b]thiophenyl (2-benzo[b]thiophenyl, 3-benzo[b]thiophenyl, 4-benzo[b]thiophenyl, 5-benzo[b]thiophenyl, 6-benzo[b]thiophenyl, 7-benzo[b]thiophenyl), 2,3-dihydro-benzo[b]thiophenyl, (2-(2,3-dihydro-benzo[b]thiophenyl), 3-(2,3-dihydro-benzo[b]thiophenyl), 4-(2,3-dihydro-benzo[b]thiophenyl), 5-(2,3-dihydro-benzo[b]thiophenyl), 6-(2,3-dihydro-benzo[b]thiophenyl), 7-(2,3-dihydro-benzo[b]thiophenyl), indolyl (1-indolyl, 2-indolyl, 3-indolyl, 4-indolyl, 5-indolyl, 6-indolyl, 7-indolyl), indazole (1-indazolyl, 3-indazolyl, 4-indazolyl, 5-indazolyl, 6-indazolyl, 7-indazolyl), benzimidazolyl (1-benzimidazolyl, 2-benzimidazolyl, 4-benzimidazolyl, 5-benzimidazolyl, 6-benzimidazolyl, 7-benzimidazolyl, 8-benzimidazolyl), benzoxazolyl (1-benzoxazolyl, 2-benzoxazolyl), benzothiazolyl (1-benzothiazolyl, 2-benzothiazolyl, 4-benzothiazolyl, 5-benzothiazolyl, 6-benzothiazolyl, 7-benzothiazolyl), carbazolyl (1-carbazolyl, 2-carbazolyl, 3-carbazolyl, 4-carbazolyl), 5H-dibenz[b,f]azepine (5H-dibenz[b,f]azepin-1-yl, 5H-dibenz[b,f]azepine-2-yl, 5H-dibenz[b,f]azepine-3-yl, 5H-dibenz[b,f]azepine-4-yl, 5H-dibenz[b,f]azepine-5-yl), 10,11-dihydro-5H-dibenz[b,f]azepine (10,11-dihydro-5H-dibenz[b,f]azepine-1-yl, 10,11-dihydro-5H-dibenz[b,f]azepine-2-yl, 10,11-dihydro-5H-dibenz[b,f]azepine-3-yl, 10,11-dihydro-5H-dibenz[b,f]azepine-4-yl, 10,11-dihydro-5H-dibenz[b,f]azepine-5-yl), and the like.

Heterocyclalkyl groups are alkyl groups as defined above in which a hydrogen or carbon bond of an alkyl group as defined above is replaced with a bond to a heterocycl group as defined above. Representative heterocycl alkyl groups include, but are not limited to, furan-2-yl methyl, furan-3-yl methyl, pyridine-3-yl methyl, tetrahydrofuran-2-yl ethyl, and indol-2-yl propyl.

Heteroarylalkyl groups are alkyl groups as defined above in which a hydrogen or carbon bond of an alkyl group is replaced with a bond to a heteroaryl group as defined above.

The term "alkoxy" refers to an oxygen atom connected to an alkyl group, including a cycloalkyl group, as are defined above. Examples of linear alkoxy groups include but are not limited to methoxy, ethoxy, propoxy, butoxy, pentyloxy, hexyloxy, and the like. Examples of branched alkoxy include but are not limited to isopropoxy,

sec-butoxy, tert-butoxy, isopentyloxy, isohexyloxy, and the like. Examples of cyclic alkoxy include but are not limited to cyclopropyloxy, cyclobutyloxy, cyclopentyloxy, cyclohexyloxy, and the like. An alkoxy group can include one to about 12-20 carbon atoms bonded to the oxygen atom, and can further include double or triple bonds, and
5 can also include heteroatoms. For example, an allyloxy group is an alkoxy group within the meaning herein. A methoxyethoxy group is also an alkoxy group within the meaning herein, as is a methylenedioxy group in a context where two adjacent atoms of a structures are substituted therewith.

The terms "halo" or "halogen" or "halide" by themselves or as part of another
10 substituent mean, unless otherwise stated, a fluorine, chlorine, bromine, or iodine atom, preferably, fluorine, chlorine, or bromine.

A "haloalkyl" group includes mono-halo alkyl groups, poly-halo alkyl groups wherein all halo atoms can be the same or different, and per-halo alkyl groups, wherein all hydrogen atoms are replaced by halogen atoms, such as fluoro. Examples of
15 haloalkyl include trifluoromethyl, 1,1-dichloroethyl, 1,2-dichloroethyl, 1,3-dibromo-3,3-difluoropropyl, perfluorobutyl, and the like.

A "haloalkoxy" group includes mono-halo alkoxy groups, poly-halo alkoxy groups wherein all halo atoms can be the same or different, and per-halo alkoxy groups, wherein all hydrogen atoms are replaced by halogen atoms, such as fluoro. Examples of
20 haloalkoxy include trifluoromethoxy, 1,1-dichloroethoxy, 1,2-dichloroethoxy, 1,3-dibromo-3,3-difluoropropoxy, perfluorobutoxy, and the like.

The term "(C_x-C_y)perfluoroalkyl," wherein $x < y$, means an alkyl group with a minimum of x carbon atoms and a maximum of y carbon atoms, wherein all hydrogen atoms are replaced by fluorine atoms. Preferred is -(C₁-C₆)perfluoroalkyl, more
25 preferred is -(C₁-C₃)perfluoroalkyl, most preferred is -CF₃.

The term "(C_x-C_y)perfluoroalkylene," wherein $x < y$, means an alkyl group with a minimum of x carbon atoms and a maximum of y carbon atoms, wherein all hydrogen atoms are replaced by fluorine atoms. Preferred is -(C₁-C₆)perfluoroalkylene, more
preferred is -(C₁-C₃)perfluoroalkylene, most preferred is -CF₂-.

30 The terms "aryloxy" and "arylalkoxy" refer to, respectively, an aryl group bonded to an oxygen atom and an aralkyl group bonded to the oxygen atom at the alkyl moiety. Examples include but are not limited to phenoxy, naphthyloxy, and benzyloxy.

An "acyl" group as the term is used herein refers to a group containing a carbonyl moiety wherein the group is bonded via the carbonyl carbon atom. The carbonyl carbon

atom is also bonded to another carbon atom, which can be part of an alkyl, aryl, aralkyl, cycloalkyl, cycloalkylalkyl, heterocyclyl, heterocyclalkyl, heteroaryl, heteroarylalkyl group or the like. In the special case wherein the carbonyl carbon atom is bonded to a hydrogen, the group is a "formyl" group, an acyl group as the term is defined herein. An
5 acyl group can include 0 to about 12-20 additional carbon atoms bonded to the carbonyl group. An acyl group can include double or triple bonds within the meaning herein. An acryloyl group is an example of an acyl group. An acyl group can also include heteroatoms within the meaning here. A nicotinoyl group (pyridyl-3-carbonyl) group is an example of an acyl group within the meaning herein. Other examples include acetyl,
10 benzoyl, phenylacetyl, pyridylacetyl, cinnamoyl, and acryloyl groups and the like. When the group containing the carbon atom that is bonded to the carbonyl carbon atom contains a halogen, the group is termed a "haloacyl" group. An example is a trifluoroacetyl group.

The term "amine" includes primary, secondary, and tertiary amines having, e.g.,
15 the formula $N(\text{group})_3$ wherein each group can independently be H or non-H, such as alkyl, aryl, and the like. Amines include but are not limited to $R-NH_2$, for example, alkylamines, arylamines, alkylarylamines; R_2NH wherein each R is independently selected, such as dialkylamines, diarylamines, aralkylamines, heterocyclamines and the like; and R_3N wherein each R is independently selected, such as trialkylamines,
20 dialkylarylamines, alkyl diarylamines, triarylamines, and the like. The term "amine" also includes ammonium ions as used herein.

An "amino" group is a substituent of the form $-NH_2$, $-NHR$, $-NR_2$, $-NR_3^+$, wherein each R is independently selected, and protonated forms of each, except for $-NR_3^+$, which cannot be protonated. Accordingly, any compound substituted with an
25 amino group can be viewed as an amine. An "amino group" within the meaning herein can be a primary, secondary, tertiary or quaternary amino group. An "alkylamino" group includes a monoalkylamino, dialkylamino, and trialkylamino group.

An "ammonium" ion includes the unsubstituted ammonium ion NH_4^+ , but unless otherwise specified, it also includes any protonated or quaternarized forms of amines.
30 Thus, trimethylammonium hydrochloride and tetramethylammonium chloride are both ammonium ions, and amines, within the meaning herein.

The term "amide" (or "amido") includes C- and N-amide groups, i.e., $-C(O)NR_2$, and $-NRC(O)R$ groups, respectively. Amide groups therefore include but are not limited to primary carboxamide groups ($-C(O)NH_2$) and formamide groups ($-NHC(O)H$). A

"carboxamido" group is a group of the formula $C(O)NR_2$, wherein R can be H, alkyl, aryl, etc.

The term "azido" refers to an N_3 group. An "azide" can be an organic azide or can be a salt of the azide (N_3^-) anion. The term "nitro" refers to an NO_2 group bonded to an organic moiety. The term "nitroso" refers to an NO group bonded to an organic moiety. The term nitrate refers to an ONO_2 group bonded to an organic moiety or to a salt of the nitrate (NO_3^-) anion.

The term "urethane" ("carbamoyl" or "carbamyl") includes N- and O-urethane groups, i.e., $-NRC(O)OR$ and $-OC(O)NR_2$ groups, respectively.

The term "sulfonamide" (or "sulfonamido") includes S- and N-sulfonamide groups, i.e., $-SO_2NR_2$ and $-NRSO_2R$ groups, respectively. Sulfonamide groups therefore include but are not limited to sulfamoyl groups ($-SO_2NH_2$). An organosulfur structure represented by the formula $-S(O)(NR)-$ is understood to refer to a sulfoximine, wherein both the oxygen and the nitrogen atoms are bonded to the sulfur atom, which is also bonded to two carbon atoms.

The term "amidine" or "amidino" includes groups of the formula $-C(NR)NR_2$. Typically, an amidino group is $-C(NH)NH_2$.

The term "guanidine" or "guanidino" includes groups of the formula $-NRC(NR)NR_2$. Typically, a guanidino group is $-NHC(NH)NH_2$.

A "salt" as is well known in the art includes an organic compound such as a carboxylic acid, a sulfonic acid, or an amine, in ionic form, in combination with a counterion. For example, acids in their anionic form can form salts with cations such as metal cations, for example sodium, potassium, and the like; with ammonium salts such as NH_4^+ or the cations of various amines, including tetraalkyl ammonium salts such as tetramethylammonium, or other cations such as trimethylsulfonium, and the like. A "pharmaceutically acceptable" or "pharmacologically acceptable" salt is a salt formed from an ion that has been approved for human consumption and is generally non-toxic, such as a chloride salt or a sodium salt. A "zwitterion" is an internal salt such as can be formed in a molecule that has at least two ionizable groups, one forming an anion and the other a cation, which serve to balance each other. For example, amino acids such as glycine can exist in a zwitterionic form. A "zwitterion" is a salt within the meaning herein. The compounds of the present invention may take the form of salts. The term "salts" embraces addition salts of free acids or free bases which are compounds of the invention. Salts can be "pharmaceutically-acceptable salts." The term

“pharmaceutically-acceptable salt” refers to salts which possess toxicity profiles within a range that affords utility in pharmaceutical applications. Pharmaceutically unacceptable salts may nonetheless possess properties such as high crystallinity, which have utility in the practice of the present invention, such as for example utility in process of synthesis, purification or formulation of compounds of the invention.

Suitable pharmaceutically-acceptable acid addition salts may be prepared from an inorganic acid or from an organic acid. Examples of inorganic acids include hydrochloric, hydrobromic, hydriodic, nitric, carbonic, sulfuric, and phosphoric acids. Appropriate organic acids may be selected from aliphatic, cycloaliphatic, aromatic, araliphatic, heterocyclic, carboxylic and sulfonic classes of organic acids, examples of which include formic, acetic, propionic, succinic, glycolic, gluconic, lactic, malic, tartaric, citric, ascorbic, glucuronic, maleic, fumaric, pyruvic, aspartic, glutamic, benzoic, anthranilic, 4-hydroxybenzoic, phenylacetic, mandelic, embonic (pamoic), methanesulfonic, ethanesulfonic, benzenesulfonic, pantothenic, trifluoromethanesulfonic, 2-hydroxyethanesulfonic, p-toluenesulfonic, sulfanilic, cyclohexylaminosulfonic, stearic, alginic, β -hydroxybutyric, salicylic, galactaric and galacturonic acid. Examples of pharmaceutically unacceptable acid addition salts include, for example, perchlorates and tetrafluoroborates.

Suitable pharmaceutically acceptable base addition salts of compounds of the invention include, for example, metallic salts including alkali metal, alkaline earth metal and transition metal salts such as, for example, calcium, magnesium, potassium, sodium and zinc salts. Pharmaceutically acceptable base addition salts also include organic salts made from basic amines such as, for example, *N,N'*-dibenzylethylenediamine, chlorprocaine, choline, diethanolamine, ethylenediamine, meglumine (N-methylglucamine) and procaine. Examples of pharmaceutically unacceptable base addition salts include lithium salts and cyanate salts. Although pharmaceutically unacceptable salts are not generally useful as medicaments, such salts may be useful, for example as intermediates in the synthesis of Formula (I) compounds, for example in their purification by recrystallization. All of these salts may be prepared by conventional means from the corresponding compound according to Formula (I) by reacting, for example, the appropriate acid or base with the compound according to Formula (I). The term "pharmaceutically acceptable salts" refers to nontoxic inorganic or organic acid and/or base addition salts, see, for example, Lit et al., Salt Selection for Basic Drugs (1986), *Int J. Pharm.*, **33**, 201-217, incorporated by reference herein.

A "hydrate" is a compound that exists in a composition with water molecules. The composition can include water in stoichiometric quantities, such as a monohydrate or a dihydrate, or can include water in random amounts. As the term is used herein a "hydrate" refers to a solid form, i.e., a compound in water solution, while it may be hydrated, is not a hydrate as the term is used herein.

A "solvate" is a similar composition except that a solvent other than water replaces the water. For example, methanol or ethanol can form an "alcoholate", which can again be stoichiometric or non-stoichiometric. As the term is used herein a "solvate" refers to a solid form, i.e., a compound in solution in a solvent, while it may be solvated, is not a solvate as the term is used herein.

A "prodrug" as is well known in the art is a substance that can be administered to a patient where the substance is converted in vivo by the action of biochemicals within the patient's body, such as enzymes, to the active pharmaceutical ingredient. Examples of prodrugs include esters of carboxylic acid groups, which can be hydrolyzed by endogenous esterases as are found in the bloodstream of humans and other mammals. Conventional procedures for the selection and preparation of suitable prodrug derivatives are described, for example, in "Design of Prodrugs", ed. H. Bundgaard, Elsevier, 1985.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described. Moreover, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any combination of individual members or subgroups of members of Markush groups. Thus, for example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, and Y is described as selected from the group consisting of methyl, ethyl, and propyl, claims for X being bromine and Y being methyl are fully described.

If a value of a variable that is necessarily an integer, e.g., the number of carbon atoms in an alkyl group or the number of substituents on a ring, is described as a range, e.g., 0-4, what is meant is that the value can be any integer between 0 and 4 inclusive, i.e., 0, 1, 2, 3, or 4.

In various embodiments, the compound or set of compounds, such as are used in the inventive methods, can be any one of any of the combinations and/or sub-combinations of the above-listed embodiments.

In various embodiments, a compound as shown in any of the Examples, or among
5 the exemplary compounds, is provided. Provisos may apply to any of the disclosed categories or embodiments wherein any one or more of the other above disclosed embodiments or species may be excluded from such categories or embodiments.

The present invention further embraces isolated compounds according to formula (I). The expression "isolated compound" refers to a preparation of a compound of
10 formula (I), or a mixture of compounds according to formula (I), wherein the isolated compound has been separated from the reagents used, and/or byproducts formed, in the synthesis of the compound or compounds. "Isolated" does not mean that the preparation is technically pure (homogeneous), but it is sufficiently pure to compound in a form in which it can be used therapeutically. Preferably an "isolated compound" refers to a
15 preparation of a compound of formula (I) or a mixture of compounds according to formula (I), which contains the named compound or mixture of compounds according to formula (I) in an amount of at least 10 percent by weight of the total weight. Preferably the preparation contains the named compound or mixture of compounds in an amount of at least 50 percent by weight of the total weight; more preferably at least 80 percent by
20 weight of the total weight; and most preferably at least 90 percent, at least 95 percent or at least 98 percent by weight of the total weight of the preparation.

The compounds of the invention and intermediates may be isolated from their reaction mixtures and purified by standard techniques such as filtration, liquid-liquid extraction, solid phase extraction, distillation, recrystallization or chromatography,
25 including flash column chromatography, or HPLC.

Isomerism and Tautomerism in Compounds of the Invention

Tautomerism

Within the present invention it is to be understood that a compound of the formula (I) or a salt thereof may exhibit the phenomenon of tautomerism whereby two
30 chemical compounds that are capable of facile interconversion by exchanging a hydrogen atom between two atoms, to either of which it forms a covalent bond. Since the tautomeric compounds exist in mobile equilibrium with each other they may be regarded as different isomeric forms of the same compound. It is to be understood that the formulae drawings within this specification can represent only one of the possible

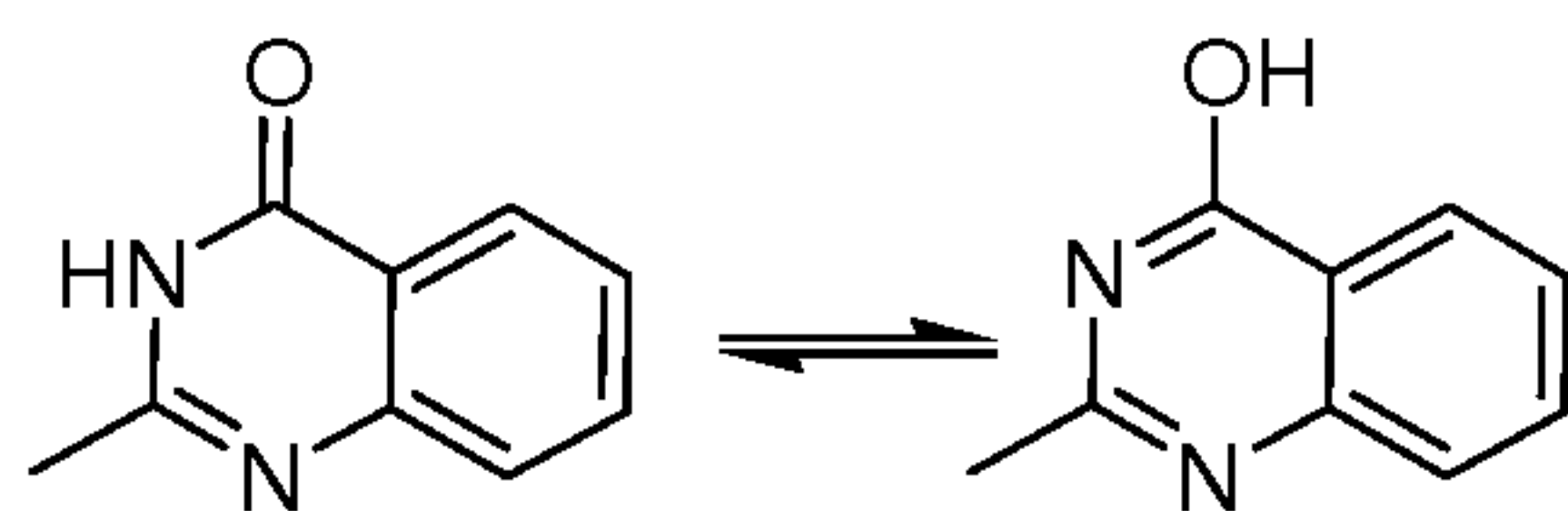
tautomeric forms. However, it is also to be understood that the invention encompasses any tautomeric form, and is not to be limited merely to any one tautomeric form utilized within the formulae drawings. The formulae drawings within this specification can represent only one of the possible tautomeric forms and it is to be understood that the specification encompasses all possible tautomeric forms of the compounds drawn not just those forms which it has been convenient to show graphically herein. For example, tautomerism may be exhibited by a pyrazolyl group bonded as indicated by the wavy line. While both substituents would be termed a 4-pyrazolyl group, it is evident that a different nitrogen atom bears the hydrogen atom in each structure.

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Such tautomerism can also occur with substituted pyrazoles such as 3-methyl, 5-methyl, or 3,5-dimethylpyrazoles, and the like. Another example of tautomerism is amido-imido (lactam-lactim when cyclic) tautomerism, such as is seen in heterocyclic compounds bearing a ring oxygen atom adjacent to a ring nitrogen atom. For example, the equilibrium:

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is an example of tautomerism. Accordingly, a structure depicted herein as one tautomer is intended to also include the other tautomer.

Optical Isomerism

It will be understood that when compounds of the present invention contain one or more chiral centers, the compounds may exist in, and may be isolated as pure enantiomeric or diastereomeric forms or as racemic mixtures. The present invention therefore includes any possible enantiomers, diastereomers, racemates or mixtures thereof of the compounds of the invention.

The isomers resulting from the presence of a chiral center comprise a pair of non-superimposable isomers that are called “enantiomers.” Single enantiomers of a pure compound are optically active, *i.e.*, they are capable of rotating the plane of plane polarized light. Single enantiomers are designated according to the *Cahn-Ingold-Prelog* system. The priority of substituents is ranked based on atomic weights, a higher atomic weight, as determined by the systematic procedure, having a higher priority ranking. Once the priority ranking of the four groups is determined, the molecule is oriented so

that the lowest ranking group is pointed away from the viewer. Then, if the descending rank order of the other groups proceeds clockwise, the molecule is designated (*R*) and if the descending rank of the other groups proceeds counterclockwise, the molecule is designated (*S*). In the example in Scheme 14, the *Cahn-Ingold-Prelog* ranking is $A > B > C > D$. The lowest ranking atom, D is oriented away from the viewer.



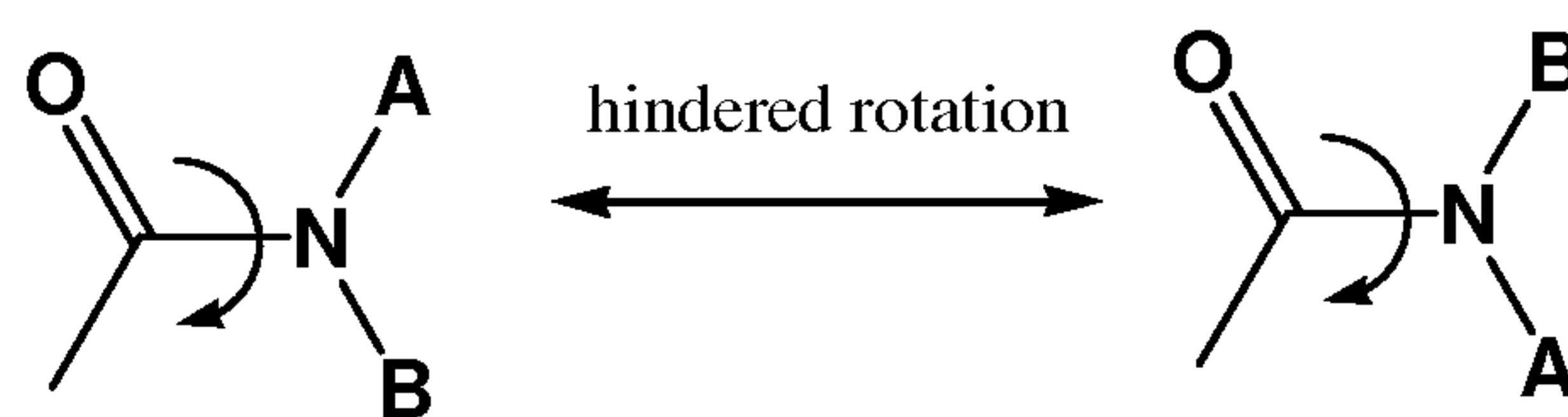
The present invention is meant to encompass diastereomers as well as their racemic and resolved, diastereomerically and enantiomerically pure forms and salts thereof. Diastereomeric pairs may be resolved by known separation techniques including normal and reverse phase chromatography, and crystallization.

“Isolated optical isomer” means a compound which has been substantially purified from the corresponding optical isomer(s) of the same formula. Preferably, the isolated isomer is at least about 80%, more preferably at least 90% pure, even more preferably at least 98% pure, most preferably at least about 99% pure, by weight.

Isolated optical isomers may be purified from racemic mixtures by well-known chiral separation techniques. According to one such method, a racemic mixture of a compound of the invention, or a chiral intermediate thereof, is separated into 99% wt.% pure optical isomers by HPLC using a suitable chiral column, such as a member of the series of DAICEL[®] CHIRALPAK[®] family of columns (Daicel Chemical Industries, Ltd., Tokyo, Japan). The column is operated according to the manufacturer’s instructions.

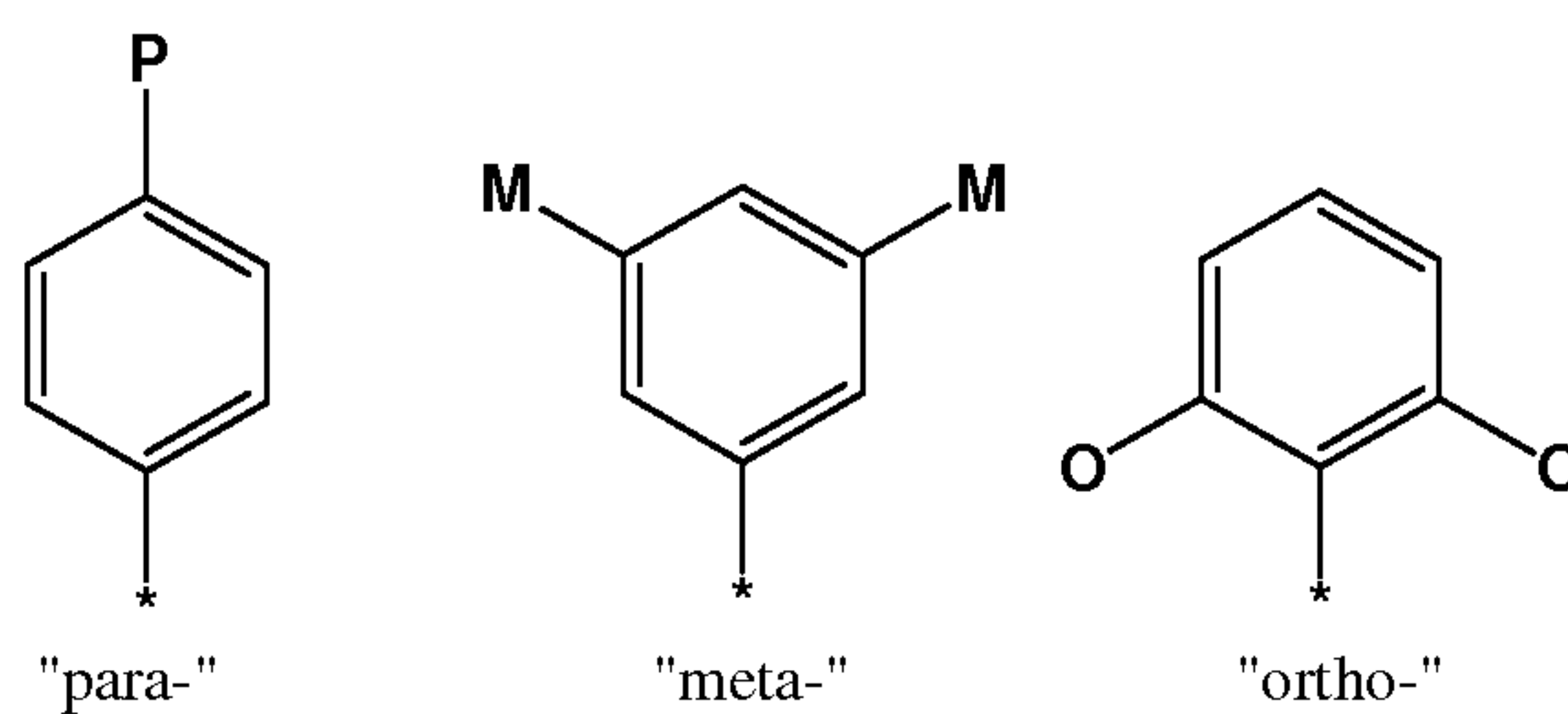
Rotational Isomerism

It is understood that due to chemical properties (*i.e.*, resonance lending some double bond character to the C-N bond) of restricted rotation about the amide bond linkage (as illustrated below) it is possible to observe separate rotamer species and even, under some circumstances, to isolate such species (see below). It is further understood that certain structural elements, including steric bulk or substituents on the amide nitrogen, may enhance the stability of a rotamer to the extent that a compound may be isolated as, and exist indefinitely, as a single stable rotamer. The present invention therefore includes any possible stable rotamers of formula (I) which are biologically active in the treatment of cancer or other proliferative disease states.



Regioisomerism

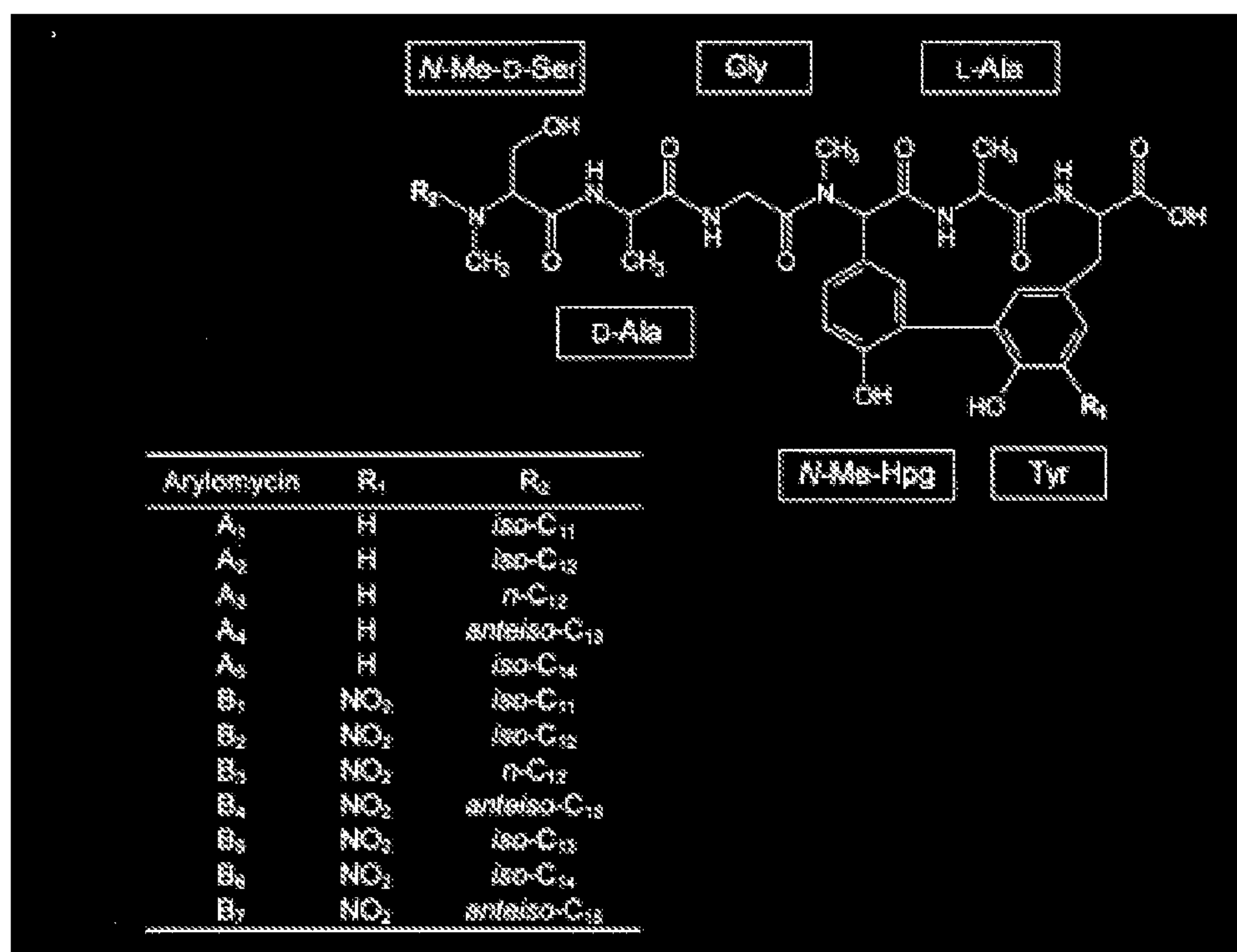
The preferred compounds of the present invention have a particular spatial arrangement of substituents on the aromatic rings, which is related to the structure activity relationship demonstrated by the compound class. Often such substitution arrangement is denoted by a numbering system; however, numbering systems are often not consistent between different ring systems. In six-membered aromatic systems, the spatial arrangements are specified by the common nomenclature “para” for 1,4-substitution, “meta” for 1,3-substitution and “ortho” for 1,2-substitution as shown below.



In various embodiments, the compound or set of compounds, such as are among the inventive compounds or are used in the inventive methods, can be any one of any of the combinations and/or sub-combinations of the above-listed embodiments.

Detailed Description

The present invention, in various embodiments is directed to analogs of arylomycins A and B. By arylomycins A and B are meant, respectively, the natural products of the following structures:



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The arylomycin A compounds bear a hydrogen atom in the R₁ position as defined in the above structure, and the arylomycin B compounds bear a nitro group in that position. The lipid tails, designated as group R₂ in the above structure, are n-alkyl, isoalkyl, and anteisoalkyl acyl groups with 11 to 15 total carbon atoms that form an amide bond with the N-Me-D-Ser residue. As used herein, the terms “arylomycins”, “arylomycin A”, “arylomycin B”, “arylomycin A_x”, “arylomycin natural products” and the like refer to these natural products, unless otherwise specified. The terms “arylomycin analogs”, “arylomycin derivatives”, “compounds of the invention”, and the like, refer to the compounds disclosed herein that do not fit within the herein-defined structural classes of arylomycin A or arylomycin B. Compounds of the invention are distinct from the natural products as specified above.

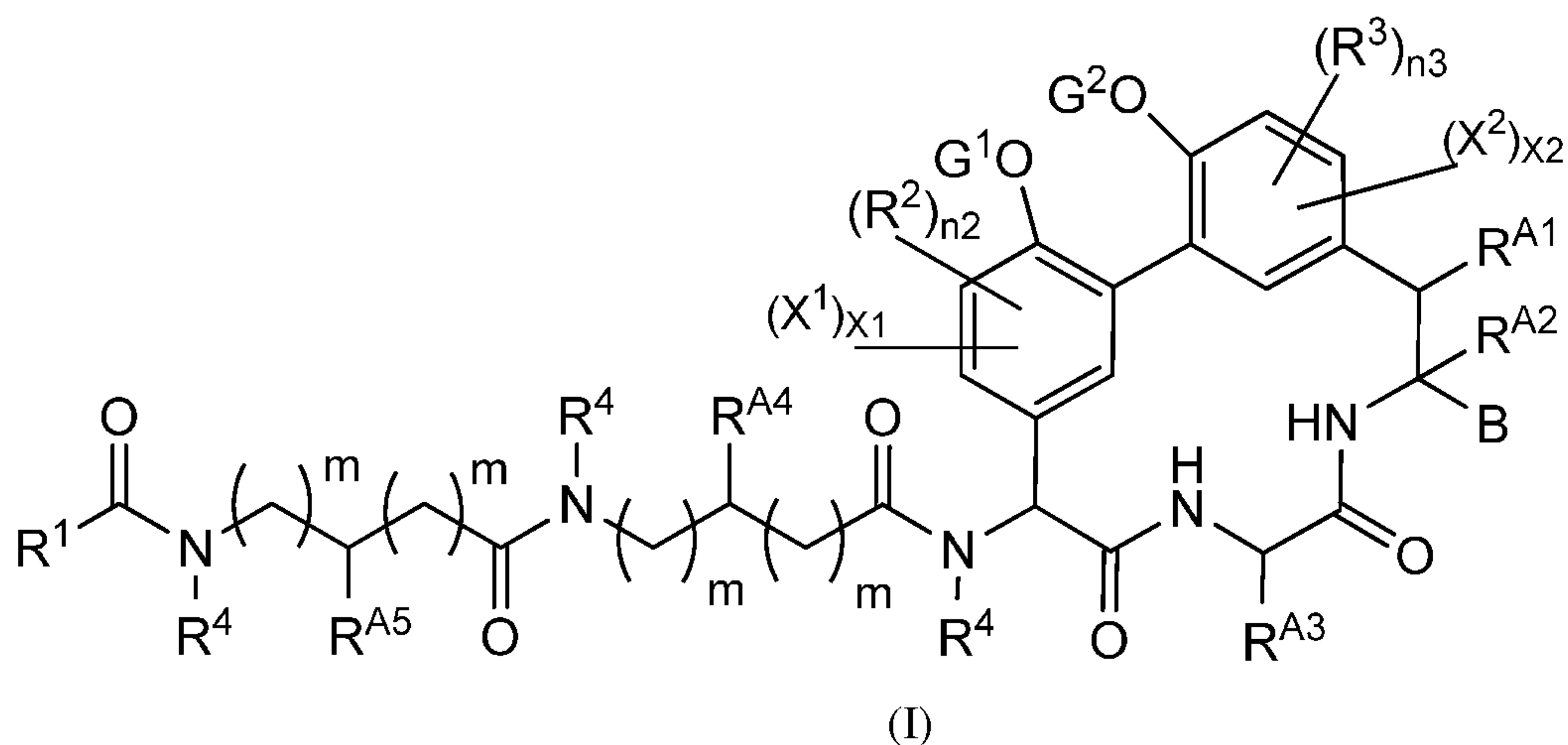
In various embodiments, the arylomycin analogs of the invention, i.e., the novel structures disclosed and claimed herein, exhibit a broader spectrum of antibiotic activity, i.e., against a wider variety of bacterial species, than do the natural products termed arylomycins A and B.

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The invention, in various embodiments, also provides methods of treatment of bacterial infections using the analogs of the invention, and using arylomycins A and B, such as against bacterial species or strains that would not be expected, based upon ordinary knowledge, to be susceptible to treatment with arylomycins A and B. In this context, the invention includes the use of the inventive arylomycin analogs and of the arylomycin A and B natural products in carrying out an inventive method as disclosed and claimed herein.

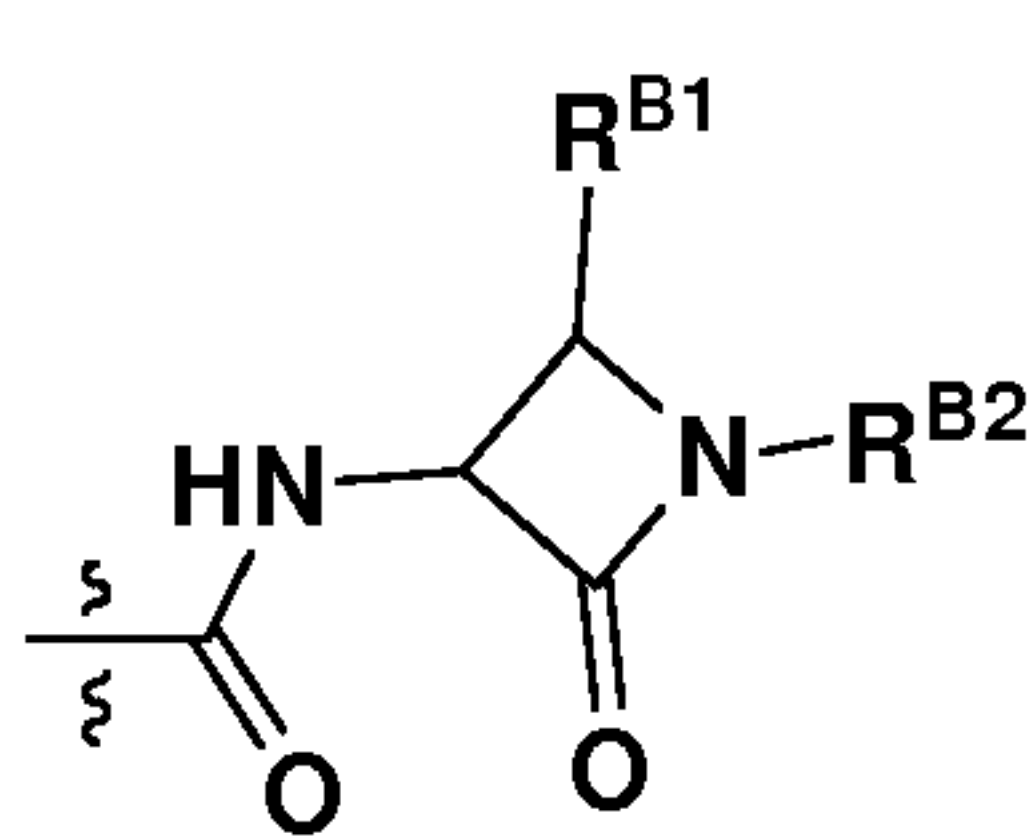
Compounds of the Invention

In various embodiments, the invention provides a compound of formula (I)

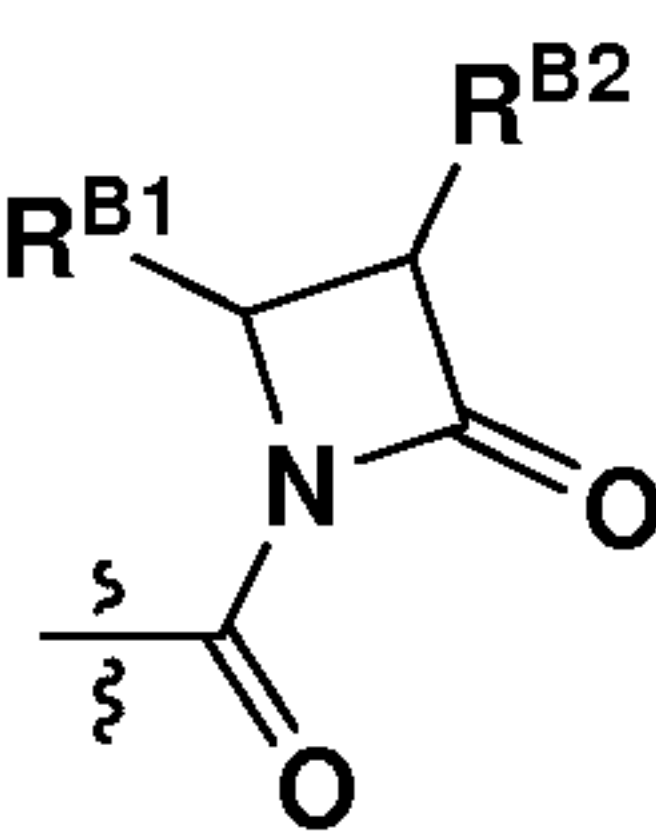


wherein

B is CO_2H , $\text{CH}_2\text{CO}_2\text{H}$, $\text{C}(=\text{O})\text{NHCH}_2\text{C}(=\text{O})\text{H}$, $\text{CH}_2\text{C}(=\text{O})\text{H}$, $\text{C}(=\text{O})\text{NHCH}_2\text{B}(\text{OR}^{\text{B}})_2$ or $\text{C}(=\text{O})\text{NHCH}_2\text{P}(=\text{O})(\text{OR}^{\text{B}})_2$ wherein R^{B} is H or $(\text{C}_1\text{-C}_6)\text{alkyl}$, or B is a group of formula



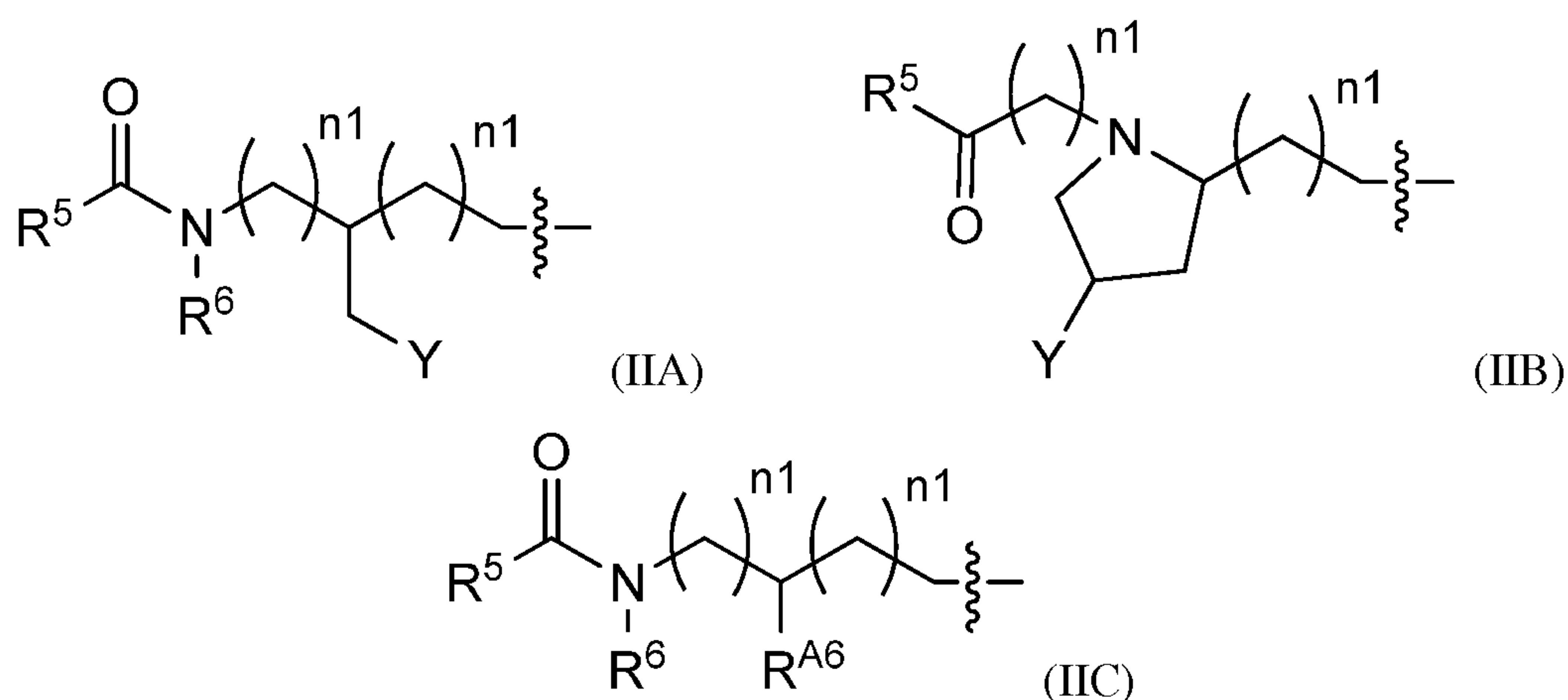
or



, wherein R^{B1} and R^{B2} are each

independently H, $(\text{C}_1\text{-C}_6)$ alkyl, $(\text{C}_3\text{-C}_6)$ cycloalkyl, OR^{C} , $\text{C}(=\text{O})\text{NR}^{\text{C}}_2$, $\text{O C}(=\text{O})\text{NR}^{\text{C}}_2$, $\text{C}(=\text{O})\text{OR}^{\text{C}}$, $\text{OC}(=\text{O})\text{OR}^{\text{C}}$, nitro, trifluoromethyl, trifluoromethoxy, $(\text{C}_1\text{-C}_6)\text{alkoxy}$, $(\text{C}_1\text{-C}_6)\text{thioalkoxy}$, NR^{C}_2 , 5-7 membered heterocyclyl or 5-7 membered heteroaryl, or $(\text{C}_6\text{-C}_{10})$ aryl; R^{C} is independently at each occurrence H or $(\text{C}_1\text{-C}_6)$ alkyl, and a wavy line indicates a point of attachment of B to a carbon of formula (I) bearing B;

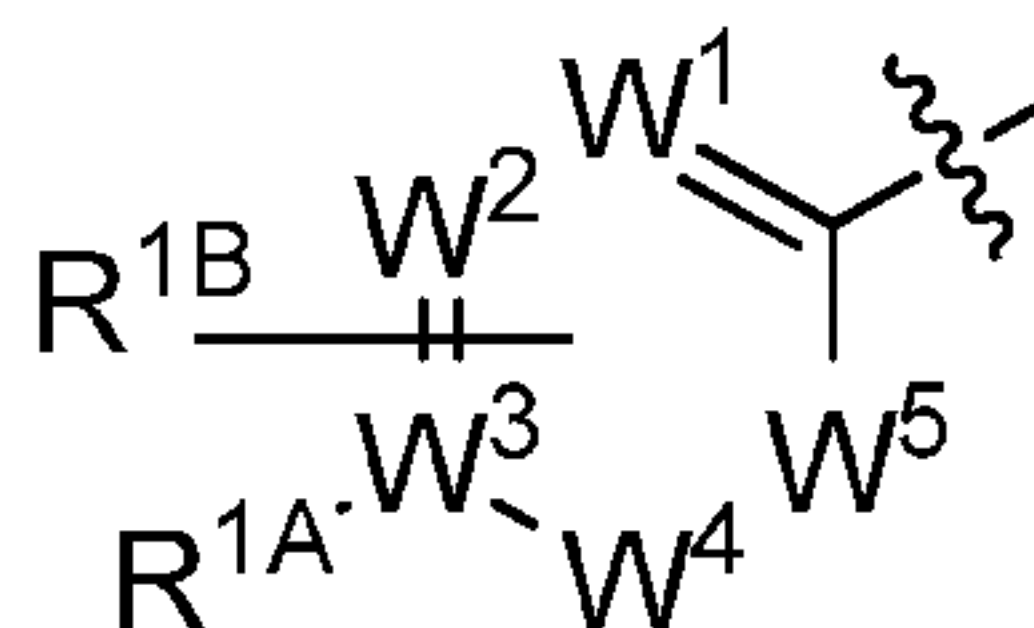
R^1 comprises a group of formula (IIA) or (IIB) or (IIC)



wherein each m is independently 0, 1, or 2, $n1$ is independently at each occurrence 0, 1, or 2; Y is $(\text{CH}_2)_{0-2}\text{H}$, $(\text{CH}_2)_{0-2}\text{OH}$, or $(\text{CH}_2)_{0-2}\text{OC}(=\text{O})(\text{C}_1\text{-C}_6)\text{alkyl}$; R^{A6} is hydrogen, $(\text{C}_1\text{-C}_6)\text{alkyl}$, $(\text{C}_3\text{-C}_7)\text{cycloalkyl}$, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or $(\text{C}_6\text{-C}_{10})$ aryl, wherein any alkyl, cycloalkyl, heterocyclyl, aryl or heteroaryl may be substituted with 1 to 3 substituents, wherein each substituent is independently selected from the group consisting of halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, cyano, trifluoromethyl, trifluoromethoxy, 5- to 7- membered heterocyclyl, $(\text{C}_1\text{-C}_6)\text{alkoxy}$, $(\text{C}_1\text{-C}_6)\text{alkyl}$, $(\text{C}_3\text{-C}_7)\text{cycloalkyl}$, $(\text{C}_1\text{-C}_6)$ -mono- or di-alkylamino, $(\text{C}_1\text{-C}_6)\text{alkoxycarbonyl}$, $(\text{C}_1\text{-C}_6)\text{alkylhydroxycarbonyl}$, $(\text{C}_1\text{-C}_6)\text{alkylaminocarbonyl}$, $(\text{C}_1\text{-C}_6)\text{alkylsulfonylamino}$, and $(\text{C}_6\text{-C}_{10})\text{-arylsulfonylamino}$; and a wavy line indicates a point of attachment of R^1 to an atom of formula (I) bearing R^1 ; and

R^5 is a linear or branched alkyl chain of about 1-22 carbon atoms, bonded to the carbonyl carbon to which it is attached directly or by an O or NR, to provide an amide, carbamate, or urea linkage respectively; optionally comprising within the chain or at a chain terminus, any of the following groups:

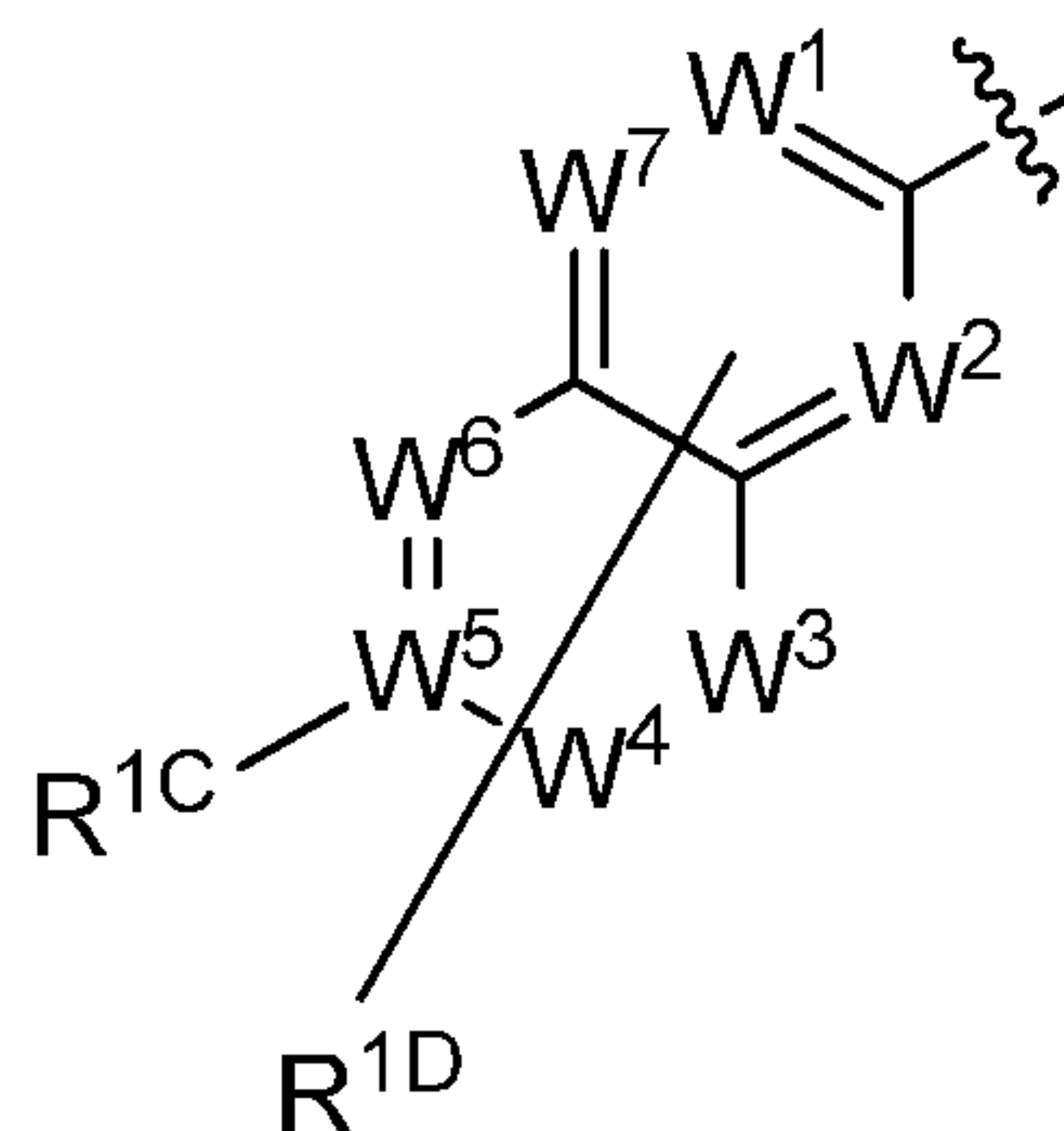
(A)



wherein W^1 , W^2 , W^3 , W^4 and W^5 are each independently C or N, provided that no more than two of W^1 , W^2 , W^3 , W^4 and W^5 are N; provided that when R^{1A} or R^{1B} is non-hydrogen, any W atom to which the R^{1A} or R^{1B} is respectively bonded is C, wherein there can be one or more R^{1B} bonded to the ring bearing the W atoms; R^{1A} is hydrogen,

halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, cyano, (C₁-C₆)-thioether, fluoroalkoxy, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1B} is hydrogen, alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1A} or R^{1B} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl groups; wherein a wavy line indicates a point of attachment;

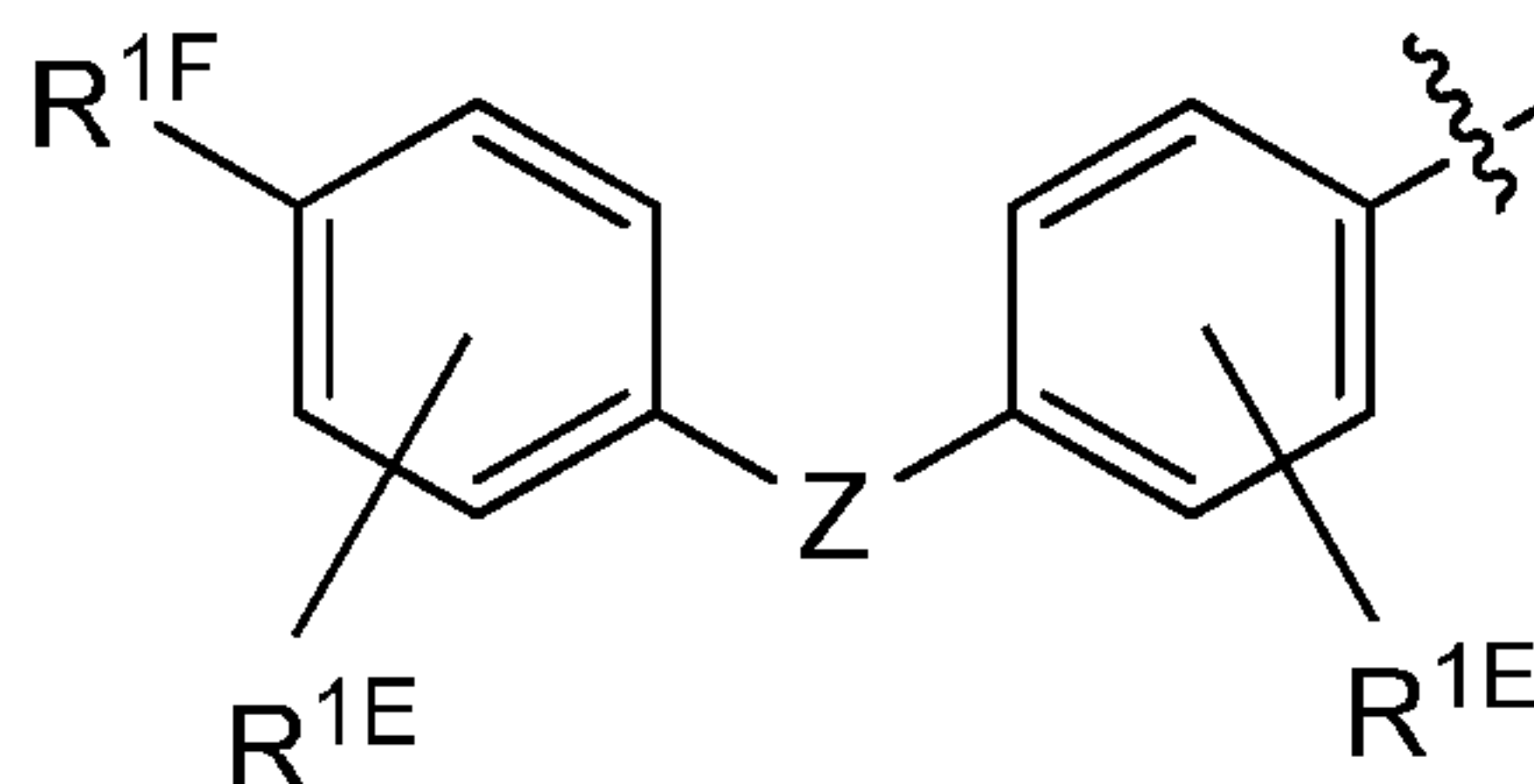
(B)



wherein W¹, W², W³, W⁴, W⁵, W⁶, and W⁷ are each independently C or N, provided that no more than three of W¹, W², W³, W⁴, W⁵, W⁶, and W⁷ are N; provided that when R^{1C} or R^{1D} is non-hydrogen, any W atom to which the R^{1C} or R^{1D} is respectively bonded is C, wherein either ring can bear one or more R^{1D}; R^{1C} is hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1D} is hydrogen, alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1C} or R^{1D} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl,

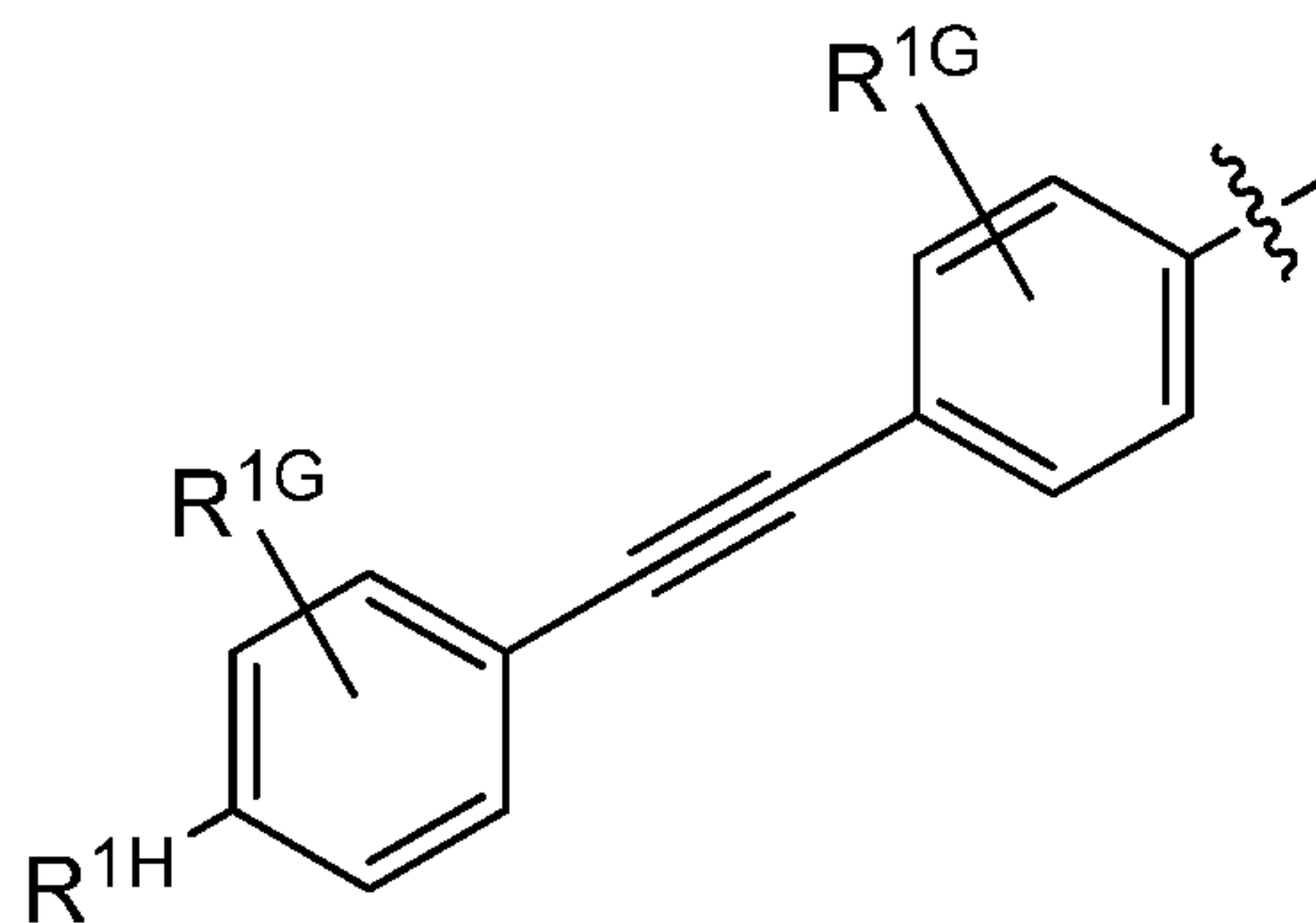
hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment;

5 (C)



wherein Z is O, S, NH or CH₂; R^{1E} at each occurrence is independently hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1F} is hydrogen or alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1E} or R^{1F} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment; or

(D)



wherein R^{1G} at each occurrence is independently hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)thioalkyl,

fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1H} is hydrogen or alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1G} or R^{1H} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment;

R² and R³ are each independently nitro, halo, cyano, hydroxy, glycosyloxy, amino, (C₁-C₄)-alkoxy, (C₁-C₄)-acyloxy, or (C₁-C₄)-alkyl, wherein any carbon atom can be unsubstituted or substituted with J, wherein n² and n³ are independently 0, 1, 2, or 3; or wherein two R² groups taken together, and/or two R³ groups taken together, can comprise fused cycloalkyl, aryl, heterocyclyl, or heteroaryl ring or rings, any of which is substituted with 0-3 J;

R⁴ and R⁶ are each independently at every occurrence hydrogen, (C₁-C₆)-alkyl, (C₃-C₇)-cycloalkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl, wherein any alkyl, cycloalkyl, heterocyclyl, aryl or heteroaryl can be substituted with 1 to 3 J;

R^{A1}, R^{A2}, R^{A3}, R^{A4}, R^{A5} are independently at each occurrence hydrogen, (C₁-C₆)-alkyl, (C₃-C₇)-cycloalkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl, wherein any alkyl, cycloalkyl, heterocyclyl, aryl or heteroaryl can be substituted with 1 to 3 J;

J is halogen, R', OR', CN, CF₃, OCF₃, O, S, C(O), S(O), methylenedioxy, ethylenedioxy, (CH₂)_{0-p}N(R')₂, (CH₂)_{0-p}SR', (CH₂)_{0-p}S(O)R', (CH₂)_{0-p}S(O)₂R', (CH₂)_{0-p}S(O)₂N(R')₂, (CH₂)_{0-p}SO₃R', (CH₂)_{0-p}C(O)R', (CH₂)_{0-p}C(O)CH₂C(O)R', (CH₂)_{0-p}C(S)R', (CH₂)_{0-p}C(O)OR', (CH₂)_{0-p}OC(O)R', (CH₂)_{0-p}C(O)N(R')₂, (CH₂)_{0-p}OC(O)N(R')₂, (CH₂)_{0-p}C(S)N(R')₂, (CH₂)_{0-p}NH-C(O)R', (CH₂)_{0-p}N(R')N(R')C(O)R', (CH₂)_{0-p}N(R')N(R')C(O)OR', (CH₂)_{0-p}N(R')N(R')CON(R')₂, (CH₂)_{0-p}N(R')SO₂R', (CH₂)_{0-p}N(R')SO₂N(R')₂, (CH₂)_{0-p}N(R')C(O)OR', (CH₂)_{0-p}N(R')C(O)R', (CH₂)_{0-p}N(R')C(S)R', (CH₂)_{0-p}N(R')C(O)N(R')₂, (CH₂)_{0-p}N(R')C(S)N(R')₂, (CH₂)_{0-p}N(COR')COR', (CH₂)₀₋

$p\text{N(OR')R'}$, $(\text{CH}_2)_{0-p}\text{C(=NH)N(R')}_2$, $(\text{CH}_2)_{0-p}\text{C(O)N(OR')R'}$, or $(\text{CH}_2)_{0-p}\text{C(=NOR')R'}$;

wherein p is about 4,

each R' is independently at each occurrence hydrogen, $(\text{C}_1\text{-C}_{12})$ -alkyl, $(\text{C}_2\text{-C}_{12})$ -alkenyl, $(\text{C}_2\text{-C}_{12})$ -alkynyl, $(\text{C}_3\text{-C}_{10})$ -cycloalkyl, $(\text{C}_3\text{-C}_{10})$ -cycloalkenyl, $[(\text{C}_3\text{-C}_{10})\text{cycloalkyl}$ or $(\text{C}_3\text{-C}_{10})\text{-cycloalkenyl}]$ - $[(\text{C}_1\text{-C}_{12})\text{-alkyl}$ or $(\text{C}_2\text{-C}_{12})\text{-alkenyl}$ or $(\text{C}_2\text{-C}_{12})\text{-alkynyl}]$, $(\text{C}_6\text{-C}_{10})$ -aryl, $(\text{C}_6\text{-C}_{10})\text{-aryl}$ - $[(\text{C}_1\text{-C}_{12})\text{-alkyl}$ or $(\text{C}_2\text{-C}_{12})\text{-alkenyl}$ or $(\text{C}_2\text{-C}_{12})\text{-alkynyl}]$, mono- or bicyclic 3-10 membered heterocyclyl, mono- or bicyclic 3-10 membered heterocyclyl- $[(\text{C}_1\text{-C}_{12})\text{-alkyl}$ or $(\text{C}_2\text{-C}_{12})\text{-alkenyl}$ or $(\text{C}_2\text{-C}_{12})\text{-alkynyl}]$, mono- or bicyclic 5-10 membered heteroaryl, or mono- or bicyclic 5-10 membered heteroaryl- $[(\text{C}_1\text{-C}_{12})\text{-alkyl}$ or $(\text{C}_2\text{-C}_{12})\text{-alkenyl}$ or $(\text{C}_2\text{-C}_{12})\text{-alkynyl}]$, wherein R' is substituted with 0-3 substituents selected independently from J;

or, when two R' are bound to a nitrogen atom or to two adjacent nitrogen atoms, the two R' groups together with the nitrogen atom or atoms to which they are bound can form a 3- to 8-membered monocyclic heterocyclic ring, or an 8- to 20-membered, bicyclic or tricyclic, heterocyclic ring system, wherein any ring or ring system can further contain 1-3 additional heteroatoms selected from the group consisting of N, NR' , O, S, S(O) and S(O)_2 , wherein each ring is substituted with 0-3 substituents selected independently from J;

wherein, in any bicyclic or tricyclic ring system, each ring is linearly fused, bridged, or spirocyclic, wherein each ring is either aromatic or nonaromatic, wherein each ring can be fused to a $(\text{C}_6\text{-C}_{10})$ aryl, mono- or bicyclic 5-10 membered heteroaryl, $(\text{C}_3\text{-C}_{10})$ cycloalkyl or mono- or bicyclic 3-10 membered heterocyclyl;

G^1 and G^2 are each independently a hydrogen or a glycosyl residue, or a group cleavable under physiological conditions to provide a compound of formula (I) wherein G^1 or G^2 respectively is hydrogen;

$(\text{X}^1)_{\text{X}1}$ and $(\text{X}^2)_{\text{X}2}$ each signify that 0, 1, or 2 ring atoms of each respective ring can be nitrogen, provided that where a non-hydrogen substituent is bonded, X^1 or X^2 , respectively, is C;

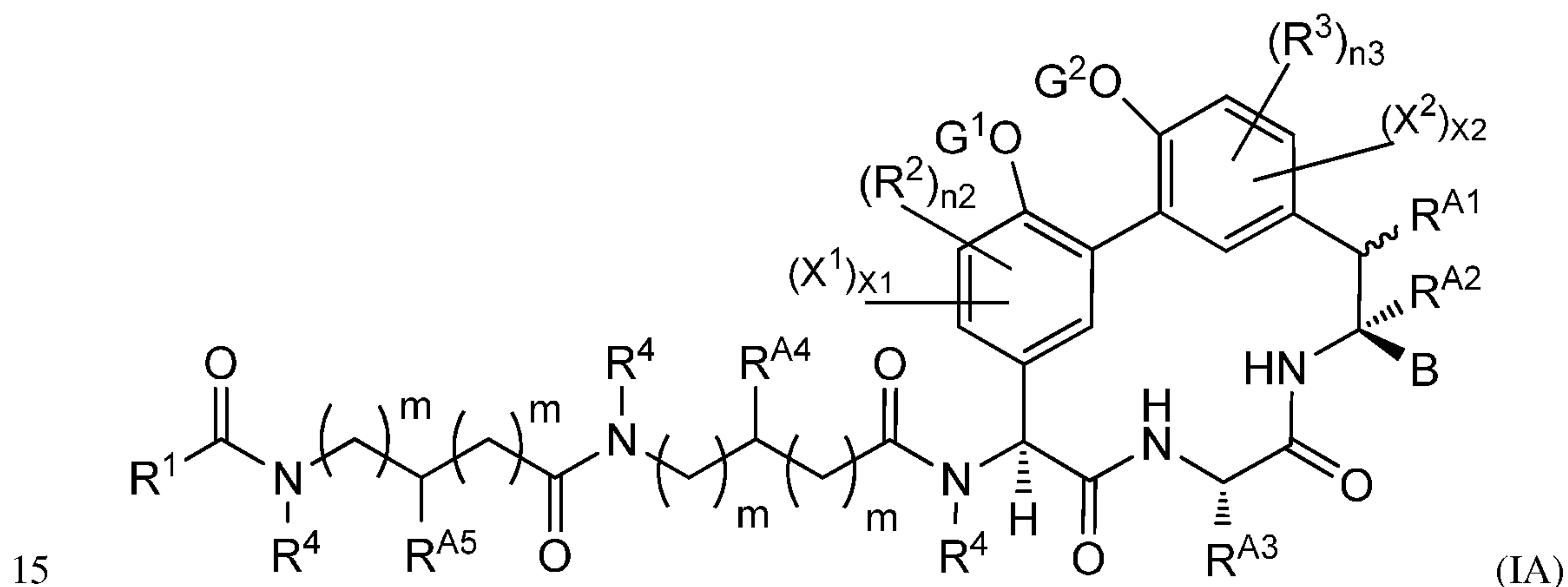
provided that when G^1 is a 6-deoxyhexopyranosyl residue, G^2 is H, R^1 is of formula (IIA), R^2 is hydrogen or hydroxy, R^3 is hydrogen, $\text{R}^{\text{A}1}$ and $\text{R}^{\text{A}2}$ and $\text{R}^{\text{A}4}$ are H, $\text{R}^{\text{A}3}$ and $\text{R}^{\text{A}5}$ are methyl, and B is CO_2H , or when G^1 and G^2 are H, R^1 is of formula (IIA), R^2 is hydrogen, R^3 is hydrogen or nitro, $\text{R}^{\text{A}1}$ and $\text{R}^{\text{A}2}$ and $\text{R}^{\text{A}4}$ are H, $\text{R}^{\text{A}3}$ and $\text{R}^{\text{A}5}$ are methyl, and B is CO_2H , then R^5 is not unsubstituted $(\text{C}_{10}\text{-C}_{16})$ -alkyl;

or a salt thereof.

In various embodiments, compounds of the invention can include atropisomeric forms due to hindered rotation about the phenyl-phenyl bond of the biphenyl (or bi-aryl or aryl-heteroaryl or bi-heteroaryl) moiety. In various embodiments, a compound of the invention can comprise the Sa atropisomer. Applicants have found that when the amide bond connecting the macrocycle to the tail is not methylated both atropisomers can be present and interconvert freely.

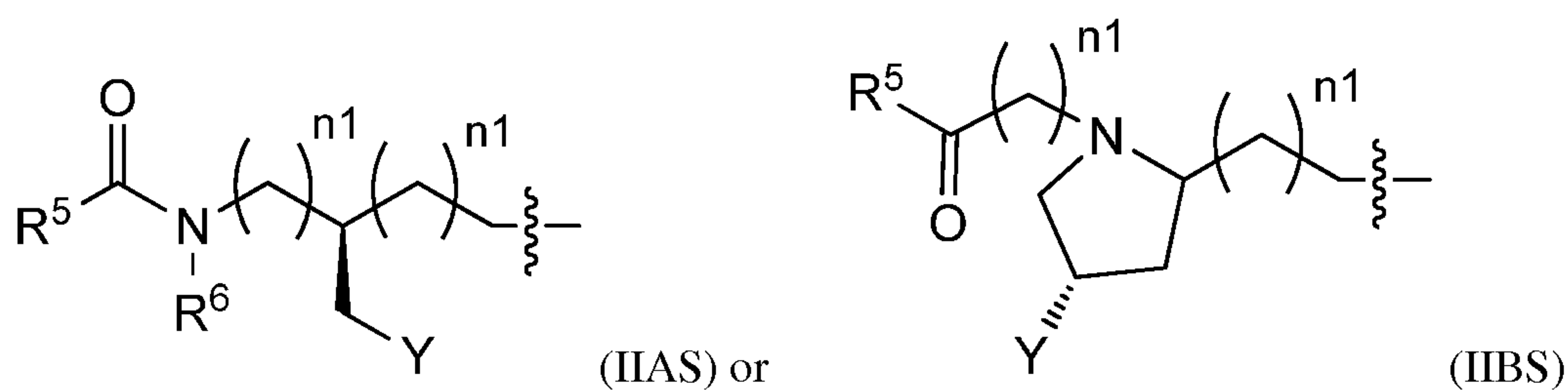
In various embodiments, the invention provides a compound of formula I of the invention wherein when G^1 is a H or a 6-deoxyhexopyranosyl residue, G^2 is H, R^1 is of formula (IIA), R^2 is hydrogen or hydroxy, R^3 is hydrogen or nitro, R^{A1} and R^{A2} and R^{A4} are H, R^{A3} and R^{A5} are methyl, and B is CO_2H , then R^5 is not unsubstituted (C_1 - C_{22})alkyl.

In various embodiments, the invention provides a compound of the invention wherein the compound is of formula (IA)



wherein R^1 , R^2 , R^3 , R^4 , R^5 , R^6 , R^{A1} , R^{A2} , R^{A3} , R^{A4} , R^{A5} , R^{A6} , R^B , R^{B1} , R^{B2} , and R^C , and m, n, n^1 , n^2 , n^3 , B, G^1 , G^2 , $(X^1)_{X1}$, $(X^2)_{X2}$, and Y, are as defined herein and a wavy line indicates a point of attachment of R^1 to an atom bonded to R^1 in formula (IA); or a salt thereof.

20 In various embodiments, the invention provides a compound of the invention wherein R^1 is a group of formula (IIAS) or (IIBS)



wherein n^1 , R^5 , R^6 , and Y, are as defined herein and a wavy line indicates a point of attachment of R^1 to an atom bonded to R^1 in formula (I);

or a salt thereof.

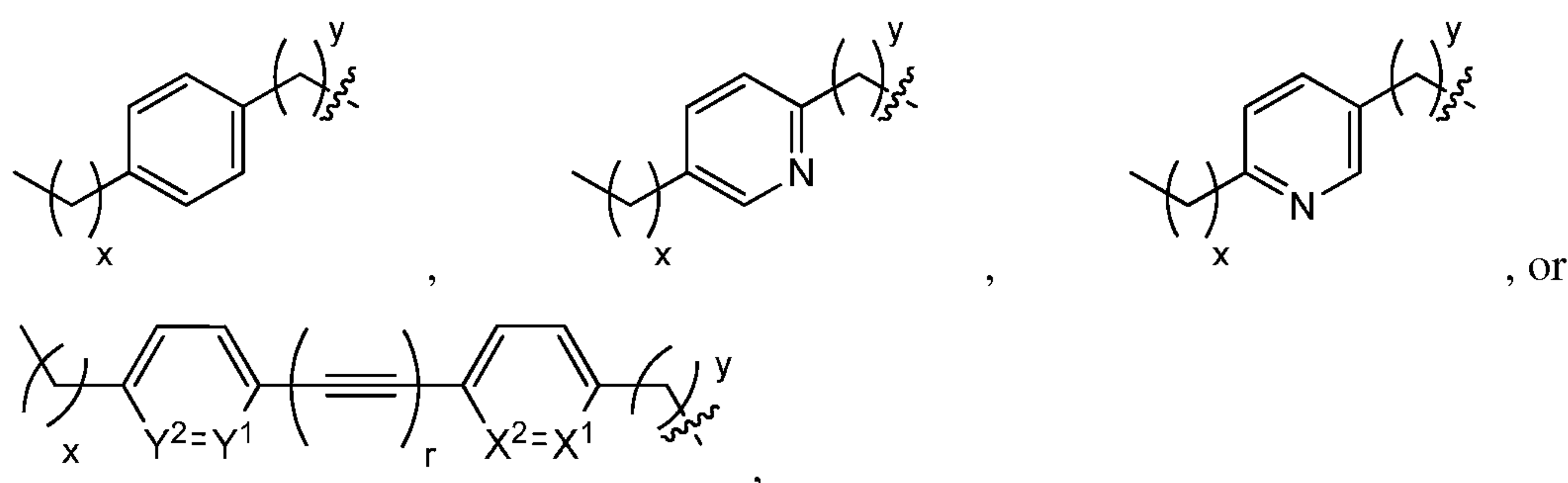
In various embodiments, the invention provides a compound of the invention
5 wherein R^5 is a (C_1-C_{22}) linear or branched alkyl.

In various embodiments, the invention provides a compound of the invention wherein R^5 is a (C_1-C_{22}) linear or branched alkyl comprising one or more of groups (A), (B), (C), or (D).

In various embodiments, the invention provides a compound of the invention
10 wherein R^5 is a (C_1-C_{22}) linear or branched alkyl.

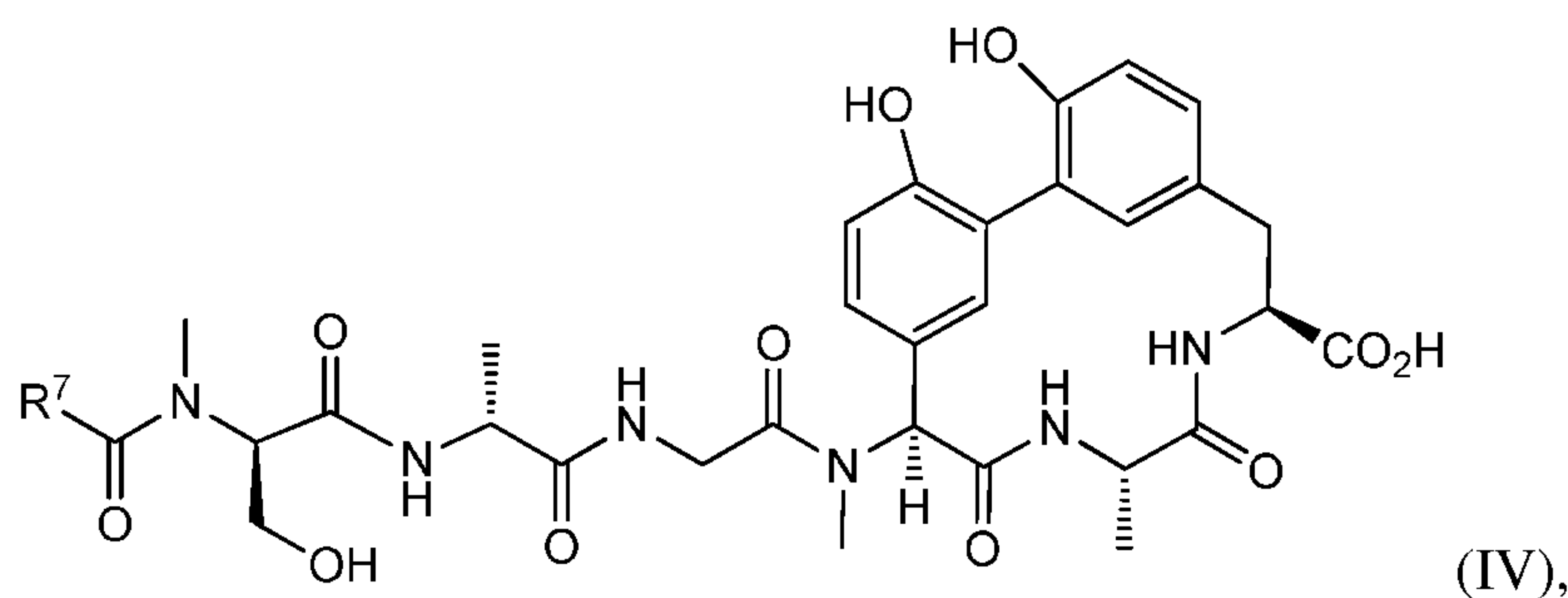
In various embodiments, the invention provides a compound of the invention wherein R^5 is a (C_1-C_{22}) linear or branched alkyl, comprising one or more of groups (A), (B), (C), or (D).

In various embodiments, the invention provides a compound of the invention
15 wherein R^5 is any of the following groups



wherein x is 0-14, y is 0-14, provided that $x + y \leq 22$, and X^1 , X^2 , Y^1 and Y^2 are
20 each independently C or N, provided that no more than one of X^1 and X^2 , and no more than one of Y^1 and Y^2 , is N, wherein a wavy line indicates a point of attachment of R^5 to an atom bonded to R^5 in formula (IIA), (IIB), or (IIC).

In various embodiments, the invention provides a compound of the invention wherein R^5 is any of the following: methyl, ethyl, (C_3-C_{22}) -n-alkyl, (C_3-C_{22}) -isoalkyl,
25 (C_4-C_{22}) -anteisoalkyl, naphthyl, (C_2-C_{10}) naphthyl, naphthylmethyl, (C_2-C_{10}) naphthylmethyl, biphenyl, (C_2-C_{10}) alkylbiphenyl, biphenylmethyl, (C_2-C_{10}) alkylbiphenylmethyl, (C_4-C_{12}) phenyl, (C_4-C_{12}) benzyl, or (C_2-C_{10}) -1,2-diphenylethynyl, wherein a wavy line indicates a point of attachment of R^5 to an atom bonded to R^5 in formula (IIA), (IIB), or (IIC).



herein R^7 is (C_8-C_{18}) -n-alkyl, (C_8-C_{18}) -isoalkyl, (C_8-C_{18}) -anteisoalkyl, any of which includes a group (A), (B), (C), (D), or (E) of claim 1; or is 2-naphthyl, 6- (C_2-C_{10}) -2-naphthyl, 2-naphthylmethyl, 6- (C_2-C_{10}) -2-naphthylmethyl, 4-biphenyl, 4-biphenylmethyl, 4'- (C_2-C_{10}) alkyl-4-biphenyl, 4'- (C_2-C_{10}) alkyl-4-biphenylmethyl, p- (C_4-C_{12}) phenyl, p- (C_4-C_{12}) benzyl, or 4'- (C_2-C_{10}) -1,2-diphenylethynyl; or a salt thereof.

In various embodiments, the invention provides a compound comprising a hydrate, solvate, prodrug, or metabolite of a compound of the invention.

In various embodiments, the invention provides a pharmaceutical composition comprising the compound of the invention and a pharmaceutically acceptable excipient.

Methods of Treatment of Bacterial Infections Using Compounds of the Invention.

The evolution of bacteria that are resistant to multiple antibiotics poses a serious threat to human health.^{1,2} Although much effort has been focused on the discovery and development of fully synthetic antibiotics,³ most of the antibiotics used in the clinic were derived from natural products, which evolved over eons of time to penetrate bacteria, avoid efflux, and inhibit essential and highly conserved biochemical processes.⁴ Unfortunately, broad-spectrum natural product antibiotics have become increasingly difficult to isolate and the more plentiful narrow-spectrum agents are limited either by unknown factors or by factors that are intrinsic to the compound, such as poor penetration or targeting proteins that are not sufficiently essential or conserved, and which are viewed as challenging to overcome by optimization.³ In contrast, there is much precedent for re-optimizing antibiotics after their spectrum has been compromised by specific resistance mechanisms acquired during clinical use, as evidenced by the development of many “next generation” antibiotics.⁵⁻⁸

The arylomycins are a class of lipopeptide antibiotics that inhibit bacterial type I signal peptidase (SPase), an essential serine-lysine dyad protease that is anchored to the outer leaflet of the cytoplasmic membrane and that removes N-terminal signal peptides

from proteins that are transported out of the cytoplasm.⁹⁻¹¹ Three related series of arylomycins have been identified, the arylomycins A and B and the lipoglycopeptides, which have similar core macrocycles, but different substituents and fatty acid tails (FIG. 1).^{12,13} Based on their novel mechanism of action, there was originally much enthusiasm
5 for these compounds, but despite their ability to inhibit SPase *in vitro*, and their *in vivo* activity against the soil bacteria *Rhodococcus opacus* and *Brevibacillus brevis* and the human pathogen *Streptococcus pneumoniae*, they were found to have no activity against a variety of other important human pathogens.^{13,14} This apparently narrow spectrum is surprising considering that SPase is located on the outer leaflet of the cytoplasmic
10 membrane and appears to be present and essential in all Eubacteria.^{10,15-17} To explore the origins of their narrow spectrum, we synthesized and evaluated arylomycin A₂, as well as several derivatives, including arylomycin C₁₆ (FIG. 1).¹⁸ Interestingly, we found that the arylomycins are as active against *Staphylococcus epidermidis* as the antibiotics used for its treatment, and importantly, we determined that *S. epidermidis* evolves resistance by
15 introducing a Pro residue into SPase at position 29, which is located in the enzyme's P5 pocket. Remarkably, all bacteria that had been shown to be resistant to the arylomycins have a Pro at the corresponding position, and we identified a wide variety of bacteria that lack this residue and showed that the majority of them are sensitive to the arylomycins, including the Gram-positive pathogens *Streptococcus pyogenes* and *Staphylococcus*
20 *haemolyticus*, and the Gram-negative pathogens *Helicobacter pylori* and *Chlamydia trachomatis*. Moreover, while the arylomycins slow the growth of *Staphylococcus aureus* strain 8325, they do not actually prevent it,¹⁸ even at concentrations as high as 128 µg/ml, however, they do prevent the growth of USA300, an epidemic MRSA isolate, with an MIC of 16 µg/ml. While this might result from unique features associated with
25 methicillin resistance, it suggests that the arylomycin scaffold has the potential for broader spectrum *S. aureus* activity. Importantly, we showed that the Pro residue imparts resistance by reducing the affinity with which the arylomycin binds, and that removing it is sufficient to render resistant *S. aureus*, *Escherichia coli*, and *Pseudomonas aeruginosa* highly sensitive. This data suggests that if the arylomycins could be
30 optimized to bind SPases regardless of the resistance-conferring Pro, they would have a remarkably broad spectrum of activity.

Despite not having activity against wild type *E. coli*, two crystal structures of arylomycin A₂ bound to a soluble fragment of *E. coli* SPase have been reported (FIG. 3A).^{19,20} The arylomycin is seen to bind in an extended β -sheet conformation that likely

mimics the binding of membrane bound pre-protein substrates.¹⁹ The C-terminal macrocycle of the arylomycin binds in a deep hydrophobic cleft and makes multiple hydrogen-bonds and hydrophobic interactions with the protein, while the C-terminal carboxyl group forms a critical salt bridge with the catalytic residues. The peptide tail
5 extends down a shallow cleft in the surface of SPase and forms two hydrogen-bonds with backbone residues of the protein. The critical resistance-conferring residue, Pro⁸⁴, interacts with the N-terminal end of the peptidic tail and appears to preclude the formation of a hydrogen-bond to a carbonyl oxygen of the arylomycin and possibly to alter the trajectory of the lipid moiety as it enters the membrane (FIG. 3A). While the
10 crystal structures are likely to reveal little information about the biologically relevant structure of the lipid tail due to the use of a soluble truncated fragment of SPase and the absence of a membrane bilayer, it most likely adopts an extended conformation to maximize packing within the outer leaflet of the cytoplasmic membrane.

As with a variety of other antibiotics with membrane-associated targets,²¹⁻²⁴ the
15 lipopeptide tail of the arylomycins has been shown to play an important role in their activity.^{13,14,21-24} Here, we report the first structure-activity relationship study of synthetic arylomycins, focusing on derivatives with altered lipopeptide tails. The activities of the arylomycin derivatives were evaluated with *S. epidermidis*, *S. aureus*, *E. coli*, and *P. aeruginosa*. With each pathogen, the derivatives were evaluated in the context of SPases
20 with and without the critical resistance-conferring Pro, to identify the changes in activity that result from altered interactions with this resistance-conferring residue and to identify the types of modifications that might be pursued to overcome resistance and thereby instill the arylomycin scaffold with broad-spectrum antibacterial activity.

SPase and the N-terminal portion of its natural substrates are embedded within
25 the bacterial cell membrane,^{26,27} suggesting that some part of the inhibitor's lipopeptide tail must also be accommodated within the membrane. To probe this interaction, and also to determine whether a positive charge at the lipid-peptide junction of arylomycin is capable of interacting with the negatively charged head groups of the phospholipid bilayer, we synthesized a derivative of the formula shown (Compound 25 of Table 2B),
30 wherein R¹ is H and R² (of FIG. 1) is a C16-n-alkyl, not an alkanoyl, chain, which serves to replace the lipid tail amide with a charged tertiary amine. This derivative has significantly reduced activity against *S. epidermidis* and sensitized *S. aureus* (MICs of 32 and 64 µg/ml, respectively), and no activity against any of the wild type or mutant Gram-negative strains examined. The decreased activity likely results from the inability of a

hydrophobic environment to accommodate the charge, suggesting that this portion of the tail is embedded in the membrane or within the interface between the membrane and SPase.

Accordingly, a series of hydrophobic tail analogs of arylomycin A2, adapted to
5 accommodate the proline residues of the resistant forms of SPase as described in the Specification and documents cited herein, were designed. Certain compounds were synthesized and tested, as shown below in the bioactivity Tables 1-4, below.

To explore the minimal tail length required for activity and to determine whether there is a limit to the tail length that can be accommodated within the cytoplasmic
10 membranes of the different bacteria, we synthesized and characterized derivatives **2 – 5** (Table 1). None of these derivatives gained activity against any of the resistant bacteria relative to arylomycin C₁₆, but significant differences were apparent with *S. epidermidis* and the genetically sensitized strains. With the sensitive strains, the C₈ derivative **2** has no activity, but the C₁₀ derivative **3** has activity against *S. epidermidis*, *S. aureus*, and *E.*
15 *coli*, while only **4** and **5** show activity against *P. aeruginosa*, revealing that at minimum a C₁₂ tail is required. In each case, activity increased with increasing tail length until it plateaued with the C₁₆ fatty acid tail (*i.e.* arylomycin C₁₆), and activity decreased slightly with the C₁₈ derivative **5** with all but *P. aeruginosa*.

To further explore the effects of increased hydrophobicity, we synthesized and
20 characterized derivatives with tails that contain one or more aromatic rings (Table 1). We first examined the series of naphthyl and biphenyl derivatives **6 – 8**. The naphthyl derivative **6** shows no activity against any of the bacteria tested, while the biphenyl derivative **7** retains some activity against wild type *S. epidermidis*. We found that compound **8**, which lacks the methylene spacer between the fatty acid carbonyl and the
25 biphenyl moiety also retains some activity against *S. epidermidis*, suggesting that flexibility of the biphenyl moiety is not essential. To further explore this biphenyl architecture, we synthesized the *p*-alkyl substituted biphenyl derivatives **9 – 12**. We observed an increase in activity with increasing alkyl substituent length against wild type *S. epidermidis* that plateaued with the C₆ and C₈ derivatives **11** and **12**, which are also
30 active against resistant *S. epidermidis*. Interestingly, several of the compounds in this series are also active against both sensitized and wild type *S. aureus*, with relative activities similar to those observed with *S. epidermidis*, but with absolute activities that were somewhat lower. None of the biphenyl derivatives have activity against the wild type or sensitized strains of *P. aeruginosa*, but they do maintain activity against

sensitized *E. coli*, again showing trends that were similar to those observed with *S. epidermidis* and *S. aureus*. Overall, the data reveal that relative to the straight chain derivatives, the biphenyl derivatives show similar activities against *S. epidermidis* and *E. coli*, less activity against *P. aeruginosa*, but greater activity against *S. aureus*.

5 We next examined the series of phenyl substituted tail mimetics **13** – **15** (Table 1). With *S. epidermidis* and the genetically sensitized strains, we again observed an increase in activity with increasing alkyl chain length. Moreover, the decylphenyl derivative **15** has activity against wild type *S. aureus*. Because the number of carbon atoms in this derivative is similar to that of arylomycin C₁₆, which has no activity against
10 wild type *S. aureus*, the data suggest that at least some of the activity is mediated by the interaction of the polarizable aromatic moiety with the membrane or with SPase.

To explore the effects of lipopeptide methylation, and to begin a more focused exploration of modifications that might overcome the deleterious effects of the resistance-conferring Pro, we synthesized and characterized derivatives with altered N-
15 methylation at d-MeSer2 and d-Ala3 (Table 2), arylomycin residues that are proximal to this critical residue when bound to SPase (FIG. 3A). The absence of the d-MeSer2 N-methyl group in **16** results in a slight decrease in activity against both the wild type and resistant *S. epidermidis* strains, and a more pronounced loss of activity against each of the other strains that is most pronounced with *P. aeruginosa*. It is unlikely that this
20 reduced activity results from specific deleterious interactions with the lipid membrane due to membrane fluidity, nor with SPase, as the structure of the *E. coli* SPase-arylomycin A₂ complex suggests that this region of the lipopeptide tail is either disordered or oriented away from the protein (although as discussed above, the N-terminally truncated form of SPase used in the structural studies renders this conclusion
25 somewhat speculative).¹⁹ Thus, the observed decrease in activity is likely the result of decreased hydrophobicity, outer membrane penetration, or protease resistance. The loss in activity is even more pronounced with compound **17** where methylation of d-Ala3 ablates activity against all organisms tested, likely resulting from replacement of a stabilizing H-bond with a destabilizing steric clash.

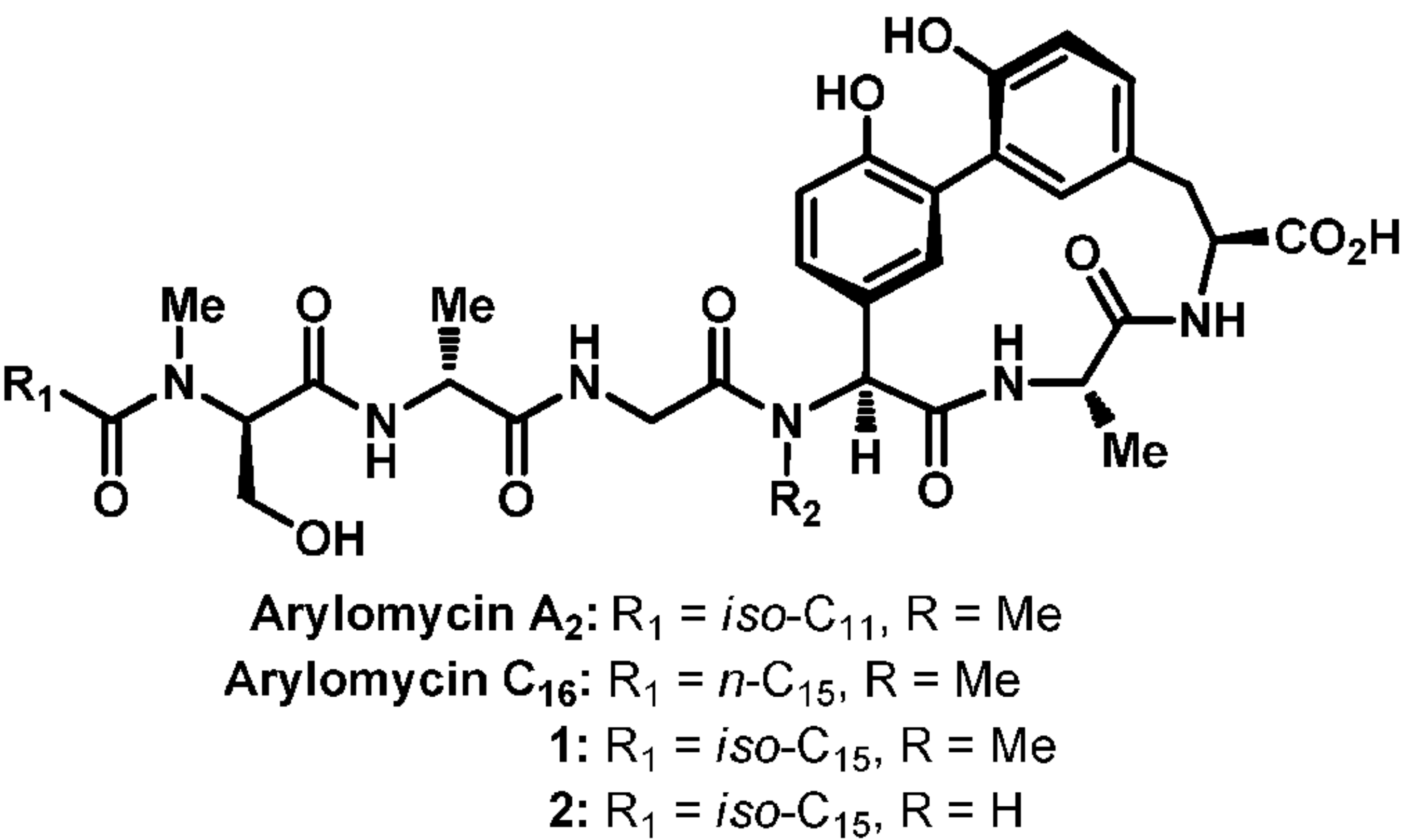
30 To explore the effects of lipopeptide tail rigidity, and to further explore modifications that might directly compensate for the resistance conferred by Pro29/84 of SPase, we designed the hydroxyproline derivative **18** (Table 2). In this compound, the side chain of d-MeSer2, which interacts with the sidechain and backbone of the SPase residue at position 29/84,¹⁹ is homologated by a methylene unit and fused with the

methyl group of the neighboring *N*-methyl amide bond. We found that this modification results in a complete loss of activity against the Gram-negative organisms but only little to moderate loss in activity against the Gram-positive organisms. Interestingly, because **18** retained full activity against resistant *S. epidermidis*, the disparity in activities against the wild type and resistant variants is greatly decreased, suggesting that at least for this organism, **18** recognizes both the Ser- and the Pro-variant SPases similarly.

To explore the effects of decreased rigidity, we synthesized derivative **19** (Table 2), which lacks the peptide bond between the serine and the fatty acid tail (and thus should impart the tail with greater rotational freedom). This molecule has significantly less activity compared to arylomycin C₁₆ against all organisms tested, with no observable activity against *E. coli*, *S. aureus*, or *P. aeruginosa*, and only moderate activity against *S. epidermidis*.

To increase flexibility without introducing or deleting other peptidic functionalities that might contribute to binding SPase, we synthesized and evaluated derivatives with one or two methylene units inserted immediately N-terminal or C-terminal to the amide bond linking d-MeSer₂ to d-Ala₃ (**20** – **23**, Table 2). These compounds did not gain activity against either of the wild type Gram-negative bacteria. With the sensitized Gram-negative strains, activity was observed only with **20**, which relative to the parent compound is 16-fold less active against *E. coli*, but only 2-fold less active against *P. aeruginosa*. The effects of methylene addition were significantly different with the Gram-positive bacteria. Relative to arylomycin C₁₆, derivatives **20** – **23** lost 8- to 16-fold activity against sensitive *S. epidermidis*, but retained activity against the resistant strain. This demonstrates that once the hydrogen-bond donor of the protein is removed (by mutation to Pro), perturbing the H-bond acceptor does not further decrease activity. The results were somewhat more complicated with *S. aureus*. As expected, relative to arylomycin C₁₆, addition of the methylene units decreased activity against the sensitized strain of *S. aureus*, 2- to 8-fold for **21** – **23**, and at least 64-fold for **20**. In the case of wild type *S. aureus*, however, no activity is observed with **20** or **21**, but interestingly, **22** and especially **23** gain activity.

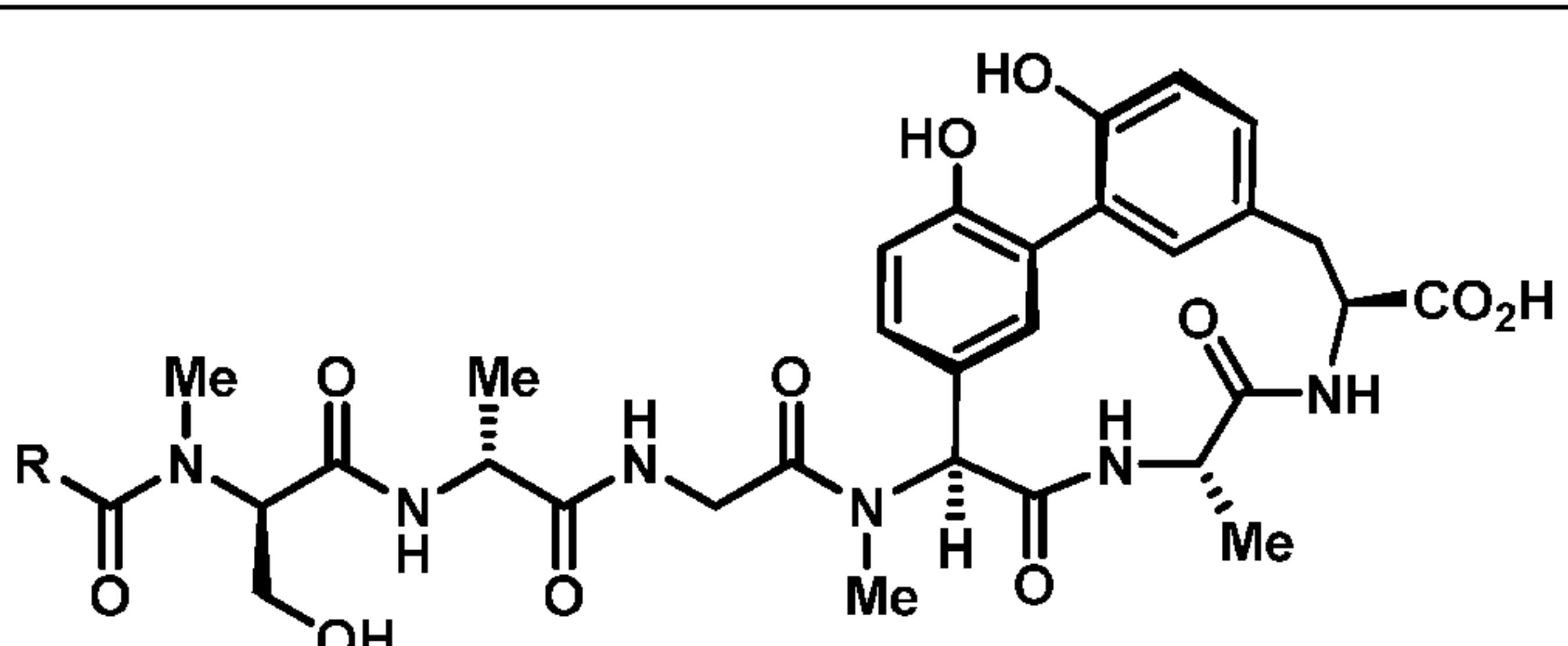
Table 1. MICs (μM) of selected compounds.



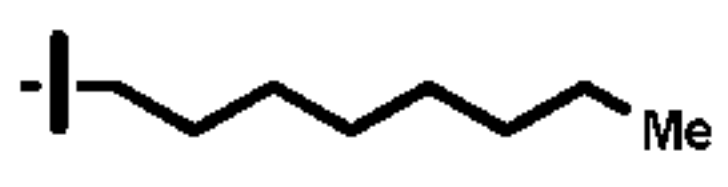
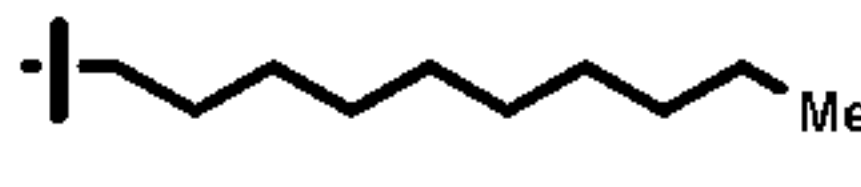
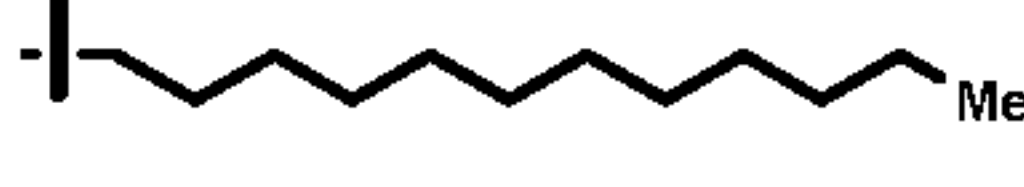
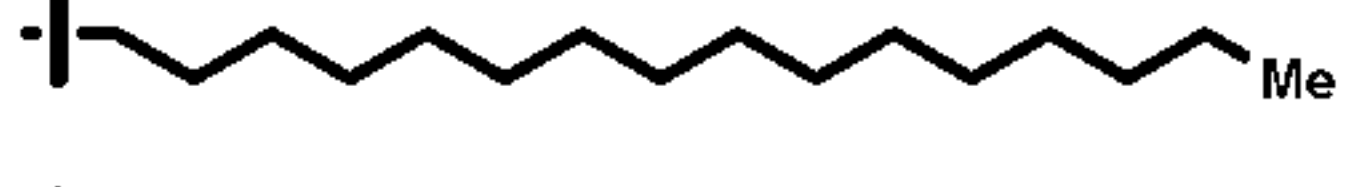
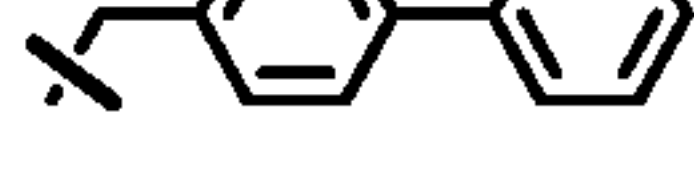
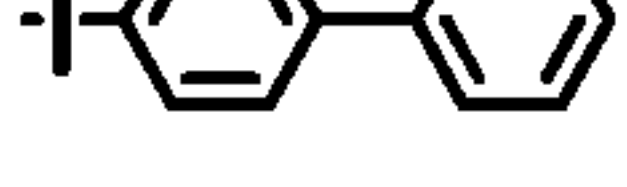
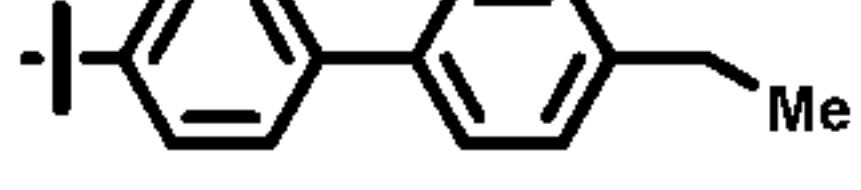
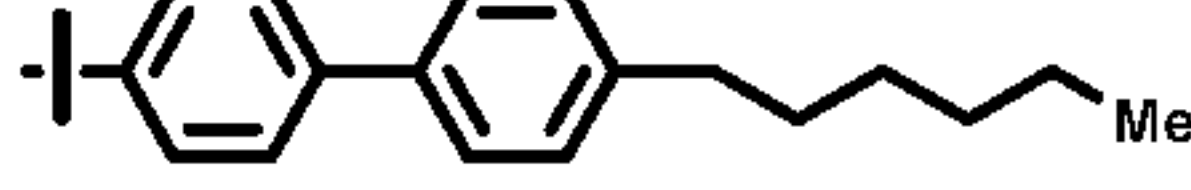
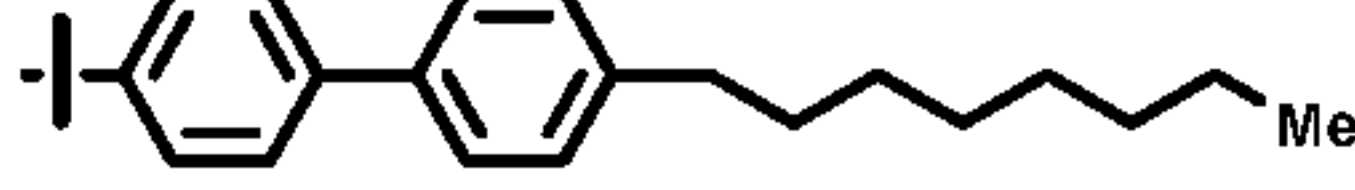
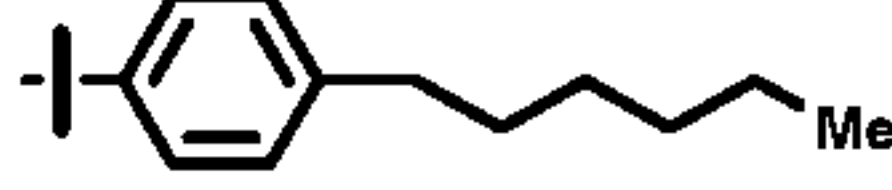
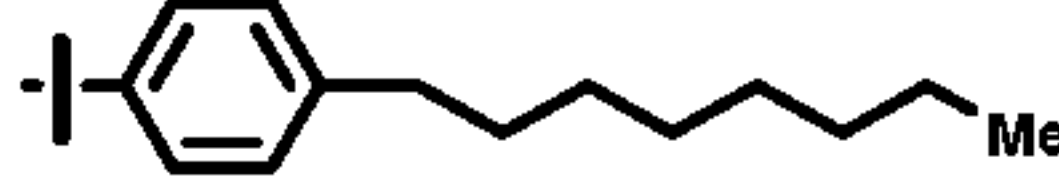
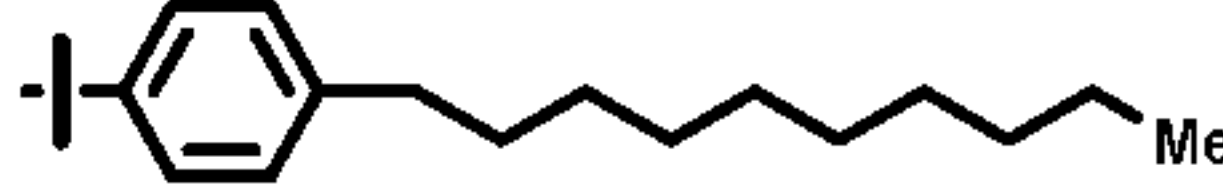
Strain	Arylomycin A ₂	Compound 1	Compound 2
<i>E. coli</i> MG1655	>128	>128	>128
<i>S. aureus</i> 8325	>128	>128	>128
<i>S. epidermidis</i> ATCC 35984	1	0.5	1
<i>B. anthracis</i> Sterne	n.d.	32	n.d.
<i>E. faecium</i> AEFA001 ^a	n.d.	>64	n.d.
<i>E. faecalis</i> ATCC 29212	n.d.	>64	n.d.
<i>E. faecalis</i> ATCC 51299	n.d.	>64	n.d.

^aPart of the Achaogen, Inc. strain collection.

Table 2A. Activity (MICs (μg/ml)) of arylomycin derivatives with altered fatty acid tails against strains of *S. epidermidis*, *S. aureus*, *E. coli*, and *P. aeruginosa* harboring SPase without (Sensitive) and with (Resistant) the arylomycin-resistance conferring Pro residue.



R	Sensitive ^b				Resistant ^c			
	<i>Se</i>	<i>Sa</i>	<i>Ec</i>	<i>Pa</i>	<i>Se</i>	<i>Sa</i>	<i>Ec</i>	<i>Pa</i>

3		>64	>64	>64	>64	>64	>64	>64	>64
4		16	64	32	>64	>64	>64	>64	>64
5		0.5	16	8	64	>64	>64	>64	>64
- ^a		0.5	2	0.5	8	8	>64	>64	>64
6		1	4	2	8	16	>64	>64	>64
7		>64	>64	>64	>64	>64	>64	>64	>64
8		32	>64	>64	>64	>64	>64	>64	>64
9		64	>64	>64	>64	>64	>64	>64	>64
10		8	64	16	>64	>64	>64	>64	>64
11		1	16	4	>64	>64	>64	>64	>64
12		0.5	8	1	>64	32	64	>64	>64
13		1	8	1	>64	16	16	>64	>64
14		8	64	32	>64	>64	>64	>64	>64
15		1	8	8	64	>64	>64	>64	>64
16		0.5	4	2	16	16	32	>64	>64

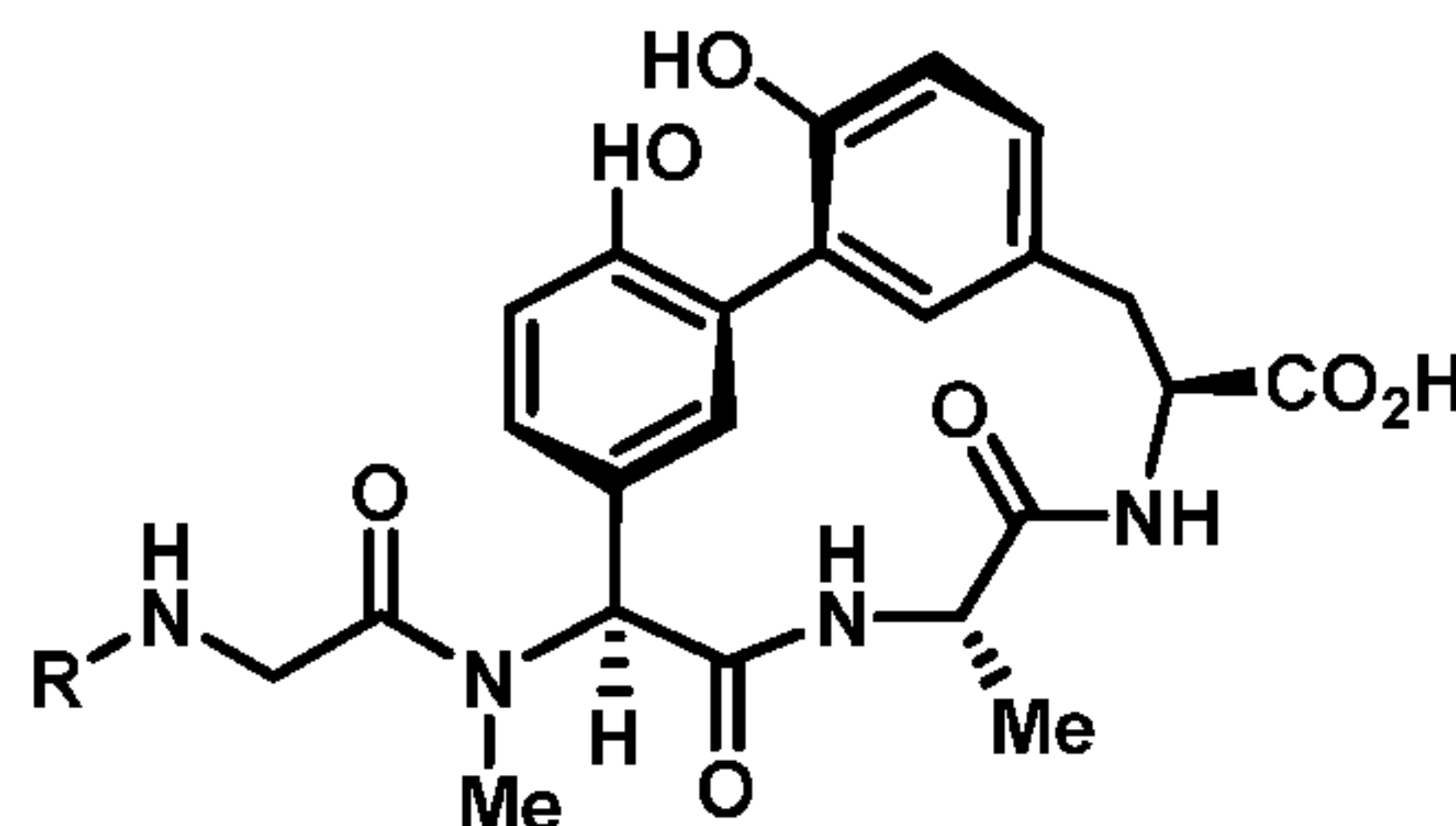
Se = *S. epidermidis*, Sa = *S. aureus*, Ec = *E. coli*, Pa = *P. aeruginosa*

^aArylomycin C₁₆ (fourth entry) included for reference.

^b Sensitive strains include wild type *S. epidermidis* RP62A, *lepB*(P29S) *S. aureus* 8325, *lepB*(P84L) *E. coli* MG1655, and *lepB*(P84L) *P. aeruginosa* PAO1.

5 ^c Resistant strains include *spsB*(S29P) *S. epidermidis* RP62A, and wild type *S. aureus* 8325, *E. coli* MG1655, and *P. aeruginosa* PAO1.

10 **Table 2B.** Activity (MICs (μg/ml)) of arylomycin derivatives with altered lipopeptide tails against strains of *S. epidermidis*, *S. aureus*, *E. coli*, and *P. aeruginosa* harboring SPase without (Sensitive) and with (Resistant) the arylomycin-resistance conferring Pro residue.



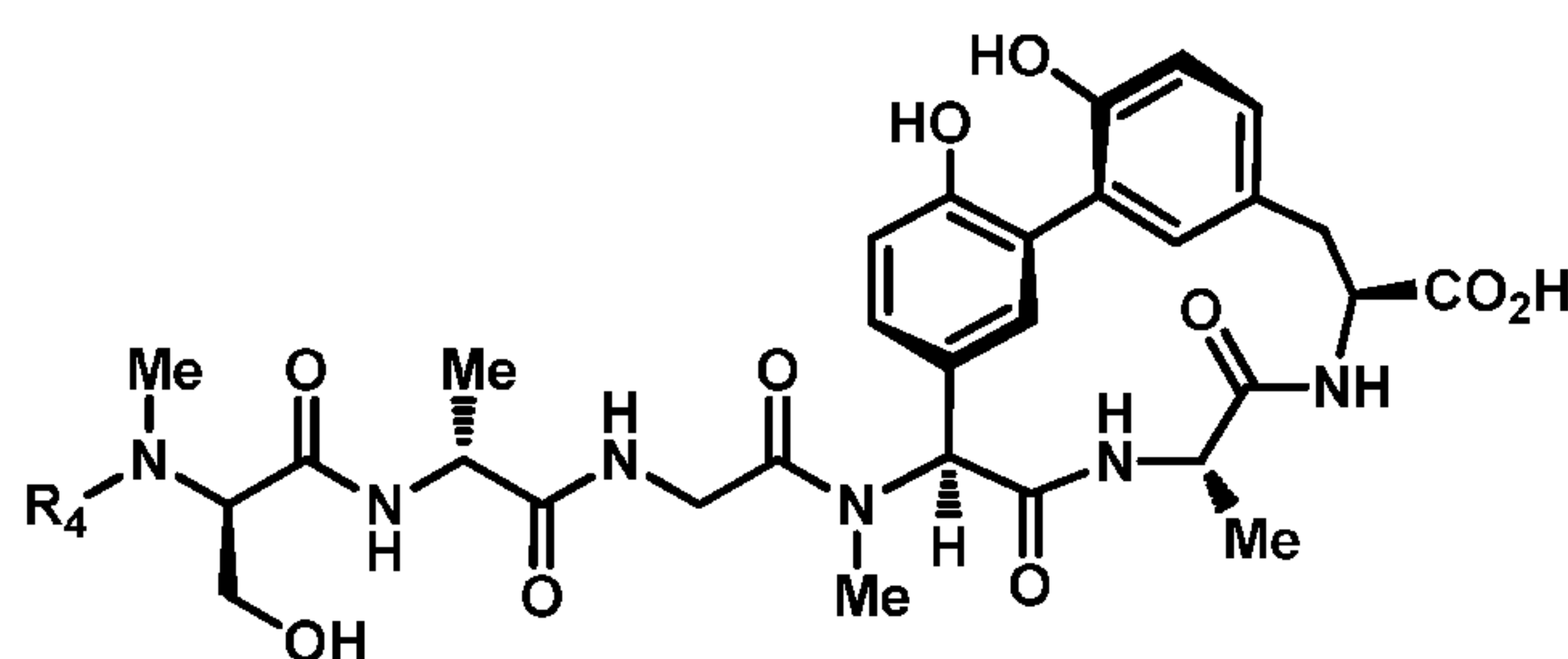
R	Sensitive ^b				Resistant ^c			
	<i>Se</i>	<i>Sa</i>	<i>Ec</i>	<i>Pa</i>	<i>Se</i>	<i>Sa</i>	<i>Ec</i>	<i>Pa</i>
^a	0.5	2	0.5	8	8	>64	>64	>64
17	1	16	4	>64	32	>64	>64	>64
18	>64	>64	>64	>64	>64	>64	>64	>64
19	4	4	>64	>64	8	>64	>64	>64
20	8	>64	>64	>64	>64	>64	>64	>64
21	8	>64	8	16	16	>64	>64	>64
22	8	8	>64	>64	8	>64	>64	>64
23	4	16	>64	>64	8	64	>64	>64
24	8	4	>64	>64	16	16	>64	>64

Se = *S. epidermidis*, *Sa* = *S. aureus*, *Ec* = *E. coli*, *Pa* = *P. aeruginosa*

^a Arylomycin C₁₆ (fourth entry) included for reference.

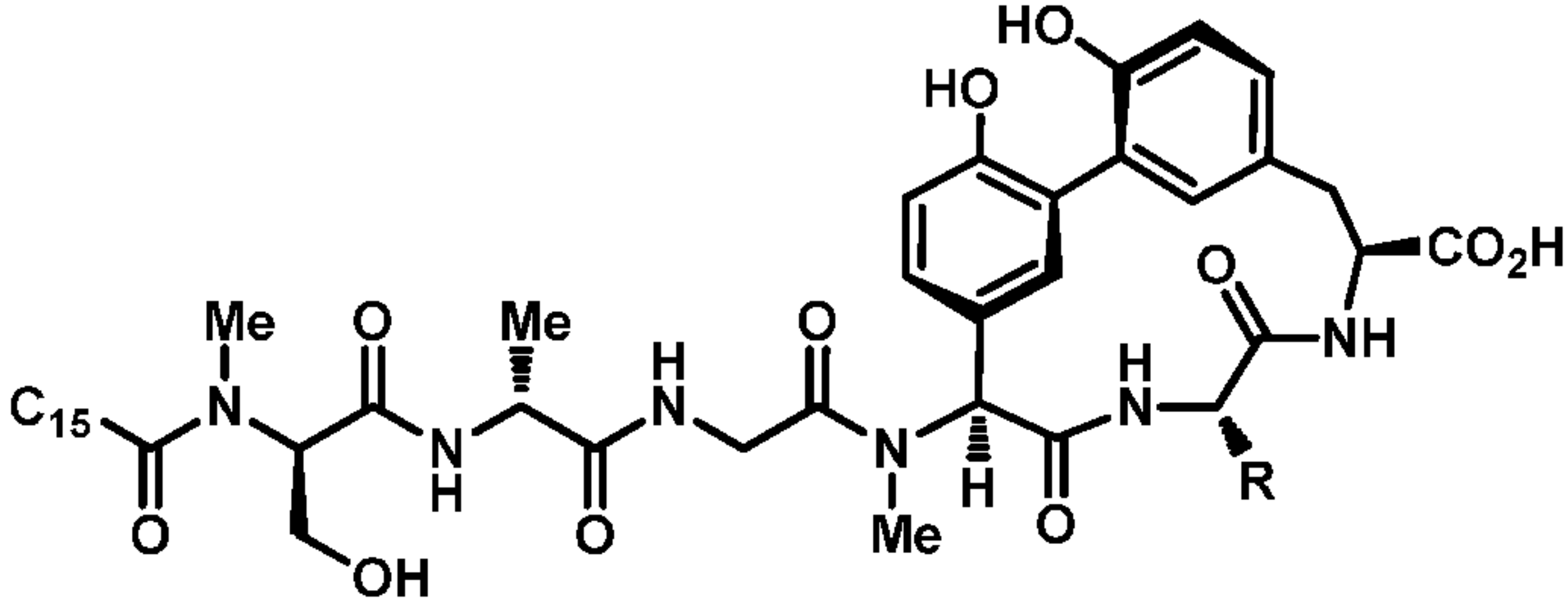
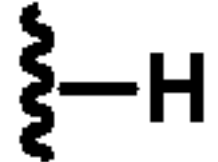
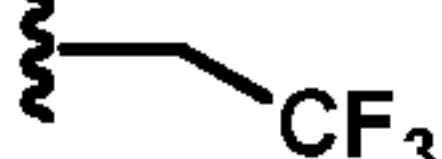
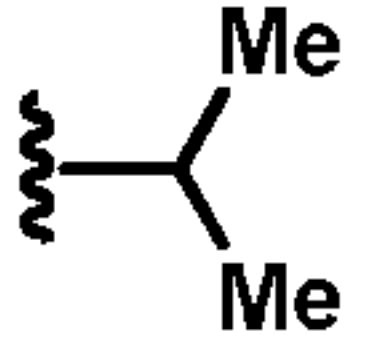
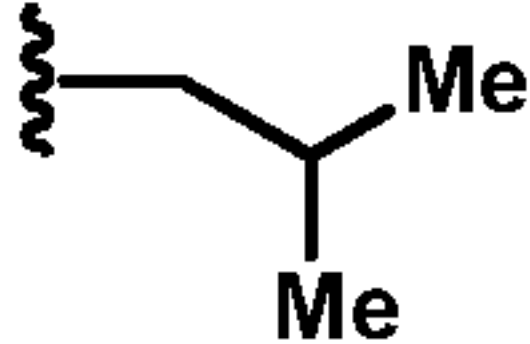
^b Sensitive strains include wild type *S. epidermidis* RP62A, *lepB*(P29S) *S. aureus* 8325, *lepB*(P84L) *E. coli* MG1655, and *lepB*(P84L) *P. aeruginosa* PAO1. See text for details.

5 ^c Resistant strains include *spsB*(S29P) *S. epidermidis* RP62A, and wild type *S. aureus* 8325, *E. coli* MG1655, and *P. aeruginosa* PAO1.



25: R₁ = H, R₂ = H
R₃ = H, R₄ = alkyl-C₁₆

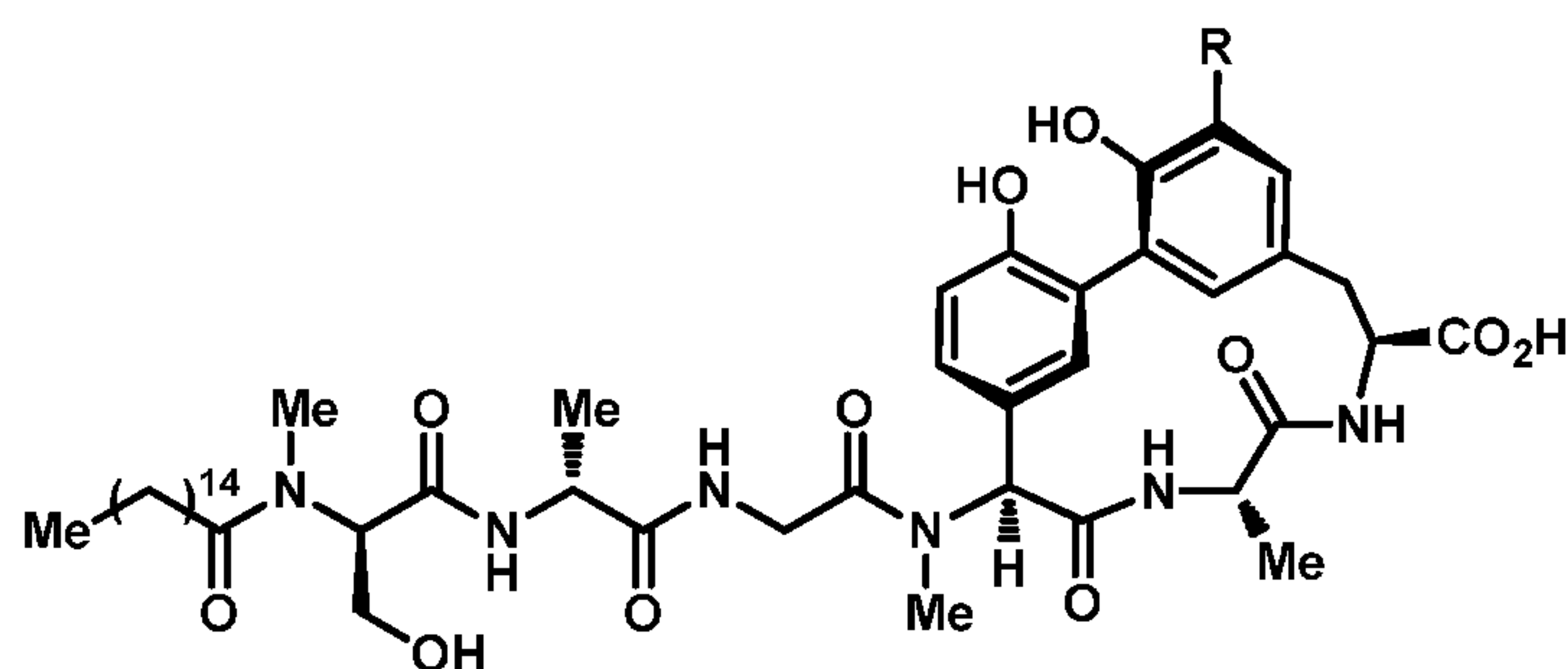
Table 3. Arylomycin P3 Position Derivatives

					
	R	<i>S. epidermidis</i> ^b	<i>S. aureus</i> ^c	<i>E. coli</i> ^d	<i>P. aeruginosa</i> ^e
26		8	>64	16	>64
- ^a		0.25	4	2	4
27		0.5	8	1	4
28		1	8	2	8
29		4	16	>128	>128
30		4	16	>128	>128
31		>64	>64	>64	>64
32		>64	>64	>64	>64
33		8	>64	16	>64
34		4	32	4	16
35		2	32	4	>64

^aArylomycin C₁₆ (fourth entry) included for reference. ^bwild type *S. epidermidis* RP62A. ^c*lepB*(P29S) *S. aureus* 8325, ^d*lepB*(P84L) *E. coli* MG1655, and *lepB*(P84L) ^e*P. aeruginosa* PAO1

5

Table 4. MICs of Arylomycin Derivatives (μg/mL)



Strain	Arylomycin C ₁₆ (R = H)	Arylomycin B-C ₁₆ (R = NO ₂)	36 (R = NH ₂)
<i>S. epidermidis</i>	0.25	0.13	8
<i>S. aureus</i> P29S	8	8	64
<i>E. coli</i> P84L	2	2	16
<i>E. coli</i>	>64	>64	>64
<i>P. aeruginosa</i> P84L	4	4	32
<i>B. brevis</i>	>64	>64	>64
<i>R. equi</i>	16	32	nd
<i>R. opacus</i>	1	4	nd
<i>S. agalactiae</i>	>128	8	nd
<i>S. pyogenes</i>	8	4	nd
<i>S. pneumoniae</i>	8	16	nd
<i>C. efficiens</i>	16	16	nd
<i>C. glutamicum</i>	2	2	nd
<i>L. lactis</i>	16	32	nd

The phenyl- and biphenyl-fatty acid tail series showed similar activities against *S. epidermidis*, *S. aureus*, and *E. coli*, with the longer *p*-alkyl derivatives having activity against both sensitive and resistant strains of *S. aureus*. Interestingly, *P. aeruginosa*

again shows unique behavior as it is not inhibited by any of the biphenyl-modified derivatives. This is particularly noteworthy considering that it is inhibited by the C₈- and C₁₀-substituted phenyl analogs, which in some cases are less hydrophobic. While some of the differences may result from altered outer membrane penetration or *in vivo* stability, the data likely reflect suboptimal insertion of the arylomycin into the plasma membrane of *P. aeruginosa*. It is interesting to speculate that this might result from unique aspects of the phospholipids that comprise the plasma membrane of *P. aeruginosa*, such as the presence of phosphatidylcholine,⁴⁶⁻⁵⁰ or from different constituent fatty acids.⁵¹⁻⁵⁴ For example, *P. aeruginosa* appears to employ a higher percentage of cis-vaccenic acid (a C₁₈ fatty acid) relative to palmitic and palmitoleic acids (which are C₁₆ fatty acids),⁵¹⁻⁵⁴ possibly resulting in a slightly thicker plasma membrane and possibly accounting for the generally longer fatty acid tail lengths that were observed to be required for *P. aeruginosa* inhibition. Overall, the data collected with the different tail derivatives suggest that the phenyl-modified derivatives are likely better scaffolds for arylomycin optimization than the natural, saturated fatty acid chains. This is most clearly highlighted by compound **15**, which retains all of the activities of the parent compound arylomycin C₁₆ but also gains activity against *S. aureus*.

N-methylation is common with non-ribosomally synthesized peptides such as the arylomycins, and is generally thought to optimize hydrophobicity, hydrogen-bonding potential, conformation, and/or resistance to proteases.⁵⁵⁻⁵⁸ The peptide portion of the arylomycin lipopeptide tail is backbone methylated at D-MeSer2 and MeHpg5, but not at D-Ala3 or Gly4. Previously, we showed that the methyl group at MeHpg5 pre-organizes the biaryl ring system for recognition of SPase.¹⁸ When we altered the backbone methylation state of D-MeSer2 and D-Ala3, which are both proximal to the critical resistance-conferring Pro in the *E. coli* SPase-arylomycin A₂ complex,¹⁹ significant activity was lost against both Gram-positive and Gram-negative bacteria. Although the specific origins of the decreased activity may differ at the two sites examined, the data suggests that natural lipopeptide tail methylation pattern is already optimized for activity.

In an effort to more directly compensate for the negative interactions introduced by the resistance-conferring Pro, we synthesized several derivatives with increased or decreased flexibility around D-MeSer2 and D-Ala3. None of the derivatives gained activity against either of the wild type Gram-negative bacteria, and while **20** retained activity against sensitized *P. aeruginosa*, it and the other derivatives lost activity against sensitized *E. coli*. The results were significantly different with the Gram-positive

pathogens. Relative to arylomycin C₁₆, derivatives **20** – **23** each lost 8 to 16-fold activity against sensitive *S. epidermidis* and 2- to >32-fold activity against the genetically sensitized *S. aureus*. This trend is consistent with the modifications shifting the register of the β -sheet formed between SPase and the inhibitor such that a stabilizing H-bond is lost. However, and more importantly, **22**, and especially **23**, gain activity against wild type *S. aureus*. As mentioned above, the structure of the *E. coli* SPase-arylomycin A₂ complex suggests that Pro84 (and by inference the homologous Pro in the other bacteria) disrupts arylomycin binding by physically occluding the lipopeptide tail from a hydrophobic groove and by disrupting an otherwise stabilizing hydrogen-bond with the carbonyl group of the lipid tail. While the precise mechanism by which these derivatives gain activity against *S. aureus* remains to be determined, the data nonetheless support the possibility that the spectrum of the arylomycins may be optimized by derivatization.

Accordingly, a series of derivatives with residues of varied side chains at the position of the macrocycle of arylomycin C₁₆ where Ala is present, adapted to compensate for binding energy lost due to the existence of the proline residues of the resistant forms of SPase as described in the specification and documents cited herein, were designed. Certain compounds were synthesized and tested, as shown below in the bioactivity Tables 3, below. The derivatives were evaluated by characterizing their minimal inhibitory concentration (MIC) against wild type *S. epidermidis* (strain RP62A), as well as mutant strains of *S. aureus* 8325, *E. coli* MG1655, and *P. aeruginosa* PAO1 that are rendered sensitive to the arylomycins via mutation of the resistance-conferring SPase Pro residue to Ser (*S. aureus*) or Leu (*E. coli*, and *P. aeruginosa*).

We initially explored the effects of removing the side chain at P3 by incorporation of Gly (**26**, Table 3). This compound lost significant activity against *S. epidermidis* (32-fold), *S. aureus* (>16 fold), *E. coli* (32-fold) and *P. aeruginosa* (>16-fold), suggesting that α -branching is required at this position either for packing within the hydrophobic environment of the S3 pocket and/or to help orient the backbone of the arylomycin, and thereby decrease the internal entropy of the macrocycle lost upon binding.

Having established the requirement for an α -substituent at the P3 position to maintain activity, we systematically explored the effect of increased side chain length with arylomycin derivatives **27** – **30**. Interestingly, the data reveal that arylomycin C₁₆, which bears a methyl group at this position, and analogs with ethyl, or *n*-propyl side chain results all have indistinguishable activities against each of the bacteria tested

(Table 5-1). In contrast, the derivatives and **29** with *n*-butyl and *n*-pentyl side chains, respectively, had significant effects that were somewhat different with the different bacteria examined. Relative to arylomycin C₁₆, both compounds **29** and **30** lost 8- to 32-fold activity against *S. epidermidis*, 32-fold against *S. aureus*, and at least 32- and 64-fold against *P. aeruginosa* and *E. coli*, respectively. The data suggest that the different SPases do not discriminate against shorter side chains at this position, but have varying abilities to tolerate increasingly longer P3 side chains.

While an inability to accommodate the longer P3 side chains is a simple explanation for the structure activity-relationships revealed with **27** – **30**, the crystal structure of the inhibitor-bound *E. coli* peptidase reveals the presence of several crystallographically observable water molecules near the P3 pocket. Thus, it is also possible that the *n*-butyl and *n*-pentyl derivatives may have lost activity by forcing a hydrophobic methyl group proximal to these water molecules, or by forcing desolvation of the protein without compensating with any stabilizing interactions. To address these possibilities, we explored the effects of increased hydrophilicity and/or hydrogen-bonding via derivatives **31** and **32** which bear *n*-propanol and *n*-butanol side chains, respectively. All activity was lost with these compounds against all bacteria tested, suggesting that the longer alkyl or hydroxyalkyl are not accommodated due to size constraints with the S3 pocket.

To further explore how changes in the hydrophobicity of the P3 side chain impact activity we examined trifluoroethyl derivative **33**. Such fluorinated derivatives are thought to be ‘superhydrophobic’²⁴ and are often used in drug optimization.²⁵ We found that compound **33** is 8-fold less active against *E. coli*, at least 16-fold less active against *P. aeruginosa* and *S. aureus*, and 32-fold less active against *S. epidermidis*.

Having explored the effect of altered length and hydrophobicity within a linear side chain, we turned our attention to the Val and Leu derivatives **34** and **35**, which possess β - and γ -branched side chains, respectively. While these compounds are also less active than the parent compound, the loss in activity was again organism dependent. Both **34** and **35** lost 8- to 16-fold activity against both Gram-positive bacteria, but they maintained activity against *E. coli*. Interestingly, *P. aeruginosa* more strongly differentiated between the branched derivatives, with **34** losing 4-fold activity, but **35** losing >16-fold activity. This data suggests that the S3 pocket of the *E. coli* SPase is relatively tolerant toward branching in general, that the Gram-positive SPase are less so,

and that the S3 pocket of *P. aeruginosa* SPase is relatively tolerant of β -branching but intolerant of γ -branching.

In summary, we have synthesized the first series of arylomycin derivatives with substitution in the backbone of the macrocycle. We found that the side chain at the P3
5 position of arylomycin contributes significantly to binding. In addition, we found that the S3 pocket of SPase can accommodate up to three linear saturated carbons from the P3 position of arylomycin however, increasing the size of the substituent filling this pocket does not increase overall activity. Arylomycin derivatives with side-chains larger than three linear saturated carbons either linearly or laterally at the P3 position lose activity
10 against most strains with larger losses of activity seen when larger substituents were present. While these derivatives did not make arylomycin more potent, they defined the limits of the S3 pocket for the inhibitor and they suggest a binding model where the arylomycins, and perhaps the recognition sequence of preproteins, are not free in solution but are bound in the lipophilic membrane before binding SPase.

15 To explore the effect of substituents on the aromatic ring affect binding of the arylomycin we synthesized and arylomycin B derivative arylomycin B C₁₆ and its amino derivative **36**. They were adapted to compensate for binding energy lost due to the existence of the proline residues of the resistant forms of SPase as described in the specification and documents cited herein, were designed. Certain compounds were
20 synthesized and tested, as shown below in the bioactivity Table 4, below.

The activity of arylomycin B-C₁₆ and its derivative **36** was characterized by determining the minimal inhibitory concentration (MIC) required to inhibit the growth of wild type *S. epidermidis* (strain RP62A), and *E. coli* (MG1655). The compounds were also tested against strains of *S. aureus* (8325), *E. coli* (MG1655), and *P. aeruginosa*
25 (PAO1) that were rendered sensitive to the arylomycins by mutation of the resistance-conferring Pro to a residue that does not confer resistance (P29S in the *S. aureus* protein, and P84L in the *E. coli*, and *P. aeruginosa* proteins).

Like arylomycin A₂ and its derivative arylomycin C₁₆, arylomycin B-C₁₆ has potent activity against *S. epidermidis* (Table 4) and no activity against wild-type *E.coli*.
30 In addition, similar to the arylomycin A compounds, arylomycin B-C₁₆ has activity against the mutant strains of *S. aureus*, *E. coli*, and *P. aeruginosa*. Thus, the activity of the B series compound is limited against natural isolates via the same mechanism as the A series compounds. In fact, the level of arylomycin B-C₁₆ activity against all strains tested is indistinguishable from that of arylomycin C₁₆ (Table 4). Surprisingly, our data

contradicts the previously reported conclusion that the arylomycins have activity against *B. brevis* and that nitro substitution increases the activity of the arylomycin scaffold.¹⁸ In our experiments, using both MHBII broth and nutrient broth (as was used in the previously reported studies) both compounds showed no activity against *B. brevis*.

5 Relative to the two natural products, we found that the amino derivative **36** is significantly less active against all bacteria tested and the loss in activity is slightly larger against the Gram-positive bacteria (32-fold) than against the Gram-negative pathogens (8-fold). The amino group is expected to be protonated and thus charged at physiological pH, and the inability of the SPase binding site to accommodate this charge
10 likely explains the decreased activity.

 To generate a broader assessment of the activity of the A- and B-series arylomycins, we examined representatives from a broad range of bacteria that are sensitive to arylomycin C₁₆²⁰ including *Rhodococcus equi*, *Rhodococcus opacus*, *Streptococcus agalactiae*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*,
15 *Corynebacterium efficiens*, *Corynebacterium glutamicum* and *Lactococcus lactis* (Table 4). For almost all of the bacteria tested the inhibitory concentrations for arylomycin C₁₆ and arylomycin B-C₁₆ were identical or within the error of the experiment. However, *Streptococcus agalactiae* showed significant differences in MICs between the compounds with arylomycin B-C₁₆ having greater than 16-fold more activity than its
20 non-nitrosylated analogue arylomycin C₁₆. This result is especially interesting given that the in neither of the two SPases of *S. agalactiae* is the resistance conferring Pro present and that identical activities were observed between the two compounds against the closely related organisms *Streptococcus pneumoniae*, and *Streptococcus pyogenes*. It is interesting to speculate that in the context of an arms race this species may have found an
25 alternative method for mediating resistance to the arylomycin A series that was overcome by the installation of a nitro group in the arylomycin B series.

 In conclusion, we have shown that aminated arylomycin loses significant activity relative to the nitrosylated variant. In addition, we have showed that arylomycin B-C₁₆ has no difference in activity against *S. epidermidis*, mutant strains of *S. aureus*, *E. coli*
30 and *P. aeruginosa* and multiple other strains of bacteria when compared to the analogous arylomycin C₁₆ of the A series. Importantly, it was found that *S. agalactiae* is uniquely sensitive to the arylomycin B-C₁₆. In addition, closely related strains of bacteria showed no difference between the A and B series arylomycins. These results support the idea that nitrosylation of the arylomycin is important for biological activity against some

bacteria and that its inclusion in the repertoire of arylomycins was possibly the result of selection on the producing organism.

Reports by other workers indicate that arylomycins (e.g., those shown in FIG. 1) have little whole cell activity against most bacterial pathogens except possibly for
 5 *Staphylococcus epidermidis*, and *Rhodococcus opacus*. See, e.g., Kulanthaivel et al., J. Biol. Chem. 279: 36250-58 (2004); Schimana et al., J. Antibiotics 55:565-70 (2002). For example, currently available reports indicate that arylomycins A and B lack activity against the Gram-negative bacteria *Escherichia coli* K12, *Proteus mirabilis* ATCC 35501, *Pseudomonas fluorescens* DSM 50090 and against the eukaryotic organisms
 10 *Saccharomyces cerevisiae* ATCC 9080, *Botrytis cinerea* Tu 157 and against the green algae *Chlorella fusca* and against the duckweed *Lemna minor*.

However, according to the invention, arylomycins actually do have activity against a variety of bacterial species. For example, the following bacterial species are susceptible to arylomycins: *Rhodococcus equi*, *Corynebacterium diphtheriae*,
 15 *Lactococcus lactis* subsp. *cremoris*, *Corynebacterium glutamicum*, *Francisella tularensis*, *Campylobacter jejuni*, *Helicobacter pylori*, *Propionibacterium acnes*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Staphylococcus carnosus*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*, *Streptococcus dysgalactiae*, *Streptococcus mitis*,
 20 *Streptococcus oralis*, and *Streptococcus pyogenes*, as illustrated in the following Table 5.

Table 5. Bacteria Predicted by sequence to be Sensitive and Confirmed Sensitive.

Predicted by sequence to be Sensitive and Confirmed Sensitive.		
Species	Aminio acid -7 from catalytic Ser ^a	MIC (μg/ml)
<i>Staphylococcus epidermidis</i>	S,S	0.25
<i>Staphylococcus haemolyticus</i>	S,S	2
<i>Staphylococcus hominis</i>	S,S	0.25
<i>Staphylococcus lugdunensis</i>	S,T	0.25
<i>Staphylococcus simulans</i>	S,?	0.25
<i>Staphylococcus cohnii</i>	S,?	8
<i>Streptococcus pneumoniae</i>	N	16
<i>Streptococcus pyogenes</i>	A	16
<i>Corynebacterium glutamicum</i>	M	2
<i>Rhodococcus opacus</i>	V	2
<i>Lactococcus lactis</i>	L	16, >128 ^b
<i>Rhodococcus equi</i>	V,I	16

<i>Helicobacter pylori</i>	A	4
<i>Chlamydia trachomatis</i>	L	6
<i>Francisella tularensis</i>	N	4 -16, >64 ^b
^a Multiple amino acids indicate where organisms express multiple SPases		
^b Range of MICs across different isolates		

Accordingly, another aspect of the invention is a method of treating a bacterial infection in an animal that includes administering any one or any combination of the arylomycin compounds (e.g., compounds of Formula I) to the animal, wherein the bacterial infection comprises an infection by *Rhodococcus equi*, *Corynebacterium diphtheriae*, *Lactococcus lactis* subsp. *cremoris*, *Corynebacterium glutamicum*, *Francisella tularensis*, *Campylobacter jejuni*, *Helicobacter pylori*, *Propionibacterium acnes*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Staphylococcus carnosus*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*, *Streptococcus dysgalactiae*, *Streptococcus mitis*, *Streptococcus oralis*, and *Streptococcus pyogenes*. The arylomycin compounds, including those of Formula I can be administered in a therapeutically effective amount.

As further described below, arylomycin antibiotics inhibit the bacterial type I signal peptidase (SPase) enzyme, particularly when the bacteria's SPase enzyme does not have a proline within about 10 amino acids N-terminal to the SPase catalytic serine, and especially when the bacteria's SPase enzyme does not have a proline at 5 to 7 amino acids N-terminal to the SPase catalytic serine. Thus, another aspect of the invention is a method of treating a bacterial infection in an animal that includes administering any one or any combination of arylomycin A, arylomycin B or the arylomycin compounds of Formula I to the animal, wherein the bacterial infection comprises an infection by a bacteria that encodes or expresses an SPase enzyme that does not have a proline within about 10 amino acids N-terminal to the SPase catalytic serine, or is an infection by *Yersinia pestis*. In some embodiments, the bacteria encodes or expresses an SPase enzyme that does not have a proline at 5 to 7 amino acids N-terminal to the SPase catalytic serine. The arylomycin A, arylomycin B and/or the compounds of Formula I can be administered in a therapeutically effective amount. Examples of organism with SPase genes that encode amino acids other than proline at residues -5 and -7 from the catalytic serine include but are not limited to *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus luganensis*, *Staphylococcus hominis* subsp. *hominis*, *Staphylococcus hominis* subsp. *novobiosepticus*, *Staphylococcus cohnii*, *Streptococcus pneumoniae*,

Streptococcus pyogenes, *Streptococcus agalactiae*, *Lactococcus lactis* subsp. *lactis*, *Rhodococcus opacus*, *Rhodococcus equi*, *Corynebacterium glutamicum*, *Helicobacter pylori*, *Chlamydia trachomatis*, and *Francisella tularensis*.

The following Table 6 provides a representative listing of bacterial species that do not have a proline at 5 to 7 amino acids N-terminal to the SPase catalytic serine.

Table 6. Bacteria Expressing a SPase enzyme that does not have a proline 5 to 7 amino acids N-terminal to the SPase catalytic serine

Species	8 residues N-terminal to and including catalytic Ser
<i>Rhodococcus equi</i>	VYLIPSES
<i>Rhodococcus opacus</i>	VYLIPSES
<i>Corynebacterium diphtheriae</i>	VYMIPSQS
<i>Lactococcus lactis</i> subsp. <i>cremoris</i>	LVVVDGHS
<i>Corynebacterium glutamicum</i>	MYMIPSGS
<i>Francisella tularensis</i>	NFLIPTAS
<i>Campylobacter jejuni</i>	AFVIPSGS
<i>Helicobacter pylori</i>	AFIIPSR
<i>Propionibacterium acnes</i>	MFVIPSKS
<i>Chlamydia trachomatis</i>	LYEVPTGS
<i>Chlamydophila pneumoniae</i>	LYEVPTGS
<i>Staphylococcus carnosus</i>	SYTVRGDS
<i>Staphylococcus haemolyticus</i>	SYTIKGDS
	SYTVSGSS
<i>Staphylococcus epidermidis</i>	SYSIKGDS
	SYTVKGAS
<i>Staphylococcus hominis</i>	SYTIKGDS
	SYTVSGSS
<i>Staphylococcus lugdunensis</i>	SYTIKGDS
	TYSVSGDS
<i>Streptococcus pneumoniae</i>	NVRVEGHS
<i>Streptococcus agalactiae</i>	VLRIYGHS
	FVKVDGHS
<i>Streptococcus dysgalactiae</i>	AVKVDGHS
<i>Streptococcus mitis</i>	NVRVEGHS
<i>Streptococcus oralis</i>	NVRVEGHS
<i>Streptococcus pyogenes</i>	AVKVDGHS

While almost all bacteria that do not have a proline within about 10 amino acids N-terminal to the SPase catalytic serine are susceptible to arylomycins (including arylomycin A, arylomycin B and the compounds of Formula I), there are a few exceptions. For example, some strains of *Staphylococcus aureus*, *Staphylococcus capitis*, *Staphylococcus caprae*

and *Yersinia pestis* are still susceptible to arylomycins even though they do have a proline residue within 10 amino acids N-terminal to the catalytic serine (see Table 7).

Table 7. Bacterial Species Susceptible to Arylomycins
but with a Proline N-terminal to the SPase Catalytic Serine

Species	Amino acid -7 from catalytic Ser ^a	MIC (μg/ml)
<i>Yersinia pestis</i>	P	4
<i>Staphylococcus capitis</i>	P,S	8
<i>Staphylococcus caprae</i>	P,S	8
^a Multiple amino acids indicate where organisms express multiple SPases		

Thus, another aspect of the invention is a method of treating a bacterial infection in an animal that includes administering arylomycin A and/or arylomycin B and/or a compound of Formula I to the animal, wherein the infection is an infection involving a bacterial species that is susceptible to arylomycin but where the bacterial species has a proline residue within 10 amino acids N-terminal to the catalytic serine (e.g., at positions -5 and/or -7 from the catalytic serine). Such organisms include certain strains of *Staphylococcus aureus*, *Staphylococcus capitis*, *Staphylococcus caprae* and *Yersinia pestis*.

For example, *Yersinia pestis* has a single SPase with a proline at position 29, but as demonstrated herein, *Yersinia pestis*, is sensitive to arylomycin compounds. *Yersinia pestis* is a significant pathogen that can infect humans and other animals – it is the causative agent of the plague. Thus, new methods of treating *Yersinia pestis* infections are highly desirable. Therefore, another aspect of the invention is a method of treating a *Yersinia pestis* infection in an animal that includes administering arylomycin A and/or arylomycin B and/or a compound of Formula I to the animal. The arylomycin A and/or arylomycin B and/or the compound of Formula I can be administered in a therapeutically effective amount.

However, according to the invention, bacterial species with a proline 5-7 amino acids N-terminal to the catalytic serine are resistance to arylomycins. Such species include those shown in Table 8.

Table 8. Bacterial Species with a Proline
within 10 amino acids N-terminal to the SPase catalytic Serine

	8 residues N-terminal to and including catalytic Ser	SEQ ID NO:
<i>Escherichia coli</i>	PFQIPSGS	87
<i>Klebsiella pneumoniae</i>	PFQIPSGS	87
<i>Salmonella enterica</i>	PFQIPSGS	87
<i>Vibrio cholerae</i>	PFQIPSGS	87
<i>Pseudomonas aeruginosa</i>	PFQIPSGS	87
<i>Acinetobacter baumannii</i>	PFNIPSDS	88
<i>Neisseria meningitidis</i>	PFQIPSSS	89
<i>Haemophilus influenzae</i>	PFQIPSGS	89
<i>Citrobacter koseri</i>	PFQIPSGS	89
<i>Shigella flexneri</i>	PFQIPSGS	89
<i>Bordetella pertussis</i>	PFHIPSGS	90
<i>Mycobacterium tuberculosis</i>	PYLIPSES	91
<i>Staphylococcus aureus</i>	PYTIKGES	92
<i>Bacillus anthracis</i>	PSLVQGES	93
	LCKVEGKS	94
<i>Streptococcus mutans</i>	PVQVDGHS	95
<i>Clostridium difficile</i>	PSIVSGES	96
	PTIVKGES	97
	PTLVNGES	98
<i>Enterococcus faecalis</i>	PAAVNGSS	99
	SYPIAGQS	100
	PVVVRGHS	101
	PVRVDGHS	102
<i>Listeria monocytogenes</i>	PVKVEGTS	103
	PVTVNGKS	104
	PILVDGIS	105

Infections of particular interest that can be treated using arylomycins include those commonly detected in humans and/or those infections that are frequently inadequately treated by other antibiotics. Examples of infections that are susceptible to arylomycin treatment include those involving *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus luganensis*, *Staphylococcus hominis* subsp. *hominis*, *Staphylococcus hominis* subsp. *novobiosepticus*, *Staphylococcus cohnii*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus agalactiae*, *Lactococcus lactis* subsp. *lactis*, *Rhodococcus opacus*, *Rhodococcus equi*, *Corynebacterium glutamicum*, *Helicobacter pylori*, *Chlamydia trachomatis*, and *Francisella tularensis*, *Rhodococcus equi*, *Corynebacterium diphtheriae*, *Lactococcus lactis* subsp. *cremoris*, *Corynebacterium glutamicum*, *Francisella tularensis*,

Campylobacter jejuni, *Helicobacter pylori*, *Propionibacterium acnes*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Staphylococcus carnosus*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*, *Streptococcus dysgalactiae*, *Streptococcus mitis*, *Streptococcus oralis*, and
5 *Streptococcus pyogenes*.

In one embodiment, the infection involves *Helicobacter pylori* (whose SPase has Ala29), which infection is readily identified by available procedures. Hence, when such infections are identified the infections can be treated by administering to the affected animal any one or any combination of arylomin A, arylomycin B and/or any of the
10 arylomycin compounds of Formula I. The arylomycin A and/or arylomycin B and/or the compound of Formula I can be administered in a therapeutically effective amount.

In other embodiments, the bacterial infection does not involve *Staphylococcus epidermidis* and/or *Rhodococcus opacus*.

The animal can be any animal suspected of suffering from a bacterial infection.
15 For example, the animal can be a human, a domesticated animal, a zoo animal or an animal under the treatment of a doctor, nurse or veterinarian. Examples of animals that can be treated include humans, dogs, cats, horses, cattle, pigs, goats, sheep, chickens, geese, turkeys, rats, mice, hamsters, ferrets, parrots, lizards and the like.

Thus, the compounds of the invention can be administered to an animal (e.g., a
20 mammal), especially a human in need of such treatment, prevention, elimination, alleviation or amelioration of a malcondition.

The compounds of the invention are effective over a wide dosage range. For example, in the treatment of adult humans, dosages from about 0.05 to about 5000 mg, preferably from about 1 to about 2000 mg, and more preferably between about 2 and
25 about 2000 mg per day can be used. A typical dosage is about 10 mg to about 1000 mg per day. In choosing a regimen for patients it can frequently be necessary to begin with a higher dosage and when the condition is under control to reduce the dosage. The exact dosage will depend upon the activity of the compound, mode of administration, on the therapy desired, form in which administered, the subject to be treated and the body
30 weight of the subject to be treated, and the preference and experience of the physician or veterinarian in charge.

Generally, the compounds of the invention are dispensed in unit dosage form including from about 0.05 mg to about 1000 mg of active ingredient together with a pharmaceutically acceptable carrier per unit dosage.

Usually, dosage forms suitable for oral, nasal, pulmonal or transdermal administration include from about 125 µg to about 1250 mg, preferably from about 250 µg to about 500 mg, and more preferably from about 2.5 mg to about 250 mg, of the compounds admixed with a pharmaceutically acceptable carrier or diluent.

5 Dosage forms can be administered daily, or more than once a day, such as twice or thrice daily. Alternatively dosage forms can be administered less frequently than daily, such as every other day, or weekly, if found to be advisable by a prescribing physician.

10 It is within ordinary skill to evaluate any compound disclosed and claimed herein for effectiveness in inhibition of susceptible and resistant variants of bacterial SPases, and in the various *in vivo* assays, using the procedures described above or found in the scientific literature. Accordingly, the person of ordinary skill can prepare and evaluate any of the claimed compounds without undue experimentation.

15 Any compound found to be an effective inhibitor of a bacterial SPase can likewise be tested in animal models and in human clinical studies using the skill and experience of the investigator to guide the selection of dosages and treatment regimens.

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Methods of Preparation

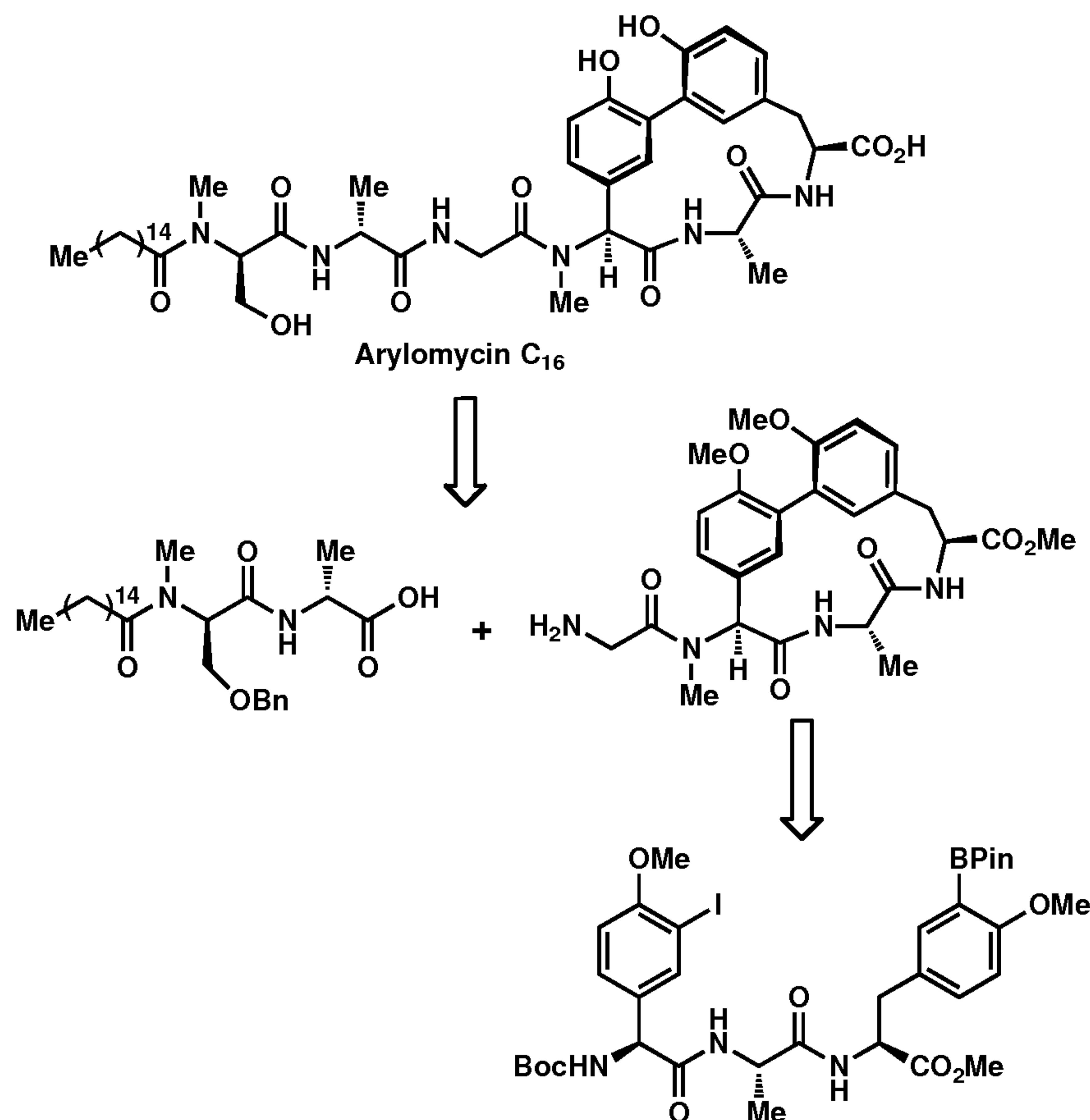
Compounds of the invention can be prepared either by semi-synthesis starting with an arylomycin compound isolated from a fermentation procedure, or by total chemical synthesis. Procedures are provided herein that, in combination with the knowledge of the synthetic organic chemist of ordinary skill in the art, can be used to prepare the full range of compounds of the invention as disclosed and claimed herein.

25

Total Chemical Synthesis

For total synthesis, a retrosynthetic analysis was carried out, as shown in Scheme 1.

30

Scheme 1. Retrosynthesis of Arylomycin C₁₆

Arylomycin derivatives can be synthesized by synthesizing tripeptides by solution phase peptide couplings and then cyclization via Suzuki-Miyaura macrocyclization (the final step shown in the above retrosynthetic analysis).

5 Alternatively, natural product arylomycins can provide a core for further synthetic elaboration in some cases, depending upon the desired substituent pattern.

Starting with a cyclic core, for example by a total synthesis approach as shown above and exemplified in the Examples section, below, the exocyclic peptide / peptidomimetic domain, and the lipophilic tail domain, can be elaborated using approaches and methods described herein and those within the knowledge of the person of ordinary skill. See, for example, T. Roberts, et al. (2007), *J. Am. Chem. Soc.* 129, 15830-15838; Dufour, J.; Neuville, L.; Zhu, J. P. *Synlett* **2008**, 2355-2359.

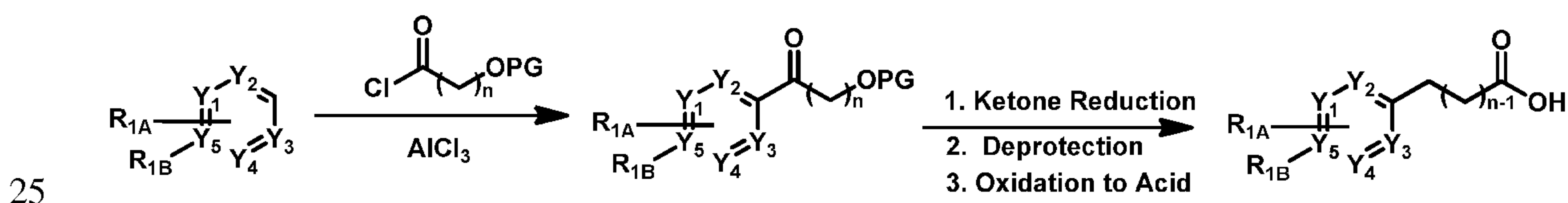
The various lipopeptide tails can be assembled via solution phase peptide couplings and then coupling to the macrocyclic core. The molecule can be considered to include three major domains: the cyclic core, an exocyclic peptide or peptidomimetic moiety, and a lipophilic tail moiety. In the natural product arylomycins, such as arylomycin A2, the lipophilic tail is an n-alkanoyl, isoalkanoyl, or anteisoalkanoyl acyl

group; in compounds of the invention groups are introduced into the lipophilic tail that are adapted to provide a more favorable binding interaction of the inventive arylomycin analog with an SPase including a proline residue at the -5 and -7 position relative to the catalytic SPase serine residue, as shown in the X-ray crystal structure of arylomycin bound to a fragment of a resistant form of SPase, shown in FIG. 3A. As discussed above, the presence of a proline residue at one of these positions has been found by the inventors herein to provide resistance of the SPase to inhibition by natural product arylomycins such as arylomycin A2. The inventive compounds can overcome this resistance by designing the lipophilic tail to bind more effectively to SPase forms having the proline residue(s).

The R⁵ group can be bonded to the exocyclic peptide moiety via acyl, carbamate, or urea linkages, which can be formed as described below, for the three classes of linkages.

For compounds where the R⁵ linkage to the peptide is an amide bond, and wherein the aromatic ring is connected directly to the carbonyl group of the amide, these compounds can be synthesized by coupling of commercially available benzoic acids or heterocyclic acids that had been substituted by electrophilic or nucleophilic aromatic substitution or palladium catalyzed processes (and appropriately protected using standard protecting groups^{S1}) to the N-terminus of the peptide chain. Heterocycles where the commercially available acids are not available will be synthesized via any one of a number of methods for synthesizing pyridines, pyrazines, pyrimidines or pyradizines^{S2}.

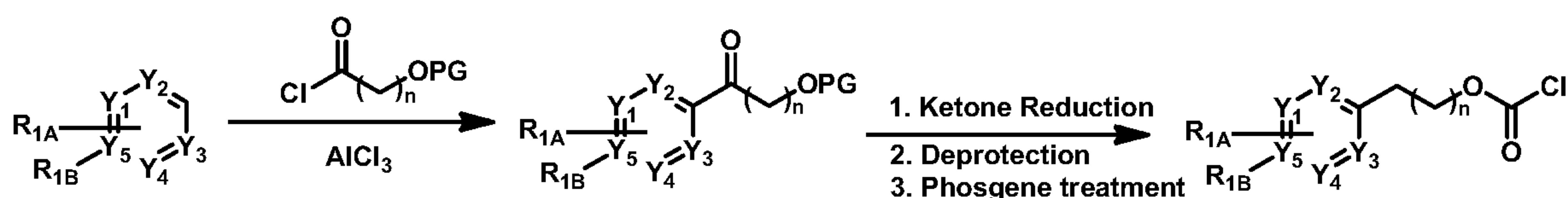
For compounds where the linkage of R⁵ to the exocyclic peptide is an amide bond, and where the aromatic ring is not connected directly to the carbonyl group of the amide, these compounds can be synthesized via the scheme:



Appropriately functionalized or unfunctionalized aryl rings (appropriately protected using standard protecting groups^{S1}) will be subjected to Friedel-Crafts acylation conditions with an alkyl chain bearing an acid chloride and a protected hydroxyl group. The ketone is then reduced, the protected hydroxyl group is deprotected, the hydroxyl is oxidized to an acid and the resulting acid is coupled to the N-terminus of the peptide.

For compounds where the R⁵ linkage to the peptide is a carbamate and the aryl ring is not attached directly to the carbamate, functionalized phenols (appropriately protected using standard protecting groups^{S1}) can be treated with phosgene to create the aryl carbamoyl chloride which can then be used to acylate the N-terminus of the peptide.

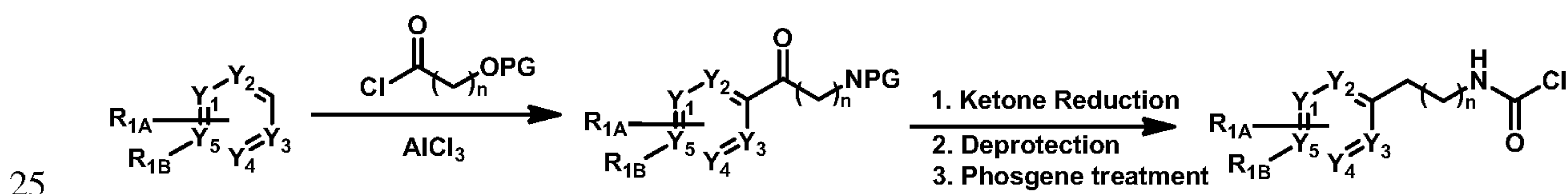
- 5 Functionalized or unfunctionalized aryl rings will be subjected to Friedel-Crafts acylation conditions with an alkyl chain bearing an acid chloride and a protected hydroxyl group. The ketone of the resulting compound will be reduced and the protecting group will be removed. The compound will then be treated with phosgene to form the carbamoyl chloride^{S3} and this compound will be used to acylate the N-terminus of the peptide as shown in the scheme:



- Heterocycles where Friedel-Crafts acylations are not possible will be halogenated (and appropriately protected using standard protecting groups^{S1}) and the appropriate length hydrocarbon chain terminated on one end with a protected alcohol and the other end with a halogen or boronic acid/ester will be attached via palladium mediated coupling.

- For compounds where the R⁵ linkage to the peptide is a urea and the aryl ring is attached directly to the nitrogen atom, functionalized aryl amines will be treated with phosgene to create the aryl ureayl chloride which will then be used to acylate the N-terminus of the peptide.

For compounds where the R⁵ linkage to the peptide is a urea and the aryl ring is not attached directly to the carbamate, the compounds will be synthesized via the scheme:



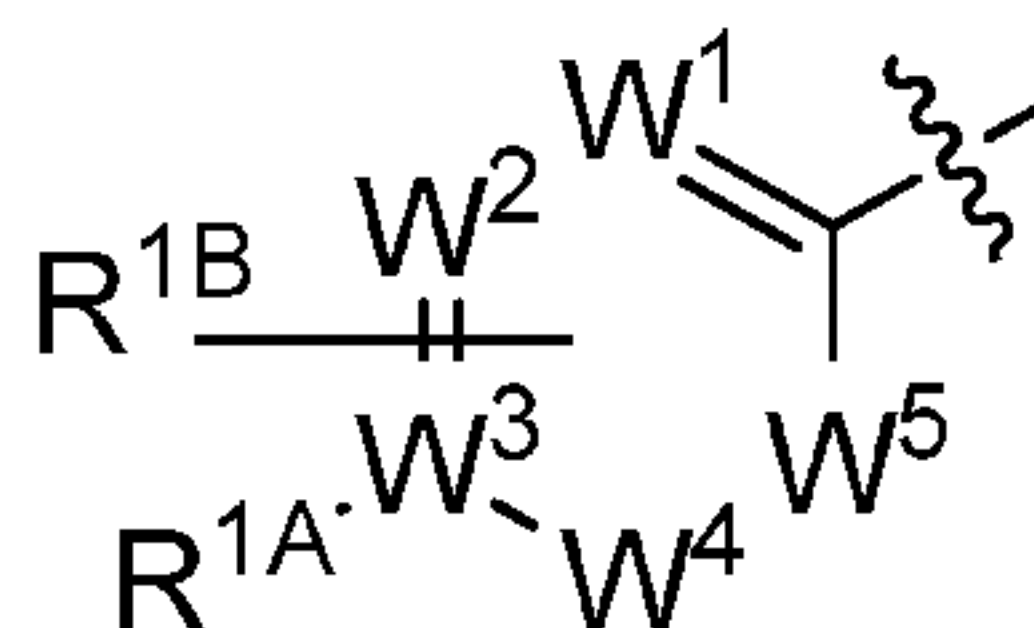
- Appropriately functionalized or unfunctionalized aryl rings (and appropriately protected using standard protecting groups^{S1}) will be subjected to Friedel-Crafts acylation conditions with an alkyl chain bearing an acid chloride and a protected amine. The ketone of the resulting compound will be reduced and the protecting group will be

removed. The compound will then be treated with phosgene to form the ureayl chloride^{S4} and this compound will be used to acylate the N-terminus of the peptide. Heterocycles where Friedel-Crafts acylations are not possible are halogenated (and appropriately protected using standard protecting groups^{S1}) and an appropriate length hydrocarbon chain terminated on one end with a protected amine and the other end with a halogen or boronic acid/ester will be attached via palladium mediated coupling.

The various embodiments of compounds of the invention with the variants of the R⁵ group can be synthesized using the above approaches, in conjunction with ordinary knowledge concerning the use of any protecting or blocking groups that may be necessary. See, for example, Protective Groups in Organic Synthesis, Greene, T.W.; Wuts, P. G. M., John Wiley & Sons, New York, NY, (3rd Edition, 1999).

In various embodiments of the invention, R⁵ can be straight chain or branched chain alkyl, wherein the chain can include any of the following groups (A) – (E). Synthetic approaches appropriate for each class of R⁵ group are provided.

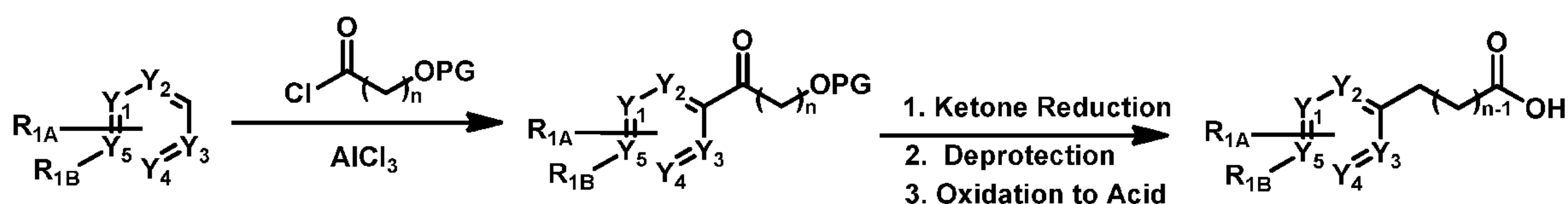
(A)



wherein W¹, W², W³, W⁴ and W⁵ are each independently C or N, provided that no more than two of W¹, W², W³, W⁴ and W⁵ are N; provided that when R^{1A} or R^{1B} is non-hydrogen, any W atom to which the R^{1A} or R^{1B} is respectively bonded is C, wherein there can be one or more R^{1B} bonded to the ring bearing the W atoms; R^{1A} is hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, cyano, (C₁-C₆)-thioether, fluoroalkoxy, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1B} is hydrogen, alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁- C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-alkylamino, (C₁- C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1A} or R^{1B} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁- C₆)-alkyl, (C₁- C₆)-alkoxy, (C₁- C₆)-alkylamino, (C₁- C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7-

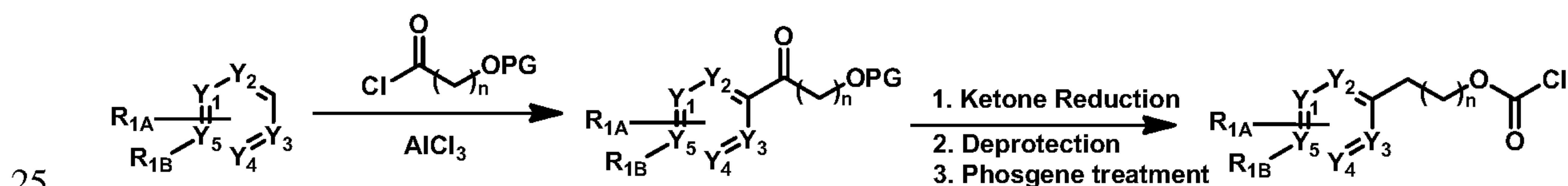
membered heterocyclyl, or (C₆-C₁₀) aryl groups; wherein a wavy line indicates a point of attachment.

For compounds where the R⁵ linkage to the peptide is an acyl group and where the aromatic ring is connected directly to the acyl group these compounds can be synthesized by peptide coupling of commercially available benzoic or heterocyclic acids that had been substituted by electrophilic aromatic substitution, nucleophilic aromatic substitution or palladium catalyzed processes (and appropriately protected using standard protecting groups^{S1}) to the N-terminus of the peptide chain. Heterocycles where the commercially available acids are not available can be synthesized via any one of a number of methods for synthesizing pyridines, pyrazines, pyrimidines or pyradizines^{S2}.



For compounds where the R⁵ linkage to the peptide is an acyl group and where the aromatic ring is not connected directly to the acyl group, these compounds can be synthesized via the above scheme. Appropriately functionalized or unfunctionalized aryl rings (appropriately protected using standard protecting groups^{S1}) can be subjected to Friedel-Crafts acylation conditions with an alkyl chain bearing an acid chloride and a protected hydroxyl group. The ketone can then be reduced, the protected hydroxyl group deprotected, the hydroxyl oxidized to an acid, and the resulting acid coupled to the N-terminus of the peptide.

For compounds where the R⁵ linkage to the peptide is a carbamate and the aryl ring is attached directly to the carbamate, functionalized phenols (appropriately protected using standard protecting groups^{S1}) can be treated with phosgene to create the aryl carbamoyl chloride which can then be used to acylate the N-terminus of the peptide.



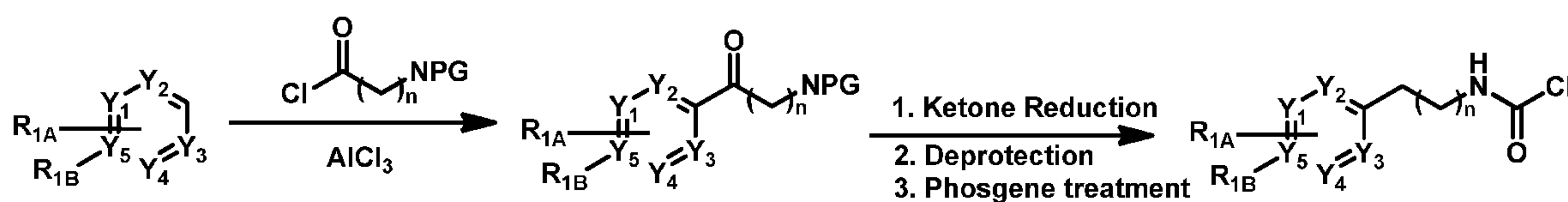
For compounds where the R⁵ linkage to the peptide is a carbamate and the aryl ring is not attached directly to the carbamate, the compounds can be synthesized via the route shown in the above scheme. Appropriately functionalized benzenes (appropriately protected using standard protecting groups^{S1}) can be subjected to Friedel-Crafts acylation conditions with an alkyl chain bearing an acid chloride and a protected hydroxyl group.

The ketone of the resulting compound can be reduced and the protecting group removed. The compound can then be treated with phosgene to form the carbamoyl chloride^{S3} and this compound can be used to acylate the N-terminus of the peptide. Heterocycles where Friedel-Crafts acylations are not possible can be halogenated (and appropriately

5 protected using standard protecting groups^{S1}) and the appropriate length hydrocarbon chain terminated on one end with a protected alcohol and the other end with a halogen or boronic acid/ester can be attached via palladium mediated coupling.

For compounds where the R⁵ linkage to the peptide is a urea and the aryl ring is attached directly to the carbamate, functionalized aryl amines can be treated with

10 phosgene to create the aryl ureayl chloride which can then be used to acylate the N-terminus of the peptide.

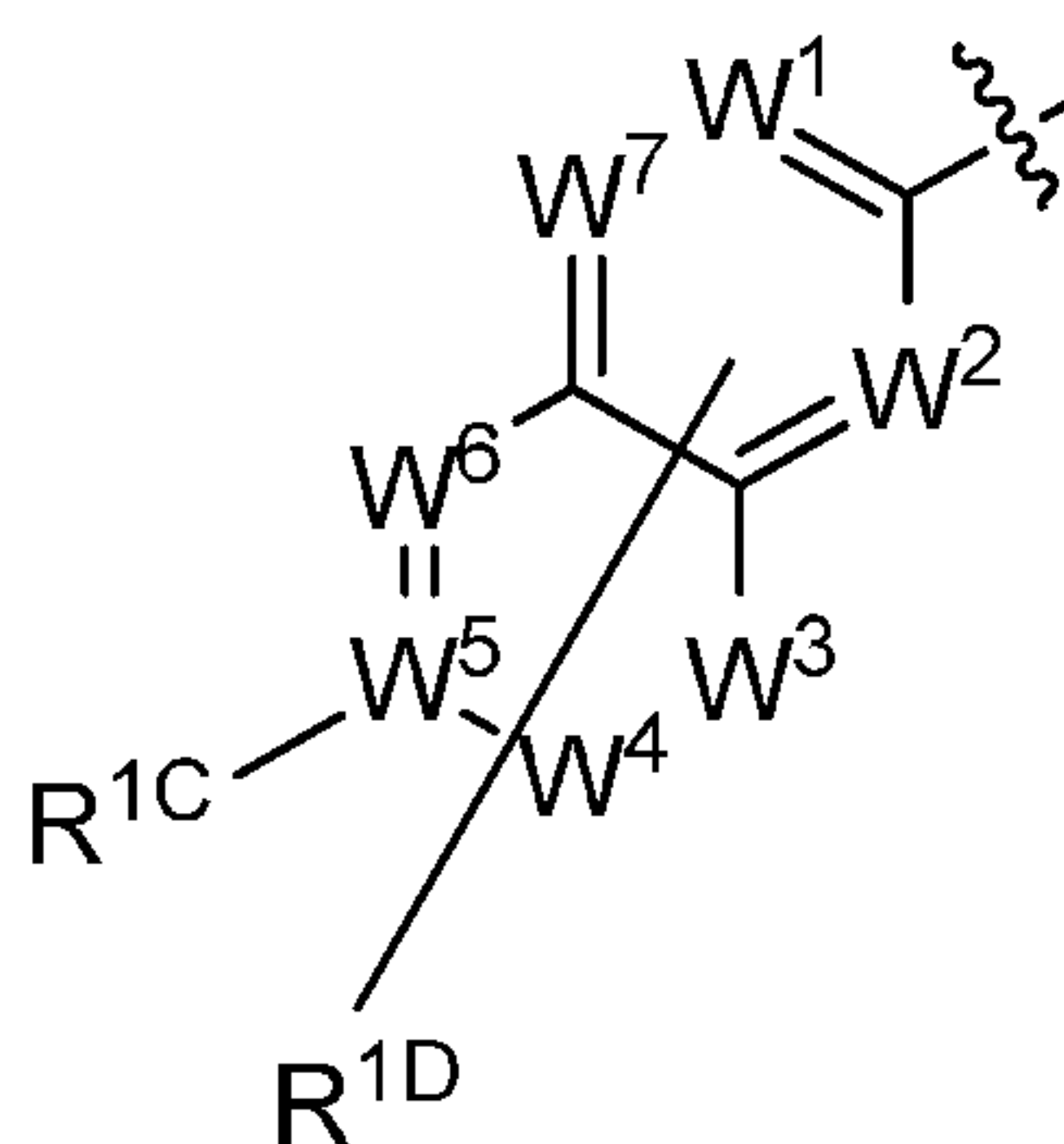


For compounds where the R⁵ linkage to the peptide is a urea and the aryl ring is

15 not attached directly to the carbamate, the compounds can be synthesized via the route shown in the above scheme. Appropriately functionalized can be subjected to Friedel-Crafts acylation conditions with an alkyl chain bearing an acid chloride and a protected amine. The ketone of the resulting compound can be reduced and the protecting group be removed. The compound can then be treated with phosgene to form the ureayl

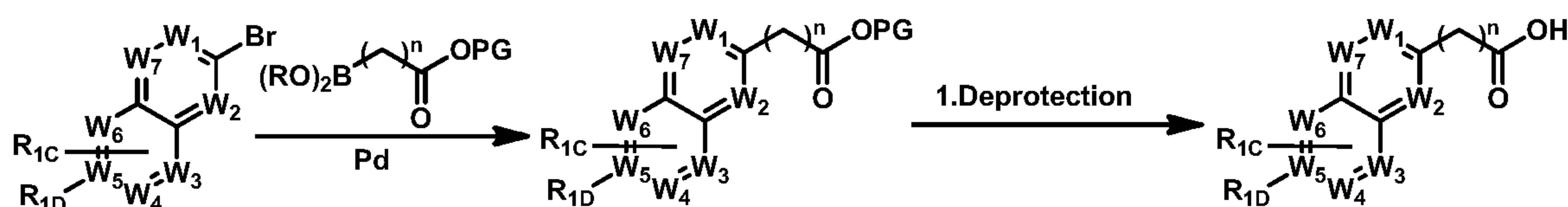
20 chloride^{S4} and this compound can be used to acylate the N-terminus of the peptide. Heterocycles where Friedel-Crafts acylations are not possible can be halogenated (and appropriately protected using standard protecting groups^{S1}) and an appropriate length hydrocarbon chain terminated on one end with a protected amine and the other end with a halogen or boronic acid/ester attached via palladium mediated coupling.

25 (B)



wherein W^1 , W^2 , W^3 , W^4 , W^5 , W^6 , and W^7 are each independently C or N, provided that no more than three of W^1 , W^2 , W^3 , W^4 , W^5 , W^6 , and W^7 are N; provided that when R^{1C} or R^{1D} is non-hydrogen, any W atom to which the R^{1C} or R^{1D} is respectively bonded is C, wherein either ring can bear one or more R^{1D} ; R^{1C} is hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1D} is hydrogen, alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1C} or R^{1D} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment.

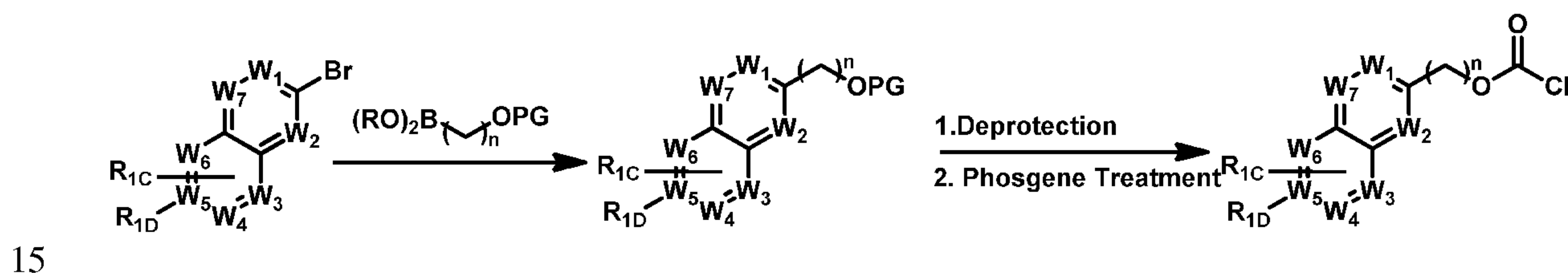
For compounds where the R^5 linkage to the peptide is an acyl group and where the aromatic rings are connected directly to the acyl group these compounds can be synthesized by peptide coupling of commercially available heterocyclic acids that are substituted by electrophilic aromatic substitution, nucleophilic aromatic substitution, heteroarylolithium formation or palladium catalyzed processes (and appropriately protected using standard protecting groups^{S1}) to the N-terminus of the peptide chain. Heterocycles where the commercially available acids are not available can be synthesized via any one of a number of methods for synthesizing quinolines, isoquinolines, quinazolines, quinoxalines or 1,8-naphthyridines^{S2}.



For compounds where the R^5 linkage to the peptide is an acyl group and where the aromatic ring is not connected directly to the acyl group, these compounds can be synthesized via the above scheme. Halogenated and appropriately functionalized or

unfunctionalized aryl rings (appropriately protected using standard protecting groups^{S1}) and an appropriate length hydrocarbon chain terminated on one end with a protected carboxylate and the other end with a halogen or boronic acid/ester can be attached via palladium mediated coupling

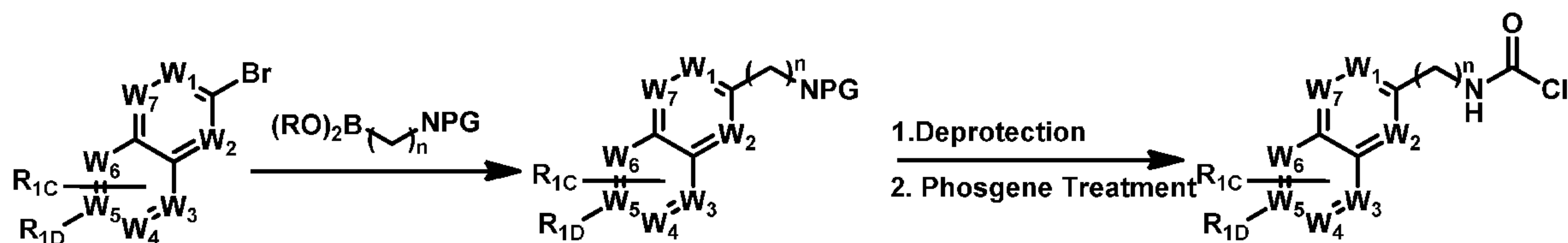
- 5 For compounds where the R⁵ linkage to the peptide is a carbamate and the aryl rings are attached directly to the carbamate, these compounds can be by peptide coupling of commercially available heterocyclic alcohols that are substituted by electrophilic aromatic substitution, nucleophilic aromatic substitution, heteroaryllithium formation or palladium catalyzed processes (and appropriately protected using standard protecting groups^{S1}) to the N-terminus of the peptide chain. Heterocycles where the commercially available alcohols are not available can be synthesized via any one of a number of methods for synthesizing quinolines, isoquinolines, quinazolines, quinoxalines or 1,8-naphthyridines^{S2}.



- For compounds where the R⁵ linkage to the peptide is a carbamate and the aryl rings are not attached directly to the carbamate, these compounds can be synthesized via the above scheme. Halogenated and appropriately functionalized or unfunctionalized aryl rings (appropriately protected using standard protecting groups^{S1}) and an appropriate length hydrocarbon chain terminated on one end with a protected alcohol and the other end with a halogen or boronic acid/ester can be attached via palladium mediated coupling. The alcohol can then be deprotected, the compound treated with phosgene and the resulting carbamoyl chloride used to acylate the N-terminus of the peptide.
- 20

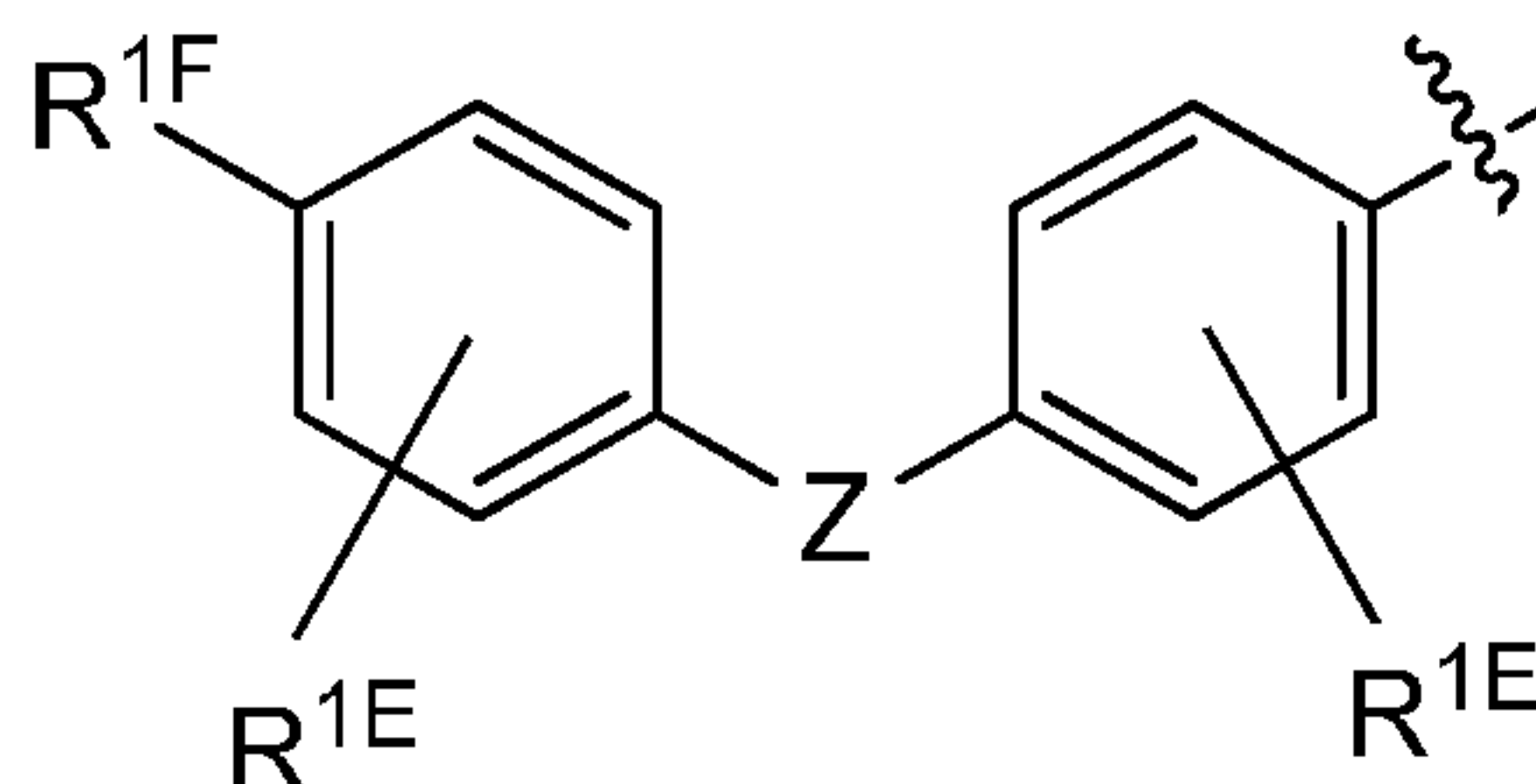
- For compounds where the R⁵ linkage to the peptide is a urea and the aryl rings are attached directly to the urea, these compounds can be synthesized by peptide coupling of commercially available heterocyclic amines that are substituted by electrophilic aromatic substitution, nucleophilic aromatic substitution, heteroaryllithium formation or palladium catalyzed processes (and appropriately protected using standard protecting groups^{S1}) then treated with phosgene^{S4} to the N-terminus of the peptide chain.
- 25
- 30 Heterocycles where the commercially available amines are not available can be

synthesized via any one of a number of methods for synthesizing quinolines, isoquinolines, quinazolines, quinoxalines or 1,8-naphthyridines^{S2}.



- 5 For compounds where the R⁵ linkage to the peptide is a urea and the aryl rings are not attached directly to the urea, these compounds can be synthesized via the above scheme. Halogenated and appropriately functionalized or unfunctionalized aryl rings (appropriately protected using standard protecting groups^{S1}) and an appropriate length hydrocarbon chain terminated on one end with a protected amine and the other end with a halogen or boronic acid/ester can be attached via palladium mediated coupling. The
- 10 a amine can then be deprotected, the compound will be treated with phosgene and the resulting carbamoyl chloride used to acylate the N-terminus of the peptide.

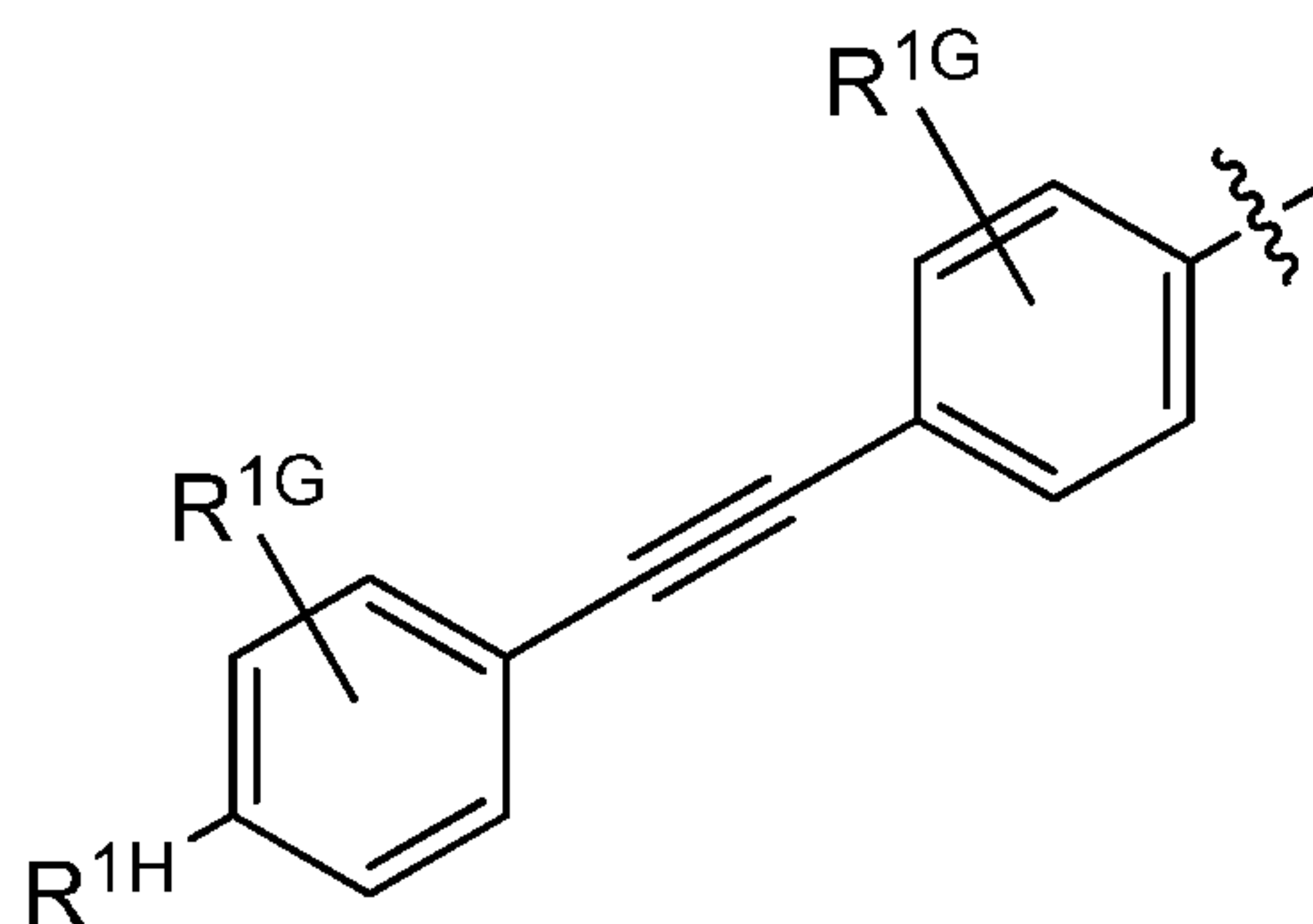
(C)



- 15 wherein Z is O, S, NH or CH₂; R^{1E} at each occurrence is independently hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁- C₆)-alkyl, (C₁- C₆)-alkoxy, (C₁- C₆)-mono- or di-alkylamino, (C₁- C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1F} is hydrogen or alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁- C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁- C₆)-alkoxy, (C₁- C₆)-mono- or di-alkylamino, (C₁- C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1E} or R^{1F} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl,
- 20 aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)thioalkyl, fluoroalkoxy, cyano, (C₁- C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment.

In addition to the procedures outlined above for attachment to the peptide, compounds of this functionality are synthesized by employment of the Buchwald-Hartwig coupling conditions^{S5} when Z = O or N. Where a para-halogen substituted protected benzoic acid, homologated benzoic acid or precursor is coupled with a phenol functionalized by electrophilic or nucleophilic aromatic substitution or palladium catalyzed processes (and appropriately protected using standard protecting groups^{S1}). When Z = S these compounds can be formed using transition metal catalyzed couplings of a para-halogen substituted protected benzoic acid, homologated benzoic acid or precursor combined with an appropriately functionalized thiophenol.

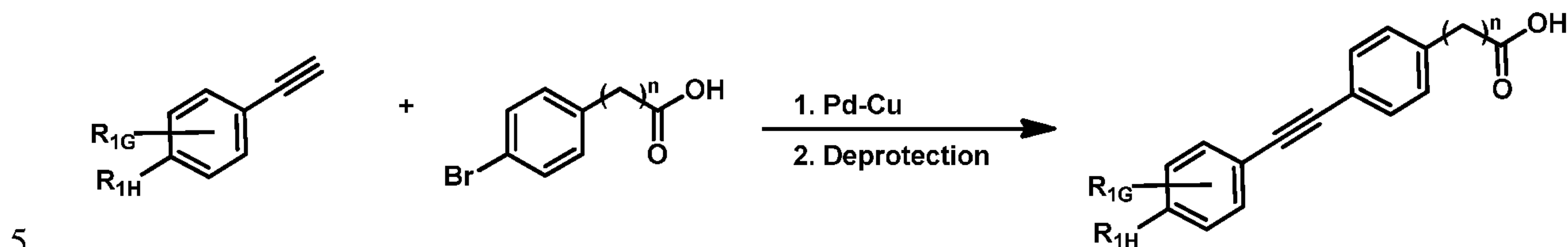
10 (D)



wherein R^{1G} at each occurrence is independently hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1H} is hydrogen or alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1G} or R^{1H} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment.

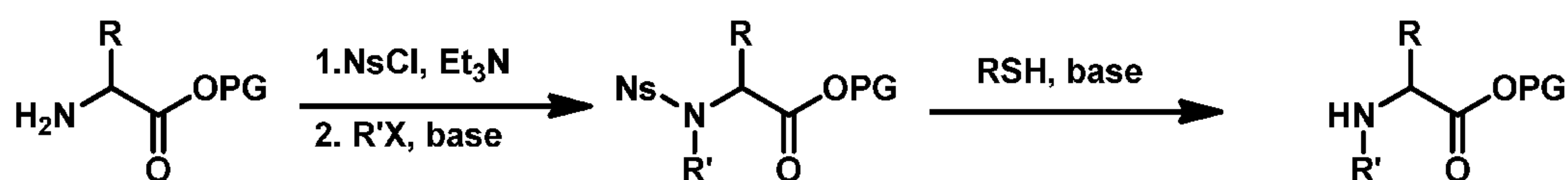
In addition to the procedures outlined above for attachment to the peptide, compounds of this functionality can be synthesized by employment of Sonagashira reaction conditions^{S6} on a para-halogen substituted protected benzoic acid, homologated

benzoic acid or precursor combined with the appropriately functionalized by electrophilic or nucleophilic aromatic substitution or palladium catalyzed processes (and appropriately protected using standard protecting groups^{S1}) aryl acetylene as shown in the below scheme.

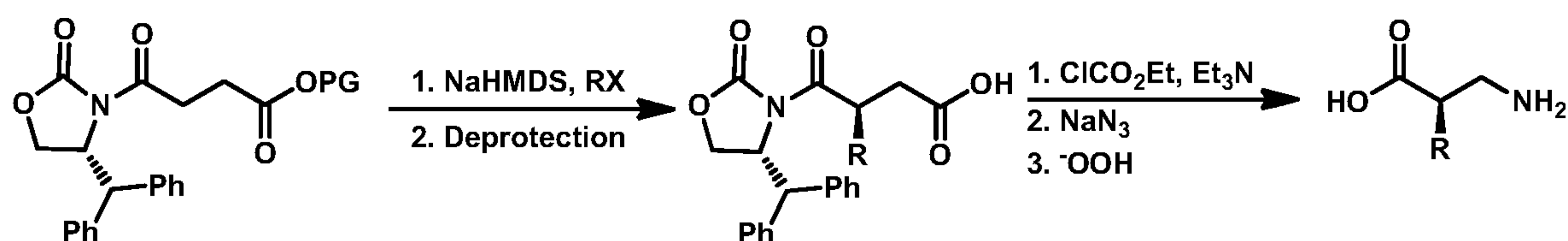


The peptidic tail can be assembled analogously to procedures described herein using standard solution or solid phase peptide couplings. Constituent amino acids containing substituents at the R^{A3}, R^{A4}, and R^{A5} positions, and the groups of formulas (IIA), (IIB), and (IIC), can either be purchased commercially or synthesized via amino acid synthesis procedures described in the literature^{S7-S9}.

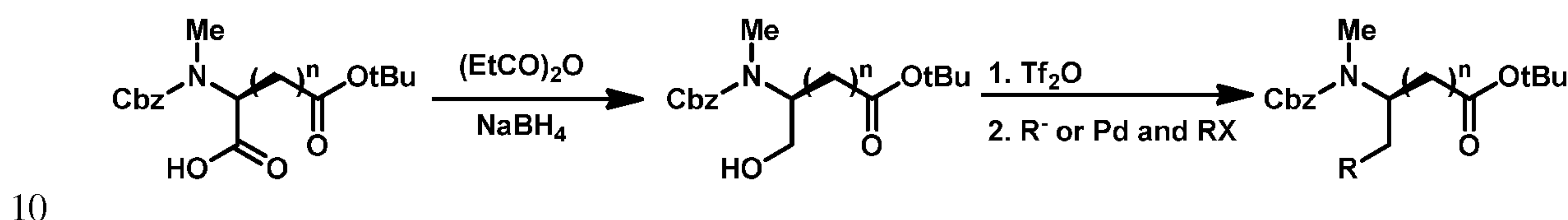
Peptidic tails where any R⁴ or R⁶ are not hydrogen can be assembled using literature protocols for peptide-peptoid conjugates^{S10}. The monomers can be synthesized using amine alkylation protocols^{S11} for example an amino acid with a protected carboxylate is protected at the amine with a nosyl group, the nosylated amine is selectively alkylated with base and an electrophile and the nosyl group is deprotected by thiolate anion.



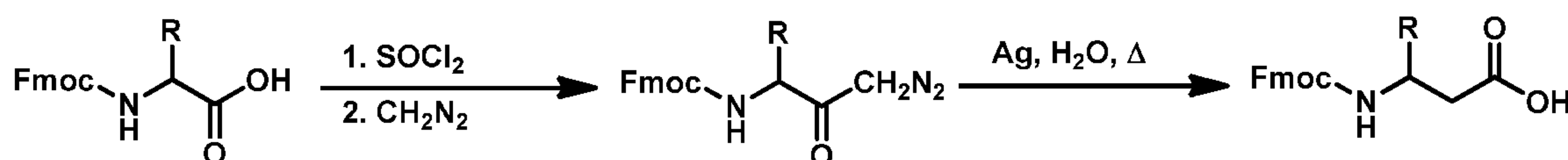
Where m, n1, or n2 are either 0 or 1, amino acids building blocks where m, n1, and n2 are equal to 1 are commercially available or can be synthesized via methods found in the literature^{S12}, for example from succinates where one acid is protected with a carboxyl protecting group and the other attached to a chiral auxiliary which then allows asymmetric monoalkylation. The protected carboxyl can then be deprotected and transformed into an amine via a Curtius rearrangement followed by cleavage of the chiral auxiliary with peroxide.



Where m, n1, and n2 are 0, 1 or 2, amino acids building blocks where m, n1, and n2 are equal to 1 or 2 can be synthesized analogously wherein the differentially protected aspartic or glutamic acid is functionalized at the free carboxylate attached to the alpha carbon by any number of strategies including but not limited to peptide coupling,
 5 reduction whereby the acid can be converted to a functionalized ketone via a Weinreb amide or reduction whereby the acid is converted to an alcohol that is subsequently converted to a tosylate and either displaced by a nucleophile or coupled to another aryl or alkyl group via a palladium mediated process:



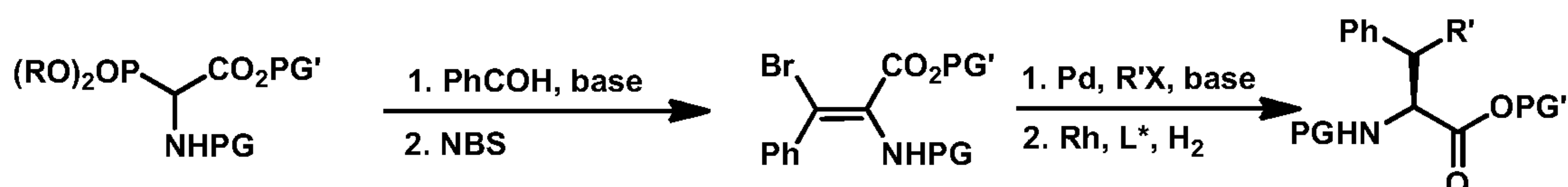
These amino acids can be synthesized via protocols found in the literature^{S12-S13} for example Arndt Eistert homologation(s) as shown in the below scheme.



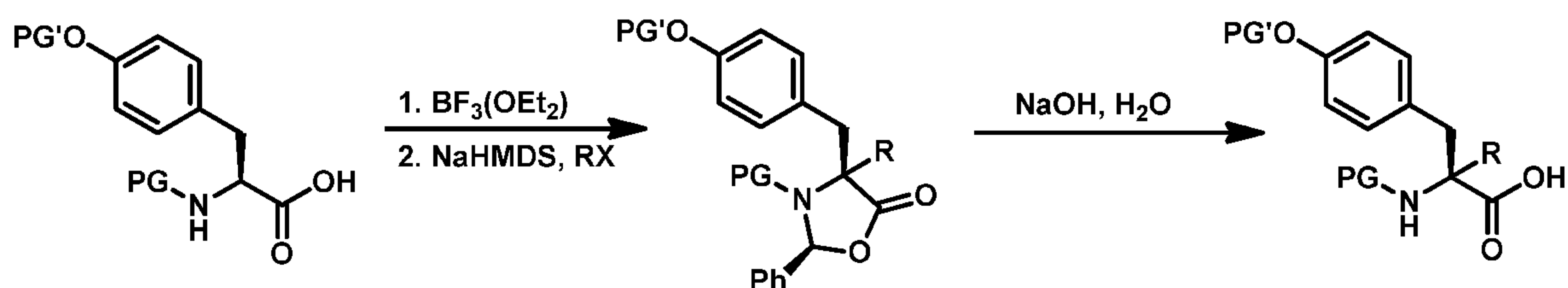
15 Amino acids building blocks for the synthesis of compounds where R² and R³ are each independently not hydrogen can either be purchased commercially or can be synthesized via amino acid synthesis procedures described in the literature^{S7-S9,S14} and appropriately protected using standard protecting groups^{S1}.

20 Where OG¹ and OG² hydroxyl, O-alkyl, or O-glycosyl, compounds can be synthesized by protocols developed for synthesis of the arylomycin natural product^{S15}.

Where R^{A1} is not hydrogen can be synthesized by the methods described for the synthesis of the arylomycin macrocycle. The tyrosine derivatives required as building blocks for that synthesis can be synthesized as described by Michaux et. al.^{S16} and the references described therein. A Horner Wadsworth Emmons reaction can be used,
 25 followed by halogenations of the alkene Suzuki coupling of the desired substituent and asymmetric catalytic hydrogenation to the desired tyrosine derivative.



Where R^{A2} is not hydrogen, compounds can be synthesized using protocols for the synthesis of the natural product and protocols for peptide coupling of disubstituted amino acids^{S17}. The amino acid building blocks can be synthesized by literature protocols^{S18}. For example the amino and carboxyl groups of an appropriately protected tyrosine can be condensed with benzaldehyde to form an oxazolidinone which can then be asymmetrically alkylated with strong base and an electrophile and hydrolyzed to yield the substituted tyrosine derivative^{S19}.



Compounds where a carbonyl group is directly attached to the scaffold at B can be synthesized from the fully deprotected arylomycin. Peptide coupling to an amino acid where the carboxylate is replaced by a protected or unprotected electrophilic moiety can install the aldehydes^{S20}, boronic acids/esters^{S21} and phosphonates^{S22}. Azetidinones that are attached to the arylomycin through an amine at the 3-position of the azetidinone ring can be synthesized via peptide coupling of the amine of the azetidinone to the carboxylate of arylomycin^{S23}. Azetidinones that are attached to the arylomycin through the cyclic nitrogen can be synthesized by peptide coupling of the cyclic NH to the arylomycin carboxylate^{S24}. The azetidinone building blocks can be synthesized via literature protocols^{S25-S26}.

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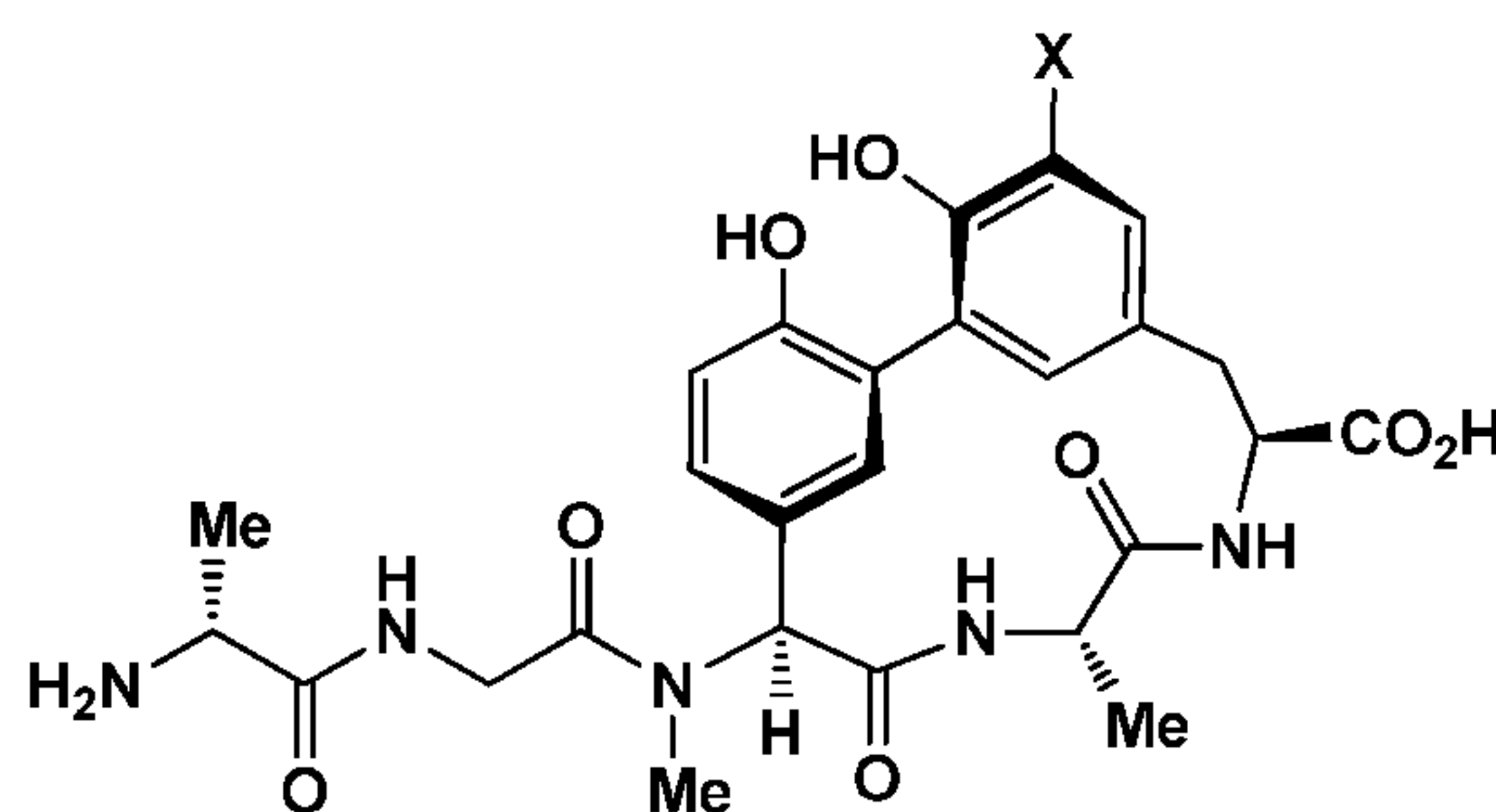
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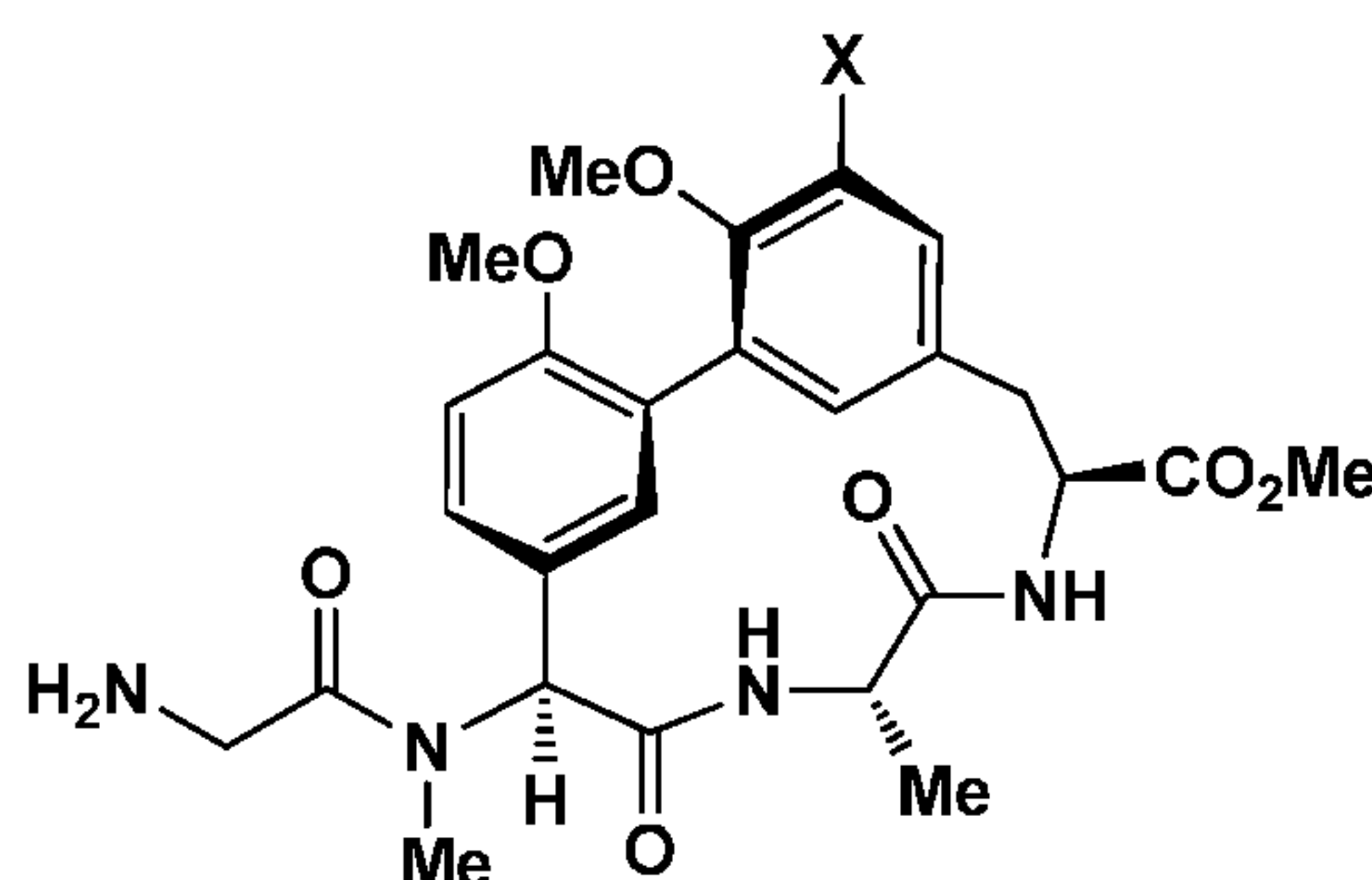
Semisynthesis

Compounds of the invention can also be prepared by semisynthesis, that is, through synthetic conversions applied to arylomycin compounds isolated from natural sources such as fermentation broths or in vitro biosynthesis systems.

- 5 It is known in the art that the natural product arylomycin, such as arylomycin A2, can be isolated and purified from its microbial source.^{N1-N2} The natural product can then be treated with a 50:50 mixture of trifluoroacetic acid and CH₂Cl₂ to cleave off the n-terminal lipid and N-Me serine residue leaving a free amine, as shown below. When the arylomycin starting material is in the A series, X is hydrogen, and when the arylomycin
- 10 starting material is in the B series, X is nitro.

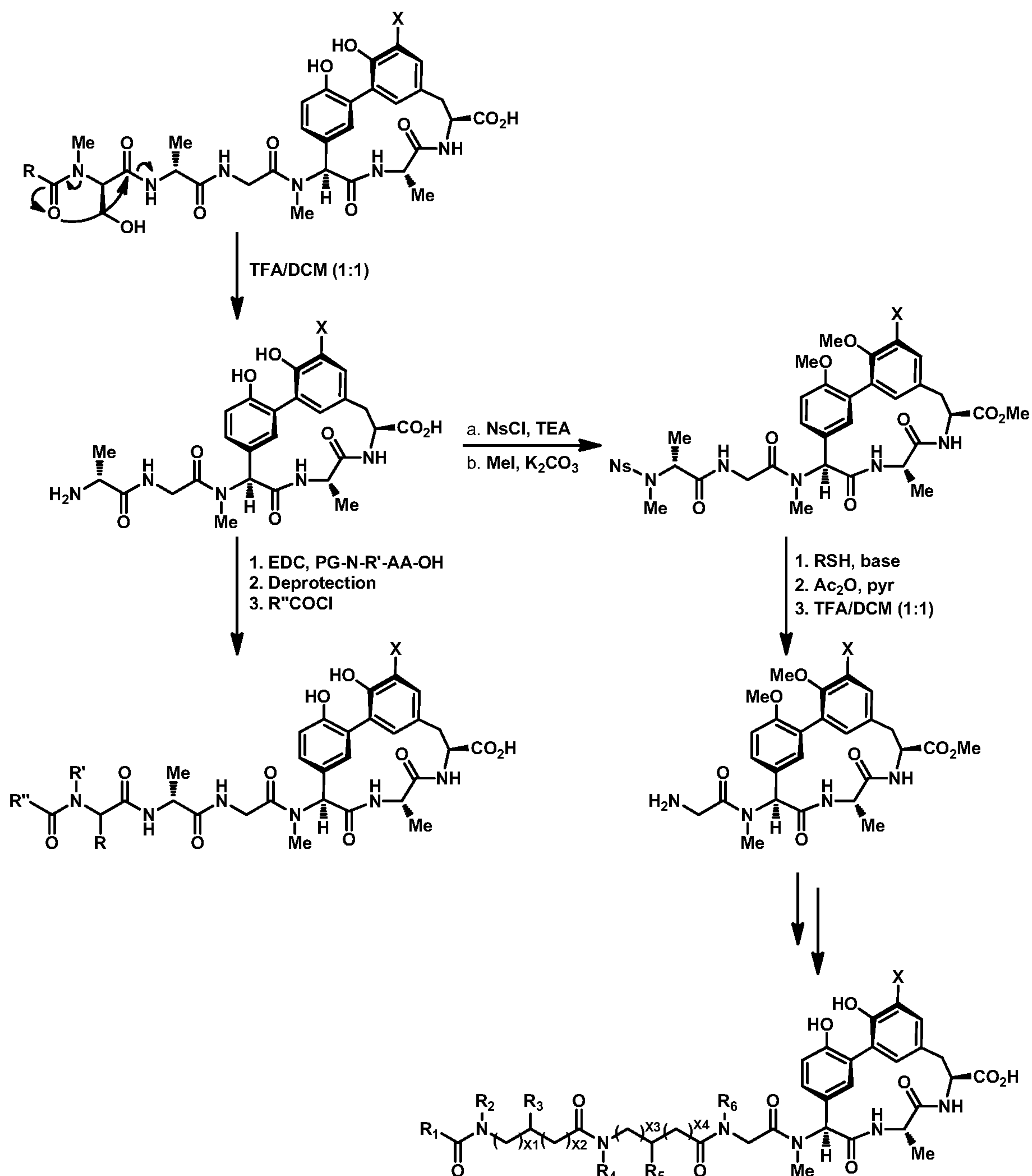


- The resulting free amine can then either be coupled to a new N-alkyl amino acid and lipid tail or protected with a nosyl group, selectively methylated, denosylated^{N3}, acetylated and treated again with a 50:50 mixture of trifluoroacetic acid and CH₂Cl₂ to
- 15 cleave off the N-terminal alanine.



The free amine of the alanine cleaved compound can then be alkylated, if desired, then coupled to an appropriately functionalized and protected lipodipeptide tail and globally deprotected^{N4} (scheme 2, below).

Scheme 2: Semisynthetic Precursor Preparation and Elaboration



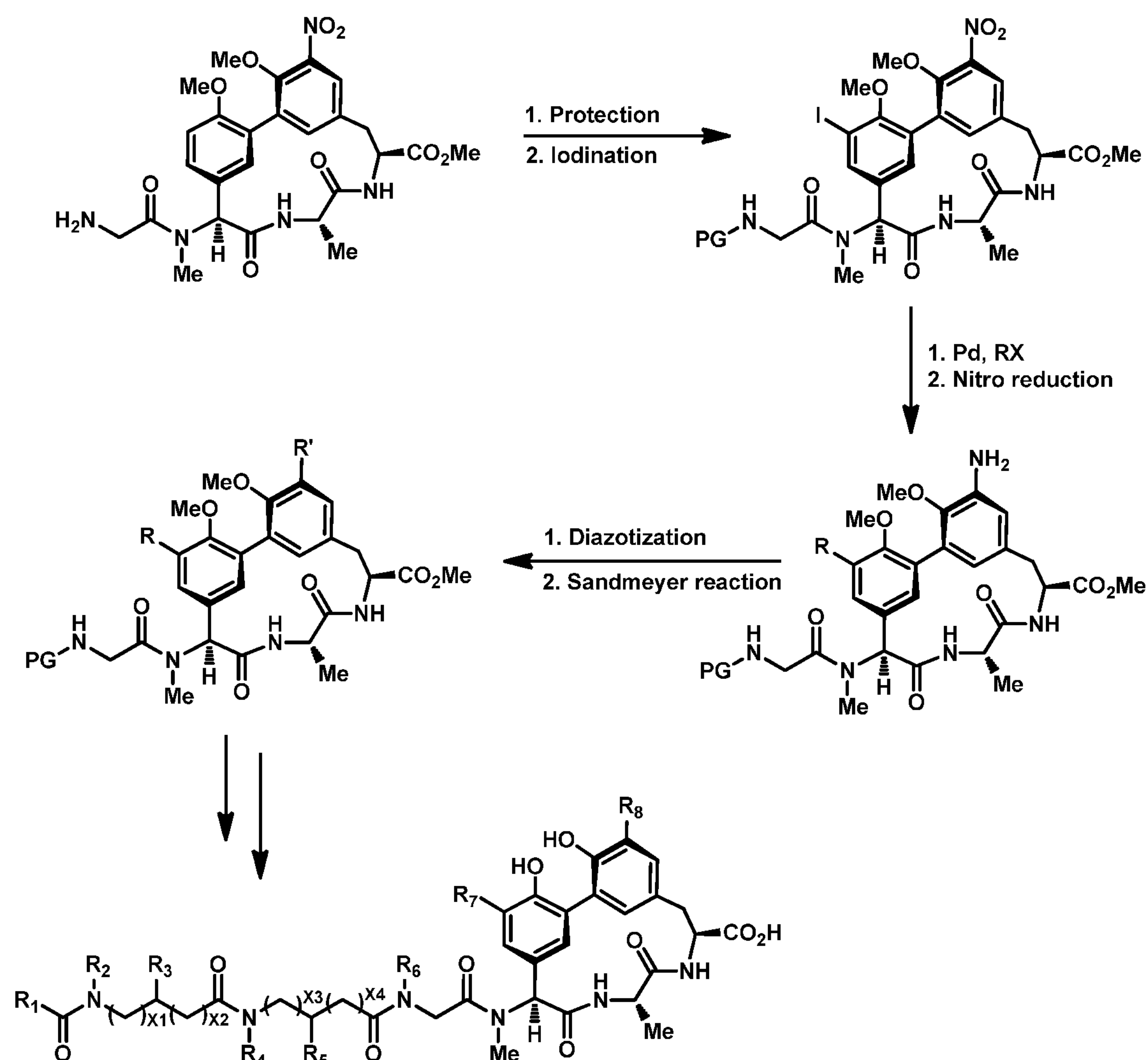
- 5 The isolated natural product of the arylomycin B series bears a nitro group on the tyrosine^{N1-N2}, so the free amine that is the result of TFA mediated cleavage of the lipid tail and N-terminal serine of this compound, or the free amine that is the result of cleavage of the lipid tail and the N-terminal serine and alanine residues of this compound, contain a nitro functionality that can then be used to prepare other

modifications of the tyrosine ring and, due to the nitro deactivation of the tyrosine ring, of the hydroxyphenylglycine ring as well. After protection or deprotection with the appropriate protecting groups^{N5} the nitro compounds of the arylomycin B derivatives can be selectively iodinated ortho to the hydroxyl of the hydroxyphenylglycine residue. This
5 compound can then be functionalized to install numerous chemical groups selectively on the hydroxyphenylglycine ring using, for example, palladium mediated coupling^{N6}. For further functionalization of the tyrosine ring, after appropriate protection or deprotection, the nitro group can be reduced to an amine and converted into a diazo salt^{N7}. This compound can be subsequently functionalized via the Sandmeyer reaction^{N8} to yield a
10 variety of different functional groups. The resulting compound can then be attached to a lipopeptide tail via peptide coupling, then globally deprotected^{N4} (scheme 3, below).

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Scheme 3: Semisynthetic Preparation of Aryl Ring Derivatives



5

Signal Peptidase (SPase)

As described and illustrated herein, arylomycin antibiotics can inhibit the bacterial type I signal peptidase (SPase) enzyme, an essential serine-lysine dyad protease that is anchored to the outer leaflet of the bacterial cytoplasmic membrane and that removes N-terminal signal peptides from proteins that are transported out of the cytoplasm. Bacterial SPase proteases appear to be present and essential in all *Eubacteria*. However, not all *Eubacteria* are susceptible to arylomycin antibiotics.

According to the invention, the sequence of a bacterial SPase is correlated with susceptibility or resistance to arylomycin antibiotics. In particular, the presence of one or more proline residues near the catalytic serine gives rise to an arylomycin-resistant

phenotype. The term "resistant" or "resistance" is used to refer to the reduced sensitivity of a strain harboring a resistance-conferring Pro relative to the isogenic strain without the Pro, and not to the absolute sensitivities of the different bacteria (*e.g.* resistant *S. epidermidis* is inhibited with an MIC of 8 µg/ml and is significantly more sensitive to
 5 arylomycin C₁₆ than the resistant mutants of the other pathogens, which are not inhibited at concentrations as high as 128 µg/ml).

Sequences for bacterial SPase nucleic acids and polypeptides are publicly available, for example, in the database maintained by the National Center for Biotechnology (ncbi.nlm.nih.gov) and can be used to make probes, primers and antigens
 10 useful for detecting arylomycin-susceptible or arylomycin-resistant bacteria.

For example, the *Staphylococcus epidermidis* RP62A signal peptidase IB has the following sequence (SEQ ID NO:1; see NCBI accession no. YP_188144.1, gi:57866486).

```

      1 MKKEILEWIV AIAVAIALIA IITKFVVGKSY SIKGDSMDPT
  15    41 LKDGERVVVN IIGYKLGGEV KGNVIVFHAN KKDDYVKRVI
      81 GTPGDSVEYK NDTLYVNGKK QSEPYLNYNE KRKQTEYITG
     121 SFKTKNLPNA NPQSNVIPKG KYLVLGDNRE VSKDSRSFGL
     161 IDKDQIVGKV SLRYWPFSEF KSNFNPNTK N
  
```

20 The underlining shows the region of the catalytic serine, which is at position 36 in this SPase sequence. A nucleic acid sequence for the SEQ ID NO:1 *Staphylococcus epidermidis* RP62A signal peptidase IB can have the following sequence (SEQ ID NO:2, see NCBI accession no. NC_002976.3, GI:57865352).

```

      1 TTGAAAAAAG AAATTTTAGA GTGGATTGTT GCCATAGCCG
  25    41 TTGCCATTGC ACTTATTGCC ATAATCACTA AATTTGTCGG
      81 AAAATCATAT TCTATTAAAG GTGATTCAAT GGATCCTACA
     121 TTAAAAGATG GGGAGCGTGT AGTGGTAAAT ATTATTGGCT
     161 ATAAATTAGG TGGCGTTGAA AAAGGAAATG TCATTGTATT
     201 TCATGCTAAT AAAAAGATG ATTATGTTAA AAGAGTTATT
  30    241 GGAAGTCCAG GAGATAGTGT TGAATATAAA AATGATACAC
      281 TCTATGTTAA TGGTAAAAAG CAATCAGAAC CATACTTGAA
     321 CTATAATGAA AAACGTAAGC AAAGTGAAGT TATCACAGGT
     361 AGTTTCAAAA CAAAAAATTT ACCAAATGCT AATCCTCAAT
     401 CTAATGTTAT TCCTAAAGGT AAATATTTAG TTTTGGGGGA
  35    441 TAACCGTGAG GTAAGTAAAG ATAGTCGTTC ATTCGGTTTA
      481 ATTGACAAAG ACCAAATTGT TGGAAAGGTA TCGCTCAGAT
     521 ATTGGCCTTT CAGTGAATTT AAATCTAACT TTAATCCAAA
     561 TAACACTAAA AATTAA
  
```

According to the invention, a bacterium having a mutant SPase gene is resistant to arylomycin antibiotics when one or more proline residues are present near the catalytic serine (e.g., at position 36 in SEQ ID NO:1) of the SPase polypeptide, for example, within about 10 amino acid positions on the N-terminal side of the catalytic serine of the SPase polypeptide. Thus, as illustrated herein, a bacterium with a proline between about amino acid position 28 to about amino acid position 35 of the SEQ ID NO:1 SPase amino acid sequence tends to exhibit resistance to arylomycin antibiotics. In some embodiments, the proline residue that gives rise to arylomycin resistance is present at about position -7 relative to catalytic serine. In other embodiments, the proline residue that gives rise to arylomycin resistance is present at about position -5 relative to catalytic serine. For example, in the SEQ ID NO:1 SPase sequence, a proline at position 29 or a proline at position 31 gives rise to arylomycin resistance.

One aspect of the invention therefore includes a method for detecting whether bacterial cells susceptible to arylomycin compounds are present in a test sample. Such susceptibility can be detected by detecting whether a SPase polypeptide is present that does not have a proline near the catalytic serine, for example, within about 10 amino positions on the N-terminal side of the catalytic serine and about two positions on the C-terminal side of the bacterial SPase polypeptide (e.g., within about positions 26-38 of SEQ ID NO:1). The absence of such a proline within the SPase polypeptide sequence indicates that bacterial cells within the sample are susceptible to arylomycin treatment.

In some embodiments, the method may also include detecting whether bacteria are present in a test sample. The presence or absence of a proline in the SPase polypeptides can be simultaneously or subsequently detected to ascertain whether bacterial cells in the test sample are resistant or susceptible, respectively, to arylomycin compounds.

The presence of bacterial resistance to arylomycin compounds can be detected by determining whether a proline is present within about 10-12 amino acids of the catalytic serine in a SPase polypeptide. For example, an antibody that is specific for the proline-containing SPase polypeptide can be employed. Such a specific antibody binds with detectably greater affinity to a SPase polypeptide having one or more prolines than to a corresponding SPase polypeptide that does not have any such proline residues.

Conversely, the presence of susceptibility to arylomycin compounds can be detected by determining whether no proline residues are present within about 10-12 amino acids of the catalytic serine in a SPase polypeptide. An antibody specific for a SPase polypeptide that does not have a proline within about 10-12 amino acids of the

catalytic serine in a SPase polypeptide can, for example, be used to detect whether a bacteria cell in a test sample is susceptible to arylomycin treatment.

Alternatively, such antibiotic resistance or susceptibility can be detected by detecting a nucleic acid encoding a SPase protein with such a proline residue. Thus, for example, nucleic acids in a test sample can be isolated using available procedures and the presence of a nucleic acid can be detected that encodes a SPase protein with or without such a proline residue. These isolated nucleic acids can be tested by available hybridization and/or nucleic acid amplification procedures to ascertain whether proline-encoding or non-proline-encoding SPase nucleic acids are present in the test sample.

Probes, primers and antigenic peptides useful for detecting the presence or absence of a proline within a SPase nucleic acid or polypeptide can readily be designed by one of ordinary skill in the art. For example, the following description illustrates how the SEQ ID NO:1 and 2 sequences can be used to design such probes, primers and/or antigenic peptides.

When the SEQ ID NO:1 and 2 sequences are aligned as illustrated below, the nucleic acid and amino acid sequences near the catalytic serine become apparent, as well as the sequences and codons that can become proline residue(s) in arylomycin resistant SPases (e.g., the underlined sequences).

DNA: ATGAAAAAAGAAATTTTAGAGTGGATTGTTGCCATAGCCGTTGCCATTGCA
1: M K K E I L E W I V A I A V A I A

DNA: CTTATTGCCATAATCACTAAATTTGTCGGAAAATCATATTCTATTAAAGGT
18: L I A I I T K F V G K S Y S I K G

DNA: GAT**TCA**ATGGATCCTACATTAAAAGATGGGGAGCGTGTAGTGGTAAATATT
35: D **S** M D P T L K D G E R V V V N I

DNA: ATTGGCTATAAATTAGGTGGCGTTGAAAAAGGAAATGTCATTGTATTTTCAT
+1: I G Y K L G G V E K G N V I V F H

DNA: GCTAATAAAAAAGATGATTATGTTAAAAGAGTTATTGGAACCTCCAGGAGAT
+1: A N K K D D Y V K R V I G T P G D

DNA: AGTGTTGAATATAAAAATGATACACTCTATGTTAATGGTAAAAAGCAATCA
35 +1: S V E Y K N D T L Y V N G K K Q S

DNA: GAACCATACTTGAACCTATAATGAAAAACGTAAGCAAACCTGAGTATATCACA
+1: E P Y L N Y N E K R K Q T E Y I T

DNA: GGTAGTTTCAAAACAAAAAATTTACCAAATGCTAATCCTCAATCTAATGTT
40 +1: G S F K T K N L P N A N P Q S N V

DNA: ATTCCTAAAGGTAAATATTTAGTTTTGGGGGATAACCGTGAGGTAAGTAAA
 +1: I P K G K Y L V L G D N R E V S K

5 DNA: GATAGTCGTTTCATTCGGTTTAATTGACAAAGACCAAATTGTTGGAAAGGTA
 +1: D S R S F G L I D K D Q I V G K V

DNA: TCGCTCAGATATTGGCCTTTTCAGTGAATTTAAATCTAACTTTAATCCAAAT
 +1: S L R Y W P F S E F K S N F N P N

10 DNA: AACACTAAAAATTAA
 +1: N T K N *

As described herein, when position -7 or position -5 from the catalytic serine is occupied by a proline rather than a serine, bacteria containing such a SPase enzyme are arylomycin resistant. When no such proline is present in the SPase enzyme, the bacteria are arylomycin susceptible. In the SEQ ID NO:1 SPase amino acid sequence, the -7 position is at position 29 and the -5 position is at position 31 -- serine is typically present in both positions within the wild type, arylomycin-susceptible SEQ ID NO:1 sequence.

Examples of shorter SPase peptide and nucleotide sequences from SEQ ID NO:1 and 2 that are correlated with arylomycin resistance or susceptibility include the following, where the position of the mutation in the nucleotide sequence is noted with a small arrow.

	DNA: <u>GTCGGAAAATCATATTCTATTAAAGGTGATTCA</u>	Arylomycin
	Susceptible	
25	28: <u>V G K S Y S I K G D S</u>	SEQ ID NOs:3 and 4
	↓	
	DNA: <u>GTCGGAAAACCATATTCTATTAAAGGTGATTCA</u>	Arylomycin
	Resistant	
30	28: <u>V G K P Y S I K G D S</u>	SEQ ID NOs:5 and 6
	↓ ↓	
	DNA: <u>GTCGGAAAACCGTATTCTATTAAAGGTGATTCA</u>	Arylomycin
	Resistant	
35	28: <u>V G K P Y S I K G D S</u>	SEQ ID NOs:7 and 6
	↓ ↓	
	DNA: <u>GTCGGAAAACCCTATTCTATTAAAGGTGATTCA</u>	Arylomycin
	Resistant	
40	28: <u>V G K P Y S I K G D S</u>	SEQ ID NOs:8 and 6
	↓ ↓	
	DNA: <u>GTCGGAAAACCTTATTCTATTAAAGGTGATTCA</u>	Arylomycin
	Resistant	
45	28: <u>V G K P Y S I K G D S</u>	SEQ ID NOs:9 and 6

5	DNA: <u>GTCGGAAAATCATATCCTATTAAAGGTGATTCA</u> Resistant 28: <u>V G K S Y P I K G D S</u>	Arylomycin SEQ ID NOs:10 and 11
10	DNA: <u>GTCGGAAAATCATATCCCATTAAAGGTGATTCA</u> Resistant 28: <u>V G K S Y P I K G D S</u>	Arylomycin SEQ ID NOs:12 and 11
15	DNA: <u>GTCGGAAAATCATATCCAATTAAAGGTGATTCA</u> Resistant 28: <u>V G K S Y P I K G D S</u>	Arylomycin SEQ ID NOs:13 and 11
20	DNA: <u>GTCGGAAAATCATATCCGATTAAAGGTGATTCA</u> Resistant 28: <u>V G K S Y P I K G D S</u>	Arylomycin SEQ ID NOs:14 and 11

25

The first set of nucleotide and peptide sequences are just short sequences taken from the wild type, arylomycin susceptible SEQ ID NO:1 and 2 SPase sequences. Note that proline is encoded by four different codons (CCT, CCC, CCA, CCG), so four different SPase nucleotide sequences (e.g., SEQ ID NOs: 5, 7, 8 and 9) can exist for each proline-containing SPase polypeptide (e.g., a SPase polypeptide containing SEQ ID NO:6).

30

Primers and probes can readily be designed that are complementary to nucleic acids encoding SPase-susceptible (non-proline containing) or SPase-resistant (proline-encoding) polypeptides. Such primers and probes can be designed to have sufficient sequence identity and/or sufficient complementary sequence identity to selectively hybridize with bacterial nucleic acids that encode SPase-susceptible (non-proline containing) or SPase-resistant (proline-encoding) polypeptides, and thereby permit detection of whether bacteria are arylomycin susceptible or arylomycin resistant. For example, to detect whether *S. epidermidis* bacteria in a test sample are arylomycin susceptible or arylomycin resistant primers or probes are designed to selectively hybridize to regions of nucleic acids that include any of SEQ ID NOs:3, 5, 7-10, 12, 13 or 14. Further information is provided below on selective hybridization and on the selection of probes and primers to detect bacterial nucleic acids that encode SPase-

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susceptible (non-proline containing) or SPase-resistant (proline-encoding) polypeptides, and thereby permit detection of whether bacteria are arylomycin susceptible or arylomycin resistant. For example, the Examples provide specific primer sequences that can be used to detect an/or isolate SPase nucleic acids.

5 One of skill in the art can also readily generate antibodies that selectively bind to bacterial SPase-susceptible (non-proline containing) polypeptides or SPase-resistant (proline-encoding) polypeptides, and to use those antibodies to detect whether bacteria are arylomycin susceptible or arylomycin resistant. For example, peptides or polypeptides that contain any of SEQ ID NOs:4, 6 or 11 can be used to generate such
10 antibodies. These antibodies can be screened to identify antibody preparations that selectively bind to bacterial SPase-susceptible (non-proline containing) polypeptides or SPase-resistant (proline-encoding) polypeptides. Further information is provided below on making and using antibodies for detecting SPase-susceptible (non-proline containing) or SPase-resistant (proline-encoding) polypeptides, to thereby detect whether bacteria
15 with such polypeptides are arylomycin susceptible or arylomycin resistant.

Primers and/or probes can be made from other bacterial SPase polypeptide and nucleic acid sequences, for example, any of those described herein or available in sequence databases. For example, the *Staphylococcus epidermidis* RP62A signal peptidase I has the following sequence, where the catalytic serine is identified in bold
20 and with underlining (SEQ ID NO:15; see NCBI accession no.YP_187624.1, gi:57865986).

```

1  MKKEIIIEWIV AIIVAIVIVT LVQKFLFASY TVKGASSMHPT
41 FENREKVIVS RIAKTLDHID TGDVVIFHAN AKQDYIKRLI
81 GKPGDSVEYK KDQLYLNK GK VDEPYLSENK KHKVGEYLTE
25 121 NFKSRDLKGT NGNMKIPSGK YLVLGDNRQN SIDSRMDEVG
161 LLDKNQVVVGK VVLRYPFNR WGGSFNPGTF PN

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The nucleotide sequence for the SEQ ID NO:15 *Staphylococcus epidermidis* RP62A signal peptidase I has the following sequence (SEQ ID NO:16; see NCBI accession no.
30 NC_002976.3 GI:57865352).

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1  ATGAAGAAAG AAATAATAGA ATGGATTGTA GCCATAATCG
41 TTGCAATTGT TATCGTCACA CTTGTGCAA AGTTTTTATT
81 TGCTTCTTAT ACAGTCAAAG GAGCATCTAT GCATCCAACA
121 TTTGAAAATC GAGAAAAAGT GATAGTAAGT CGTATAGCAA
35 161 AAACGCTTGA TCATATTGAT ACAGGAGATG TAGTGATTTT
201 TCATGCTAAC GCGAAGCAAG ATTATATTAA GCGACTTATT

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241 GGTAACCCAG GTGATTCAGT AGAATATAAA AAAGATCAAC
 281 TATATTTAAA CGGTAAAAAA GTAGATGAGC CTTATTTAAG
 321 TGAAAATAAA AAACATAAAG TTGGAGAATA TCTAACGGAA
 361 AACTTTAAGT CTAGAGATCT TAAGGGTACG AATGGCAATA
 5 401 TGAAAATTCC TAGTGGTAAA TACTTGGTTT TAGGTGATAA
 441 TCGTCAAAAC AGTATTGACA GTCGCATGGA TGAAGTAGGT
 481 CTTTTAGATA AAAATCAAGT TGTGGAATA GTAGTTTTGA
 521 GATACTGGCC ATTTAATCGG TGGGGCGGTA GTTTTAATCC
 561 TGGAACATTT CCTAACTAA
 10

Additional bacterial SPase sequences are available, for example, in the NCBI sequence database.

Genetically Modified Bacterial Signal Peptidases

15 Another aspect of the invention is a modified bacterial SPase and/or a bacterial host cell that includes a modified bacterial SPase. Such modified SPases are useful for identifying arylomycin compounds that can inhibit the activity of modified and/or naturally occurring SPases. For example, when a proline is present within about 10 amino acids N-terminal to the catalytic serine, the SPase does not effectively bind an
 20 arylomycin and the arylomycin does not effectively inhibit the activity of the SPase. The presence of the proline reduces arylomycin binding to such an extent that the effects of structural changes in the arylomycin compound structure cannot readily be detected.

According to the invention, one way to detect improved arylomycin structures during structure-activity studies is to observe the binding of a test arylomycin compound
 25 to an SPase that has been modified by replacement of the proline at position 5 to 7 N-terminal to the catalytic serine with another amino acid (e.g., a serine or other amino acid). Alternatively, improved arylomycin structures can be identified by observing the binding of a test arylomycin compound to an SPase that has been modified by replacement of a naturally occurring amino acid at position 5 to 7 N-terminal to the
 30 catalytic serine with a proline (thereby converting an arylomycin-susceptible SPase into an arylomycin-resistant SPase). These types of modified SPase enzymes therefore permit evaluation of test compounds against non-proline containing “arylomycin resistant” SPase sequences so that secondary sites of potential (minor) resistance can be identified and the arylomycin structure can be modified to address any such secondary
 35 sites of resistance. Similarly, SPases that are naturally resistant to arylomycin, due to the absence of a proline within about 10 amino acids of the catalytic serine, are modified by

substitution to place a proline at -5 to -7 positions N-terminal to the catalytic serine so that the test compounds can be identified that effectively bind and inhibit such an SPase even though there is a proline in what is otherwise an "arylomycin-susceptible" SPase structure.

5 Therefore, another aspect of the invention is a method of identifying a compound that can bind to and/or inhibit the activity of a bacterial SPase that involves contacting a modified SPase with a test compound and observing whether the test compound binds to and/or inhibits the activity of the modified SPase, wherein the modified SPase has a natural bacterial SPase amino acid sequence that has been modified at position -5 to -7
10 relative to the catalytic serine by substitution or replacement of a proline at that position. In some embodiments, a proline at position -5 and/or at position -7 is replaced with another amino acid (e.g., a serine). In other embodiments, the amino acid that is naturally present at position -5 and/or at position -7 is replaced with a proline. Test compounds that bind and/or inhibit the activity of the modified SPase are compounds of
15 interest.

 In another embodiment, test compounds that have antibiotic activity against bacteria are identified by contacting a culture of bacteria with the test compound and identifying whether the test compound inhibits the growth of the bacteria, wherein the bacteria express a modified SPase that has a natural bacterial SPase amino acid sequence
20 that has been modified at position -5 to -7 relative to the catalytic serine by substitution or replacement of a proline at that position. In some embodiments, a proline at position -5 and/or at position -7 is replaced with another amino acid (e.g., a serine). In other embodiments, the amino acid that is naturally present at position -5 and/or at position -7 is replaced with a proline. Test compounds that inhibit the growth of a bacterium
25 expressing such modified SPase have antibiotic activity.

 The bacteria can be modified by recombinant techniques available to those of skill in the art so that the bacteria express a modified SPase. Such techniques can include removal, replacement or mutation of an endogenous SPase gene so that endogenous SPase gene is not expressed, thereby allowing expression of only the
30 modified SPase enzyme. Such "knockout" procedures for removal, replacement and/or mutation of an endogenous gene in a bacterium are available in the art, and can readily be employed to generate bacterial populations that express a selected modified SPase enzyme.

Examples of procedures for generating such modified SPase enzymes and modified bacterial populations are provided, for example, in the Examples and in the art. A "knockout cassette" can be employed. Such a knockout cassette refers to a fragment of native chromosomal DNA having a foreign DNA piece that may provide a selectable
5 marker. In one embodiment "knock-out mutation cassettes" are created by interrupting a fragment of genomic DNA with a foreign piece of DNA, and replacing the wild-type chromosomal copy of the sequence with the knock-out cassette. In this embodiment, the knock-out protocol involves cloning a modified SPase DNA segment into a target DNA such that "tails" comprising the target site DNA remain at the 5' and 3' ends of the knock-
10 out cassette. The tails may be at least 50 base pairs and preferably greater than 200 to 500 base pairs for efficient recombination and/or gene conversion. For convenience, the foreign DNA cloned into the target DNA also provides a selectable marker, for example, an antibiotic resistance gene. Where the target DNA is disrupted with a marker antibiotic resistance gene, selection of transformants is carried out on agar plates containing
15 suitable levels of an appropriate antibiotic. Following transformation, a fraction of cells that have taken up the knockout cassette will have undergone homologous recombination or gene conversion across the genomic DNA tails of the cassette, resulting in replacement of the wild-type genomic sequence by the knock-out cassette. Knock-out recombination events are easily confirmed by, for example, Southern blot hybridization,
20 or by PCR.

Detection and/or Amplification of SPase Nucleic Acids

The presence of bacterial species susceptible or resistant to arylomycin antibiotics can be detected by detecting SPase nucleic acids in a test sample suspected of
25 containing bacteria. As described and illustrated herein arylomycin antibiotic resistance or susceptibility can be detected by detecting a nucleic acid encoding a SPase protein with a proline residue near the catalytic serine residue.

Nucleic acids in a test sample can be isolated using available procedures. For example, bacterial nucleic acids can be isolated from a test sample by lysing the bacterial
30 cells using detergents, heat, proteases and/or phenol extraction and alcohol preceipitation.

The presence of a nucleic acid can be detected that encodes a SPase protein with or without such a proline residue by employing available hybridization, single nucleotide polymorphism and/or nucleic acid amplification procedures to ascertain whether proline-

encoding or non-proline-encoding SPase nucleic acids are present in the test sample. In general, selective hybridization conditions are employed to facilitate detection of the proline-encoding and/or non-proline-encoding SPase nucleic acids and these procedures.

The term “selectively hybridize” includes hybridization, under stringent
 5 hybridization conditions, of a nucleic acid sequence to a specified nucleic acid target sequence (e.g., SEQ ID NO:2 or any SPase nucleic acid) to a detectably greater degree (e.g., at least 2-fold over background) than its hybridization to non-target nucleic acid sequences and to the substantial exclusion of non-target nucleic acids. Selectively
 10 hybridizing sequences typically have about at least 40% sequence identity, or 60-90% sequence identity, or 90-95% sequence identity, or 90-99% sequence identity, or 95-97% sequence identity, or 98-99% sequence identity, or 100% sequence identity (or complementarity) with each other. In some embodiments, a selectively hybridizing sequence has about at least about 70% sequence identity with SEQ ID NO:2. Note that if
 15 a value of a variable that is necessarily an integer, e.g., the number of nucleotides or amino acids in a nucleic acid or protein, is described as a range, e.g., or 90-99% sequence identity, or 100% sequence identity, what is meant is that the value can be any integer between 90 and 99 inclusive, i.e., 90, 91, 92, 93, 94, 95, 96, 97, 98 or 99.

The probes and primers of the invention include those with about 10-100 of the same nucleotides as either strand of a bacterial SPase DNA or RNA (e.g., SEQ ID
 20 NOs:2), or about 12-50, or about 13-40, or about 14-30 of the same nucleotides as either strand of a bacterial SPase DNA or RNA (e.g., SEQ ID NO:2). The probes and primers of the invention also include those with about 10-30 of the same nucleotides as either strand of any of SEQ ID NOs: 2, 5, 7, 8, 9 or the other SPase nucleic acids disclosed herein or available in a public data. The identical nucleotides or amino acids can be
 25 distributed throughout the nucleic acid or the protein, and need not be contiguous. Based on such methodologies, a person skilled in the art can readily design primers in suitable regions 5' and 3' to the signal peptidase segment that may encode the proline.

The terms “stringent conditions” or “stringent hybridization conditions” include conditions under which a probe will hybridize to its target sequence to a detectably
 30 greater degree than other sequences (e.g., at least 2-fold over background). Stringent conditions are somewhat sequence-dependent and can vary in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences can be identified which can be up to 100% complementarity to the probe (homologous probing). Alternatively, stringency conditions can be adjusted to allow

some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing).

A probe or primer can vary in length. For example, a probe can be approximately 20-500 nucleotides in length, but can vary greatly in length from about 15, or about 16, or about 17, or about 18 nucleotides to equal to the entire length of the target sequence. In some embodiments, the probe is about 10-50 nucleotides in length, or about 15-40 nucleotides in length, or about 18-50 nucleotides in length, or about 18-100 nucleotides in length.

In some embodiments, primers are shorter than probes. For example, a primer may be about 12 to 50 nucleotides in length, or about 13 to 40 nucleotides in length, or about 14 to 35 nucleotides in length.

In some embodiments, stringent hybridization conditions and procedures are employed. Typically, stringent conditions will be those where the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30 °C. for short probes or primers (e.g., 10 to 50 nucleotides) and at least about 60 °C. for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide or Denhardt's. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1M NaCl, 1% SDS (sodium dodecyl sulphate) at 37 °C., and a wash in 1 x SSC to 2 x SSC (where 20 x SSC is 3.0 M NaCl, 0.3 M trisodium citrate) at 50 to 55 °C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1M NaCl, 1% SDS at 37 °C., and a wash in 0.5 x SSC to 1 x SSC at 55 to 60 °C. Exemplary high stringency conditions include hybridization in 50% formamide, 1M NaCl, 1% SDS at 37° C., and a wash in 0.1 x SSC at 60 to 65 °C. Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl (Anal. Biochem. 138:267-84 (1984)):

$$T_m = 81.5\text{ }^{\circ}\text{C} + 16.6 (\log M) + 0.41 (\% \text{ GC}) - 0.61 (\% \text{ formamide}) - 500/L$$

where M is the molarity of monovalent cations; % GC is the percentage of guanosine and cytosine nucleotides in the DNA, % formamide is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. The T_m is reduced by about 1

°C. for each 1% of mismatching. Thus, the T_m , hybridization and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with greater than or equal to 90% sequence identity are sought, the T_m can be decreased 10 °C. Generally, stringent conditions are selected to be about 5 °C. lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or a wash at 1, 2, 3 or 4° C. lower than the thermal melting point (T_m). Moderately stringent conditions can utilize a hybridization and/or a wash at 6, 7, 8, 9 or 10 °C. lower than the thermal melting point (T_m). Low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15 or 20 °C. lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m , those of ordinary skill can identify and isolate nucleic acids with sequences related to SEQ ID NO:1. Those of skill in the art also understand how to vary the hybridization and/or wash solutions. If the desired degree of mismatching results in a T_m of less than 45 °C. (aqueous solution) or 32 °C. (formamide solution) it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Laboratory Techniques in Biochemistry and Molecular Biology – Hybridization with Nucleic Acid Probes, part 1, chapter 2, “Overview of principles of hybridization and the strategy of nucleic acid probe assays,” Elsevier, N.Y. (1993); and Current Protocols in Molecular Biology, chapter 2, Ausubel, et al., eds, Greene Publishing and Wiley-Interscience, New York (1995). Unless otherwise stated, in the present application high stringency is defined as hybridization in 4 x SSC, 5 x Denhardt’s (5 g Ficoll, 5 g polyvinylpyrrolidone, 5 g bovine serum albumin in 500 ml of water), 0.1 mg/ml boiled salmon sperm DNA, and 25 mM Na phosphate at 65 °C., and a wash in 0.1 x SSC, 0.1% SDS at 65 °C.

Therefore hybridization procedures can be used to detect the presence or absence of an encoded proline in bacterial signal peptidase nucleic acids. In addition, the presence or absence of such an encoded proline can be detected by nucleic acid amplification, single nucleotide polymorphism (SNP), sequencing and other procedures available to one of skill in the art.

Amplification methods available in the art can be utilized, including polymerase chain reaction (PCR) (U.S. Pat. Nos. 4,683,195; and 4,683,202; PCR Technology: Principles and Applications for DNA Amplification, ed. H. A. Erlich, Freeman Press, NY, N.Y., 1992), ligase chain reaction (LCR) (Wu and Wallace, Genomics 4:560, 1989;

Landegren et al., Science 241:1077, 1988), strand displacement amplification (SDA) (U.S. Pat. Nos. 5,270,184; and 5,422,252), transcription-mediated amplification (TMA) (U.S. Pat. No. 5,399,491), linked linear amplification (LLA) (U.S. Pat. No. 6,027,923), and the like, and isothermal amplification methods such as nucleic acid sequence based
 5 amplification (NASBA), and self-sustained sequence replication (Guatelli et al., Proc. Natl. Acad. Sci. USA 87: 1874, 1990).

A variety of single nucleotide polymorphism (SNP) genotyping methods are available including those described in Chen et al., "Single nucleotide polymorphism genotyping: biochemistry, protocol, cost and throughput", Pharmacogenomics J. 2003;
 10 3(2):77-96; Kwok et al., "Detection of single nucleotide polymorphisms", Curr Issues Mol. Biol. 2003 April; 5(2):43-60; Shi, "Technologies for individual genotyping: detection of genetic polymorphisms in drug targets and disease genes", Am J. Pharmacogenomics. 2002; 2(3):197-205; and Kwok, "Methods for genotyping single nucleotide polymorphisms", Annu Rev Genomics Hum Genet 2001; 2:235-58; see also,
 15 U.S. Patent Application Publication No. 20100216154, contents of which publications are incorporated by reference in their entirety. Exemplary techniques for high-throughput SNP genotyping are described in Marnellos, "High-throughput SNP analysis for genetic association studies", Curr Opin Drug Discov Devel. 2003 May; 6(3):317-21, which is incorporated herein by reference in its entirety. Common SNP genotyping
 20 methods include, but are not limited to, TaqMan assays, molecular beacon assays, nucleic acid arrays, allele-specific primer extension, allele-specific PCR, arrayed primer extension, homogeneous primer extension assays, primer extension with detection by mass spectrometry, pyrosequencing, multiplex primer extension sorted on genetic arrays, ligation with rolling circle amplification, homogeneous ligation, OLA (U.S. Pat. No.
 25 4,988,167, which is incorporated herein by reference in its entirety), multiplex ligation reaction sorted on genetic arrays, restriction-fragment length polymorphism, single base extension-tag assays, and the Invader assay. Such methods may be used in combination with detection mechanisms such as, for example, luminescence or chemiluminescence detection, fluorescence detection, time-resolved fluorescence detection, fluorescence
 30 resonance energy transfer, fluorescence polarization, mass spectrometry, and electrical detection.

Various methods for detecting polymorphisms include, but are not limited to, methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA duplexes (Myers et al., Science 230:1242 (1985); Cotton et al.,

PNAS 85:4397 (1988); and Saleeba et al., Meth. Enzymol. 217:286-295 (1992)), comparison of the electrophoretic mobility of variant and wild type nucleic acid molecules (Orita et al., PNAS 86:2766 (1989); Cotton et al., Mutat. Res. 285:125-144 (1993); and Hayashi et al, Genet. Anal. Tech. Appl. 9:73-79 (1992)), and assaying the
5 movement of polymorphic or wild-type fragments in polyacrylamide gels containing a gradient of denaturant using denaturing gradient gel electrophoresis (DGGE) (Myers et al., Nature 313:495 (1985)); the contents of which publications are incorporated herein by reference in their entirety. Sequence variations at specific locations can also be assessed by nuclease protection assays such as RNase and S1 protection or chemical
10 cleavage methods.

For example, in some embodiments, SNP genotyping is performed using the TaqMan assay, which is also known as the 5' nuclease assay (U.S. Pat. Nos. 5,210,015 and 5,538,848, which are incorporated herein by reference in their entirety). The TaqMan assay detects the accumulation of a specific amplified product during PCR. The TaqMan
15 assay utilizes an oligonucleotide probe labeled with a fluorescent reporter dye and a quencher dye. The reporter dye is excited by irradiation at an appropriate wavelength, it transfers energy to the quencher dye in the same probe via a process called fluorescence resonance energy transfer (FRET). When attached to the probe, the excited reporter dye does not emit a signal. The proximity of the quencher dye to the reporter dye in the intact
20 probe maintains a reduced fluorescence for the reporter. The reporter dye and quencher dye may be at the 5' most and the 3' most ends, respectively, or vice versa. Alternatively, the reporter dye may be at the 5' or 3' most end while the quencher dye is attached to an internal nucleotide, or vice versa. In yet another embodiment, both the reporter and the quencher may be attached to internal nucleotides at a distance from each other such that
25 fluorescence of the reporter is reduced.

In another aspect of the invention, the signal peptidase sequences of various bacterial species are determined and compared to generate bacterial phylogenetic profiles of drug resistance useful for identifying drugs that can readily be modified to overcome such drug resistance.

30 To generate such drug resistance phylogenetic profiles, the degree of sequence similarity and difference is determined. The following terms are used to describe the sequence relationships between two or more nucleic acids or nucleic acids or polypeptides: (a) "reference sequence," (b) "comparison window," (c) "sequence identity," (d) "percentage of sequence identity" and (e) "substantial identity." As used

herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. The reference sequence can be a nucleic acid sequence (e.g., SEQ ID NO:2) or an amino acid sequence (e.g., SEQ ID NO:1). A reference sequence may be a subset or the entirety of a specified sequence. For example, the reference sequence can be an
5 entire SPase DNA, RNA or polypeptide sequence, or a segment of a full-length SPase DNA, RNA or polypeptide sequence, or a peptide, DNA or RNA including/encoding just the region of the catalytic serine and/or a region that is N-terminal to catalytic serine (e.g., from about amino acid position -10 to about amino acid +2 relative to the catalytic serine).

10 As used herein, "comparison window" means includes reference to a contiguous and specified segment of a nucleic acid or an amino acid sequence, wherein the nucleic acid/amino acid sequence may be compared to a reference sequence and wherein the portion of the nucleic acid/amino acid sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which
15 does not comprise additions or deletions) for optimal alignment of the two sequences. The comparison window can vary for nucleic acid and polypeptide sequences. Generally, for nucleic acids, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 22, 25, 30, 35, 40, 50, 100 or more nucleotides. For amino acid sequences, the comparison window is at least about 10 to 15 amino acids, and can
20 optionally be 20, 22, 25, 30, 35, 40, 50, 100 or more amino acids. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the nucleic acid or amino acid sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of nucleotide and amino acid sequences for comparison are
25 well known in the art. The local homology algorithm (BESTFIT) of Smith and Waterman, (1981) Adv. Appl. Math 2:482, may conduct optimal alignment of sequences for comparison; by the homology alignment algorithm (GAP) of Needleman and Wunsch, (1970) J. Mol. Biol. 48:443-53; by the search for similarity method (Tfasta and Fasta) of Pearson and Lipman, (1988) Proc. Natl. Acad. Sci. USA 85:2444; by
30 computerized implementations of these algorithms, including, but not limited to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View, Calif., GAP, BESTFIT, BLAST, FASTA and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG™ programs (Accelrys, Inc., San Diego, Calif.)). The CLUSTAL program is well described by Higgins and Sharp,

(1988) Gene 73:237-44; Higgins and Sharp, (1989) CABIOS 5:151-3; Corpet, et al., (1988) Nucleic Acids Res. 16:10881-90; Huang, et al., (1992) Computer Applications in the Biosciences 8:155-65 and Pearson, et al., (1994) Meth. Mol. Biol. 24:307-31. The preferred program to use for optimal global alignment of multiple sequences is PileUp
5 (Feng and Doolittle, (1987) J. Mol. Evol., 25:351-60 which is similar to the method described by Higgins and Sharp, (1989) CABIOS 5:151-53 and hereby incorporated by reference). The BLAST family of programs which can be used for database similarity searches includes: BLASTN for nucleotide query sequences against nucleotide database sequences; BLASTX for nucleotide query sequences against protein database sequences;
10 BLASTP for protein query sequences against protein database sequences; TBLASTN for protein query sequences against nucleotide database sequences; and TBLASTX for nucleotide query sequences against nucleotide database sequences. See, Current Protocols in Molecular Biology, Chapter 19, Ausubel, et al., eds., Greene Publishing and Wiley-Interscience, New York (1995).

15 GAP uses the algorithm of Needleman and Wunsch, (1970) J. Mol. Biol. 48:443-53, to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. GAP considers all possible alignments and gap positions and creates the alignment with the largest number of matched bases and the fewest gaps. It allows for the provision of a gap creation penalty and a gap extension
20 penalty in units of matched bases. GAP must make a profit of gap creation penalty number of matches for each gap it inserts. If a gap extension penalty greater than zero is chosen, GAP must, in addition, make a profit for each gap inserted of the length of the gap times the gap extension penalty. Default gap creation penalty values and gap
25 extension penalty values in Version 10 of the Wisconsin Genetics Software Package are 8 and 2, respectively. The gap creation and gap extension penalties can be expressed as an integer selected from the group of integers consisting of from 0 to 100. Thus, for example, the gap creation and gap extension penalties can be 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50 or greater.

GAP presents one member of the family of best alignments. There may be many
30 members of this family, but no other member has a better quality. GAP displays four figures of merit for alignments: Quality, Ratio, Identity and Similarity. The Quality is the metric maximized in order to align the sequences. Ratio is the quality divided by the number of bases in the shorter segment. Percent Identity is the percent of the symbols that actually match. Percent Similarity is the percent of the symbols that are similar.

Symbols that are across from gaps are ignored. A similarity is scored when the scoring matrix value for a pair of symbols is greater than or equal to 0.50, the similarity threshold. The scoring matrix used in Version 10 of the Wisconsin Genetics Software Package is BLOSUM62 (see, Henikoff and Henikoff, (1989) Proc. Natl. Acad. Sci. USA 89:10915).

Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using the BLAST 2.0 suite of programs using default parameters (Altschul, et al., (1997) Nucleic Acids Res. 25:3389-402). As those of ordinary skill in the art will understand, BLAST searches assume that proteins can be modeled as random sequences. However, many real proteins comprise regions of nonrandom sequences, which may be homopolymeric tracts, short-period repeats, or regions enriched in one or more amino acids. Such low-complexity regions may be aligned between unrelated proteins even though other regions of the protein are entirely dissimilar. A number of low-complexity filter programs can be employed to reduce such low-complexity alignments. For example, the SEG (Wooten and Federhen, (1993) Comput. Chem. 17:149-63) and XNU (C.sub.1-ayerie and States, (1993) Comput. Chem. 17:191-201) low-complexity filters can be employed alone or in combination.

Anti-SPase Antibodies

Another aspect of the invention is an antibody that can distinguish between a SPase that contains or does not contain a proline within about 10-12 amino acids of the catalytic serine in the SPase polypeptide. Thus, in some embodiments, the antibody binds with specificity to a bacterial SPase epitope that contains a proline within about 10-12 amino acids of the catalytic serine in the SPase polypeptide. In other embodiments, the antibody binds with specificity to a bacterial SPase epitope that does not contain a proline within about 10-12 amino acids of the catalytic serine in the SPase polypeptide.

Antibodies that selectively bind to a SPase polypeptide can be isolated using conventional methods. Such antibodies can be polyclonal or monoclonal antibodies. In some embodiments, the anti-SPase antibodies are monoclonal antibodies.

For example, antibodies of the invention can be obtained from the blood or spleen of a animal that has been immunized with an SPase peptide or polypeptide that contains a selected amino acid sequence (e.g., SPase that contains or does not contain a proline within about 10-12 amino acids of the catalytic serine in the SPase polypeptide). The SPase polypeptide can be obtained using conventional methods, for example, as

described in the Examples. Peptides from SPase polypeptides can be obtained by proteolytic cleavage of a SPase polypeptide or by recombinant expression of the SPase peptide. The animal can be, for example, a rabbit, goat, rat, horse or mouse. At the appropriate time after immunization, antibody molecules can be isolated from the
5 animal, e.g. from the blood, spleen or other fluid of the animal, and further purified using standard techniques that include, without limitation, precipitation using ammonium sulfate, gel filtration chromatography, ion exchange chromatography or affinity chromatography using protein A. Antibodies that bind to SPase-specific antigens, can be identified using ELISA. Antibodies that bind to proline-containing epitopes on SPase
10 proteins, but do not bind to non-proline-containing epitopes (or vice versa) can be identified by screening methods available in the art.

Antibodies specific for proline-containing and non-proline-containing SPase polypeptides can also be obtained using various methods. Non-limiting examples include: (1) the generation of an antibody from an antibody-producing cell of a animal
15 that has been immunized with a SPase polypeptide or peptide using single human B cell RT-PCR and expression vector cloning; (2) isolation from immortalized antibody-secreting B cells; and (3) isolation from an antibody-producing hybridoma generated by fusion of an antibody-producing cell with a myeloma cell. These techniques are known in the art. See, for example, Kohler & Milstein, *Nature* 256:495-97 (1975); Kozbor et al.
20 *Immunol Today* 4: 72 (1983); Tiller et al., *J Immunol Methods* 329:112-124 (2008) and Traggiai et al., *Nat Med* 10:871-875(2004).

Antibodies specific for proline-containing and non-proline-containing SPase polypeptides can also be prepared using other methods known in the art, such as, for example, screening of a recombinant combinatorial immunoglobulin library such as an
25 antibody phage display library using antigenic epitope of the SPase polypeptide. See, for example, Barbas, C.F. et al., *PHAGE DISPLAY – A LABORATORY MANUAL* (2001) Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press; and Kontermann & Dubel, *ANTIBODY ENGINEERING* (2001) Berlin, Heidelberg: Springer-Verlag.

Nucleic acids encoding antibodies specific for the SPase polypeptides of the
30 invention can be derived from an animal immunized with the SPase polypeptide or a peptide fragment thereof by generating an expression library using the RNA of the animal's B cells or plasma cells and then screening for antibody-coding sequences. See, for example, in *Antibodies, A Laboratory Manual*, by Harlow and Lane, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1988, and in *Molecular Cloning, A*

Laboratory Manual by Sambrook, et al., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. 1989, the disclosures of which are incorporated herein by reference.

For example, antibodies can be used that specifically detect any of the following peptides, where the proline(s) that give rise to arylomycin-resistance are shown as a P within a box (i.e., $\boxed{\text{P}}$) and the catalytic serine is shown at the C-terminus.

Table 9: Peptide Epitopes

Bacterial Strain	Mutant or Wild type	SPase peptide sequence	SEQ ID NO:
<i>S. epidermidis</i> RP62A	WT	VGKSYSIKGDS	17
<i>S. epidermidis</i> PAS9001	S29P	VGK $\boxed{\text{P}}$ YSIKGDS	18
<i>S. epidermidis</i> PAS9002	S31P	VGKSY $\boxed{\text{P}}$ IKGDS	19
<i>S. aureus</i> NTCT 8325	WT	VAKPYTVKGDS	20
<i>S. aureus</i> PAS8001	P29S	VAK $\boxed{\text{S}}$ YTVKGDS	21
<i>E. coli</i> MG1655	WT	IYEPFQIPSGS	22
<i>E. coli</i> PAS0232	P84S	IYE $\boxed{\text{S}}$ FQIPSGS	23
<i>P. aeruginosa</i> PAO1	WT	LFEPFQIPSGS	24
<i>P. aeruginosa</i> PAS2006	P84S	LFES $\boxed{\text{S}}$ FQIPSGS	25

Compositions and Combinations

Another aspect of an embodiment of the invention provides compositions of the compounds of the invention, alone or in combination with another medicament. As set forth herein, compounds of the invention include stereoisomers, tautomers, solvates, prodrugs, pharmaceutically acceptable salts and mixtures thereof. Compositions containing a compound of the invention can be prepared by conventional techniques, e.g. as described in Remington: *The Science and Practice of Pharmacy*, 19th Ed., 1995, or later versions thereof, incorporated by reference herein. The compositions can appear in conventional forms, for example capsules, tablets, aerosols, solutions, suspensions or topical applications.

Typical compositions include a compound of the invention and a pharmaceutically acceptable excipient which can be a carrier or a diluent. For example, the active compound will usually be mixed with a carrier, or diluted by a carrier, or enclosed within a carrier which can be in the form of an ampoule, capsule, sachet, paper, or other container. When the active compound is mixed with a carrier, or when the carrier serves as a diluent, it can be solid, semi-solid, or liquid material that acts as a vehicle, excipient, or medium for the active compound. The active compound can be adsorbed on a granular solid carrier, for example contained in a sachet. Some examples of suitable carriers are water, salt solutions, alcohols, polyethylene glycols, polyhydroxyethoxylated castor oil, peanut oil, olive oil, gelatin, lactose, terra alba, sucrose, dextrin, magnesium carbonate, sugar, cyclodextrin, amylose, magnesium stearate, talc, gelatin, agar, pectin, acacia, stearic acid or lower alkyl ethers of cellulose, silicic acid, fatty acids, fatty acid amines, fatty acid monoglycerides and diglycerides, pentaerythritol fatty acid esters, polyoxyethylene, hydroxymethylcellulose and polyvinylpyrrolidone. Similarly, the carrier or diluent can include any sustained release material known in the art, such as glyceryl monostearate or glyceryl distearate, alone or mixed with a wax.

The formulations can be mixed with auxiliary agents that do not deleteriously react with the active compounds. Such additives can include wetting agents, emulsifying and suspending agents, salt for influencing osmotic pressure, buffers and/or coloring substances preserving agents, sweetening agents or flavoring agents. The compositions can also be sterilized if desired.

Moreover, the compositions can include other therapeutic agents such as analgesics, other antibiotics, antihistamines, anti-inflammatory agents and the like. In some embodiments, the compositions include a second type of antibiotic, for example, a non-arylomycin antibiotic.

The route of administration can be any route which effectively transports the active compound of the invention to the appropriate or desired site of action, such as oral, nasal, pulmonary, buccal, subdermal, intradermal, transdermal, topical or parenteral, e.g., rectal, depot, subcutaneous, intravenous, intraurethral, intramuscular, intranasal, ophthalmic solution or an ointment, the oral route being preferred. In some embodiments, the compositions containing any of the compounds described herein are administered topically. For example, compositions containing arylomycon A and/or

arylomycin B (with or without some of the compounds of formula I may advantageously be administered topically.

If a solid carrier is used for oral administration, the preparation can be tableted, placed in a hard gelatin capsule in powder or pellet form or it can be in the form of a troche or lozenge. If a liquid carrier is used, the preparation can be in the form of a syrup, emulsion, soft gelatin capsule or sterile injectable liquid such as an aqueous or non-aqueous liquid suspension or solution.

Injectable dosage forms generally include aqueous suspensions or oil suspensions which can be prepared using a suitable dispersant or wetting agent and a suspending agent. Injectable forms can be in solution phase or in the form of a suspension, which is prepared with a solvent or diluent. Acceptable solvents or vehicles include sterilized water, Ringer's solution, or an isotonic aqueous saline solution. Alternatively, sterile oils can be employed as solvents or suspending agents. Preferably, the oil or fatty acid is non-volatile, including natural or synthetic oils, fatty acids, mono-, di- or tri-glycerides.

For injection, the formulation can also be a powder suitable for reconstitution with an appropriate solution as described above. Examples of these include, but are not limited to, freeze dried, rotary dried or spray dried powders, amorphous powders, granules, precipitates, or particulates. For injection, the formulations can optionally contain stabilizers, pH modifiers, surfactants, bioavailability modifiers and combinations of these. The compounds can be formulated for parenteral administration by injection such as by bolus injection or continuous infusion. A unit dosage form for injection can be in ampoules or in multi-dose containers.

The formulations of the invention can be designed to provide quick, sustained, or delayed release of the active ingredient after administration to the patient by employing procedures well known in the art. Thus, the formulations can also be formulated for controlled release or for slow release.

Compositions contemplated by the present invention can include, for example, micelles or liposomes, or some other encapsulated form, or can be administered in an extended release form to provide a prolonged storage and/or delivery effect. Therefore, the formulations can be compressed into pellets or cylinders and implanted intramuscularly or subcutaneously as depot injections. Such implants can employ known inert materials such as silicones and biodegradable polymers, e.g., polylactide-polyglycolide. Examples of other biodegradable polymers include poly(orthoesters) and poly(anhydrides).

For nasal administration, the preparation can contain a compound of the invention, dissolved or suspended in a liquid carrier, preferably an aqueous carrier, for aerosol application. The carrier can contain additives such as solubilizing agents, e.g., propylene glycol, surfactants, absorption enhancers such as lecithin

5 (phosphatidylcholine) or cyclodextrin, or preservatives such as parabens.

For parenteral application, particularly suitable are injectable solutions or suspensions, preferably aqueous solutions with the active compound dissolved in polyhydroxylated castor oil.

Tablets, dragees, or capsules having talc and/or a carbohydrate carrier or binder
10 or the like are particularly suitable for oral application. Preferable carriers for tablets, dragees, or capsules include lactose, corn starch, and/or potato starch. A syrup or elixir can be used in cases where a sweetened vehicle can be employed.

A typical tablet that can be prepared by conventional tableting techniques can contain:

15

Core:

	Active compound (as free compound or salt thereof)	250 mg
	Colloidal silicon dioxide (Aerosil)®	1.5 mg
	Cellulose, microcryst. (Avicel)®	70 mg
20	Modified cellulose gum (Ac-Di-Sol)®	7.5 mg
	Magnesium stearate	Ad.

Coating:

	HPMC approx.	9 mg
	*Mywacett 9-40 T approx.	0.9 mg

25

*Acylated monoglyceride used as plasticizer for film coating.

A typical capsule for oral administration contains compounds of the invention (250 mg), lactose (75 mg) and magnesium stearate (15 mg). The mixture is passed through a 60 mesh sieve and packed into a No. 1 gelatin capsule. A typical injectable
30 preparation is produced by aseptically placing 250 mg of compounds of the invention into a vial, aseptically freeze-drying and sealing. For use, the contents of the vial are mixed with 2 mL of sterile physiological saline, to produce an injectable preparation.

The following non-limiting Examples illustrate aspects of the invention.

Examples

EXAMPLE 1: General Chemical Methods

¹H and ¹³C NMR spectra were recorded on Bruker AMX 400, Bruker DRX 500,
5 or Bruker DRX 600 spectrometers. Chemical shifts are reported relative to either
chloroform (δ 7.26), methanol (δ 3.31), or dimethylsulfoxide (DMSO) (δ 2.50) for ¹H
NMR and either chloroform (δ 77.16), methanol (δ 49.00), or DMSO (δ 39.52) for ¹³C
NMR. IR measurements were taken using a Nicolet 6700 ATR FT-IR. High resolution
mass spectra were measured at the Scripps Center for Mass Spectrometry. All assigned
10 structures are consistent with spectral data obtained.

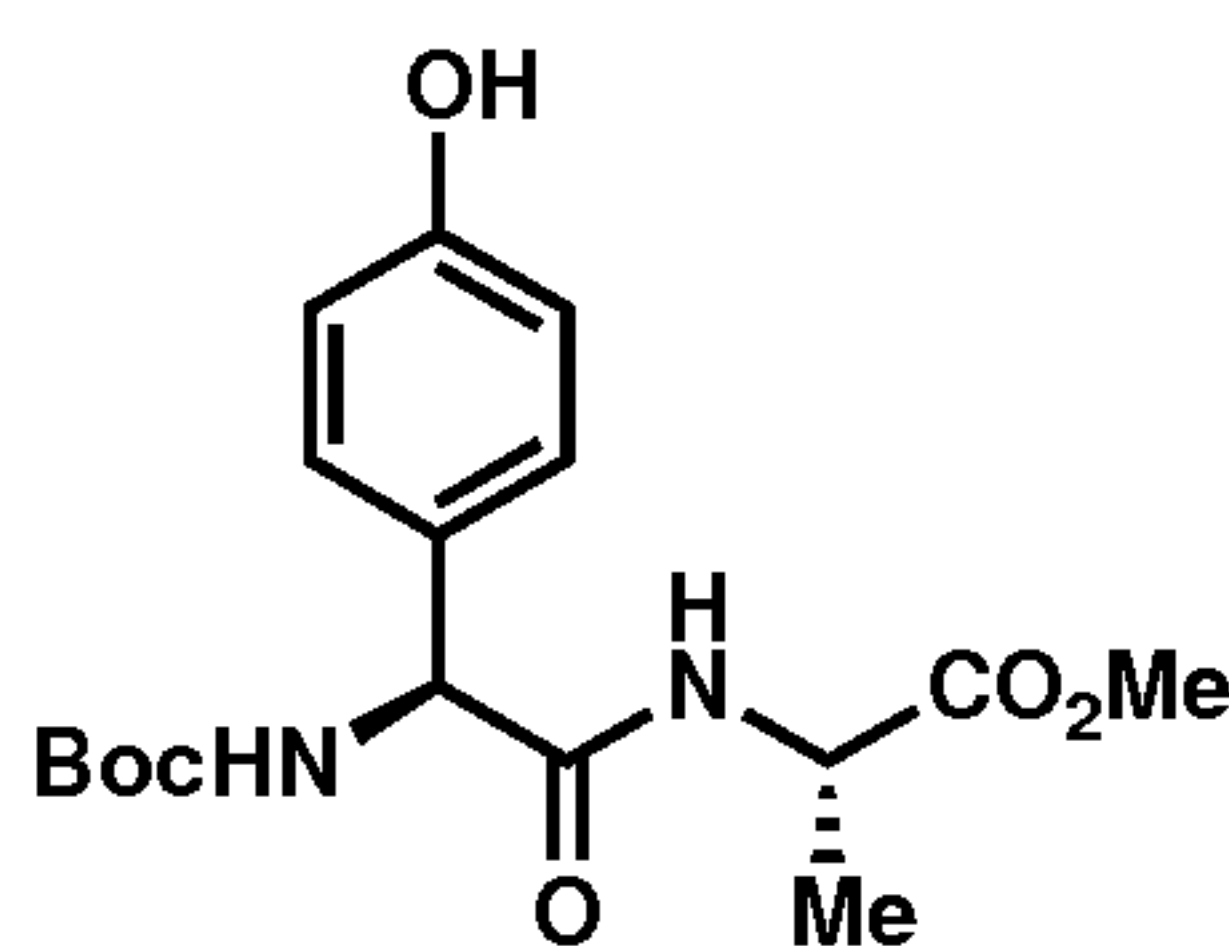
Optical rotations were measured on a Perkin Elmer model 341 polarimeter.
Yields refer to chromatographically and spectroscopically pure compounds unless
otherwise stated. Reactions were magnetically stirred, and monitored by thin layer
chromatography (TLC) with 0.25 mm Whatman pre-coated silica gel (with fluorescence
15 indicator) plates. Flash chromatography was performed with silica gel (particle size 40-
63 μ m, EMD chemicals). Acetone was dried over anhydrous potassium carbonate, and
all other dry solvents were purchased from Acros. H-D-Ser(Bzl)-OH and H-Ala-OBzl
HCl were purchased from Bachem.

4-Nitrobenzenesulfonylchloride, and 1,1'-bis(diphenylphosphino)ferrocene
20 palladium(II) chloride complex with dichloromethane (PdCl₂(dppf)) were purchased
from Alfa Aesar and Strem Chemicals, respectively. Boc-Gly-OH was purchased from
Novabiochem. Anhydrous 1-hydroxybenzotriazole (HOBT) was purchased from Chem-
Impex. Diazomethane was prepared according to Arndt, F. *Org. Synth.* 1934, 2:165. All
other chemicals were purchased from Fisher/Acros or Aldrich. Abbreviations: THF,
25 tetrahydrofuran; EtOH, ethanol; MeOH, methanol; AcOH, acetic acid; DCM,
dichloromethane; DMF, N,N-dimethylformamide; EDC, 1-(3-dimethylaminopropyl)-3-
ethylcarbodiimide hydrochloride; EtOAc, ethyl acetate; Ar, argon; DBU, 1,8-
diazabicyclo[5.4.0]undec-7-ene; TFA, trifluoroacetic acid.

All preparative reverse phase chromatography was performed using Dynamax
30 SD-200 pumps connected to a Dynamax UV-D II detector (monitoring at 220 nm). The
column used was a Phenomenex Jupiter C₁₈ (10 μ m, 2.12 $\times$ 25 cm, 300 Å pore size).
All solvents contained 0.1% TFA; Solvent A, H₂O; Solvent B, acetonitrile with 10%
H₂O. All samples were loaded onto the column at 0% B and the column was allowed to

equilibrate for ~10 min. before a linear gradient was started. Retention values are reported according to the linear gradient used and the %B at the time the sample eluted.

Procedures and Characterization



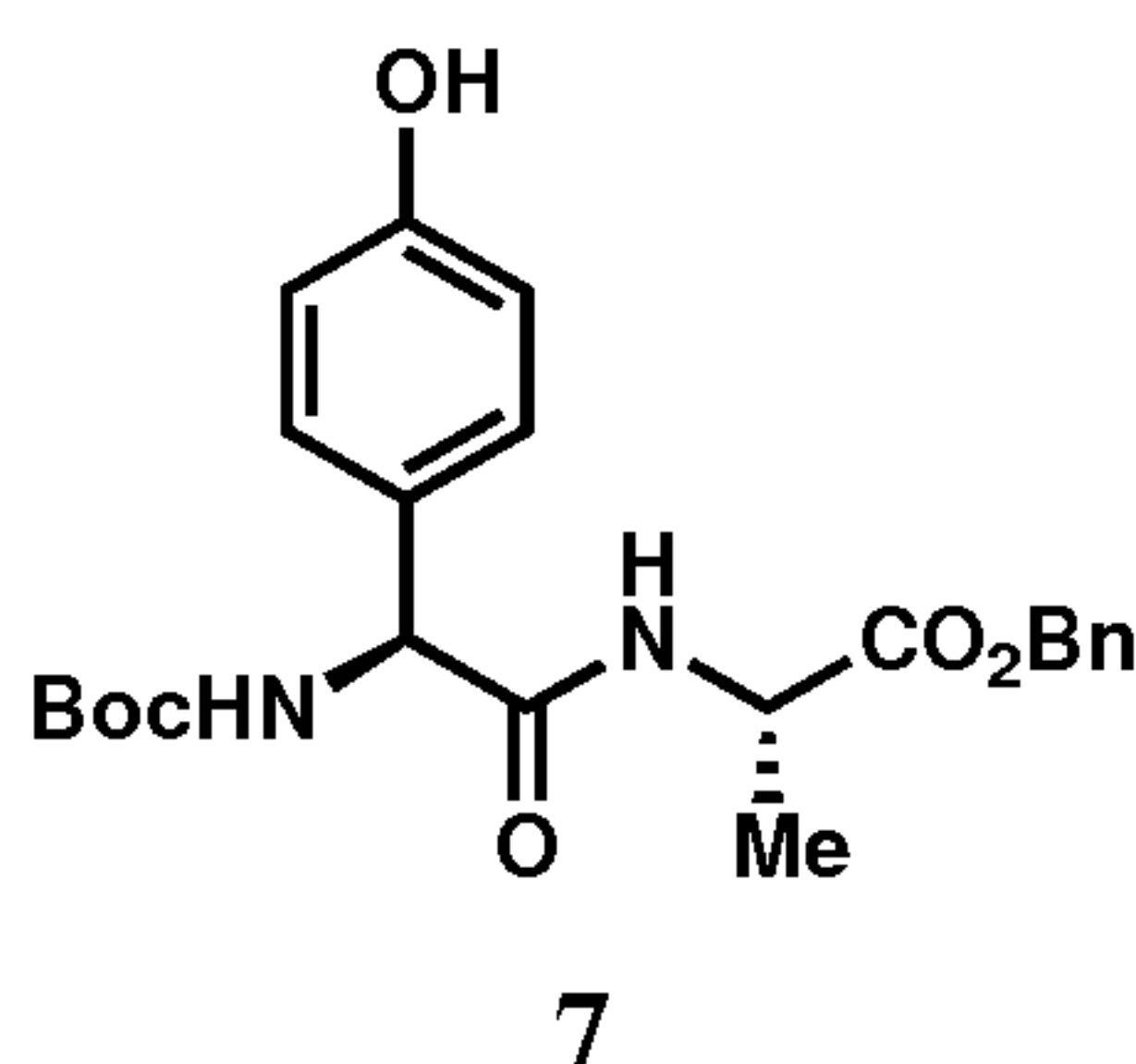
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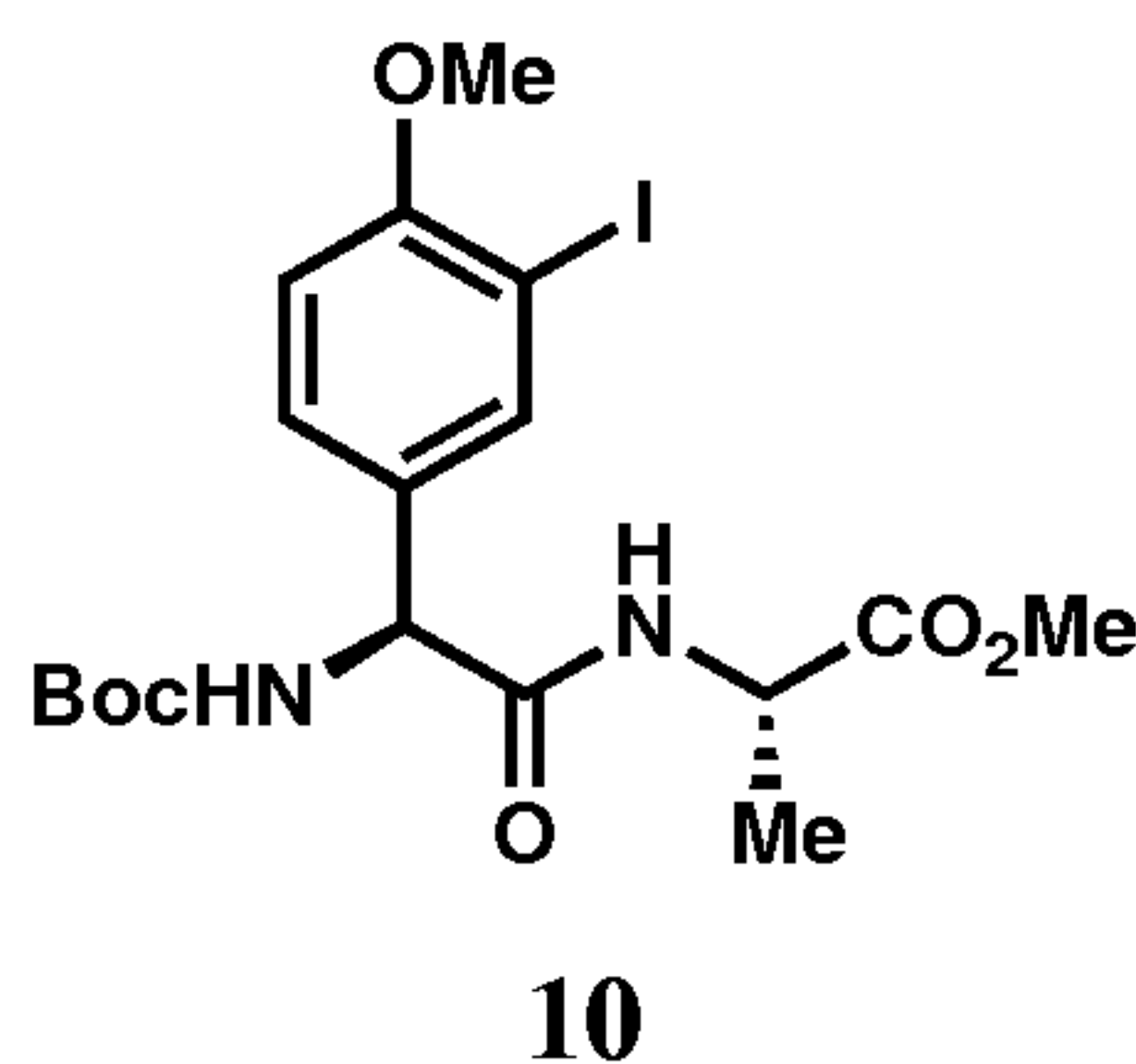
To a solution of 4-hydroxyphenylglycine (12 g, 71.8 mmol) in a 1:1 mixture of acetone and water was added di-*tert*-butyldicarbonate (16.5 mL, 71.8 mmol, 1 eq) and sodium bicarbonate (6.03 g, 0.11 mol, 1.5 eq). The solution was allowed to stir overnight, and then was quenched with the addition of citric acid (pH 3) to pH 4. The aqueous layer was then extracted 2× with EtOAc and the combined organic layers were washed with brine, dried over Na₂SO₄ and concentrated to a white foam. The crude material (18.43 g, 69 mmol (assumed)) was used without further purification by dissolving it in anhydrous DMF and treating sequentially with triethylamine (12.6 mL, 75.9 mmol, 1.3 eq), HOBT (9.32 g, 69 mmol, 1 eq) and Ala-OMe HCl (9.63 g, 69 mmol, 1 eq). The solution was then cooled to 0 °C and EDC (19.55 g, 0.1 mol, 1.5 eq) was added in one portion. The reaction was allowed to warm to room temperature and stirred overnight. Water and EtOAc were added, the aqueous layer was extracted 3×, and the combined organic layers were washed with brine, dried over Na₂SO₄ and concentrated. The residue was purified by flash chromatography (6% MeOH, 0.6% AcOH in DCM) to give a clear residue (17.82 g, 71% yield). *R_f* = 0.39 (7% MeOH in DCM). ¹H NMR (CDCl₃, 600 MHz) δ (ppm) 7.11 (d, *J* = 8.4 Hz, 2H), 6.64 (d, *J* = 8.4 Hz, 2H), 6.51 (br d, *J* = 6.6 Hz, 1H), 5.71 (br s, 1H), 5.07 (br s, 1H), 4.57-4.52 (m, 1H), 3.69 (s, 3H), 1.42-1.40 (m, 12H). ¹³C NMR (CDCl₃, 600 MHz) δ (ppm) 173.2, 170.5, 156.6, 155.4, 129.0, 128.7 (2 C), 116.1 (2 C), 80.5, 58.2, 52.7, 48.5, 28.4 (3 C), 18.4. IR (film) *v*_{max} = 1655, 1512, 1450, 1365, 1215, 1157, 1049 cm⁻¹. ESI HRMS calcd for [(M+Na)⁺] C₁₇H₂₄N₂O₆: 375.1526, found: 375.1532.

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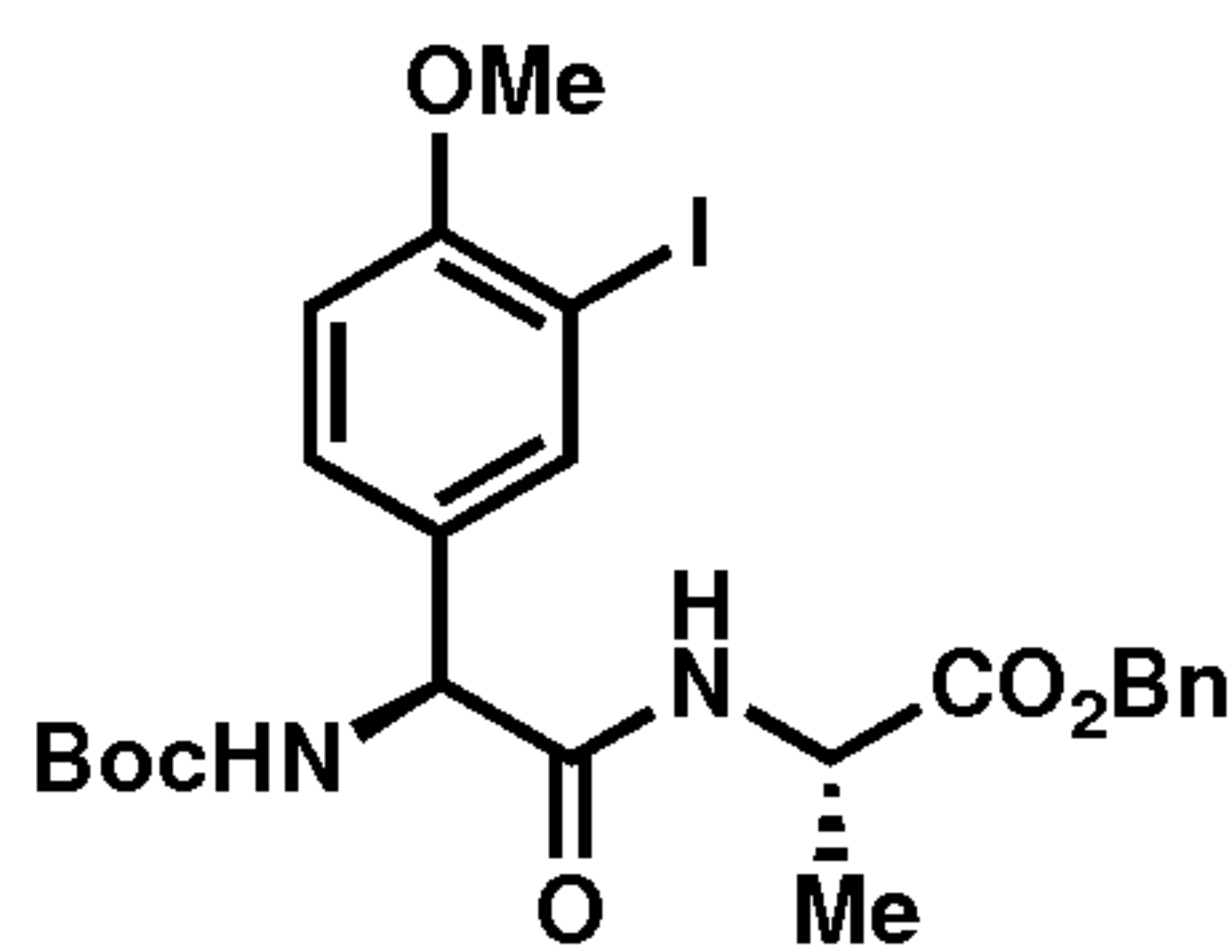
Compound **7** was synthesized in the same manner as compound **6**. $R_f = 0.3$ (4.5% MeOH in DCM). ^1H NMR (CDCl_3 , 600 MHz) δ (ppm) 7.38-7.31 (m, 3H), 7.29-7.26 (m, 2H), 7.11 (d, $J = 8.5$ Hz, 2H), 6.63 (d, $J = 8.3$ Hz, 2H), 6.44-6.38 (m, 2H), 5.69 (br s, 1H), 5.15-4.99 (m, 3H), 4.59 (p, $J = 7.2$ Hz, 1H), 1.44-1.39 (m, 12H). ^{13}C NMR (CDCl_3 , 600 MHz) δ (ppm) 172.5, 170.4, 162.8, 156.4, 135.2, 128.8 (2 C), 128.7, 128.6 (2 C), 128.3 (2 C), 116.1 (2 C), 99.7, 67.5, 48.7, 36.7, 31.7, 28.5 (3 C), 18.5. IR (film) $\nu_{\text{max}} = 1655, 1510, 1209, 1153, 1045, 696\text{ cm}^{-1}$. ESI HRMS calcd for $\text{C}_{23}\text{H}_{28}\text{N}_2\text{O}_6$ [(M+H) $^+$] 429.2020, found 429.2025.



A mixture of **6** (20.6 g, 58 mmol) dissolved in dry acetone (390 mL) and potassium carbonate (40.4 g, 0.29 mol, 5 eq) under Ar was treated with iodomethane (25.4 mL, 0.41 mol, 7 eq) and heated to reflux. After 17 h, the solution was cooled, filtered and concentrated to the crude product ($R_f = 0.35$ (2% MeOH in DCM)). To a solution of the crude compound (16.68 g, 45.6 mmol (assumed)) in MeOH (607 mL) was added AgSO_4 (14.9 g, 47.8 mmol, 1.05 eq) and I_2 (12.1 g, 47.8 mmol, 1.05 eq) consecutively. The reaction was stirred vigorously until TLC analysis (starting material stains with cerium(IV)sulfate; product does not) showed no remaining starting material (~30 min) solid $\text{Na}_2\text{S}_2\text{O}_3$ (large excess) was then added. The solids were filtered, the filtrate was concentrated, and the crude residue was purified via flash column chromatography (2% MeOH in DCM). The product was a white solid (21.19 g, 76% yield). $R_f = 0.50$ (3% MeOH in DCM). ^1H NMR (CDCl_3 , 600 MHz) δ (ppm) 7.76 (d, $J = 1.8$ Hz, 1H), 7.33 (d, $J = 7.8$ Hz, 1H), 6.78 (d, $J = 8.4$ Hz, 1H), 6.31 (d, $J = 7.2$ Hz, 1H), 5.69 (br s, 1H), 5.07 (br s, 1H), 4.56-4.51 (m, 1H), 3.86 (s, 3H), 3.70 (s, 3H), 1.41-1.40

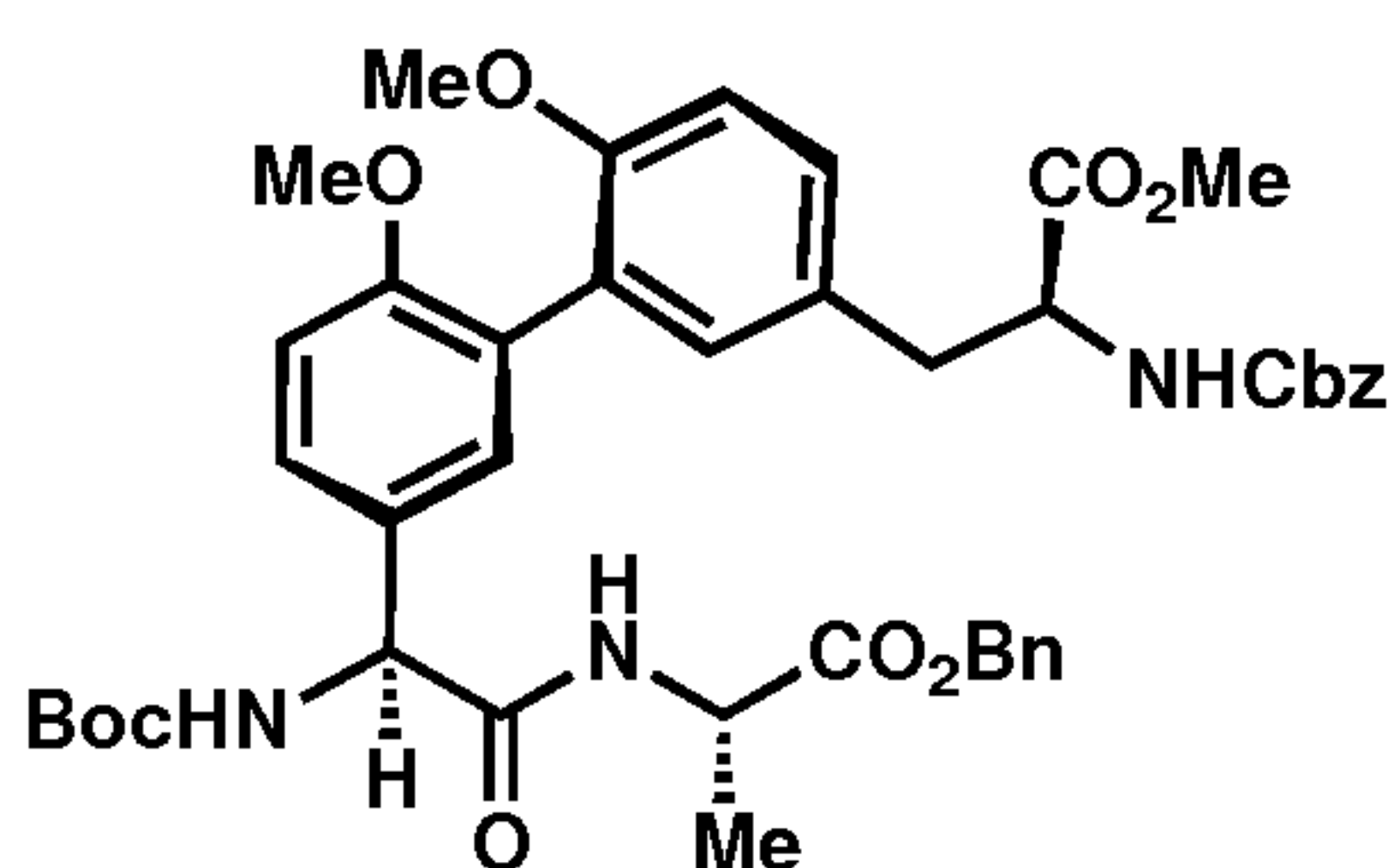
(m, 12H). ^{13}C NMR (CDCl_3 , 600 MHz) δ (ppm) 172.9 (2 C), 169.5, 158.3, 138.3, 132.2, 128.9, 111.1, 86.6, 80.4, 57.4, 56.5, 52.7, 48.6, 28.4 (3 C), 18.4. IR (film) ν_{max} = 1655, 1489, 1363, 1248, 1155, 1047, 1016, 548 cm^{-1} . ESI HRMS calcd for $\text{C}_{18}\text{H}_{25}\text{IN}_2\text{O}_6$ $[(\text{M}+\text{H})^+]$ 493.0830, found 493.0829.

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11

Compound **11** was synthesized in the same manner as compound **10**. R_f = 0.59 (2% MeOH in DCM). ^1H NMR (CDCl_3 , 600 MHz) δ (ppm) 7.76 (s, 1H), 7.38-7.23 (m, 6H), 6.72 (d, J = 8.4 Hz, 1H), 6.32 (d, J = 6.6 Hz, 1H), 5.68 (s, 1H), 5.16-5.02 (m, 3H), 4.61-4.55 (m, 1H), 3.84 (s, 3H), 1.45-1.35 (m, 12H). ^{13}C NMR (MeOD, 600 MHz) δ (ppm) 173.5, 172.4, 159.5, 157.3, 139.6, 137.1, 133.1, 129.9, 129.5 (2 C), 129.1, 129.0 (2 C), 114.9, 111.9, 86.3, 80.9, 67.8, 58.1, 56.8, 28.7 (3 C), 17.3. IR (film) ν_{max} = 1655, 1489, 1246, 1153, 1045, 735, 696 cm^{-1} . ESI HRMS calcd for $\text{C}_{24}\text{H}_{29}\text{IN}_2\text{O}_6$ $[(\text{M}+\text{H})^+]$ 569.1143, found 569.1149.

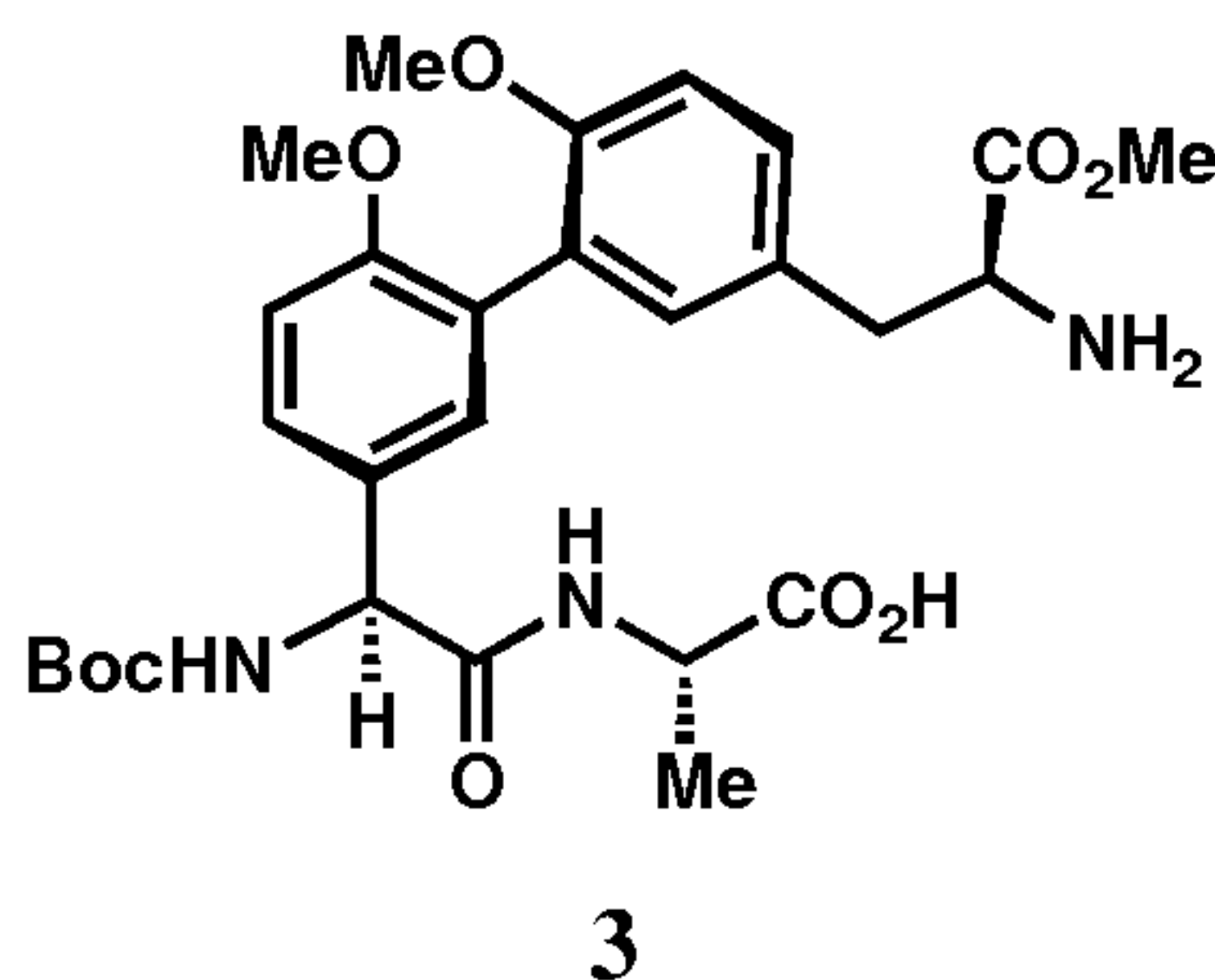


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To a mixture of compound **11** (200 mg, 350 μmol), compound **15** (198 mg, 420 μmol , 1.2 eq) and K_2CO_3 (243 mg, 1.35 mmol, 5 eq) under Ar was added an Ar sparged suspension of $\text{PdCl}_2(\text{dppf})$ (57.5 mg, 70 μmol , 0.2 eq) in DMSO (3.5 mL) via cannula. The reaction was allowed to stir at 80 $^\circ\text{C}$ for 36 hrs. then was cooled and dilute $\text{NH}_4\text{Cl}_{(\text{aq})}$ and EtOAc were added. The aqueous layer was extracted 2 $\times$ with EtOAc and the combined organic fractions were dried over Na_2SO_4 and concentrated. Purification by flash column chromatography (30% EtOAc in hexanes) yielded compound **17** (99.9 mg, 36% yield). R_f = 0.14 (35% EtOAc in hexanes). ^1H NMR (CDCl_3 , 600 MHz) multiple

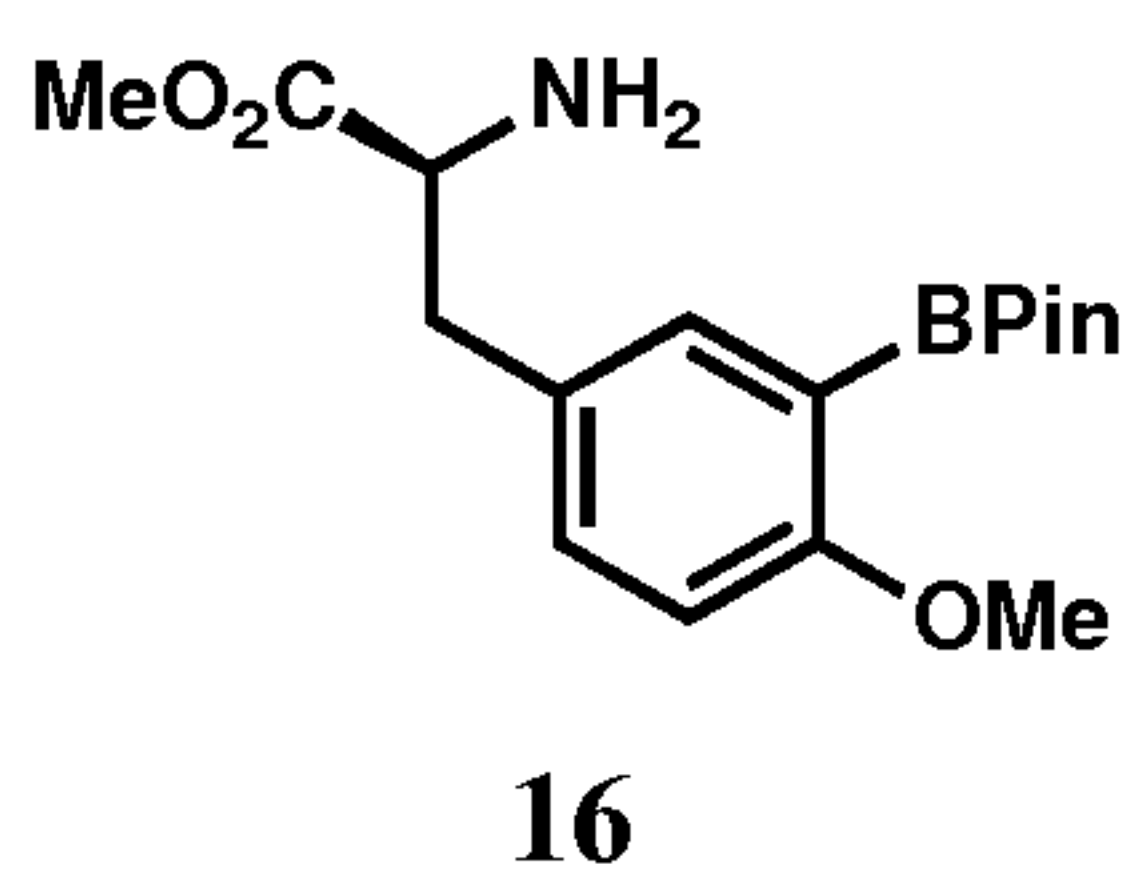
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isomers. ^{13}C NMR (CDCl_3 , 600 MHz) multiple isomers. IR (film) $\nu_{\text{max}} = 1707, 1666, 1500, 1452, 1242, 1209, 1151, 1049, 1022, 742, 696 \text{ cm}^{-1}$. ESI HRMS calcd for $\text{C}_{43}\text{H}_{49}\text{N}_3\text{O}_{11}$ $[(\text{M}+\text{H})^+]$ 783.3440, found 783.3444.



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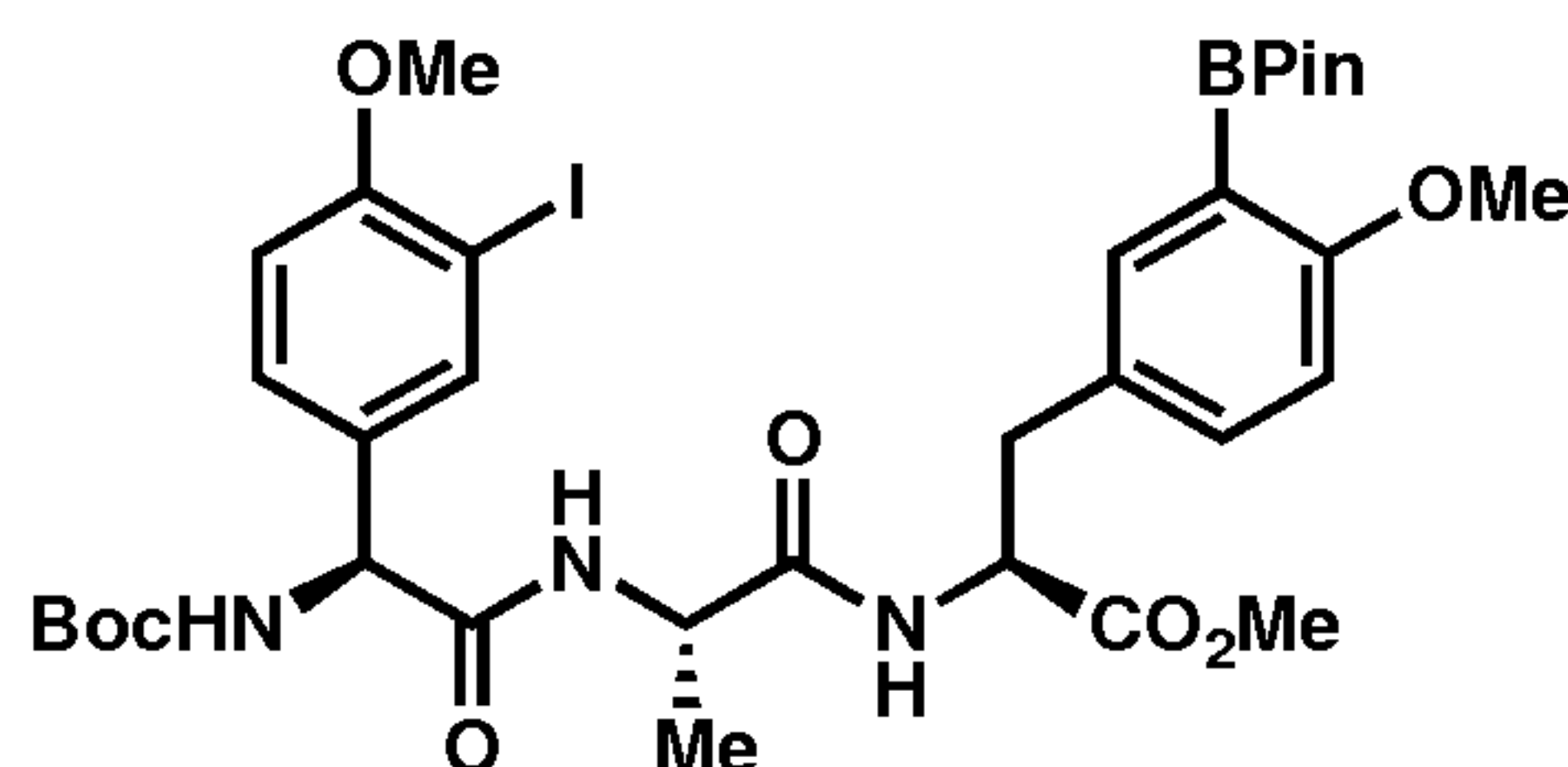
A solution of compound **17** (51.3 mg, 66 μmol) in 95% EtOH (16 mL) was treated with 10% Pd/C (17 mg) and allowed to stir until the presence of starting material could no longer be detected by TLC (~3 hrs). The reaction mixture was filtered through
 10 Celite, washed with ethyl acetate, and concentrated. The product was taken forward with no further purification. ^1H NMR (MeOD, 600 MHz) multiple isomers. IR (film) $\nu_{\text{max}} = 1497, 1246, 1155, 1132, 1045, 1024 \text{ cm}^{-1}$. ESI HRMS calcd for $\text{C}_{28}\text{H}_{37}\text{N}_3\text{O}_9$ $[(\text{M}+\text{H})^+]$ 560.2602, found 560.2597.



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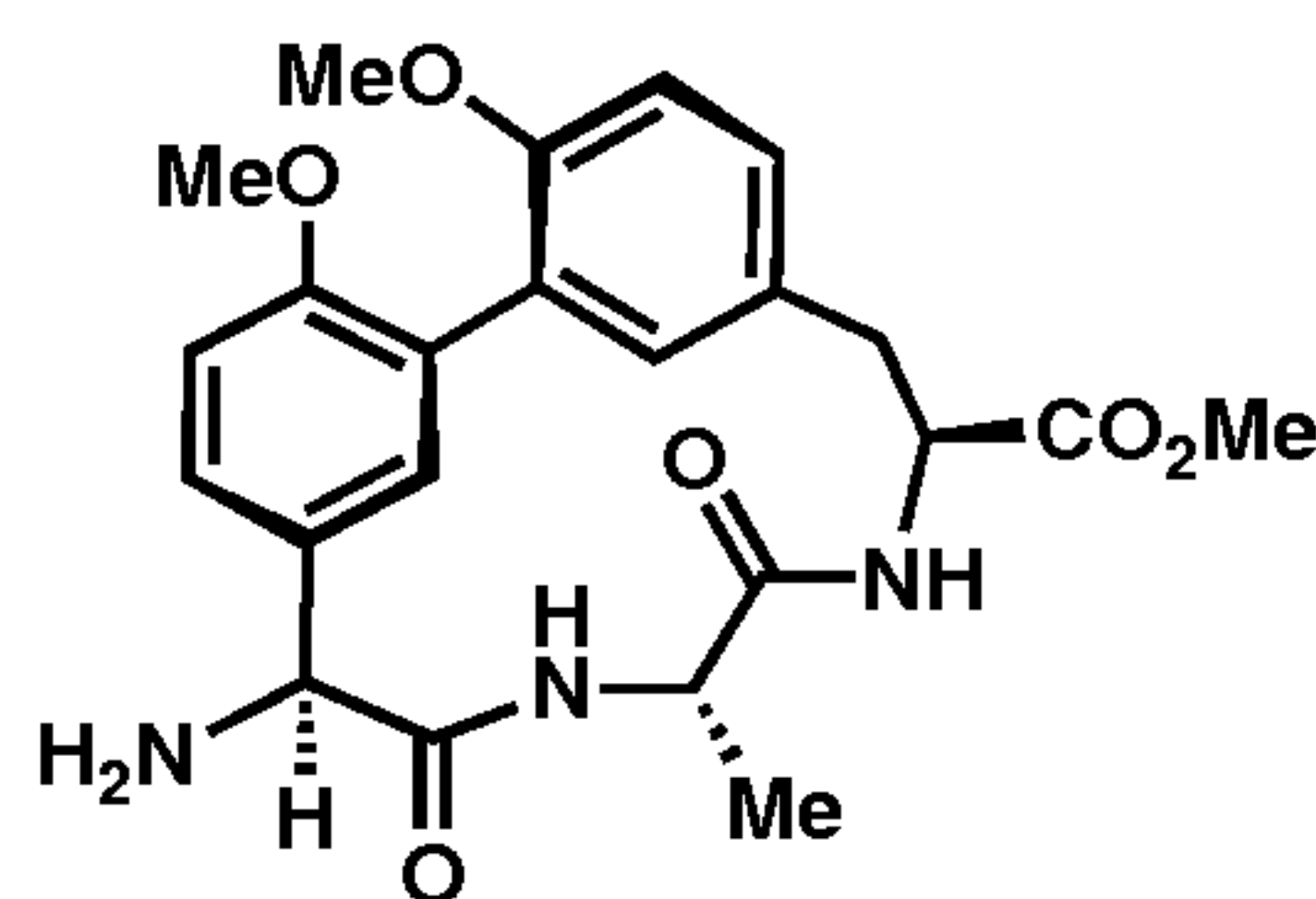
Compound **15** could not be purified completely due to instability on silica gel. A solution of semi-pure compound **15** (646 mg, 1.38 mmol) in 95% EtOH (70 mL) was treated with 10% Pd/C (215 mg) and allowed to stir until the presence of starting
 20 material could no longer be detected by TLC (35% EtOAc in Hex) (~4 hrs). The reaction mixture was filtered through Celite, washed with ethyl acetate, and concentrated. The product, a yellow oil, was taken forward with no further purification (431 mg, 93% yield). ^1H NMR (CDCl_3 , 400 MHz) δ (ppm) 7.48 (d, $J = 2.3 \text{ Hz}$, 1H), 7.21 (dd, $J = 8.4, 2.3 \text{ Hz}$, 1H), 6.80 (d, $J = 8.5 \text{ Hz}$, 1H), 3.81 (s, 3H), 3.76-3.68 (m, 4H),
 25 3.03 (dd, $J = 13.7, 4.9 \text{ Hz}$, 1H), 2.78 (dd, $J = 13.6, 8.1 \text{ Hz}$, 1H), 1.39-1.32 (m, 12H) ^{13}C NMR (CDCl_3 , 600 MHz) δ (ppm) 175.6, 163.4, 137.6, 133.4, 128.5, 110.8, 83.6 (2 C), 83.2, 56.1, 56.0, 52.1, 40.2, 25.0 (3 C). IR (film) $\nu_{\text{max}} = 1605, 1493, 1417, 1335, 1248,$

1142, 1070, 1022, 852, 796, 673, 538 cm^{-1} . ESI HRMS calcd for $\text{C}_{17}\text{H}_{26}\text{BNO}_5$ $[(\text{M}+\text{H})^+]$ 336.1977, found 336.1973.

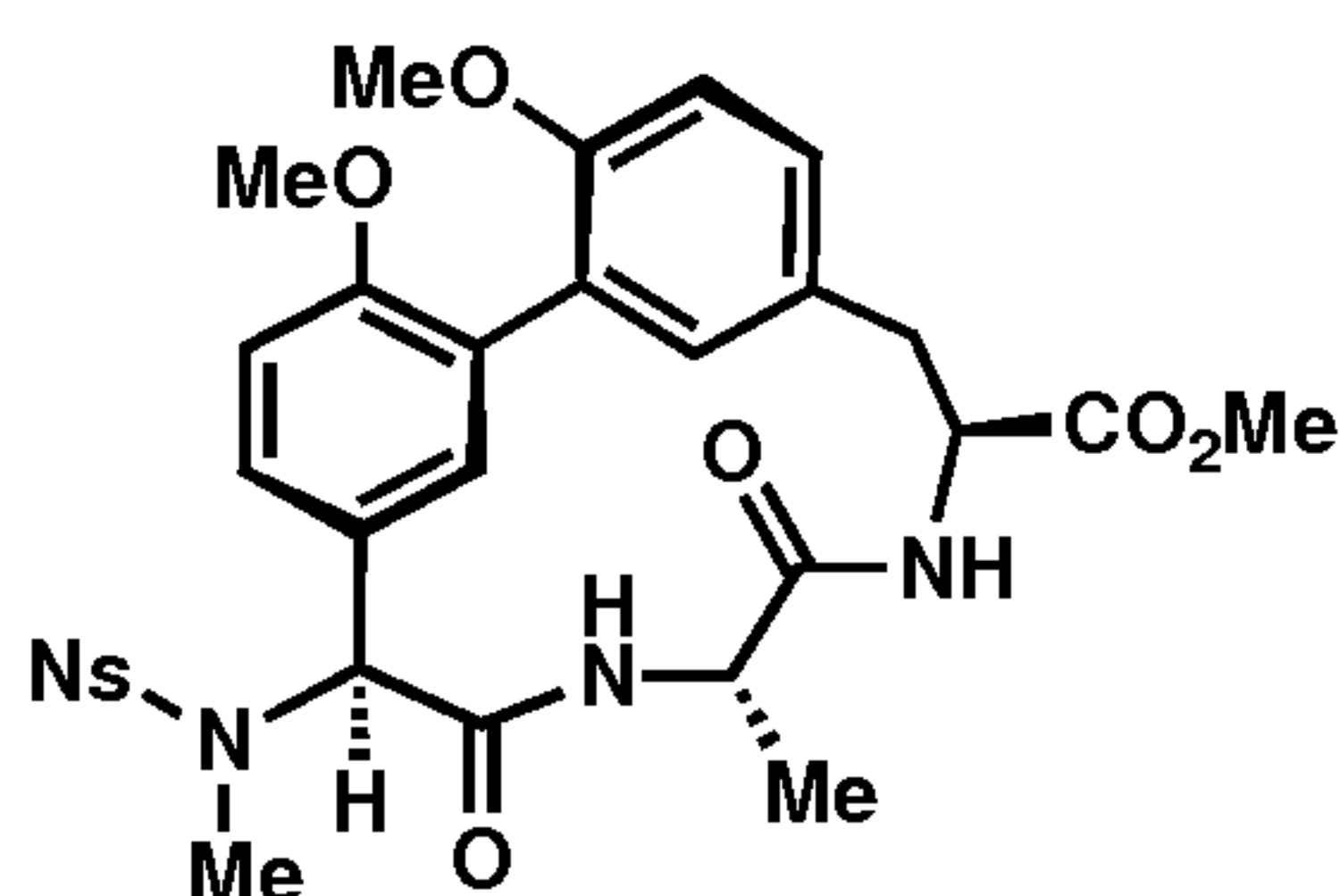


4

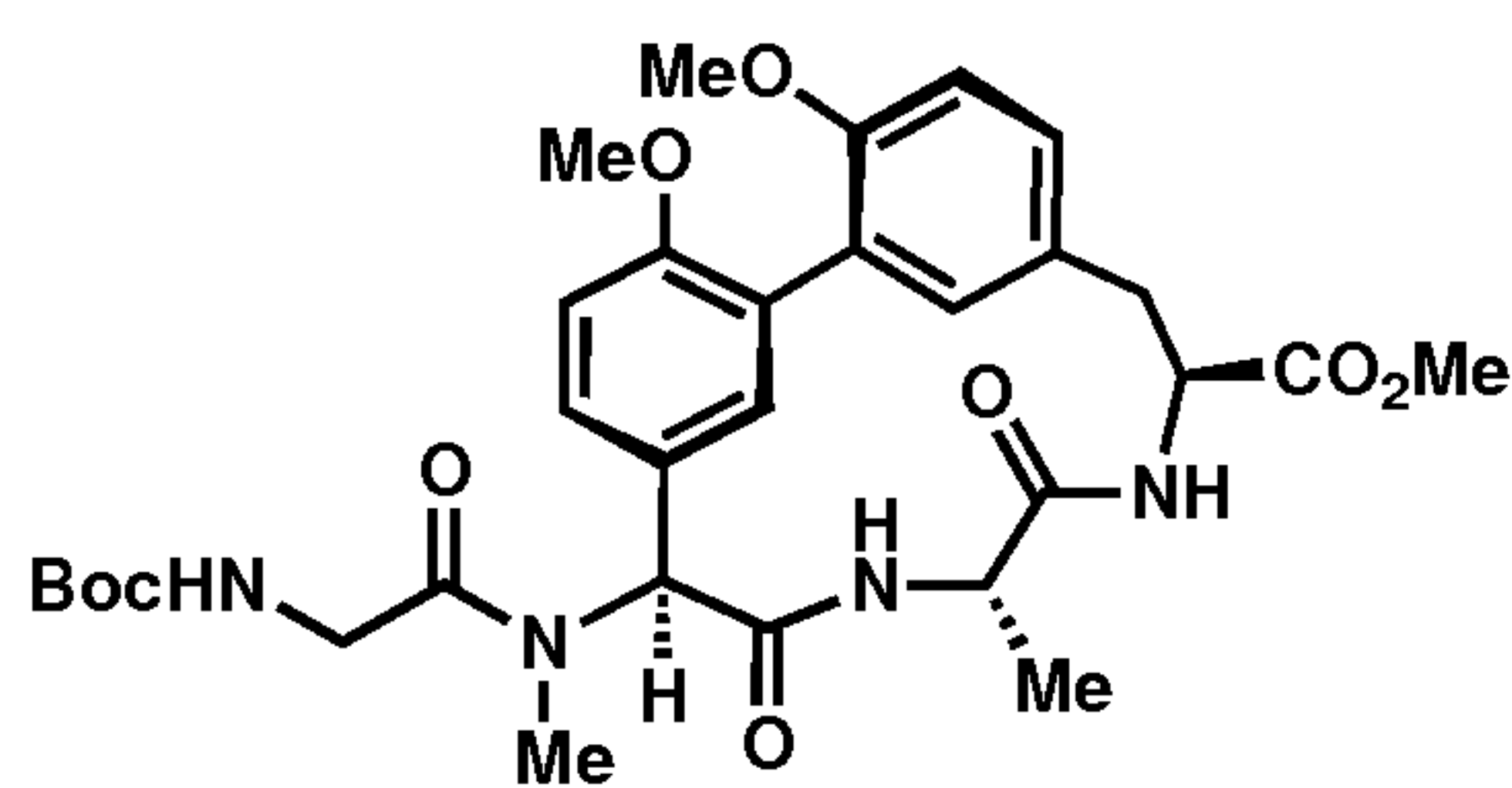
To a solution of compound **10** (1 g, 2.0 mmol) in THF (100 mL) was added 17 mL of 0.2 M $\text{LiOH}_{(\text{aq})}$ (3.4 mmol, 1.7 eq). The reaction was allowed to stir until TLC indicated all starting material had been consumed. The reaction was then quenched by the addition of 5% NH_4Cl and most of the THF was blown off under a stream of nitrogen. Water and EtOAc were added and the aqueous phase was extracted 2 $\times$ with EtOAc. The combined organic layers were then washed with brine, dried over Na_2SO_4 , and concentrated. Compound **19** (1.9 g, 4.36 mmol) was dissolved in a 2.2:1 mixture of acetonitrile and DMF (25.7 mL). The compound was then treated sequentially with NaHCO_3 (catalytic), HOBT (1.5 g, 10.9 mmol, 2.5 eq), compound **16** (1.61 g, 4.8 mmol, 1.1 eq), and EDC (1.8 g, 9.59 mmol, 2.2 eq) and stirred under Ar overnight. The volatiles were evaporated, the residue was taken up in ethyl acetate and washed with 5% $\text{NaHCO}_{3(\text{aq})}$, citric acid $_{(\text{aq})}$, water, and brine. The organic layer was dried over Na_2SO_4 and concentrated. Abbreviated column chromatography (2.5% MeOH in DCM) yielded a semi-pure product as a yellow foam (1.22 g, 79% yield). The product could not be purified further due to instability upon prolonged exposure to silica gel or a C_{18} HPLC column. Crude spectra were used to characterize the compound. $R_f = 0.32$ (3% MeOH in DCM). ^1H NMR (CDCl_3 , 600 MHz) δ (ppm) 7.85 (s, 1H), 7.30 (d, $J = 10.8$ Hz, 1H), 7.11 (d, $J = 8.2$ Hz, 1H), 6.81-6.71 (m, 3H), 6.23 (br s, 1H), 5.81 (br s, 1H), 5.15 (br s, 1H), 4.74-4.68 (m, 1H), 4.58-4.51 (m, 1H), 3.87 (s, 3H), 3.85 (s, 3H), 3.73 (s, 3H), 3.05-3.02 (m, 1H), 2.87-2.80 (m, 1H), 1.52-1.36 (m, 24H). ^{13}C NMR (CDCl_3 , 600 MHz) δ (ppm) 171.5, 171.0, 169.9, 163.5, 158.2, 155.1, 138.1, 137.7, 133.4, 132.3, 128.5, 127.0, 111.3, 110.8, 86.7, 83.9 (2 C), 80.3, 57.4, 56.5, 56.0, 53.5, 52.4, 49.0, 36.8, 28.4 (3 C), 25.2 (4 C), 18.2 (no signal was observed for the carbon attached to the boron). IR (film) $\nu_{\text{max}} = 1645, 1489, 1344, 1248, 1144, 1072, 1047, 1018, 854, 656, 550$ cm^{-1} . ESI HRMS calcd for $[(\text{M}+\text{H})^+]$ $\text{C}_{34}\text{H}_{47}\text{BIN}_3\text{O}_{10}$: 796.2472, found: 796.2465.

**20**

A solution of compound **4** (100 mg, 126 μ mol) and K_2CO_3 (174 mg, 1.26 mmol, 10 eq) in acetonitrile (1.9 mL, 20 mM final) was stirred in a sealed vial and purged extensively with Ar. The mixture was then treated via syringe with a suspension of $PdCl_2(dppf)$ (10.3 mg, 12.6 μ mol, 10 mol%) in acetonitrile (1.3 mL, 5 mM) that had been sparged with Ar. The vial was then heated to 80 $^{\circ}C$, and allowed to stir for 21 hrs. The reaction mixture was cooled, EtOAc and dilute $NH_4Cl_{(aq)}$ were added. The aqueous phase was extracted 2 $\times$ with EtOAc and the combined organic phases were washed with brine, dried over Na_2SO_4 , and concentrated. The crude residue was then filtered through an abbreviated silica column (4% MeOH in DCM) to remove palladium species yielding a semipure residue. A solution of crude compound **18** (R_f = 0.36 (4% MeOH in DCM)) was then taken up in anhydrous CH_2Cl_2 (2 mL) under Ar and treated dropwise with trifluoroacetic acid (0.5 mL). The reaction was allowed to stir until TLC indicated complete disappearance of starting material (~50 min). The volatiles were then evaporated under a stream of nitrogen, the crude material was purified via column chromatography (9.5% MeOH in DCM with trace triethylamine) and the purified material was filtered through basic alumina to give compound **20** (26mg, 48% yield). R_f = 0.44 (10% MeOH in DCM with 1 drop of TEA/10 mL). ^1H NMR (MeOD, 600 MHz) multiple isomers. ^{13}C NMR (MeOD, 600 MHz) multiple isomers. IR (film) ν_{max} = 1624, 1508, 1269, 1246, 1176, 1022, 795, 582 cm^{-1} . ESI HRMS calcd for $C_{23}H_{27}N_3O_6$ [(M+H) $^+$] 442.1973, found 442.1966.

**22**

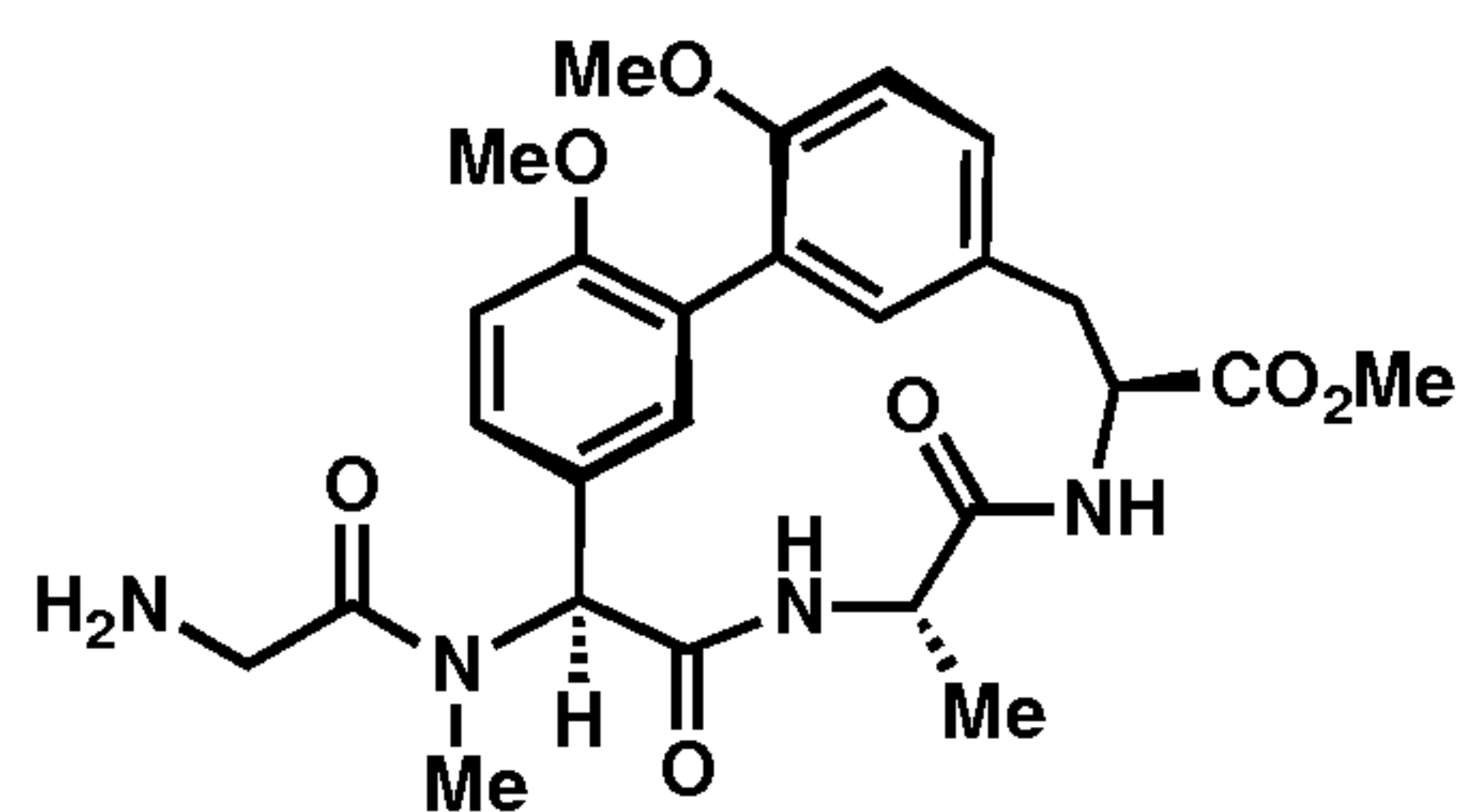
A solution of compound **20** (94 mg, 223 μ mol) in acetonitrile (3 mL) was treated with nosyl chloride (76 mg, 335 μ mol, 1.5 eq) and triethylamine (91 μ L, 669 μ mol, 3 eq). After stirring for 2 hrs all starting material was consumed as determined by TLC and a white precipitate had formed. The solvent was then evaporated, purged with Ar, and crude compound **21** (R_f = 0.36 (7% MeOH in DCM)) was taken up in dry acetone (4 mL). The dissolved material was treated with K_2CO_3 (314 mg, 2.3 mmol 10 eq), the reaction tube was sealed, and iodomethane (129 μ L, 2.3 mmol, 10 eq) was added. The mixture was stirred at 65 $^{\circ}C$ overnight then cooled, filtered, and concentrated. The residue was then subjected to flash column chromatography (2.5% MeOH in DCM) yielding compound **22** (54 mg, 37% yield). R_f = 0.32 (2.5% MeOH in DCM). ^1H NMR ($CDCl_3$, 600 MHz) δ (ppm) 8.34 (d, J = 7.2 Hz, 1H), 8.02 (d, J = 7.2 Hz, 1H), 7.38 (d, J = 8.3 Hz, 1H), 6.94 (d, J = 8.2 Hz, 1H), 6.82 (d, J = 8.2 Hz, 1H), 6.67-6.59 (m, 2H), 6.56 (s, 1H), 6.24 (d, J = 4.8 Hz, 1H), 5.81 (s, 1H), 4.85-4.80 (m, 1H), 4.52-4.44 (m, 1H), 3.84-3.76 (m, 9H), 3.44 (d, J = 15.3 Hz, 1H), 2.99 (dd, J = 15.5, 5.7 Hz, 1H), 2.83 (s, 3H), 1.30 (d, J = 5.3 Hz, 3H) ^{13}C NMR ($CDCl_3$, 600 MHz) δ (ppm) 172.0, 171.8, 169.0, 157.4, 156.1, 150.1, 145.1, 134.5, 134.5, 129.7, 128.9, 128.7 (2 C), 128.6, 128.3, 127.0, 125.1, 124.2 (2 C), 112.3, 111.8, 62.6, 56.1 (2 C), 53.1, 53.0, 49.8, 34.5, 32.0, 19.9. IR (film) ν_{max} = 1645, 1527, 1504, 1348, 1269, 1173, 1146, 735, 606 cm^{-1} . ESI HRMS calcd for $C_{30}H_{32}N_4O_{10}S$ [(M+Na) $^+$]: 663.1731, found: 663.1724.

**23**

To a solution of compound **22** (20 mg, 31.3 μ mol) in acetonitrile (1 mL) under Ar was added sequentially 2-mercaptoacetic acid (6.5 μ L, 94 μ mol, 3 eq) and DBU (23 μ L, 157 μ mol, 5 eq). The reaction was monitored by TLC for the disappearance of starting material and the volatiles were evaporated under a stream of nitrogen when the starting material had been completely consumed (~30 min). The residue was taken up in EtOAc and 1 N HCl was added. The organic layer was extracted 2 $\times$ with 1 N HCl and the combined aqueous layers were basified with saturated $NaHCO_3$. The aqueous layer was then extracted 2 $\times$ with EtOAc and the combined organic layers were dried over sodium

sulfate and concentrated. The product ($R_f = 0.29$ (8% MeOH in DCM with 1 drop of TEA/10 mL)) was not further purified and was taken directly to the next reaction. A solution of the crude material in CH_2Cl_2 :DMF (3:1, 1 mL) was treated sequentially with HoBT (11.1 mg, 82.5 μmol , 3.3 eq), Boc-Gly-OH (4.8 mg, 27.5 μmol , 1.1 eq), and EDC (14.4 mg, 75 μmol , 3 eq). The reaction was stirred overnight, then the volatiles were evaporated and EtOAc and water were added. The aqueous layer was extracted (2 $\times$) with EtOAc and the combined organic layers were washed with brine, dried over Na_2SO_4 and concentrated. The crude material was purified via column chromatography (4% MeOH in DCM) to yield a white foam (14.1 mg, 74% yield). $R_f = 0.32$ (5% MeOH in DCM). ^1H NMR (CDCl_3 , 600 MHz) δ (ppm) 7.15 (d, $J = 7.9$ Hz, 1H), 6.99 (d, $J = 7.1$ Hz, 1H), 6.93 (d, $J = 8.3$ Hz, 1H), 6.86 (d, $J = 8.3$ Hz, 1H), 6.80 (s, 1H), 6.71 (s, 1H), 6.44-6.26 (m, 3H), 5.57 (s, 1H), 4.96-4.89 (m, 1H), 4.74-4.66 (m, 1H), 4.13 (d, $J = 16.3$ Hz, 1H), 4.00 (d, $J = 16.7$ Hz, 1H), 4.86-4.80 (m, 9H), 4.13 (d, $J = 16.3$ Hz, 1H), 4.00 (d, $J = 16.7$ Hz, 1H), 3.54 (d, $J = 15.9$ Hz, 1H), 3.04 (dd, $J = 15.7, 7.0$ Hz, 1H), 2.79 (s, 3H), 1.46 (s, 9H), 1.38 (d, $J = 6.53$ Hz, 3H). ^{13}C NMR (CDCl_3 , 600 MHz) δ (ppm) 172.3, 172.0, 170.2, 170.0, 157.2, 156.1, 156.0, 135.3, 134.3, 129.9, 129.0, 129.0, 128.4, 127.2, 125.9, 112.1, 111.8, 79.7, 60.3, 56.1, 53.0, 52.7, 49.9, 46.0, 42.9, 34.5, 31.7, 28.5 (3 C), 19.7. IR (film) $\nu_{\text{max}} = 1639, 1508, 1269, 1246, 1163, 1024$ cm^{-1} . ESI HRMS calcd for $\text{C}_{31}\text{H}_{40}\text{N}_4\text{O}_9$ $[(\text{M}+\text{H})^+]$: 613.2868, found: 613.2860.

20

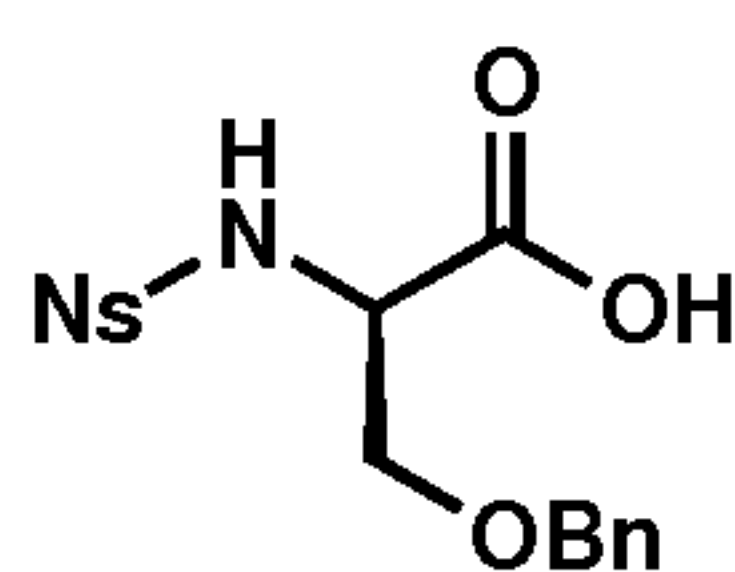


1

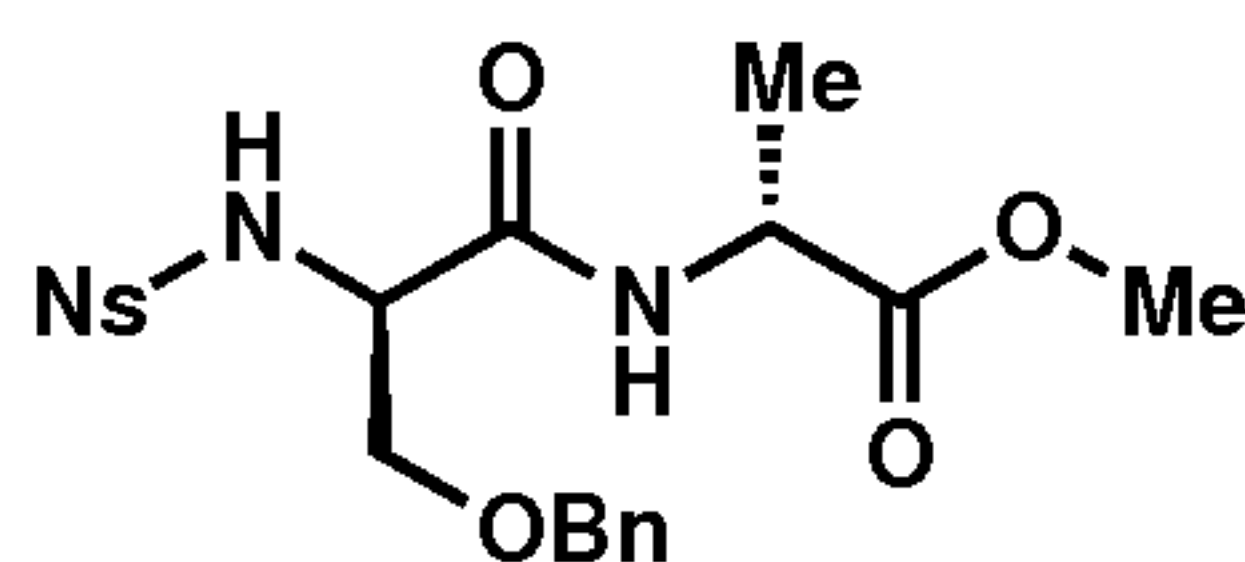
A solution of compound **23** (29.2 mg, 47.7 μmol) in CH_2Cl_2 (0.66 mL) was treated with TFA (0.33 mL) while stirring at 0 $^\circ\text{C}$ in a sealed vial. After 30 min, the reaction was found to be complete by TLC analysis, the vial was warmed to room temperature, a small amount of ethyl acetate was added, and the volatiles were evaporated under a stream of dry N_2 gas and dried *in vacuo*. The residue was then taken up in ethyl acetate and K_2CO_3 solid was added. The mixture was then filtered, concentrated, and purified by column chromatography (10% MeOH in DCM w/trace TEA). The product was obtained as a white residue (69 mg, 96% yield). $R_f = 0.33$ (14%

30

MeOH in DCM with 1 drop of TEA/10 mL). ^1H NMR (MeOD, 400 MHz) multiple isomers, see page S34. ^{13}C NMR (CDCl_3 , 600 MHz) δ (ppm) 172.3, 172.0, 170.5, 157.1, 156.1, 135.3, 134.4, 129.8, 128.9, 128.9, 128.4, 127.3, 126.3, 112.1, 111.8, 60.4, 56.1, 56.1, 53.0, 52.7, 49.8, 43.6, 34.5, 31.6, 19.6. IR (film) ν_{max} = 1639, 1506, 1269, 1202, 1175, 1128, 1022, 800, 719 cm^{-1} . ESI HRMS calcd for $\text{C}_{26}\text{H}_{32}\text{N}_4\text{O}_7$ $[(\text{M}+\text{H})^+]$: 513.2344, found: 513.2340.

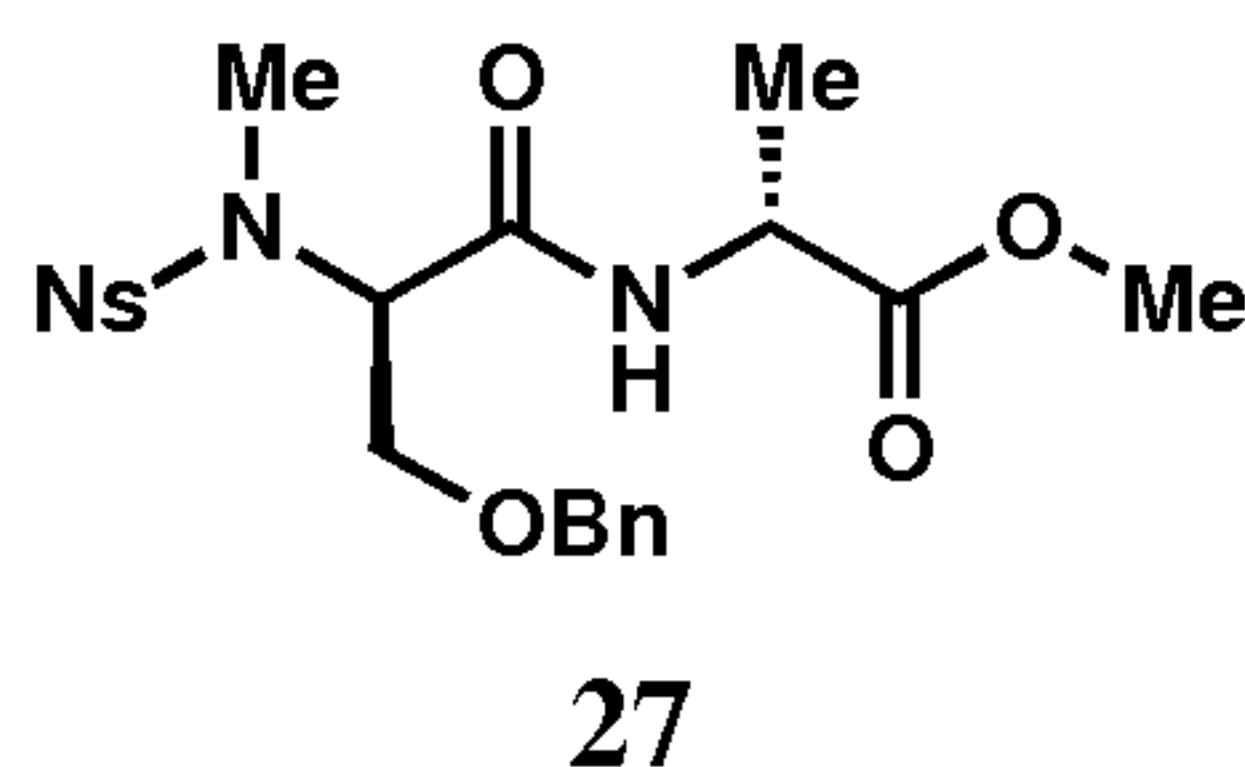
**25**

A solution of D-Ser-(OBzl)-OH (1.47 g, 15.4 mmol) in 1 N NaOH (14.7 mL) was treated dropwise with 4-nitrobenzenesulfonyl chloride (1.85 g, 7.9 mmol, 1.05 eq) in THF (1.4 mL). The solution was allowed to stir overnight then neutralized with citric acid (pH-3.5) and extracted with ethyl acetate (3 $\times$). The organic layers were combined, dried over Na_2SO_4 , and concentrated. Flash column chromatography (6% MeOH in DCM w/trace AcOH) gave compound **25** as an off-white powder (62% yield). R_f = 0.42 (7% MeOH in DCM w/1 drop/10 mL AcOH). ^1H NMR (CDCl_3 , 600 MHz) δ (ppm) 8.24 (d, J = 11.0 Hz, 2H), 7.98 (d, J = 11.0 Hz, 2H), 7.32-7.19 (m, 5H), 5.82 (d, J = 11.0 Hz, 1H), 4.50-4.43 (m, 2H), 4.23 (m, 1H), 3.85 (dd, J = 14.4 Hz, J = 4.5 Hz, 1H), 3.65 (dd, J = 14.4 Hz, J = 4.5 Hz, 1H). ^{13}C NMR (CDCl_3 , 600 MHz) δ (ppm) 173.3, 150.2, 146.0, 136.7, 128.7 (2 C), 128.4, 128.4 (2 C), 128.0 (2 C), 124.4 (2 C), 73.8, 70.1, 56.0. IR (film) ν_{max} = 1740, 1529, 1350, 1173, 1086, 856, 737, 656, 609, 554 cm^{-1} . ESI HRMS calcd for $\text{C}_{16}\text{H}_{16}\text{N}_2\text{O}_7\text{S}$ $[(\text{M}+\text{Na})^+]$: 403.0570, found: 403.0566.

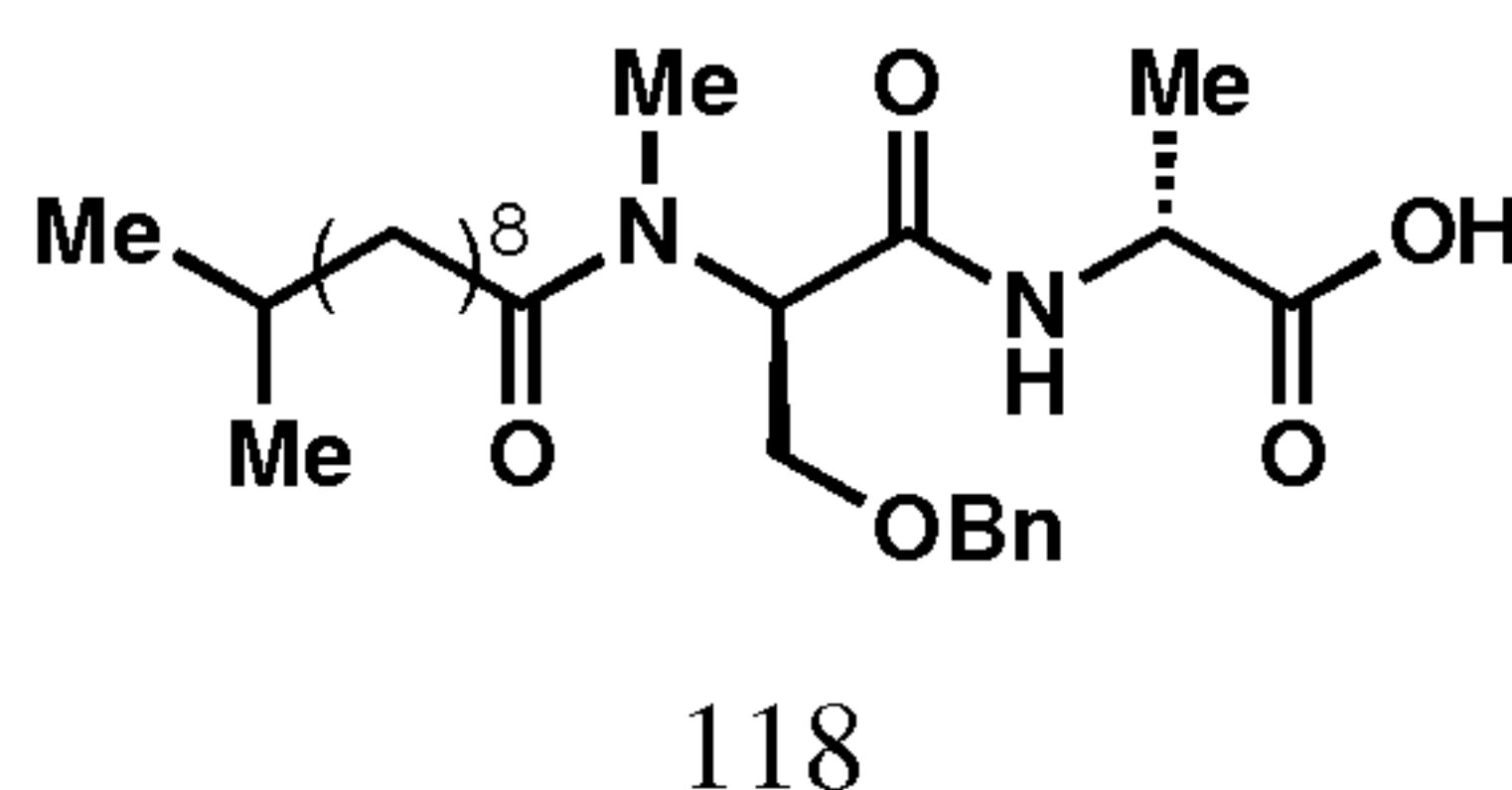
**26**

A solution of D-Ala-OMe HCl (147 mg, 1.05 mmol) in a 3:1 mixture of dichloromethane and DMF (30 mL) under Ar at 0 $^{\circ}\text{C}$ was treated sequentially with NaHCO_3 (88 mg, 1.05 mmol, 1 eq), anhydrous HoBT (468 mg, 3.5 mmol, 3.3 eq.), compound **25** (400 mg, 1.05 mmol, 1 eq.), and EDC (604 mg, 3.15 mmol, 3 eq.). The

solution was allowed to warm to room temperature and stirred overnight. All volatiles were then evaporated, and the mixture was diluted with EtOAc and water. The aqueous layer was extracted (2×) and the combined organic layers were dried over Na₂SO₄ and concentrated. Flash column chromatography (1% MeOH in DCM) afforded the product in 88% yield. $R_f = 0.20$ (1% MeOH in DCM with 1 drop of AcOH/10 mL). ¹H NMR (CDCl₃, 500 MHz) δ (ppm) 8.27 (d, $J = 8.9$ Hz, 2H), 7.99 (d, $J = 8.9$ Hz, 2H), 7.37-7.30 (m, 3H), 7.28-7.23 (m, 2H), 7.18 (d, $J = 7.3$ Hz, 1H), 5.85 (d, $J = 5.7$ Hz, 1H), 4.51 (s, 1H), 4.47-4.40 (m, 1H), 3.89-3.83 (m, 2H), 3.72 (s, 3H), 3.54-3.49 (m, 1H), 1.29 (d, $J = 7.2$ Hz, 1H) ¹³C NMR (CDCl₃, 600 MHz) δ (ppm) 172.7, 168.1, 150.3, 145.1, 136.8, 128.8 (2 C), 128.7 (2 C), 128.5, 128.2 (2 C), 124.5 (2 C), 73.9, 70.1, 55.4, 52.7, 48.6, 18.2. IR (film) $\nu_{\max} = 1645, 1525, 1450, 1348, 1310, 1165, 1119, 1092, 852, 733, 617, 546, 525$ cm⁻¹. ESI HRMS calcd for C₂₀H₂₃N₃O₈S [(M+Na)⁺]: 488.1098, found: 488.1095.



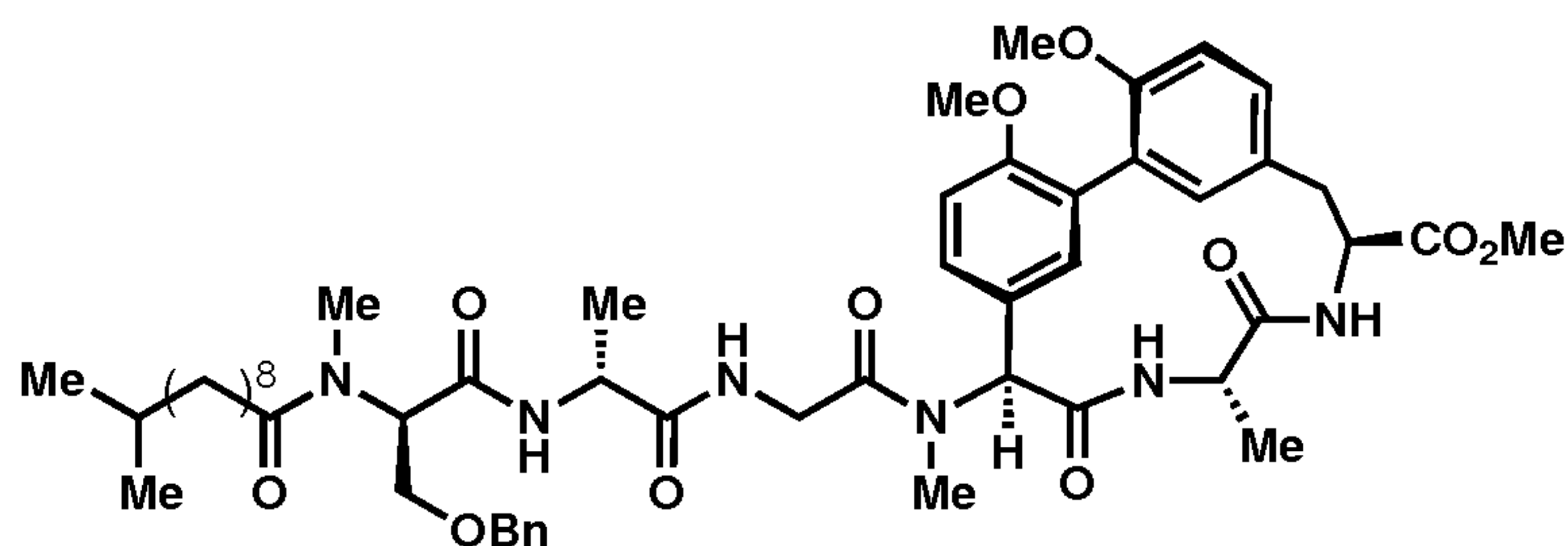
A solution of compound **26** (417 mg, 0.90 mmol) in dry CH₂Cl₂ (15 mL) under Ar was treated with diazomethane (0.66 M in ether, 16.3 mL, 12 eq, 11 mmol). The solution was monitored by TLC and when all starting material had been consumed, the volatiles were evaporated under a stream of dry nitrogen. Flash column chromatography (1% MeOH in DCM) yielded the product (86mg, 90% yield). $R_f = 0.57$ (2% MeOH in DCM). ¹H NMR (CDCl₃, 400 MHz) δ (ppm) 8.05 (d, $J = 9$ Hz, 2H), 7.92 (d, $J = 9$ Hz, 2H), 7.30-7.26 (m, 3H), 7.12-7.02 (m, 3H), 4.50 (p, $J = 7$ Hz, 1H), 4.29 (dd, $J = 40.0$ Hz, 11.0 Hz, 2H), 3.90-3.84 (m, 1H), 3.78-3.70 (m, 4H), 2.89 (s, 3H), 1.41 (d, $J = 7.2$ Hz, 3H). ¹³C NMR (CDCl₃, 600 MHz) δ (ppm) 172.8, 167.6, 149.9, 144.4, 136.7, 128.9 (2 C), 128.6 (2 C), 128.5, 128.3 (2 C), 123.9 (2 C), 73.9, 67.1, 59.7, 52.8, 48.4, 30.7, 18.2. IR (film) $\nu_{\max} = 1740, 1670, 1525, 1346, 1153, 1107, 1086, 854, 741, 604$ cm⁻¹. ESI HRMS calcd for C₂₁H₂₅N₃O₈S [(M+H)⁺]: 480.1435; found 480.1445.



2

A solution of compound **27** (86.2 mg, 180 μ mol) in anhydrous acetonitrile under Ar was treated sequentially with 2-mercaptoacetic acid (38 μ L, 540 μ mol, 3 eq) and DBU (135 μ L, 900 μ mol, 5 eq). The compound was allowed to stir until TLC indicated all of the starting material had been consumed. At this point, HCl (0.5 N) and EtOAc were added, the aqueous layer was extracted and then basified with saturated NaHCO₃. The aqueous layer was then extracted again with EtOAc (2 $\times$) and the combined organic layers from this extraction were pooled, dried over Na₂SO₄, and concentrated yielding compound **28**. A 9% NaHCO₃ solution was then added to the crude material and stirred.

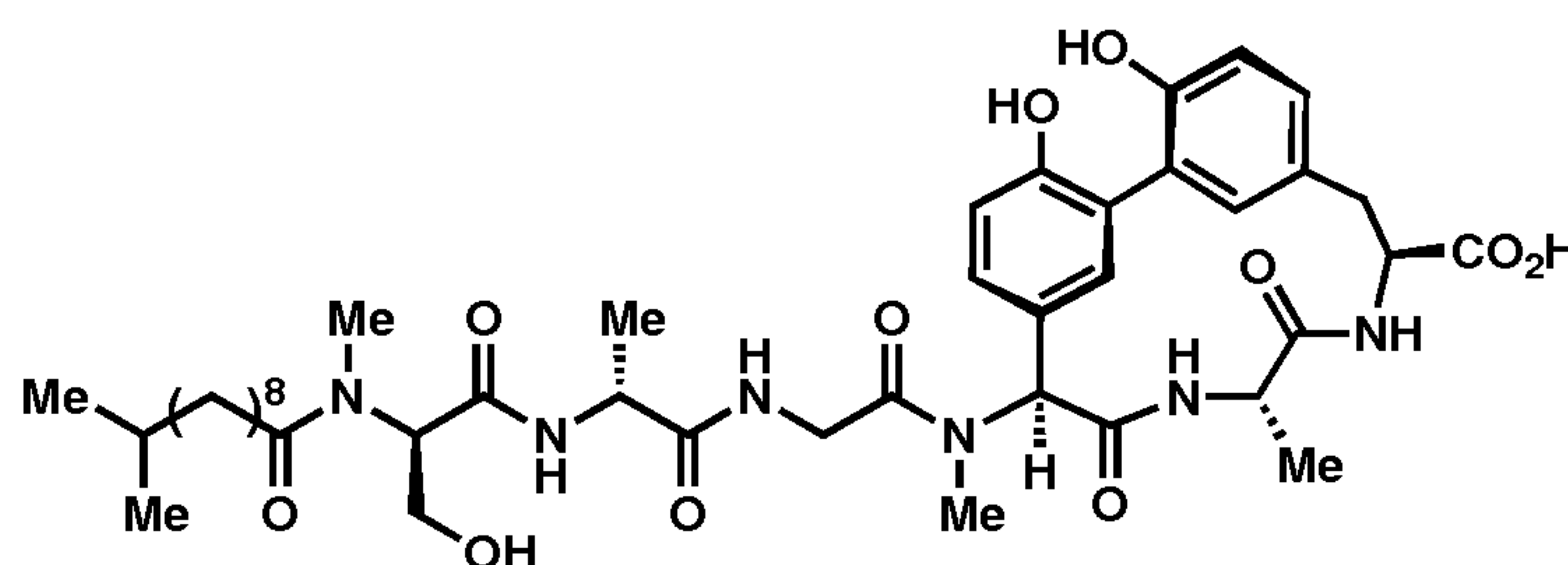
In a separate reaction, isolauric acid (34 mg, 170 mmol) in anhydrous CH₂Cl₂ (1.5 mL) was treated with SOCl₂ (148 μ L, 2.0 mmol, 12 eq) and refluxed for ~45min. The volatiles were then blown off under a stream of N₂ and pumped off *in vacuo*. The resulting white film was taken up in 2 mL of anhydrous CH₂Cl₂ and this solution was added to the freshly deprotected compound **28** in 9% NaHCO₃. This mixture was stirred vigorously for ~5 hrs. The organic layer was removed and the water layer was extracted 2 $\times$ with additional CH₂Cl₂. The combined organic layers were then dried over Na₂SO₄ and concentrated. This crude material was then dissolved in THF (2mL), treated with 0.2 N LiOH (0.98 ml, 1.15 eq) and allowed to stir for 3 hrs. Then 5% NH₄Cl_(aq) and EtOAc were added the aqueous phase was extracted 2 $\times$ with EtOAc, the combined organic layers were dried over Na₂SO₄, and concentrated. The crude material was purified using column chromatography (8% MeOH in DCM w/trace AcOH) yielding compound **2** (15.2 mg, 19% yield). R_f = 0.35 (8% MeOH in DCM with 1 drop of AcOH/10 mL). ¹H NMR (CDCl₃, 600 MHz) multiple isomers, see page S42. IR (film) ν_{max} = 2924, 2850, 1726, 1624, 1529, 1454, 1402, 1205, 1105, 733, 696 cm⁻¹. ESI HRMS calcd for C₂₆H₄₂N₂O₅ [(M+H)⁺] 463.3166, found 463.3158.



29

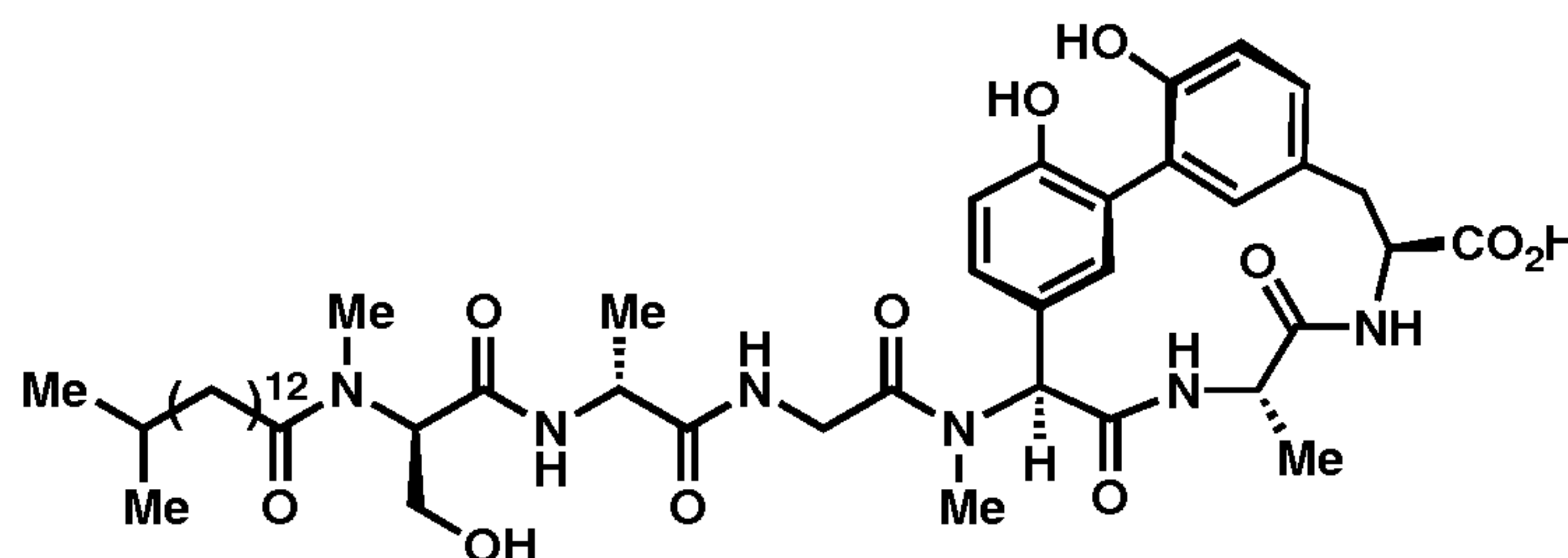
To a solution of compound **1** (16.5 mg, 0.03 mmol) in a 2.2:1 mixture of AcCN and DMF (1.5 mL) was added sequentially HOBt (13.5 mg, 0.1 mmol, 3.1 eq),

compound **2** (14.9 mg, 0.03 mmol, 1 eq) and EDC (18.5 mg, 0.97 mmol, 3 eq) under Ar. The reaction was allowed to stir overnight. Water and EtOAc were then added and the aqueous layer was extracted 2× with EtOAc. The combined organic layers were then washed with brine, dried over Na₂SO₃, and concentrated. Flash column chromatography (4.5% MeOH in DCM) afforded the product (19.5 mg, 63% yield). $R_f = 0.25$ (3% MeOH in DCM). ¹H NMR (CDCl₃, 600 MHz) multiple isomers. ¹³C NMR (CDCl₃, 600 MHz) multiple isomers. IR (film) $\nu_{\max} = 1630, 1506, 1265, 1103, 1026, 798, 696 \text{ cm}^{-1}$. ESI HRMS calcd for C₅₂H₇₂N₆O₁₁ [(M+H)⁺] 957.5332, found 957.5334.



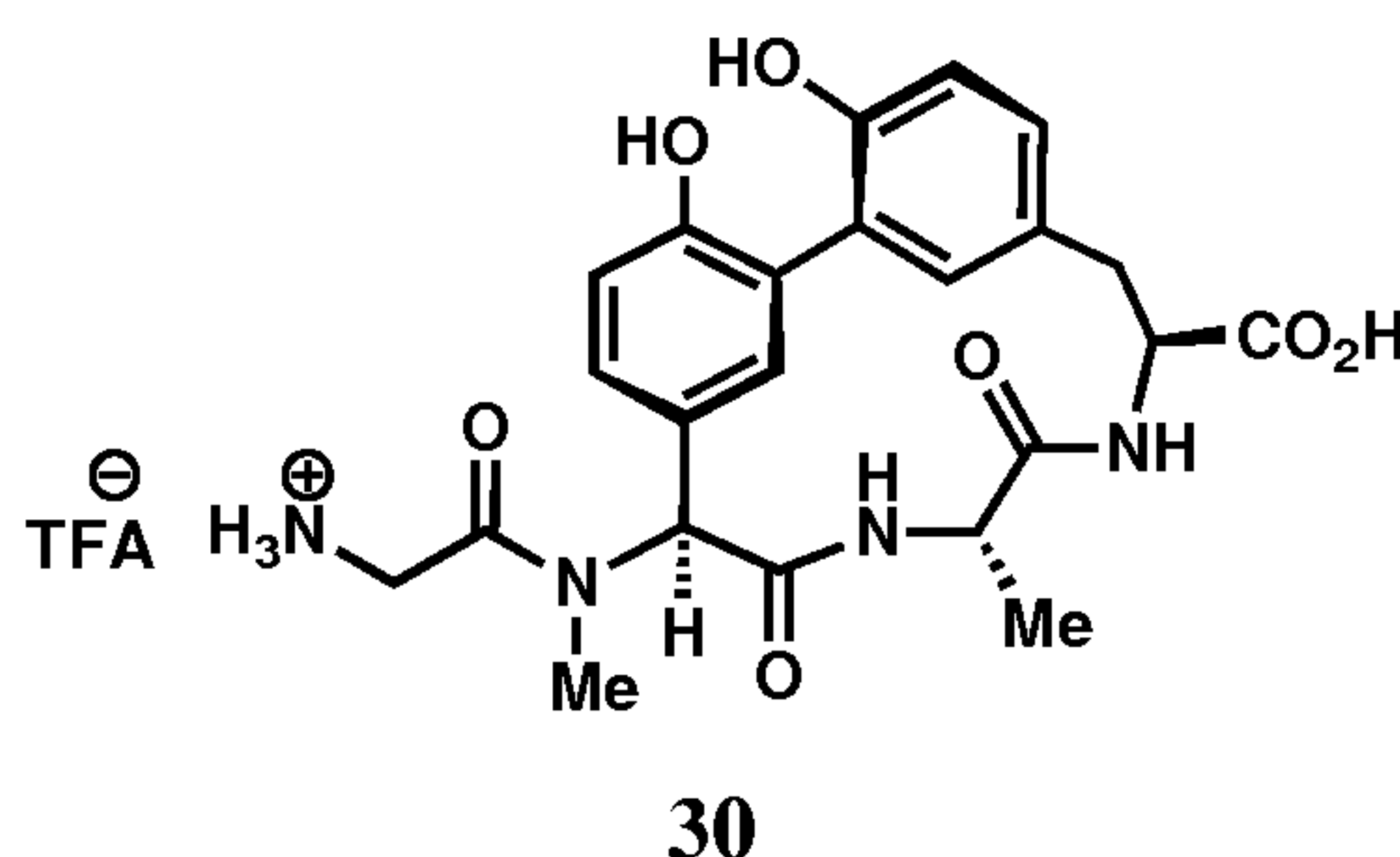
Arylomycin A₂

To a solution of compound **29** (8 mg, 8.4 μmol) in ethanethiol (0.4 mL) under Ar was added AlBr₃ in a 1.0 M solution of CH₂Br₂ (0.21 mL, 25 eq) via syringe. The reaction was then heated to 50 °C for 4 hrs. Upon cooling, water and EtOAc were added and the aqueous layer was extracted (2×) with EtOAc. The aqueous layer was then extracted (2×) with acetonitrile and the combined organic layers were dried over Na₂SO₄ and concentrated. The residue was then taken up in 100% B (1 mL) and this solution and the aqueous layer were purified by HPLC column (linear gradient, 0.5% B per minute, product eluted at 58.3% B) to yield a white powder after lyophilization (7.2 mg, 46% yield). ¹H NMR (MeOD, 600 MHz) δ (ppm) multiple isomers, see page S45. ¹³C NMR (MeOD, 600 MHz) multiple isomers. IR (film) $\nu_{\max} = 1630, 1506, 1408, 1230, 810 \text{ cm}^{-1}$. ESI HRMS calcd for C₄₂H₆₀N₆O₁₁ [(M+H)⁺] 825.4393, found 825.4397. $[\alpha]_D^{20}$ (c 3.4, MeOH): +85.1°.

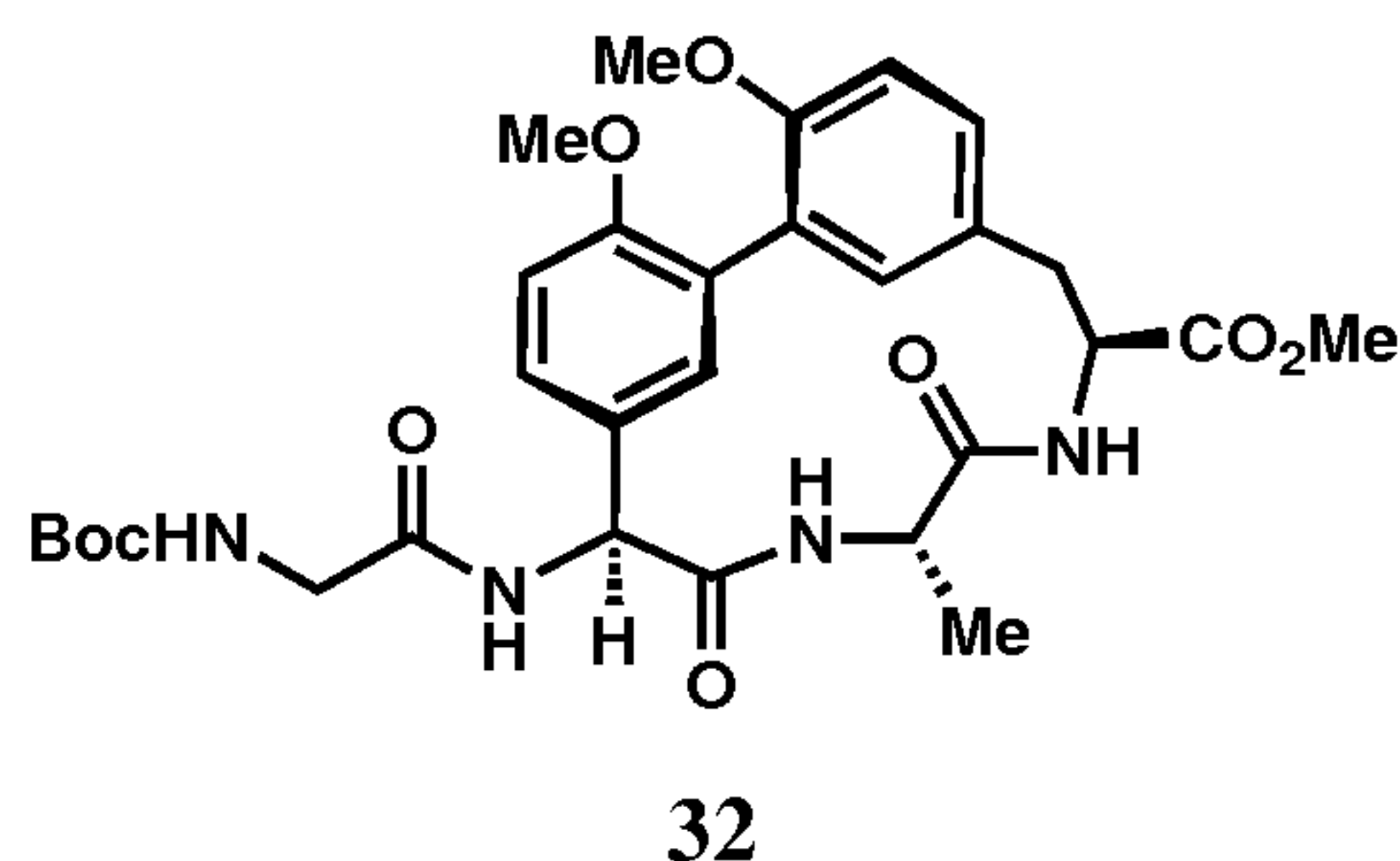


37

Compound **37** was synthesized in the same manner as arylomycin A₂. ¹H NMR (MeOD, 600 MHz) δ (ppm) multiple isomers. ¹³C NMR (MeOD, 600 MHz) δ (ppm) multiple isomers. IR (film) $\nu_{\max}$ = 3275, 2922, 2852, 1632, 1506, 1410, 1230, 810 cm⁻¹. ESI HRMS calcd for C₄₆H₆₈N₆O₁₁ [(M+H)⁺] 881.5019, found 881.5025. [α]_D²⁰ (c 1.8, MeOH): +64.9°.

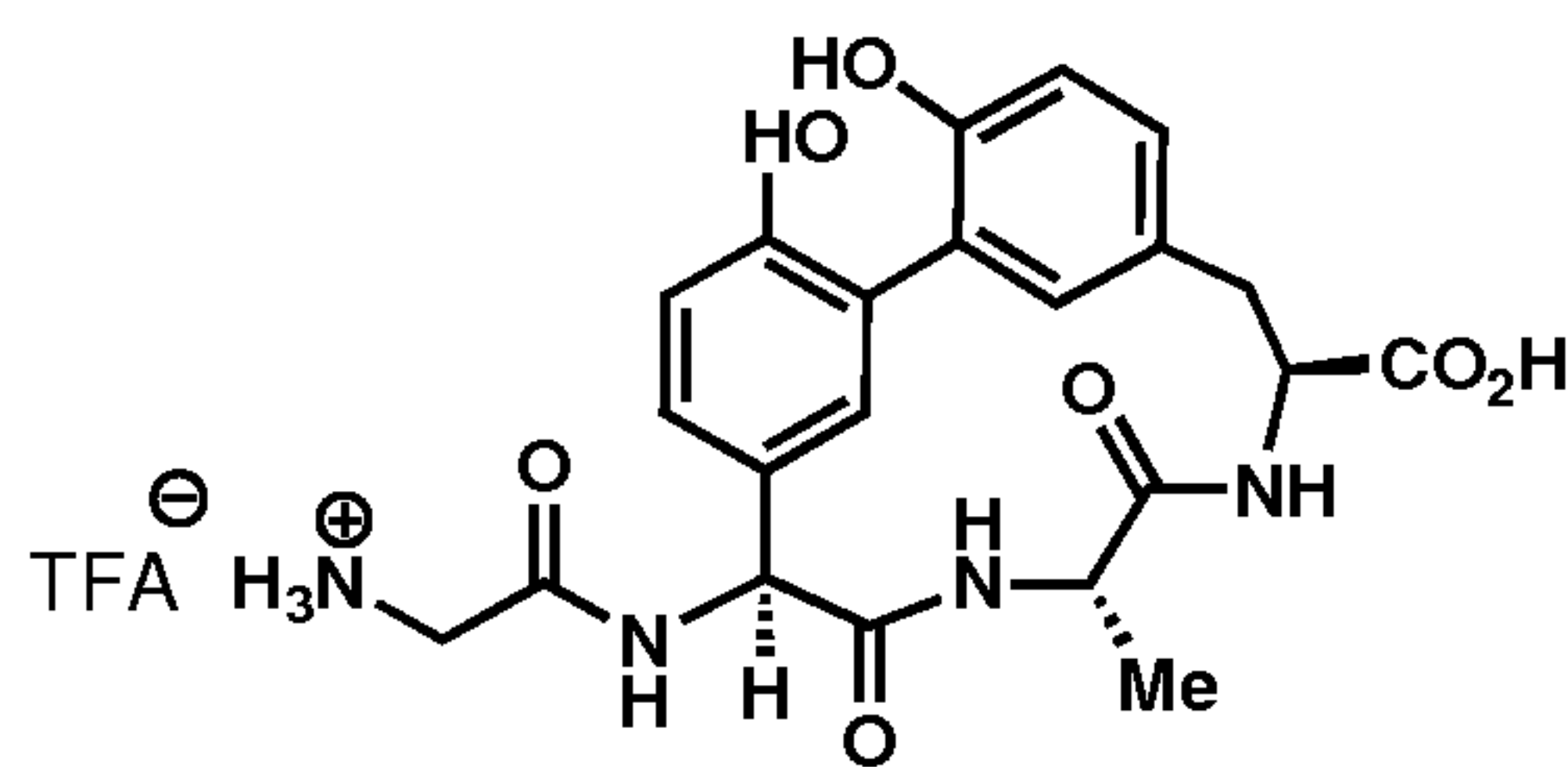


To a solution of compound **1** (49 mg, 0.08 mmol) in ethanethiol (2 mL) under Ar in a sealed tube was added AlBr₃ in CH₂Br₂ (1.0 M, 2 mL, 25 eq). The reaction was heated to 50 °C and allowed to stir for five hours. The reaction was then cooled to room temperature, a small amount of water was added, and the volatiles were evaporated under a stream of nitrogen. Additional water was added, followed by EtOAc, and the aqueous layer was extracted, filtered through a 0.22 μ m syringe filter and purified by HPLC (linear gradient, 0.5% B per minute, product eluted at 17.9% B). Lyophilization afforded the product as the TFA salt. (30 mg, 63% yield). ¹H NMR (DMSO, 500 MHz) multiple isomers. ¹³C NMR (DMSO, 600 MHz) multiple isomers. IR (film) $\nu_{\max}$ = 1639, 1509, 1416, 1184, 1134, 798, 721, 511 cm⁻¹. ESI HRMS calcd for C₂₃H₂₆N₄O₇ [(M+H)⁺] 471.1874, found 471.1880.



To a solution of compound **17** (30 mg, 0.073 mmol) in AcCN:DMF (2:1, 1.5 mL) under Ar was added consecutively HOBt (30 mg, 0.22 mmol, 3 eq), Boc-Gly-OH (14 mg, 0.08 mmol, 1.1 eq), and EDC (42 mg, 0.22 mmol, 3 eq). The reaction was stirred overnight then water and EtOAc were added. The water layer was extracted (2 $\times$), and the combined organic layers were washed with brine, dried over Na₂SO₄, and

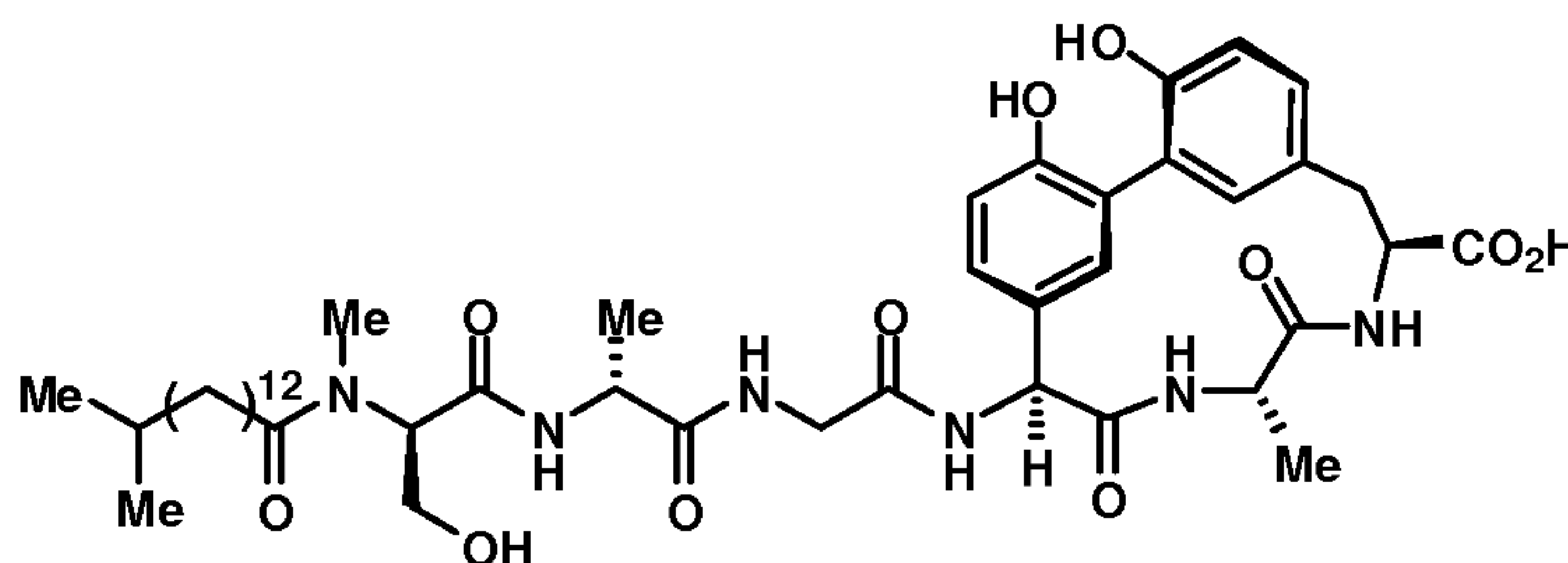
concentrated. Flash column chromatography (5.5% MeOH in DCM) yielded the product as a white flaky solid (30 mg, 68% yield). $R_f = 0.37$ (7% MeOH in DCM). ^1H NMR (DMSO, 500 MHz) multiple isomers. ^{13}C NMR (DMSO, 600 MHz) multiple isomers. IR (film) $\nu_{\text{max}} = 1633, 1506, 1267, 1246, 1163, 1026, 580\text{ cm}^{-1}$. ESI HRMS calcd for $\text{C}_{30}\text{H}_{38}\text{N}_4\text{O}_9$ $[(\text{M}+\text{H})^+]$ 599.2711, found 599.2701.



31

To a solution of compound **32** (15 mg, 0.025 mmol) in ethanethiol (0.6 mL) under Ar in a sealed tube was added AlBr_3 in CH_2Br_2 (1.0 M, 0.6 mL, 25 eq). The reaction was heated to $50\text{ }^\circ\text{C}$ and allowed to stir for five hours. The reaction was then cooled to room temperature, a small amount of water was added and the volatiles were blown off under a stream of nitrogen. Additional water was added and the aqueous layer was extracted with EtOAc, the aqueous layer was filtered through a $0.22\text{ }\mu\text{m}$ syringe filter and purified by HPLC (linear gradient = 0.67% B per minute, product eluted at 17.9% B). Lyophilization afforded the product as the TFA salt. (5.8 mg, 52% yield). ^1H NMR (MeOD, 600 MHz) δ (ppm) 7.24 (dd, $J = 8.4, 2.2\text{ Hz}$, 1H), 7.15-7.10 (m, 2H), 7.06 (d, $J = 2.00\text{ Hz}$, 1H), 6.92 (d, $J = 8.41\text{ Hz}$, 1H), 6.86 (d, $J = 8.26\text{ Hz}$, 1H), 5.80 (s, 1H), 4.97-4.92 (m, 1H), 4.74 (dd, $J = 10.96, 2.27\text{ Hz}$, 1H), 3.84-3.76 (m, 2H), 3.35-3.30 (m, 1H), 3.02 (dd, $J = 15.82, 11.05\text{ Hz}$, 1H), 1.37 (d, $J = 6.83\text{ Hz}$, 3H) (^{13}C NMR (DMSO, 600 MHz) δ (ppm) 182.8, 181.1, 179.0, 175.9, 163.2, 162.4, 141.3, 140.9, 139.1, 138.7, 138.3, 136.0, 135.9, 135.8, 125.6, 63.9, 62.6, 58.2, 57.8, 50.1, 43.9, 28.8. IR (film) $\nu_{\text{max}} = 3271\text{ (br)}, 1633, 1543, 1500, 1236, 1188, 1136, 798, 683, 563\text{ cm}^{-1}$. ESI HRMS calcd for $\text{C}_{22}\text{H}_{24}\text{N}_4\text{O}_7$ $[(\text{M}+\text{H})^+]$ 457.1718, found 457.1721.

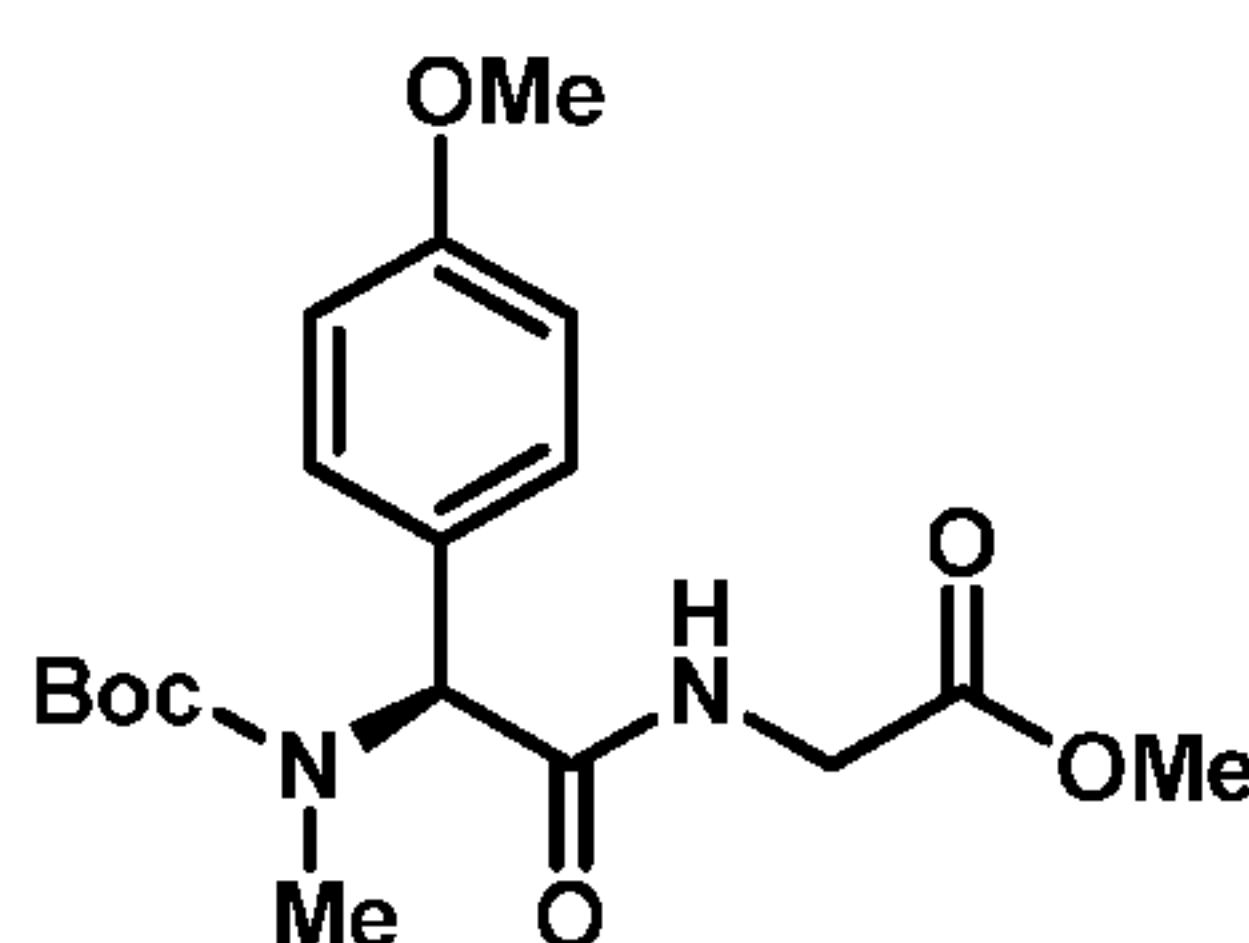
25



122

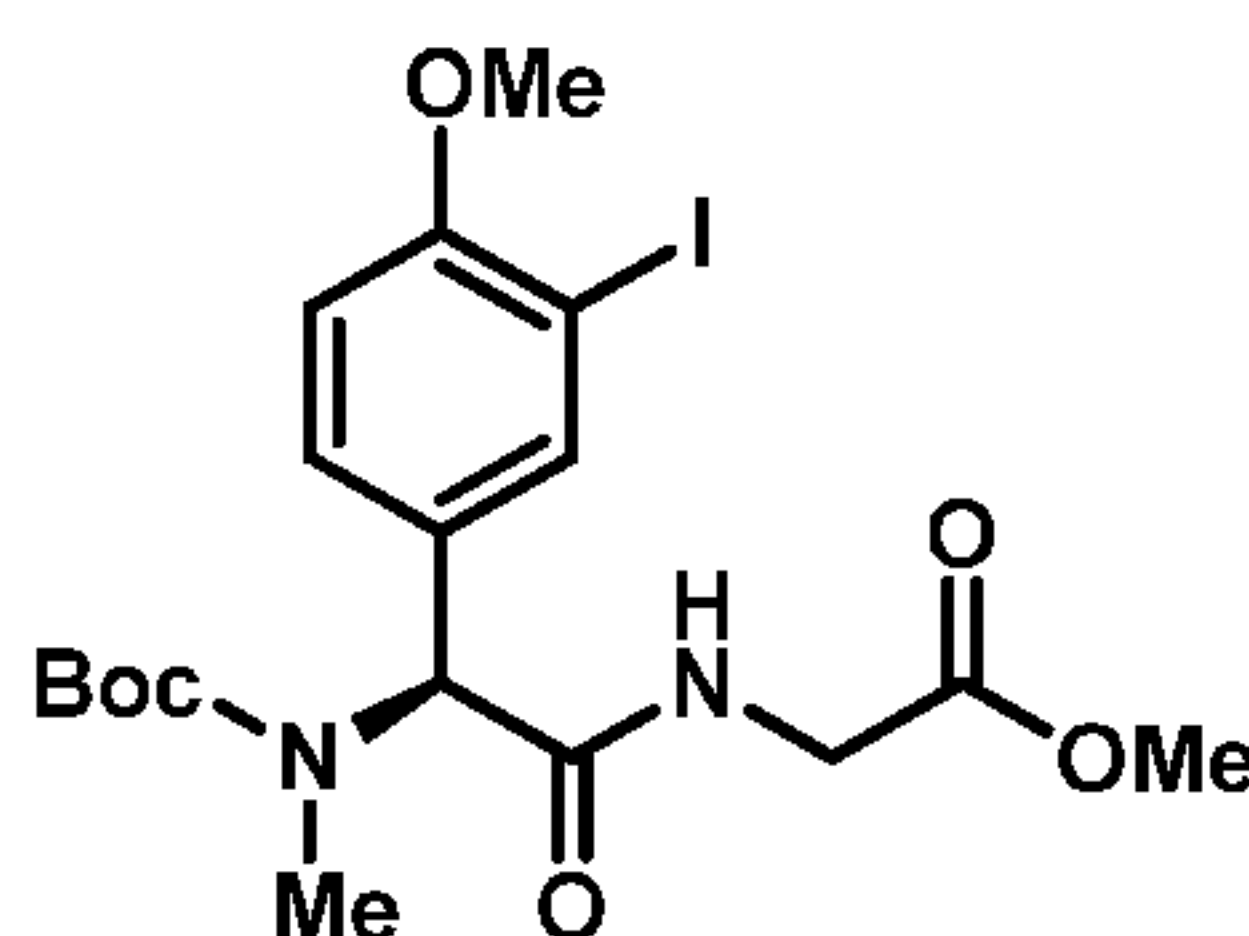
39

Compound **29** was synthesized in the same manner as arylomycin A₂. ¹H NMR (MeOD, 600 MHz) δ (ppm) multiple isomers. ¹³C NMR (MeOD, 600 MHz) δ (ppm) multiple isomers. ESI HRMS calcd for C₄₅H₆₆N₆O₁₁ [(M+H)⁺] 867.4862, found 867.4853.



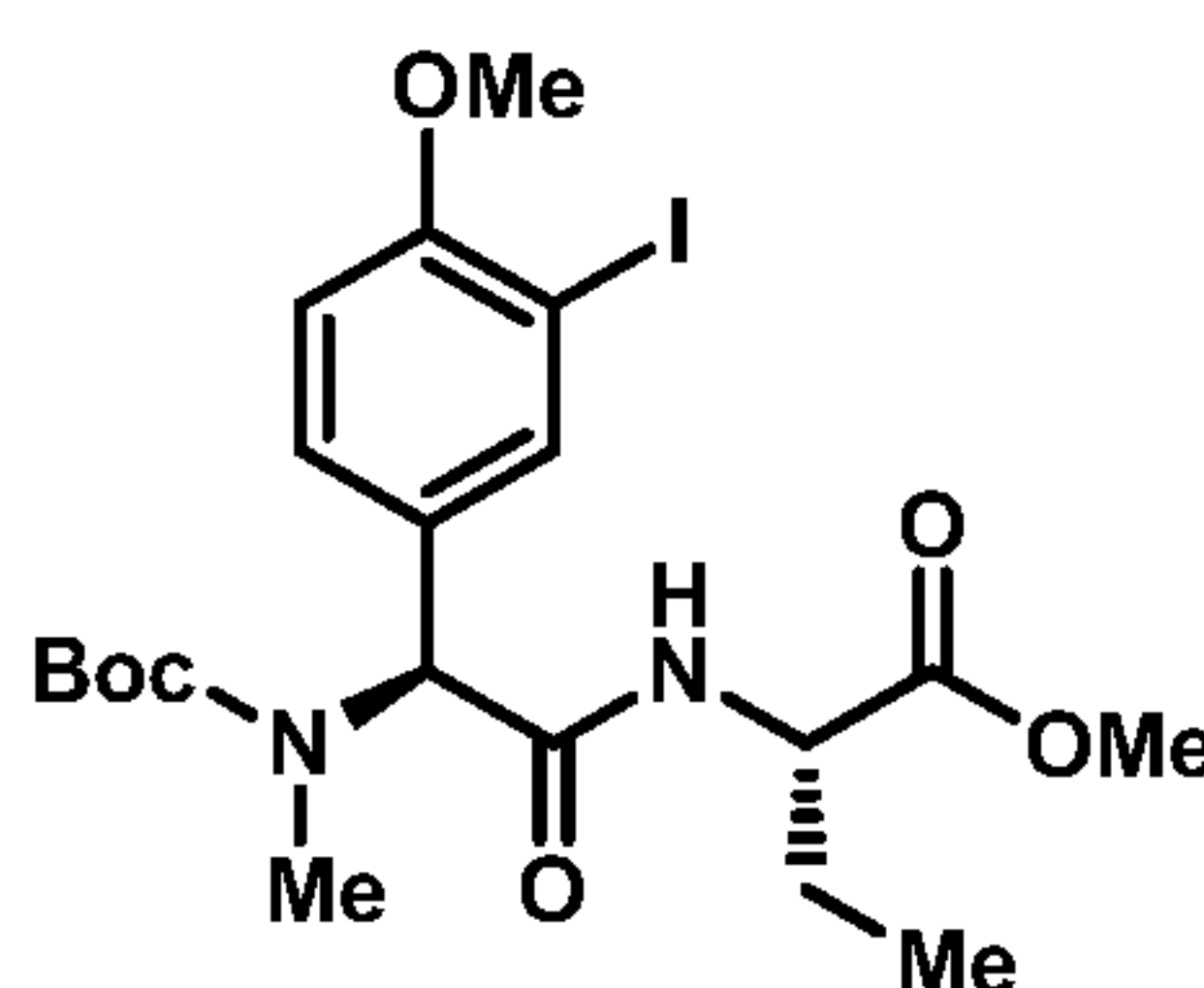
4.11

To a solution of H-Gly-OMe HCl (40 mg, 0.32mmol, 1 eq) in DMF (3 mL) was added sequentially Boc-N-Me-Hydroxyphenylglycine (122 mg, 1.35 eq), HOBT (43 mg, 1 eq), EDC (67 mg, 1.1 eq) and TEA (49 μL, 1.1 eq). The solution was allowed to stir overnight then dilute NaHCO_{3(aq)} and EtOAc, the aqueous phase was extracted 3x with EtOAc and the combined organic fractions were washed with 5% citric acid (pH – 3), water and brine. The organics were dried over sodium sulfate, concentrated then the crude was taken on directly without further purification. The crude residue (113 mg) was taken up in acetone (3.5 mL), treated with MeI (139 μL, 7 eq) and K₂CO₃ (221 mg, 5 eq) and heated at reflux in a sealed vial overnight. The reaction was then allowed to warm to room temperature, the volatiles were blown off and water and EtOAc were added. The aqueous layer was extracted 3x with EtOAc and the combined organic layers were dried over sodium sulfate and concentrated. Column chromatography (3% MeOH in DCM) yielded the product (64.3 mg, 55% yield over two steps). ¹H NMR (CDCl₃, 500 MHz) δ (ppm) 7.27 (d, *J* = 8.5 Hz, 2H), 6.89 (d, *J* = 8.5 Hz, 2H), 6.49 (br s, 1H), 5.84 (br s, 1H), 4.09-4.08 (m, 2H), 3.80 (s, 3H), 3.75 (s, 3H), 2.71 (s, 3H), 1.47 (s, 9H). ¹³C NMR (CDCl₃, 500 MHz) δ (ppm) 170.6, 170.2, 159.6, 130.6, 127.2, 114.1, 80.6, 55.3, 52.4, 41.3, 31.5, 32.1, 28.4. MS (ESI) *m/z* 389.2 (M + Na⁺).



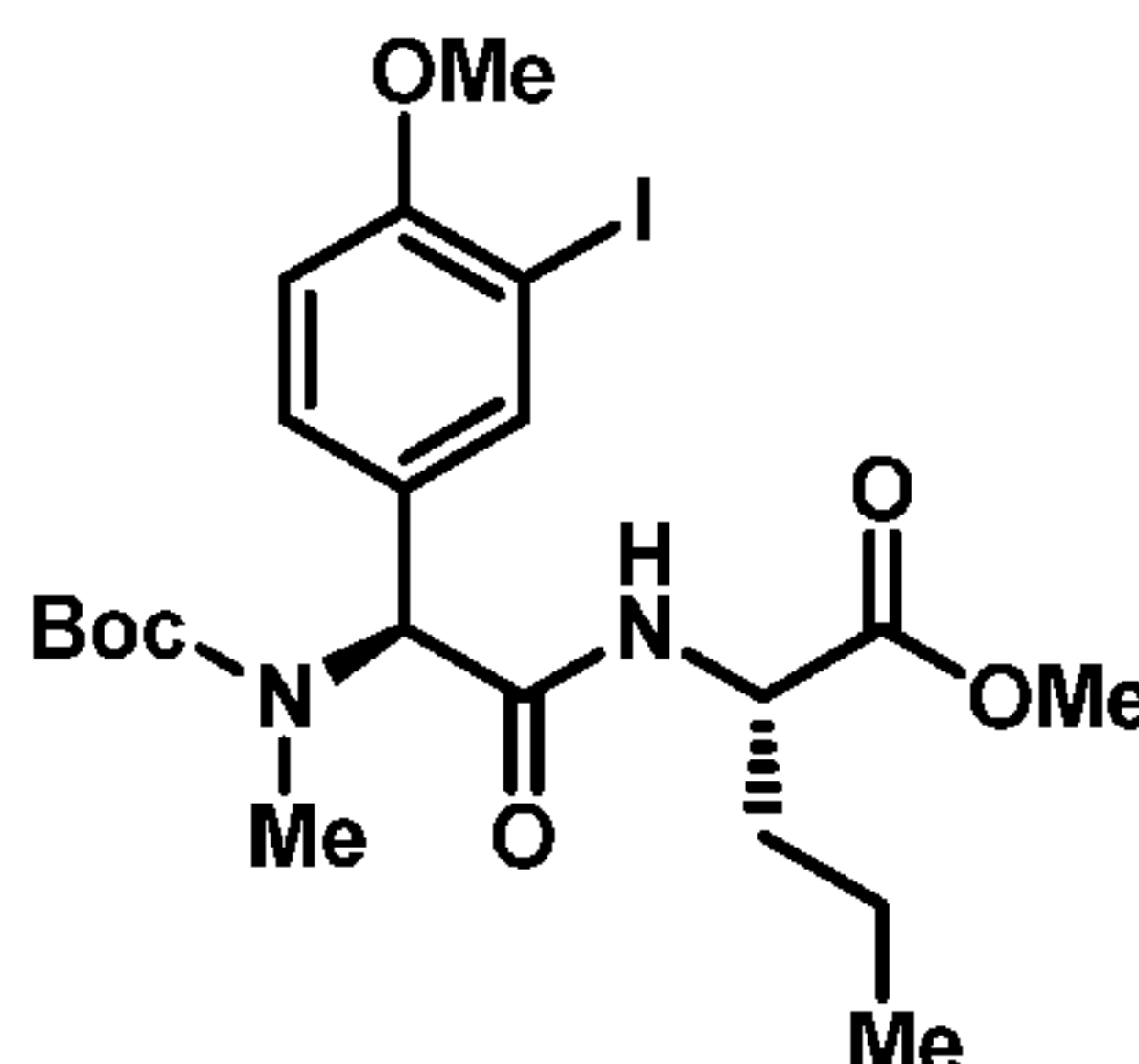
4.12

To a solution of Compound **4.11** (63 mg, 0.17 mmol, 1 eq) in MeOH (2 mL) was added sequentially AgSO₄ (56 mg, 1.05 eq) and I₂ (46 mg, 1.05 eq). The reaction mixture was allowed to stir for 2 hrs then an excess of solid sodium thiosulfate was added, the reaction was filtered through glass wool and concentrated by rotary evaporation. The crude material was purified via column chromatography (2% MeOH in DCM) to yield the product (74 mg, 88% yield). ¹H NMR (CDCl₃, 500 MHz) δ (ppm) 7.72 (d, *J* = 2.0 Hz, 1H), 7.30 (dd, *J* = 8.5 Hz, *J* = 1.5 Hz, 1H), 6.78 (d, *J* = 8.5 Hz, 1H), 6.54 (br s, 1H), 5.78 (br s, 1H), 4.06-4.05 (m, 2H), 3.85 (s, 3H), 3.74 (s, 3H), 2.70 (s, 3H), 1.45 (s, 9H). ¹³C NMR (CDCl₃, 500 MHz) δ (ppm) 170.1, 170.0, 158.1, 140.2, 130.6, 129.3, 110.7, 86.1, 80.9, 56.5, 52.5, 41.3, 31.7, 28.4. MS (ESI) *m/z* XX (M + H⁺).

**4.13**

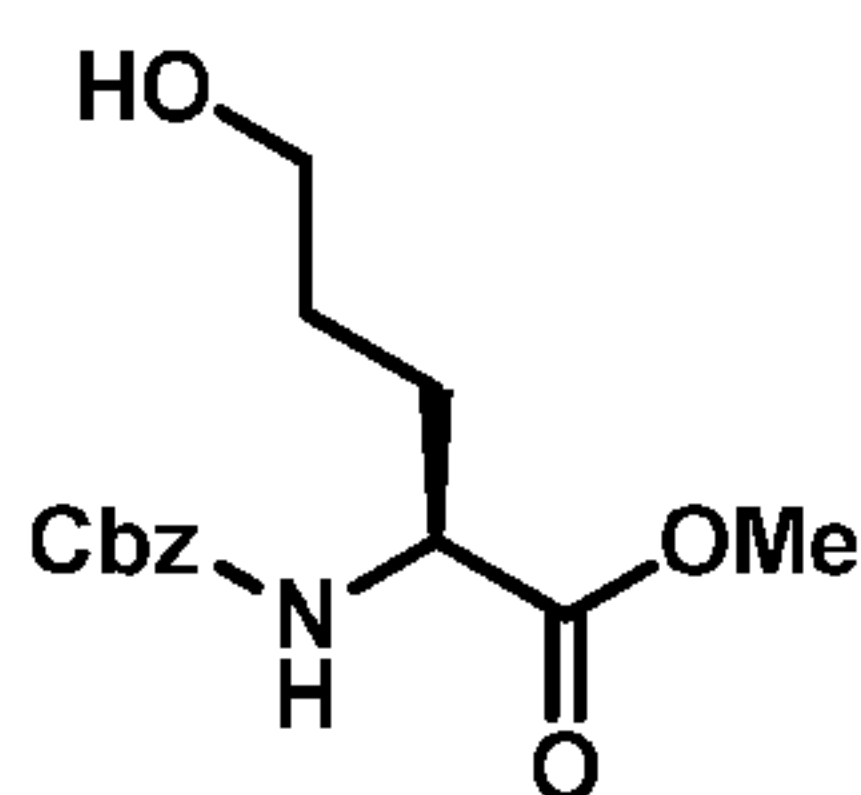
To a solution of Boc-N-Me-3-Iodo-Hydroxyphenylglycine (150 mg, 0.37 mmol, 1 eq) in DMF (3.5 mL) was added sequentially L-2-aminobutyric acid HCl (48 mg, 1.1 eq), HOBt (50 mg, 1 eq), EDC (78 mg, 1.1 eq) and NaHCO₃ (34 mg, 1.1 eq). The solution was allowed to stir overnight then was diluted with NaHCO_{3(aq)} and EtOAc. The aqueous phase was extracted 3x with EtOAc and the combined organic layers were washed with 5% citric acid (pH = 3), water and brine. The organics were then dried over sodium sulfate then concentrated. TLC analysis of the crude mixture showed one major product so the crude material (105 mg, 0.20 mmol (assumed), 1 eq) was taken up in acetone (2.5 mL) and treated with MeI (63 μL, 5 eq) and K₂CO₃ (138 mg, 5 eq). The reaction was stirred for 1.5 h at reflux in a sealed tube then the acetone was blown off under a stream of nitrogen. To the residue was added water and EtOAc and the aqueous was extracted 3x with EtOAc. The combined organic layers were then dried over sodium sulfate, concentrated and the crude material was purified via column chromatography (1% MeOH in DCM) to give the product (58 mg, 29% yield over 2 steps). ¹H NMR (CDCl₃, 500 MHz) δ (ppm) 7.73-7.71 (m, 1H), 7.32-7.28 (m, 1H), 6.45-6.37 (m, 1H), 5.76 (br s, 1H), 4.61-4.55 (m, 1H), 3.87 (s, 3H), 3.74 (s, 3H), 2.71-2.70 (m, 3H), 1.93-1.88 (m, 1H), 1.74-1.69 (m, 1H), 1.47-1.46 (m, 9H), 0.93-0.87 (m, 3H) ¹³C

NMR (CDCl₃, 500 MHz) δ (ppm) 172.5, 169.5, 158.1, 140.2, 130.5, 129.3, 110.8, 86.1, 80.9, 56.5, 53.6, 52.5, 31.6, 28.5, 25.5, 9.8. MS (ESI) m/z 543.1 (M + Na⁺).



4.14

5 Compound **4.14** was synthesized identically to compound **4.13** giving the product (47 mg, 15% yield over 2 steps). ¹H NMR (MeOD, 600 MHz) δ (ppm) 7.72 (s, 1H), 7.33 (d, J = 8.4 Hz, 1H), 6.98 (d, J = 8.4 Hz, 1H), 5.77 (br s, 1H), 4.45-4.42 (m, 1H), 3.88 (s, 3H), 3.75 (s, 3H), 2.64 (s, 3H), 1.80-1.78 (m, 1H), 1.69-1.67 (m, 1H), 1.53-1.29 (m, 11H), 0.95 (t, J = 7.2 Hz, 3H) ¹³C NMR (MeOD, 600 MHz) δ (ppm) 174.0, 172.7, 159.7, 157.6, 141.2, 131.9, 130.7, 111.9, 86.3, 81.8, 62.5, 56.9, 53.7, 52.8, 34.2, 32.1, 28.7, 20.2, 13.9. MS (ESI) m/z 557.1 (M + Na⁺).

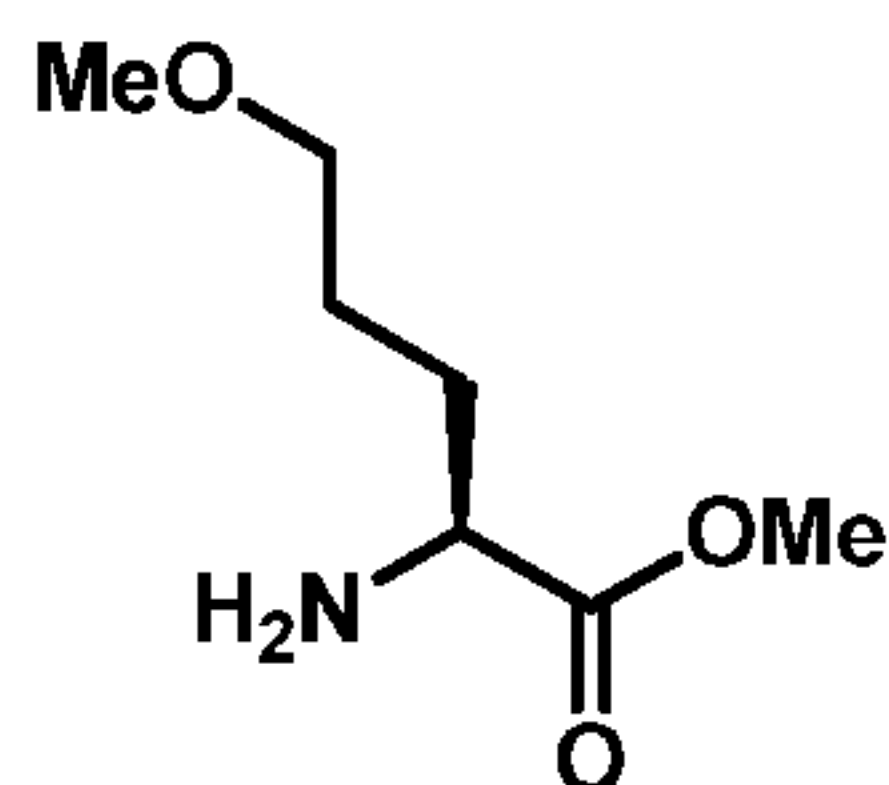


4.15

15 To a solution of Z-Glu-OMe (268 mg, 0.91 mmol, 1 eq) in THF (3 mL) at 0°C was added ethyl chloroformate (174 μ L, 2 eq), and TEA (253 μ L, 2 eq). The mixture was allowed to stir for 45 min. then filtered through glass wool (washing with THF) and the filtrate was treated with NaBH₄ (151 mg, 4.4 eq) in H₂O (1.5 mL) at 0°C. This reaction was allowed to stir for 45 min then it was warmed to rt. Next, saturated NaHCO₃, water and EtOAc were added and the aqueous phase was extracted 3x with EtOAc. The combined organic layers were washed with 5% citric acid and brine then dried over sodium sulfate and concentrated. Column chromatography (4% MeOH in DCM) yielded the product (106 mg, 41% yield). ¹H NMR (CDCl₃, 600 MHz) δ (ppm) 7.36-7.28 (m, 5H), 5.08 (s, 2H), 4.21-4.19 (m, 1H), 3.70 (s, 3H), 3.56-3.54 (m, 2H), 1.93-1.87 (m, 1H), 1.74-1.68 (m, 1H), 1.65-1.55 (m, 2H). ¹³C NMR (CDCl₃, 500

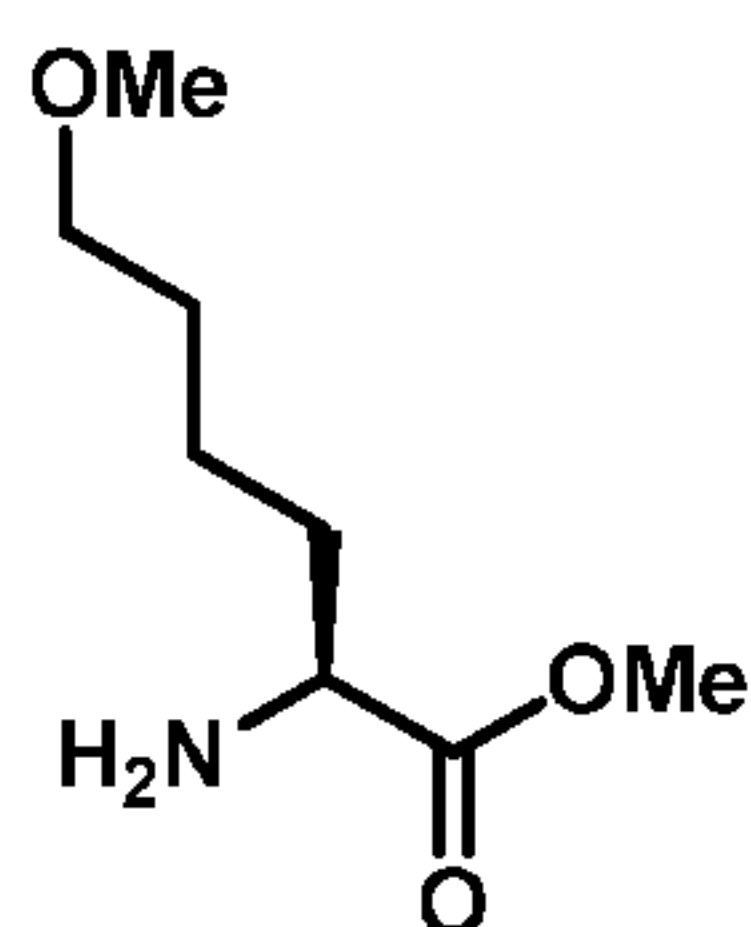
MHz) δ (ppm) 174.6, 158.6, 138.1, 129.4, 129.0, 128.8, 67.6, 62.1, 55.3, 52.6, 29.8, 29.1.

MS (ESI) m/z 304.1 ($M + Na^+$).



4.16

- 5 To a solution of compound **4.15** (104 mg, 0.37 mmol, 1 eq) in DCM (2.0 mL) was added 50% $HBF_{4(aq)}$ (23 μ L, 1 eq) and 2M $TMSCH_2N_2$ in diethyl ether (370 μ L, 2 eq) dropwise over 15 min at 0°C. The reaction was monitored by TLC for disappearance of starting material. $TMSCH_2N_2$ (190 μ L, 1 eq) was added every (~45min) four times over the course of 3 hrs. along with 50% $HBF_{4(aq)}$ (12 μ L, 0.5 eq). The reaction was
- 10 allowed to stir for an additional 30 min. then the volatiles were evaporated, water was added and the aqueous layer was washed with EtOAc 3x. The combined organic layers were dried over sodium sulfate concentrated and purified via column chromatography (35% EtOAc in Hex). This material (55mg, R_f - 0.35 in 35% EtOAc in Hex) was dissolved in MeOH, to it was added 10% Pd/C (20 mg, 1/3 by weight) and the mixture
- 15 was placed under an atmosphere of H_2 (1 atm). When TLC indicated a complete consumption of starting material the mixture was filtered through Celite and concentrated. The resulting Cbz deprotected material (30 mg, 50% yield) was used directly in the next step of the synthesis.



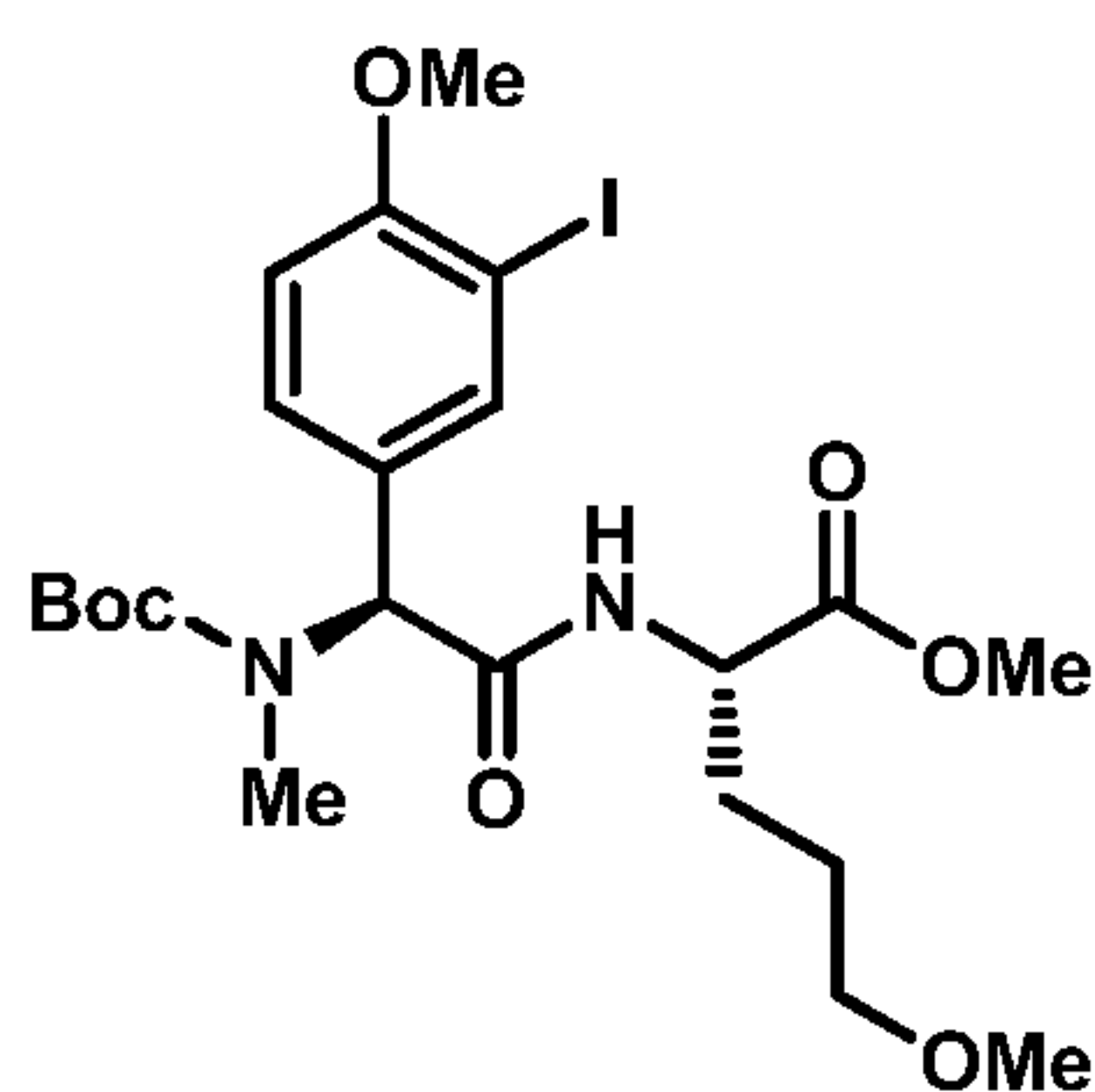
4.17

- 20
- To a solution of Boc-L-6-hydroxynorleucine (500 mg, 2 mmol, 1 eq) in a 9:1 mixture of toluene:MeOH (5 mL) was added $TMSCH_2N_2$ (1.15 mL, 1.15 eq) and the solution was allowed to stir for 1.5 hrs. The volatiles were then evaporated and the crude was purified via column chromatography (4% MeOH in DCM) to yield the product (472
- 25 mg). This material (418 mg, 1.6 mmol) was then dissolved in DCM (7 mL) and treated with 50% $HBF_{4(aq)}$ (200 μ L, 1 eq) and $TMSCH_2N_2$ in hexanes (1.6mL, 2 eq) at 0° C. After 0.5 hr the solution was treated with $TMSCH_2N_2$ in Hexanes (0.5 eq, 0.4 mL) and

COc1ccc(cc1)[C@H](C(=O)N[C@@H](CCCOC)C(=O)OC)N(C)C(=O)OC(C)(C)C

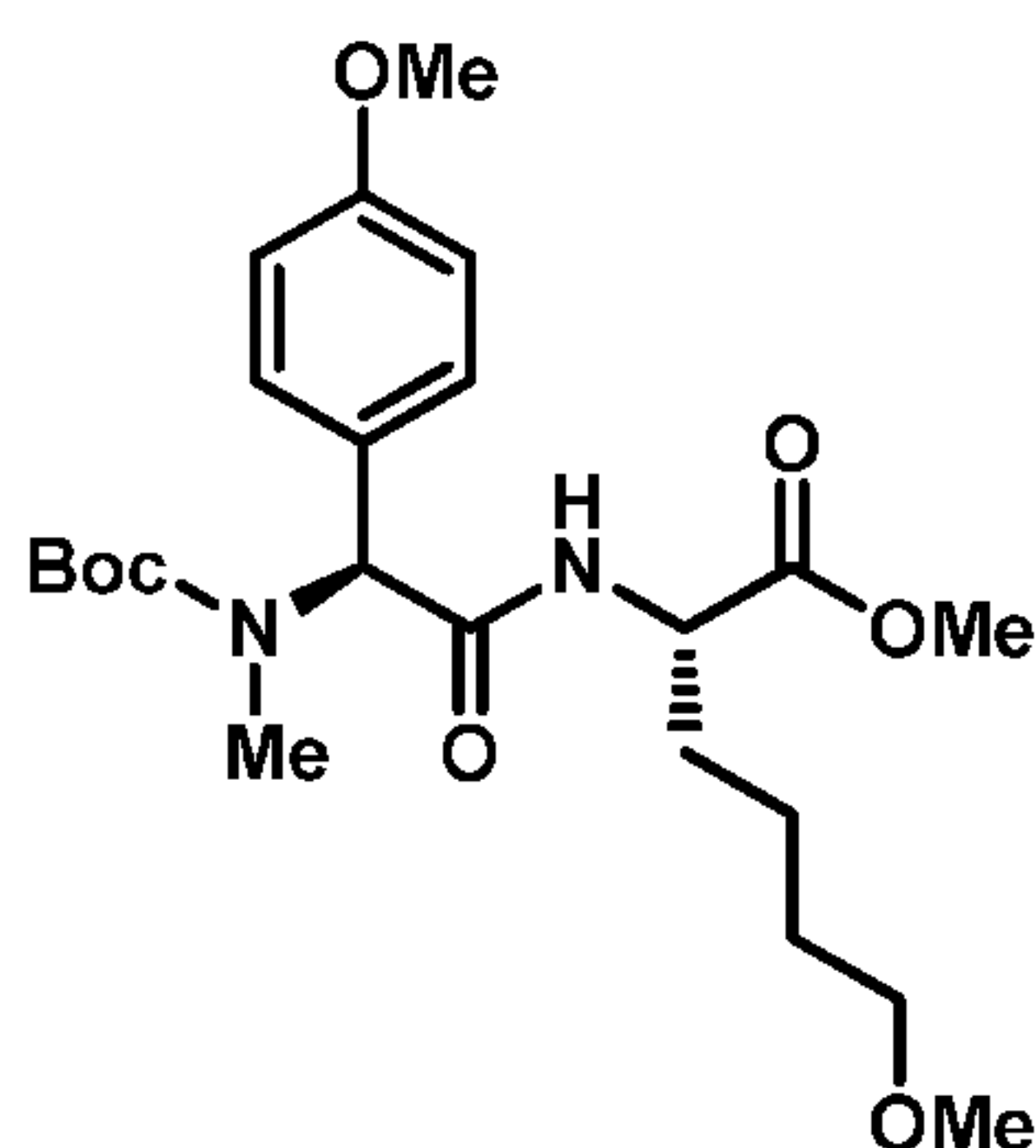
20 Boc-N-Me-Hydroxyphenylglycine (71 mg, 0.19 mmol, 1 eq) was dissolved in
DMF (1.0 mL) and treated sequentially with compound **4.16** (30 mg, 1 eq), HOBt (26
mg, 1 eq), EDC (37 mg, 1 eq) and TEA (catalytic). The reaction was allowed to stir
overnight under Ar then water and EtOAc were added. The aqueous layer was extracted
3x with EtOAc then the combined organic layers were washed with dilute NaHCO_{3(aq)}
25 and brine. The organics were dried over sodium sulfate, concentrated and the crude was
used without further purification. This material (75 mg, 0.18 mmol (assumed), 1 eq) was
dissolved in acetone (2 mL), treated with MeI (77 μ L, 7 eq) and K₂CO₃ (124 mg, 5 eq)
and heated to reflux in a sealed vial overnight. The reaction mixture was then cooled to
room temperature and the acetone was evaporated under a stream of nitrogen. Water

and EtOAc were added, the aqueous phase was extracted 3x with EtOAc, and the combined organic layers were dried over sodium sulfate. After concentrating, the crude material was purified via column chromatography (3% MeOH in DCM) to yield the product (68 mg, 81% over two steps). ¹H NMR (CDCl₃, 400 MHz) δ (ppm) 7.28 (d, *J* = 8.4 Hz, 2H), 6.88 (d, *J* = 8.8 Hz, 2H), 6.56 (d, *J* = 7.2 Hz, 1H), 5.82 (br s, 1H), 4.63-4.58 (m, 1H), 3.79 (s, 3H), 3.72 (s, 3H), 3.34 (t, *J* = 6.0 Hz, 2H) 3.22 (s, 3H), 2.67 (s, 3H) 1.94-1.79 (m, 2H), 1.63-1.42 (m, 11H) ¹³C NMR (CDCl₃, 400 MHz) δ (ppm) 172.7, 170.2, 159.6, 130.8, 127.4, 114.1, 80.5, 71.9, 58.6, 55.4, 52.4, 52.2, 31.4, 29.0, 28.5, 28.5, 25.6. MS (ESI) *m/z* 461.5 (M + Na⁺).

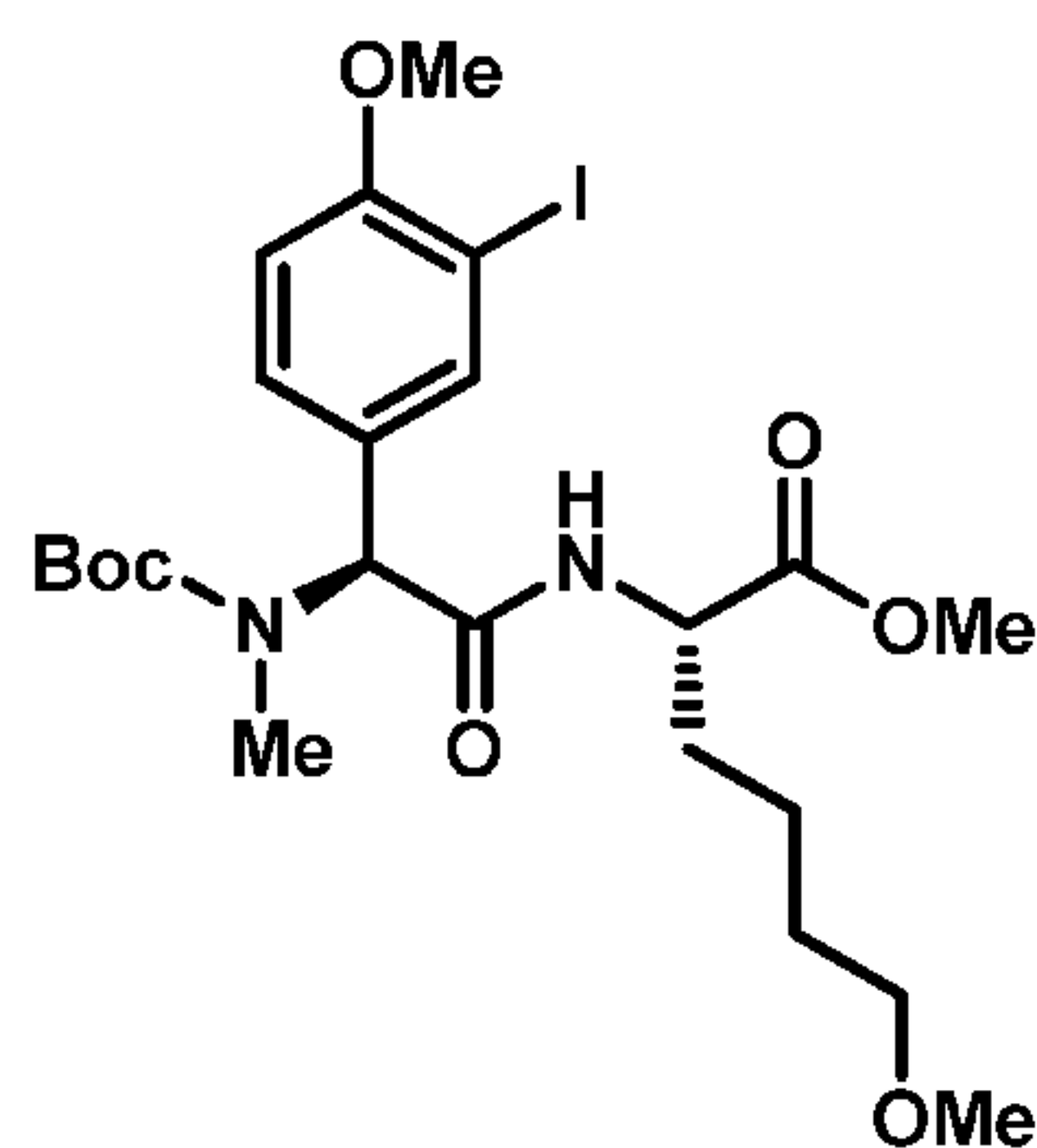


4.19

To a solution of compound **4.18** (67 mg, 0.15 mmol, 1 eq) in MeOH (3.5 mL) was added sequentially AgSO₄ (50 mg, 1.05 eq) and I₂ (41 mg, 1.05 eq). The reaction mixture was allowed to stir for 2.5 hrs then the proportion of product to starting material was checked by mass spectrometry. Seeing that starting material remained AgSO₄ (5.0 mg, 0.1 eq) and I₂ (4.0 mg, 0.1 eq). This process was repeated every 2-3 hrs for 6 hrs then 10% sodium thiosulfate was added and some of the volatiles were blown off under a stream of nitrogen. EtOAc was added, the aqueous layer was extracted 3x with EtOAc then the combined organic layers were washed with brine, dried over sodium sulfate and concentrated by rotary evaporation. The crude material was purified via column chromatography (2% MeOH in DCM) to yield the product (44 mg, 52% yield). Some NMR resonances appeared broadened or doubled (with one isomer in large excess to the other) due to slow rotation about the N-Me amide. ¹H NMR (CDCl₃, 600 MHz) δ (ppm) 7.74 (s, 1H), 7.33 (d, *J* = 7.8, 1H), 6.80 (d, *J* = 8.4 Hz, 1H), 6.67-6.66 (m, 1H), 5.77 (br s, 1H), 4.60-4.57 (m, 1H), 3.87 (s, 3H), 3.72 (s, 3H), 3.39 (t, *J* = 6.0 Hz, 2H), 3.23 (s, 3H), 2.68 (s, 3H), 1.96-1.77 (m, 2H), 1.61-1.47 (m, 11H). ¹³C NMR (CDCl₃, 600 MHz) δ (ppm) 172.5, 169.6, 158.1, 140.3, 140.2, 130.7, 129.5, 129.4, 121.6, 110.7, 86.0, 80.8, 71.9, 58.6, 56.5, 52.5, 52.3, 31.5, 28.9, 28.5, 27.8, 25.5. MS (ESI) *m/z* 587.2 (M + Na⁺).

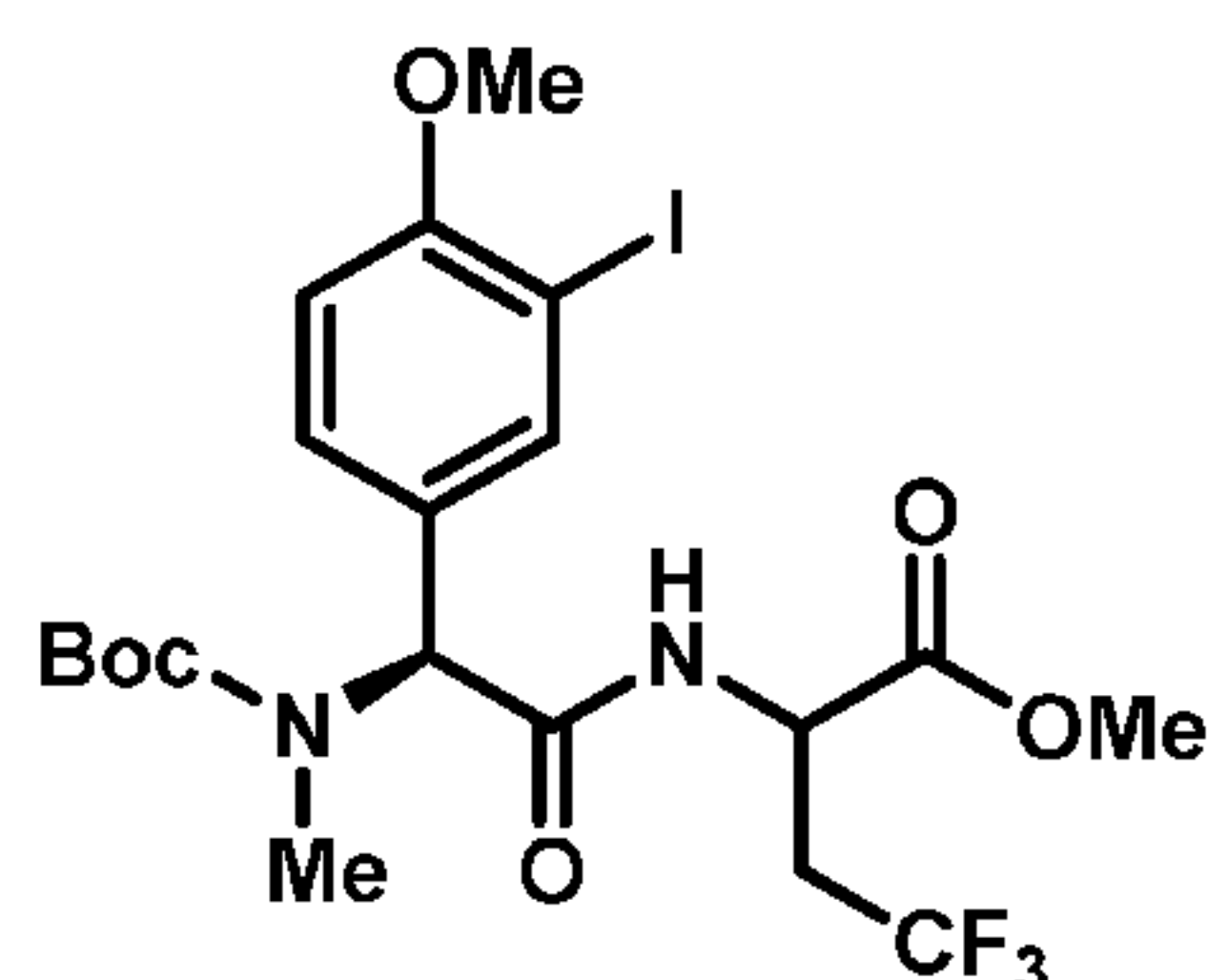
**4.20**

Boc-N-Me-Hydroxyphenylglycine (39 mg, 0.14 mmol, 1 eq) was dissolved in DMF (1.5 mL) and treated sequentially with compound **4.17** (25 mg, 1 eq), HOBt (19 mg, 1 eq), EDC (30 mg, 1 eq) and TEA (catalytic). The reaction was allowed to stir overnight under Ar then water and EtOAc were added. The aqueous layer was extracted 3x with EtOAc then the combined organic layers were washed with dilute NaHCO_{3(aq)} and brine. The organics were dried over sodium sulfate, concentrated and the crude was used without further purification. This material (61 mg, 0.14 mmol (assumed), 1 eq) was dissolved in acetone (1.5 mL), treated with MeI (88 μ L, 10 eq) and K₂CO₃ (58 mg, 3 eq) and heated to reflux in a sealed vial overnight. The reaction mixture was then cooled to room temperature and the acetone was evaporated under a stream on nitrogen. Water and EtOAc were added, the aqueous phase was extracted 3x with EtOAc, and the combined organic layers were dried over sodium sulfate. After concentrating, the crude material was purified via column chromatography (2.5% MeOH in DCM) to yield the product (46 mg, 72% over two steps). ¹H NMR (CDCl₃, 500 MHz) δ (ppm) 7.27 (d, *J* = 8.5 Hz, 2H), 6.89 (d, *J* = 8.5 Hz, 2H), 6.33 (d, *J* = 8.0 Hz, 1H), 5.81 (br s, 1H), 4.64-4.60 (m, 1H), 3.80 (s, 3H), 3.73 (s, 3H), 3.34 (t, *J* = 6.5 Hz, 2H) 3.29 (s, 3H), 2.69 (s, 3H) 1.89-1.84 (m, 1H), 1.72-1.65 (m, 1H), 1.61-1.34 (m, 13H) ¹³C NMR (CDCl₃, 500 MHz) δ (ppm) 172.7, 170.1, 159.6, 130.7, 127.2, 114.1, 80.5, 72.4, 58.6, 55.4, 52.4, 52.4, 32.0, 31.4, 29.1, 28.5, 22.3. MS (ESI) *m/z* 475.2 (M + Na⁺).



4.21

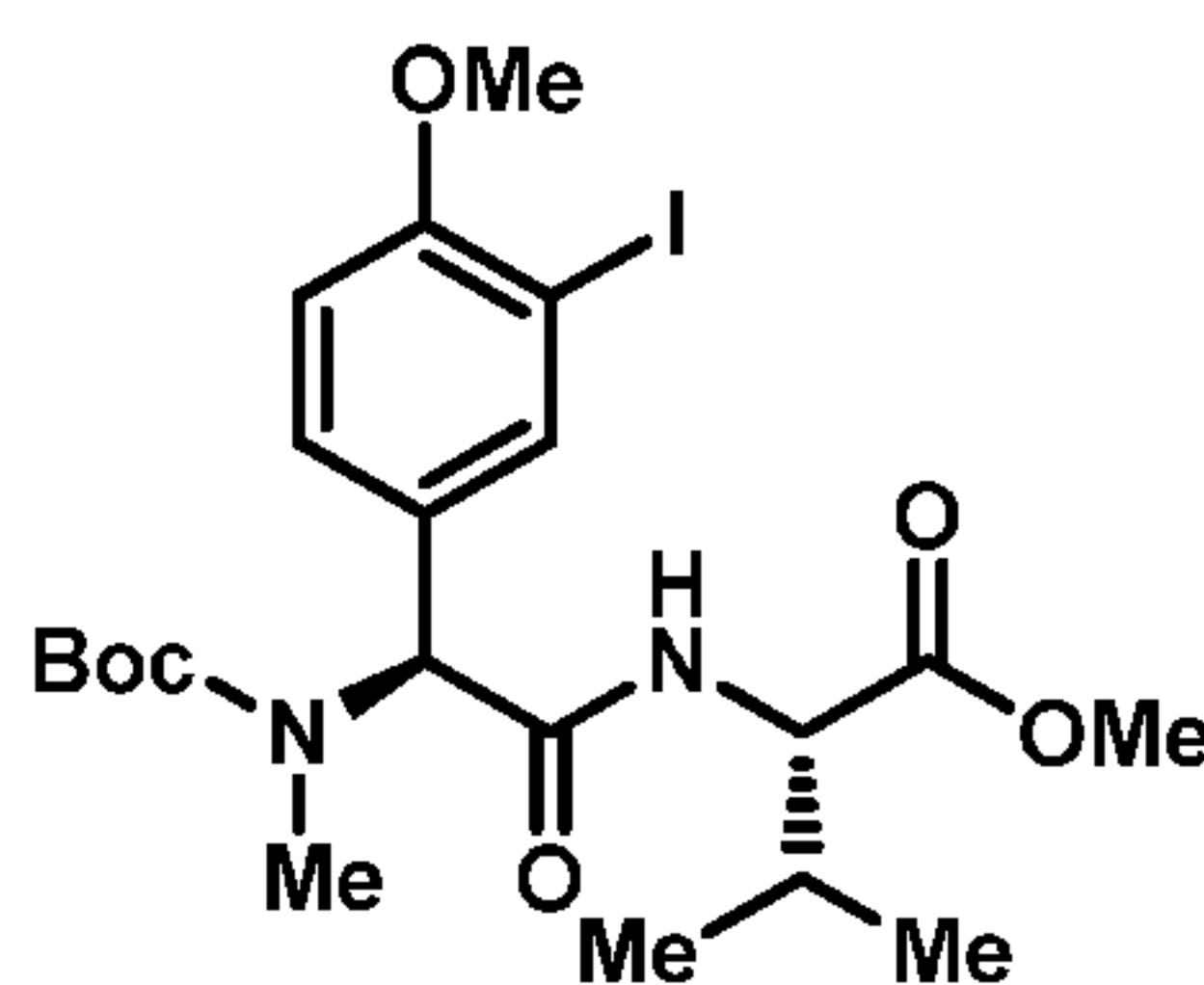
To a solution of compound **4.20** (44 mg, 0.097 mmol, 1 eq) in MeOH (1.5 mL) was added sequentially AgSO₄ (32 mg, 1.05 eq) and I₂ (26 mg, 1.05 eq). The reaction mixture was allowed to stir for 2.5 hrs then the proportion of product to starting material was checked by mass spectrometry. Seeing that starting material remained AgSO₄ (3.0 mg, 0.1 eq) and I₂ (3.0 mg, 0.1 eq). This process was repeated every 2-3 hrs for 6hrs then 10% sodium thiosulfate was added and some of the volatiles were blown off under a stream of nitrogen. EtOAc was added, the aqueous layer was extracted 3x with EtOAc then the combined organic layers were washed with brine, dried over sodium sulfate and concentrated by rotary evaporation. The crude material was purified via column chromatography (2.5% MeOH in DCM) to yield the product (46 mg, 81% yield). Some NMR resonances appeared broadened or doubled (with one isomer in large excess to the other) due to slow rotation about the N-Me amide. ¹H NMR (CDCl₃, 500 MHz) δ (ppm) 7.73 (d, *J* = 1.5 Hz, 1H), 7.31 (d, *J* = 8.5, 1H), 6.79 (d, *J* = 8.5 Hz, 1H), 6.38 (d, *J* = 7.5 Hz, 1H), 5.74 (br s, 1H), 4.61-4.57 (m, 1H), 3.86 (s, 3H), 3.73 (s, 3H), 3.33 (t, *J* = 6.5 Hz, 2H), 3.27 (s, 3H), 2.69 (s, 3H), 1.90-1.85 (m, 1H), 1.72-1.65 (m, 1H), 1.58-1.34 (m, 13H). ¹³C NMR (CDCl₃, 500 MHz) δ (ppm) 172.6, 169.5, 158.1, 140.3, 130.6, 129.3, 110.8, 86.1, 80.8, 72.4, 58.6, 56.5, 52.5, 52.5, 32.0, 31.6, 29.1, 28.5, 22.3. MS (ESI) *m/z* 601.2 (M + Na⁺).



4.22

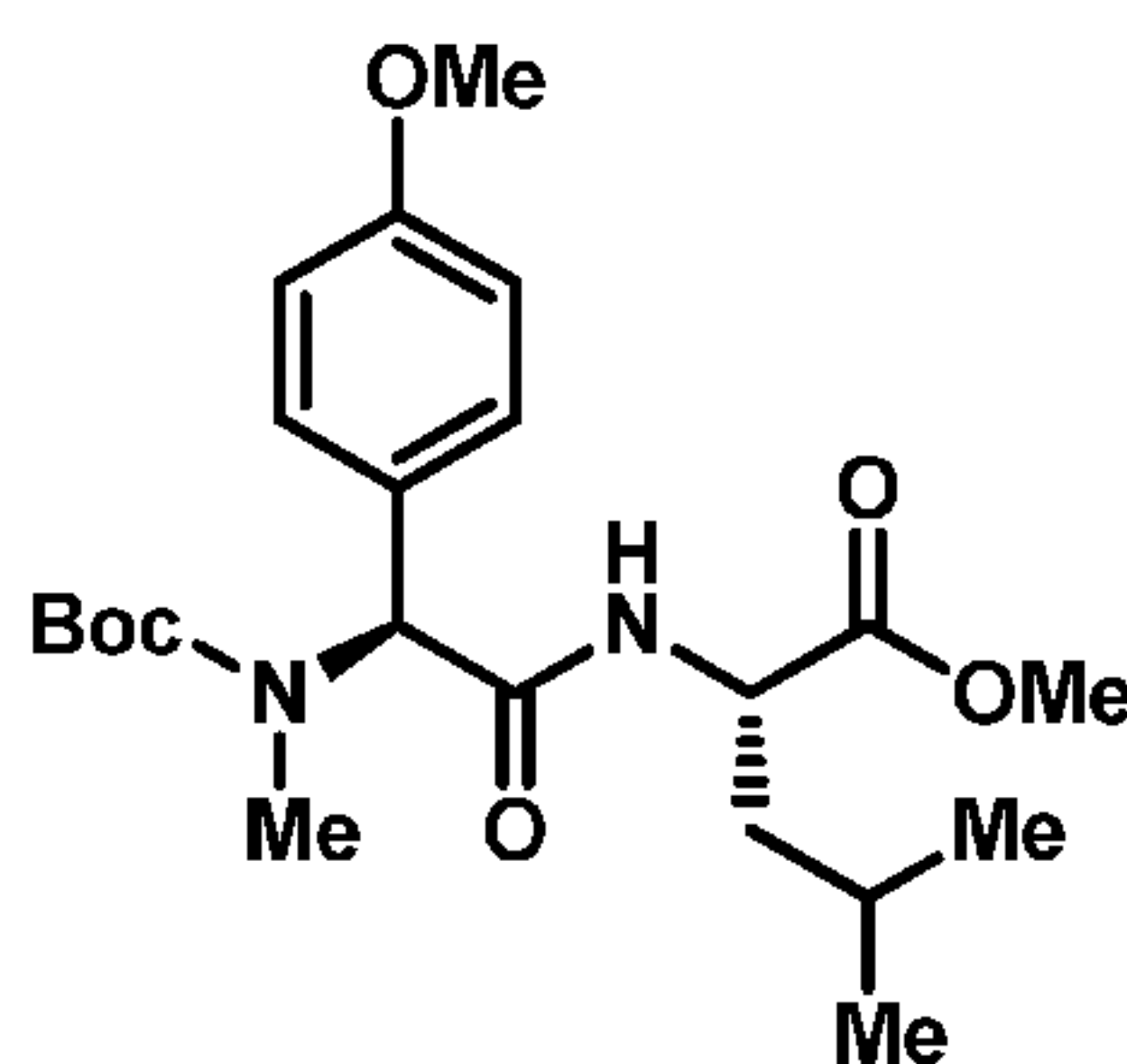
Boc-N-Me-3-Iodo-Hydroxyphenylglycine (116mg, 0.28 mmol, 1 eq) was dissolved in a 3:1 mixture of DCM:DMF (2.8mL) and treated sequentially with racemic

2-amino-4,4,4-trifluoro-butyric acid hydrochloride (59 mg, 1 eq), HOBt (38 mg, 1 eq), DIC (49 μ L, 1.1 eq) and TEA (40 μ L, 1 eq). The reaction was allowed to stir overnight under Ar then the DCM was blown off and dilute $\text{NaHCO}_{3(\text{aq})}$ and EtOAc were added. The aqueous layer was extracted 3x with EtOAc then the combined organic layers were washed with 5% citric acid (pH- 3), water and brine. The organics were dried over sodium sulfate, concentrated and purified via column chromatography (4% MeOH in DCM) to yield an oil. This material (81 mg, 0.145 mmol (assumed), 1 eq) was dissolved in acetone (2 mL), treated with MeI (45 μ L, 5 eq) and K_2CO_3 (100 mg, 5 eq) and heated to reflux in a sealed vial overnight. The reaction mixture was then cooled to room temperature and the acetone was evaporated under a stream on nitrogen. Water and EtOAc were added, the aqueous phase was extracted 3x with EtOAc, and the combined organic layers were dried over sodium sulfate. After concentrating, the crude material was purified via column chromatography (1.8% MeOH in DCM) to yield the product as a foam (47 mg, 15% over two steps). ^1H NMR (MeOD, 600 MHz) δ (ppm) 7.70 (s, 1H), 7.32-7.29 (m, 1H), 6.99-6.97 (m, 1H), 5.78 (br s, 1H), 4.82-4.68 (m, 1H), 3.88 (s, 3H), 3.80-3.79 (m, 3H), 2.94-2.86 (m, 1H), 2.74-2.66 (m, 5H), 1.49 (s, 1H) ^{13}C NMR (MeOD, 600 MHz) δ (ppm) 172.4, 172.2, 171.4, 171.3, 159.8, 141.2, 132.0, 131.9, 130.4, 128.3, 128.3, 126.5, 126.4, 112.0, 112.0, 86.3, 86.3, 82.0, 62.8, 56.9, 53.5, 53.4, 35.6, 35.4, 35.4, 35.2, 31.9, 28.6. MS (ESI) m/z 597.1 ($\text{M} + \text{Na}^+$).



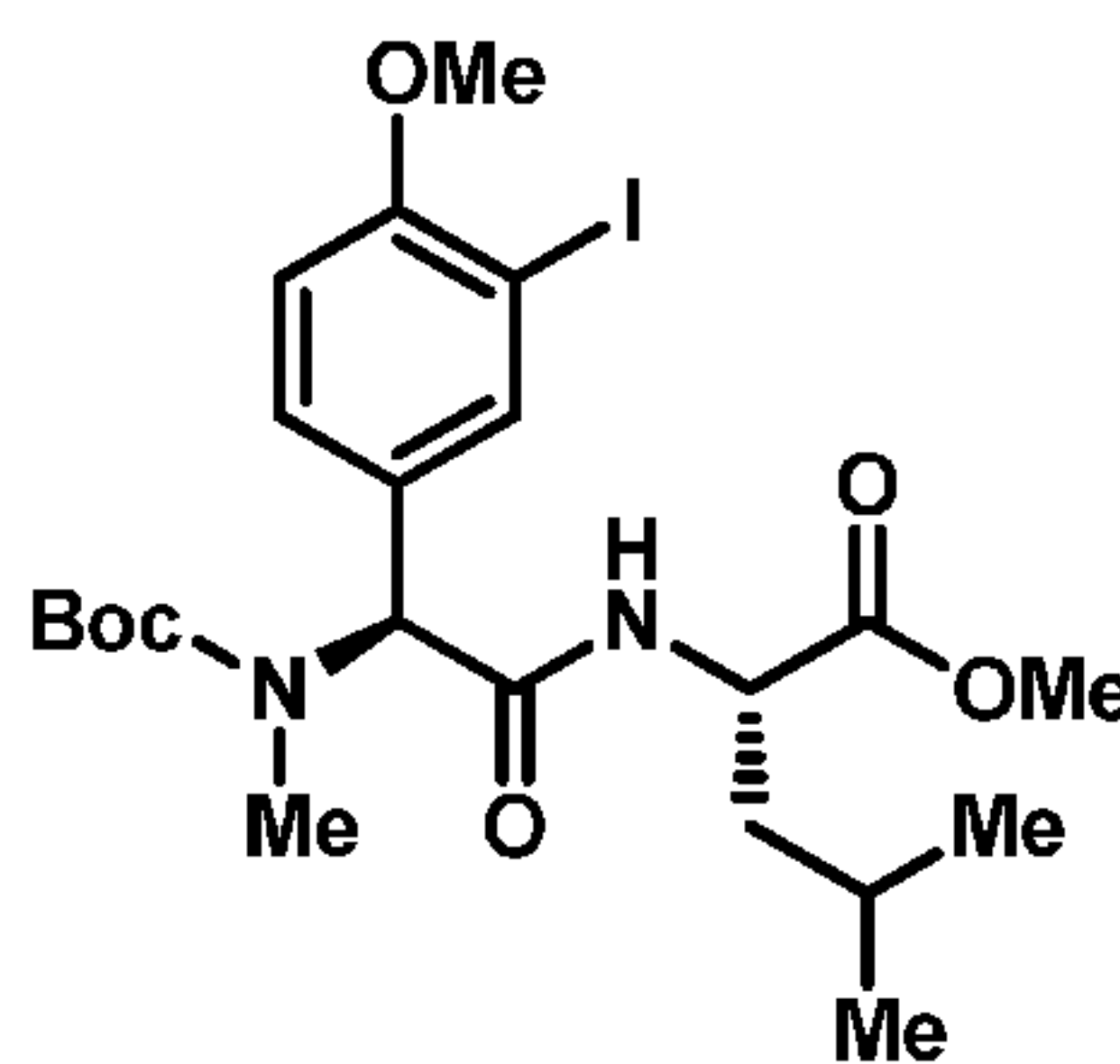
4.23

Compound **4.23** was synthesized in a manner identical to compound **4.13** (53% yield).



4.24

Boc-N-Me-Hydroxyphenylglycine (124 mg, 0.44 mmol, 1 eq) dissolved in DMF (2.0 mL) was added sequentially H-Leu-OMe (80 mg, 1 eq), HOBT (59 mg, 1 eq), EDC (93 mg, 1.1 eq) and TEA (67 μ L, 1.1 eq). The reaction was allowed to stir overnight then dilute $\text{NaHCO}_{3(\text{aq})}$ and EtOAc, the aqueous phase was extracted 3x with EtOAc and the combined organic fractions were washed with 5% citric acid (pH – 3), water and brine. The organics were then dried over sodium sulfate, concentrated and the crude was used without further purification. The crude material (170 mg, 0.42 mmol (assumed), 1 eq) was taken up in acetone (2 mL) and treated with MeI (260 μ L, 10 eq) and K_2CO_3 (172 mg, 3 eq). The reaction was stirred for overnight at reflux in a sealed tube then the acetone was blown off under a stream of nitrogen. To the residue was added water and EtOAc and the aqueous was extracted 3x with EtOAc. The combined organic layers were then dried over sodium sulfate, concentrated and the crude material was purified via column chromatography (1.5% MeOH in DCM) to give the product (130 mg, 70% yield over 2 steps). ^1H NMR (CDCl_3 , 500 MHz) δ (ppm) 7.26 (d, J = 8.5 Hz, 2H), 6.88 (d, J = 8.5 Hz, 2H), 6.49 (d, J = 8.0 Hz 1H), 5.81 (br s, 1H), 4.68-4.63 (m, 2H), 3.79 (s, 3H), 3.72 (s, 3H), 1.66-1.63 (s, 2H), 1.54-1.46 (m, 10H), 0.93 (t, J = 6.0 Hz, 3H) ^{13}C NMR (CDCl_3 , 500 MHz) δ (ppm) 173.3, 170.1, 159.6, 130.7, 127.2, 114.2, 80.5, 55.4, 52.4, 51.0, 41.5, 31.4, 28.5, 25.0, 22.9, 22.0. MS (ESI) m/z 445.2 ($\text{M} + \text{Na}^+$).

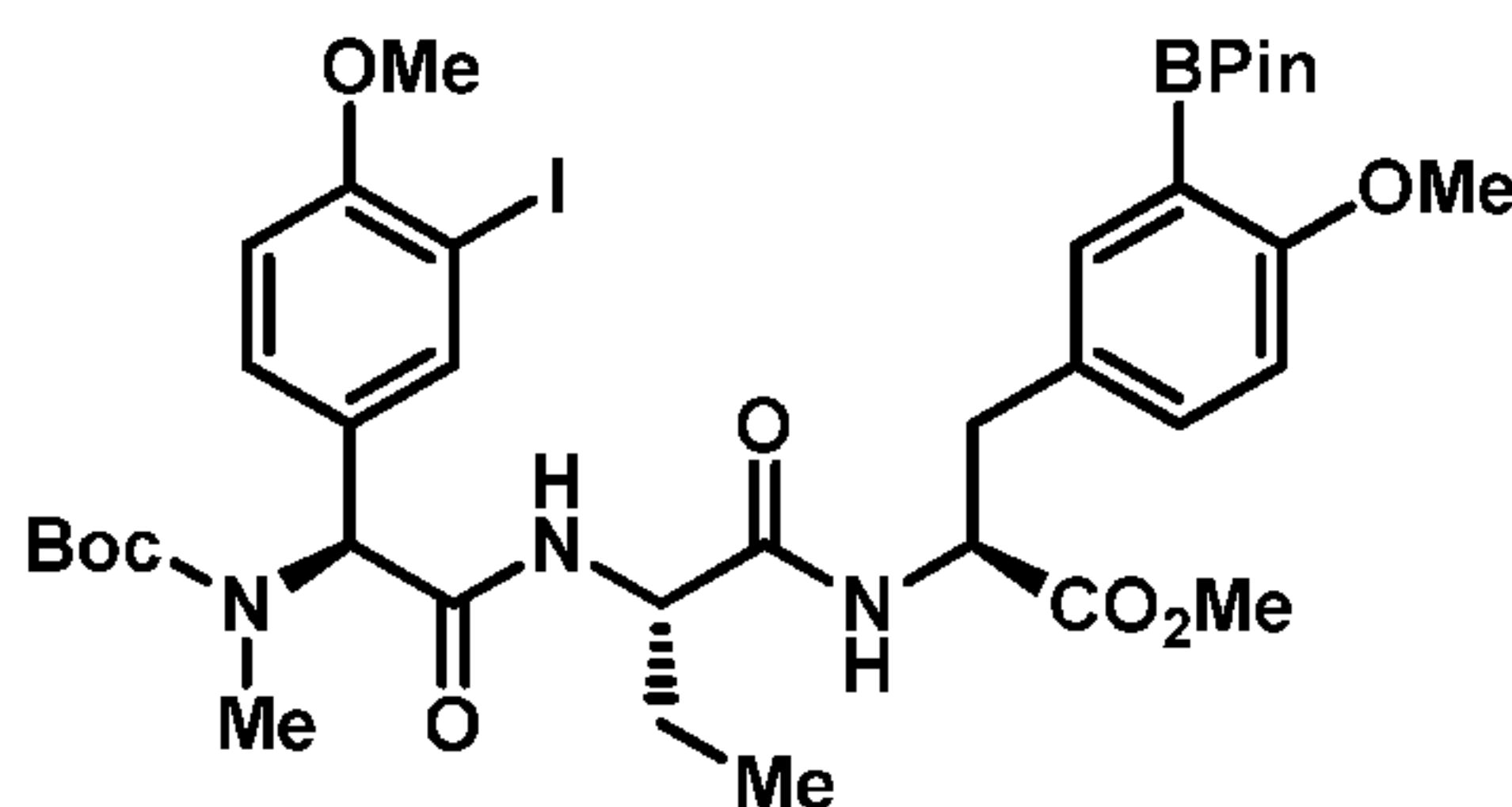


4.25

To a solution of compound **4.24** (129 mg, 0.31 mmol, 1 eq) in MeOH (2 mL) was added sequentially AgSO_4 (101 mg, 1.05 eq) and I_2 (81 mg, 1.05 eq). The reaction mixture was allowed to stir for 2.5 hrs then 10% sodium thiosulfate and some of the volatiles were blown off under a stream of nitrogen. EtOAc was added, the aqueous layer was extracted 3x with EtOAc then the combined organic layers were washed with brine, dried over sodium sulfate and concentrated by rotary evaporation. The crude material was purified via column chromatography (1% MeOH in DCM) to yield the product (135 mg, 80% yield). ^1H NMR (CDCl_3 , 500 MHz) δ (ppm) 7.72 (d, J = 2.0 Hz,

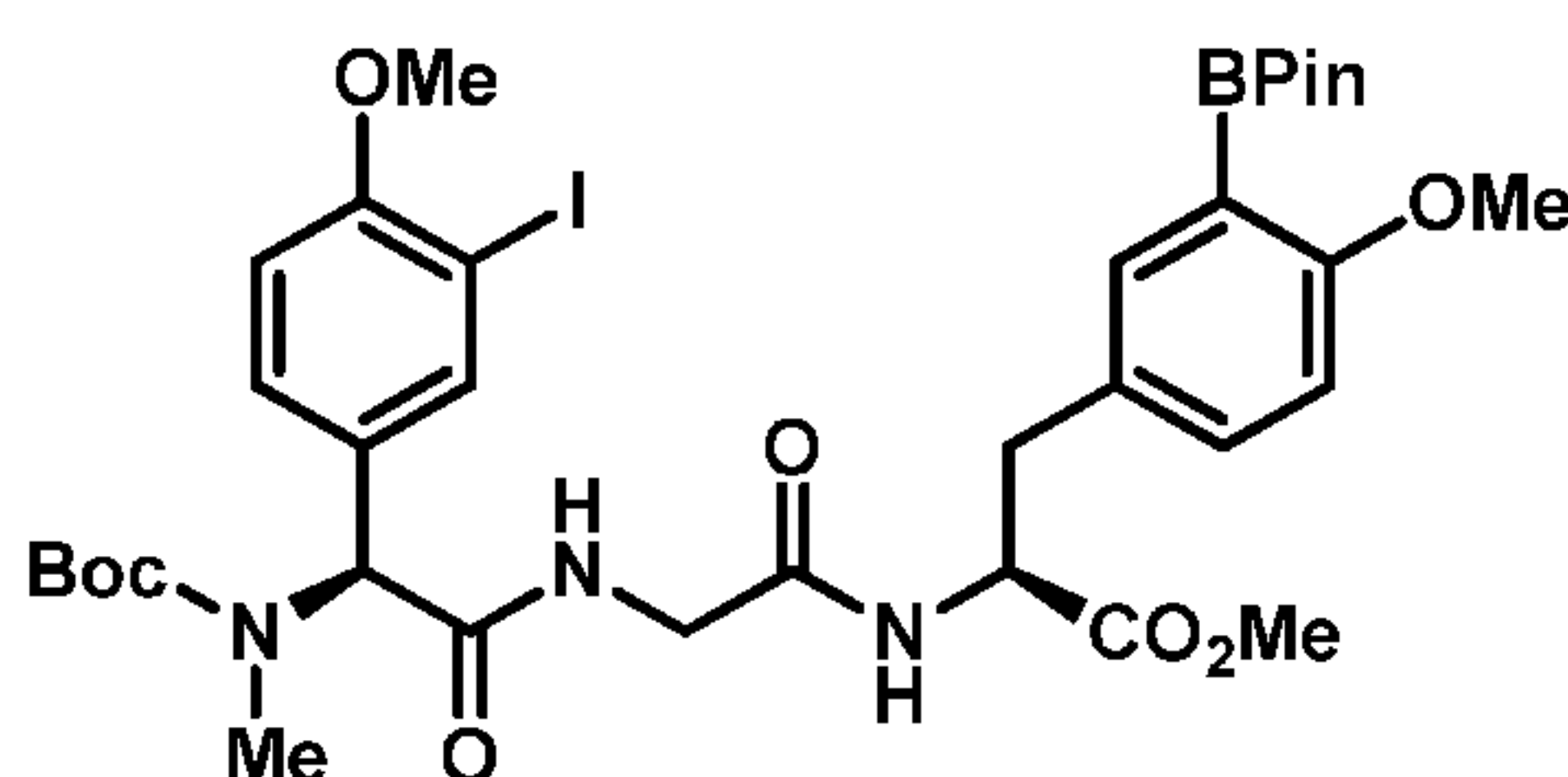
1H), 7.30 (dd, $J = 8.5$ Hz, $J = 1.5$ Hz, 1H), 6.78 (d, $J = 8.5$ Hz, 1H), 6.23 (br s, 1H), 5.74 (br s, 1H), 4.65-4.60 (m, 2H), 3.85 (s, 3H), 3.72 (s, 3H), 2.68 (s, 3H), 1.65-1.63 (m, 2H), 1.53-1.45 (m, 10H), 0.92 (t, $J = 6$ Hz, 6H). ^{13}C NMR (CDCl_3 , 500 MHz) δ (ppm) 173.1, 169.5, 158.1, 140.2, 130.5, 129.2, 110.7, 86.0, 80.8, 56.5, 52.4, 41.3, 31.6, 28.4, 24.9, 22.9, 21.9. MS (ESI) m/z XX ($\text{M} + \text{H}^+$).

General Procedure A

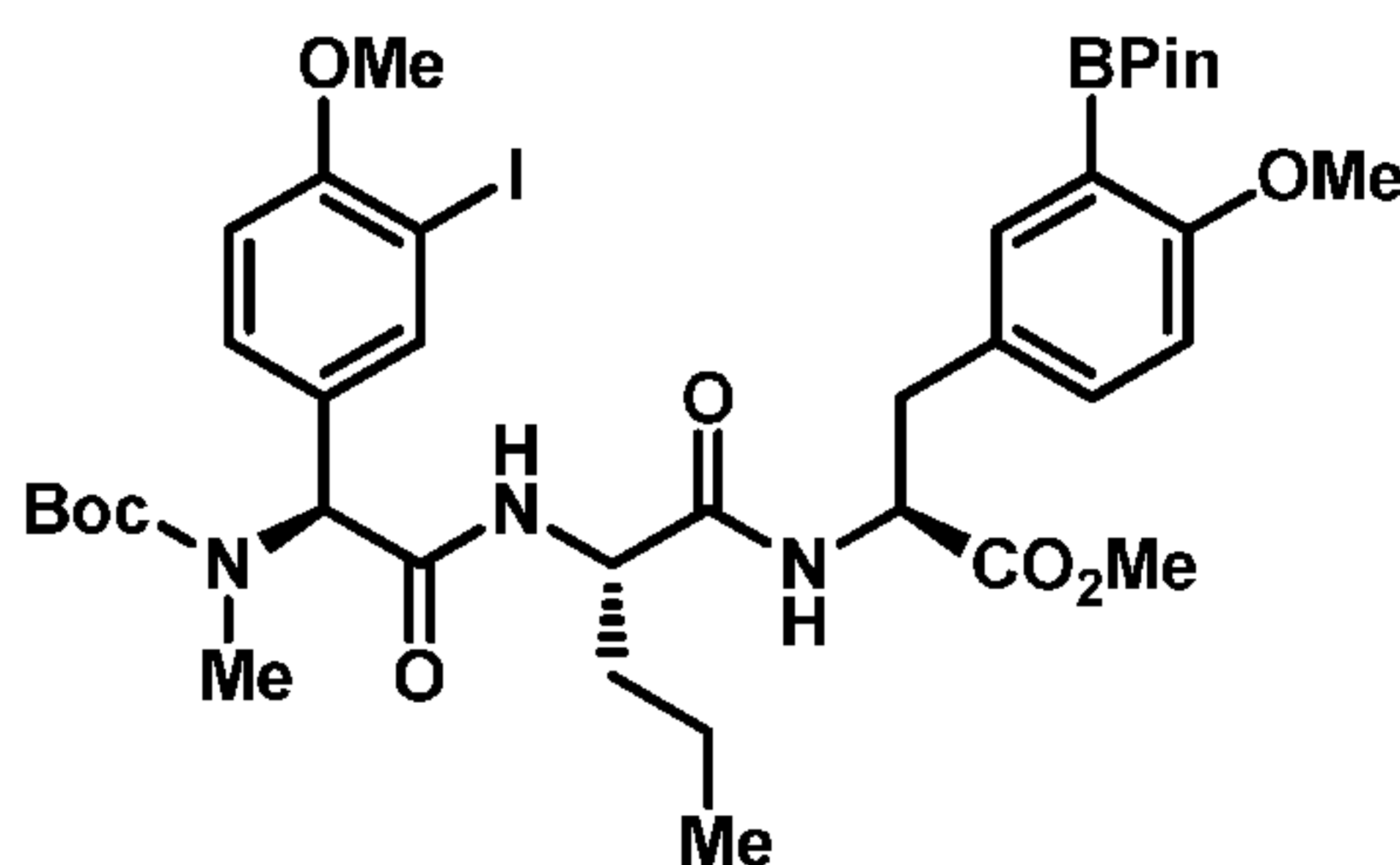


4.26

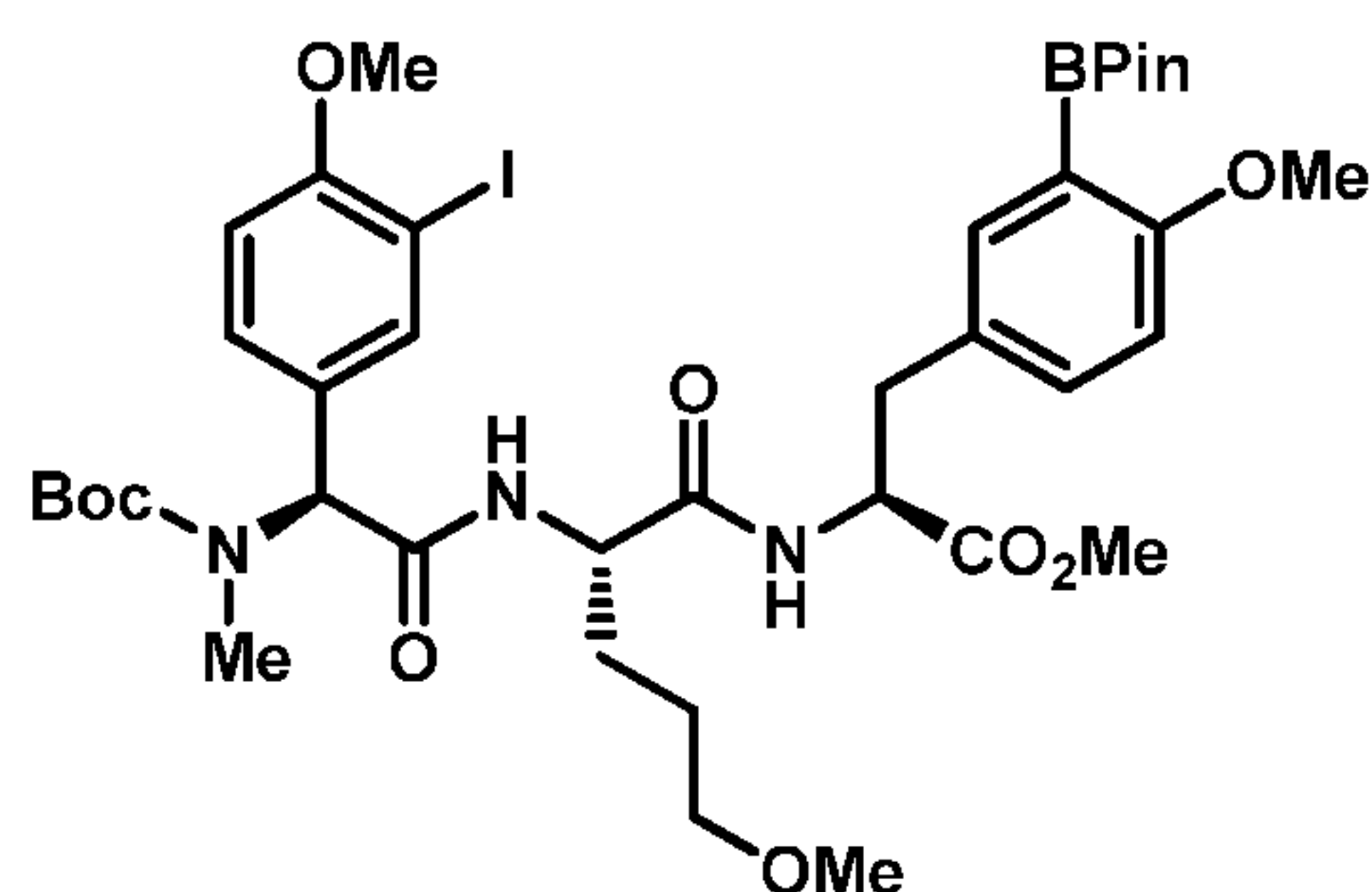
To a solution of compound **4.13** (57 mg, 0.11 mmol, 1 eq) in THF (1.3 mL) was added a 0.2 M LiOH solution (1.1 mL, 2 eq). The solution was allowed to stir until all starting material had been consumed by TLC analysis then the reaction was quenched by the addition of citric acid (pH – 3) and THF was blown off under a stream of nitrogen. The aqueous layer was extracted 3x with EtOAc and the combined organic layers were washed with brine, dried over sodium sulfate and concentrated. The resulting crude material (55 mg) was used without further purification. To a solution of this crude material (52 mg, 0.1 mmol, 1 eq) and compound XX in a 1:1 mixture of AcCN:DMF (2.6 mL) was added sequentially HOBt (24 mg, 2.5 eq) and EDC (42 mg, 2.2 eq). The reaction was allowed to stir overnight then dilute $\text{NaHCO}_3(\text{aq})$ was added and the aqueous phase was extracted 3x with EtOAc. The combined organic layers were washed with 5% citric acid (pH – 3), water and brine then dried over sodium sulfate and concentrated. The crude material was purified via abbreviated column chromatography (2.5% MeOH in DCM) due to its instability in the presence of silica gel. The purification yielded a semi-pure residue (65 mg, 77% yield). ^1H NMR (CDCl_3 , 600 MHz) δ (ppm) ^{13}C NMR (CDCl_3 , 600 MHz) δ (ppm) 171.8, 171.5, 171.0, 170.9, 170.8, 169.7, 163.7, 163.5, 163.4, 158.2, 158.1, 158.0, 140.4, 140.2, 137.8, 137.6, 133.4, 133.3, 130.7, 130.3, 130.2, 130.0, 129.2, 127.8, 127.0, 114.2, 114.1, 110.9, 110.8, 110.8, 110.6, 110.0, 86.2, 86.1, 83.7, 83.7, 81.1, 80.9, 62.2, 56.5, 56.5, 56.4, 55.9 (2C), 55.7, 55.3, 54.5 (2C), 54.4, 53.8, 53.6 (2C), 53.2, 52.5 (2C), 52.4, 37.0, 36.8, 36.6, 32.1, 28.5, 25.5, 25.0, 24.9 (2C), 10.1, 9.9 (2C), 9.8. MS (ESI) m/z 846.3 ($\text{M} + \text{Na}^+$).

**4.27**

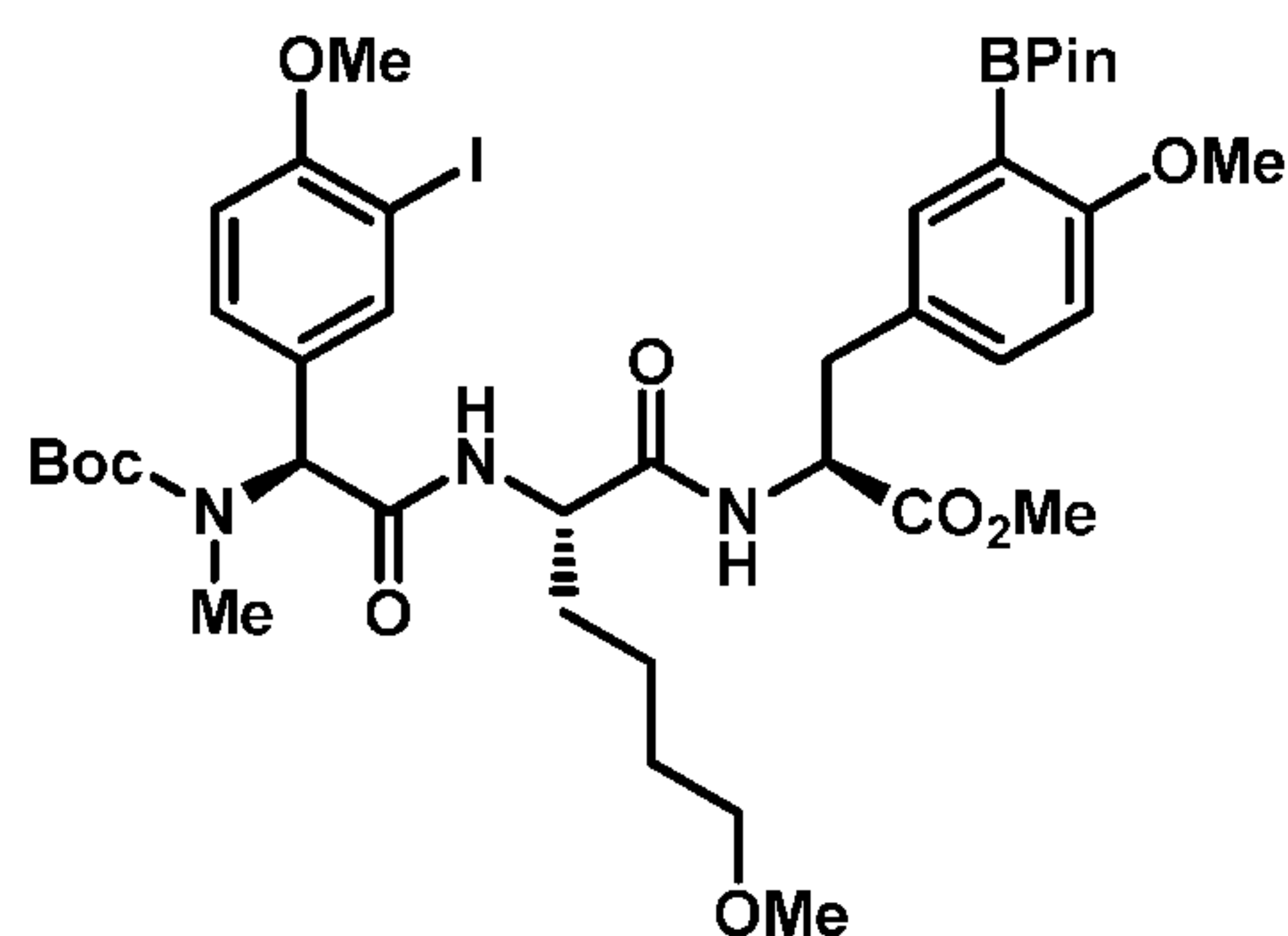
Compound **4.27** was synthesized via general procedure A starting from compound **4.12** (66% yield). R_f -0.28 (4% MeOH in DCM). ^1H NMR (CDCl_3 , 600 MHz) δ (ppm) 7.70-7.68 (m, 1H), 7.45-7.33 (m, 1H), 7.23-7.22 (m, 1H), 7.15-7.10 (m, 1H), 6.75-6.66 (m, 4H), 5.61 (br s, 1H), 4.79-4.73 (m, 1H), 4.03-3.96 (m, 1H) 3.84-3.67 (m, 9H), 3.11-2.95 (m, 2H), 2.70-2.69 (m, 3H), 1.45-1.44 (m, 9H) 1.31-1.30 (m, 10H). ^{13}C NMR (CDCl_3 , 600 MHz) δ (ppm) 171.8, 171.8, 171.6, 170.1, 168.4, 163.6, 163.4, 163.3, 158.1, 158.1, 140.3, 140.3, 140.2, 137.7, 137.6, 133.2, 134.8, 130.5, 129.2, 127.0, 110.8, 110.7, 110.6, 86.1, 83.6, 80.9, 62.4, 56.5, 56.4, 56.4, 55.9, 55.8, 55.6, 53.7, 53.5, 52.5, 52.4, 52.4, 43.0, 43.0, 36.7, 36.6, 32.2, 28.4, 27.7, 25.0, 24.9, 24.9, 24.8. MS (ESI) m/z 818.3 ($\text{M} + \text{H}^+$).

**4.28**

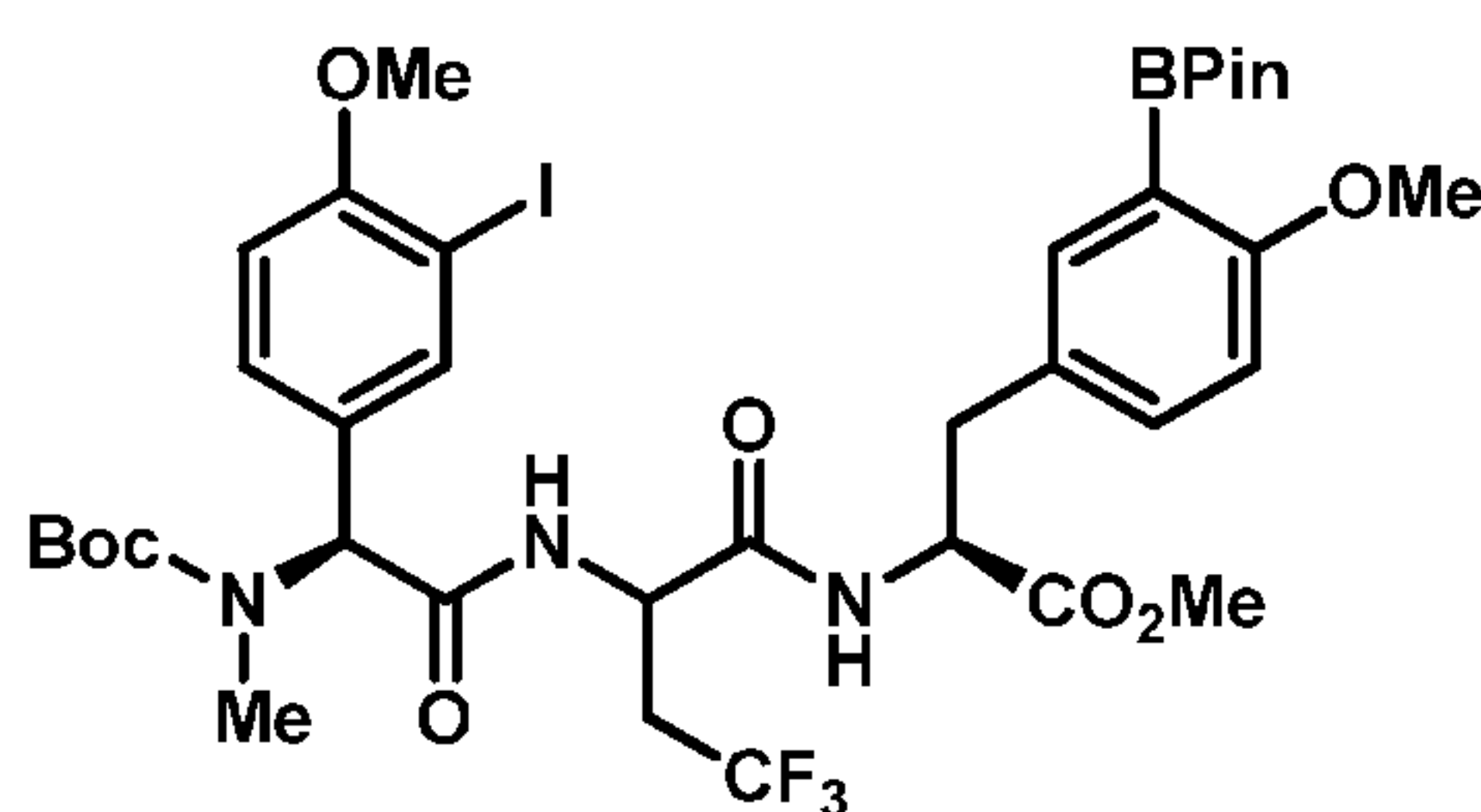
Compound **4.28** was synthesized via general procedure A using compound **4.14** (81% yield). ^1H NMR (MeOD, 600 MHz) δ (ppm) 7.69-7.64 (m, 1H), 7.45 (s, 1H), 7.29-7.26 (m, 1H), 7.16-7.07 (m, 1H), 6.97-6.81 (m, 2H), 5.68-5.64 (m, 1H), 4.62-4.59 (m, 1H), 4.45-4.43 (m, 1H) 3.87-3.67 (m, 9H), 3.09-3.06 (m, 1H), 2.89-2.93 (m, 1H), 2.66-2.64 (m, 3H), 1.75-1.69 (m, 1H) 1.62-1.27 (m, 24H), 0.95-0.88 (s, 3H). ^{13}C NMR (MeOD, 600 MHz) δ (ppm) 174.0, 173.3, 172.2, 164.8, 164.8, 141.3, 141.2, 138.7, 138.6, 134.8, 134.8, 132.0, 131.6, 131.3, 130.6, 129.3, 114.9, 112.1, 112.0, 111.7, 111.6, 86.5, 86.3, 84.8, 81.9, 57.0, 56.9, 55.9, 55.8, 55.7, 55.6, 54.3, 52.7, 52.6, 37.6, 37.4, 35.2, 32.4, 28.7, 28.7, 25.2, 25.1, 20.0, 19.9, 14.1. MS (ESI) m/z 860.3 ($\text{M} + \text{Na}^+$).

**4.29**

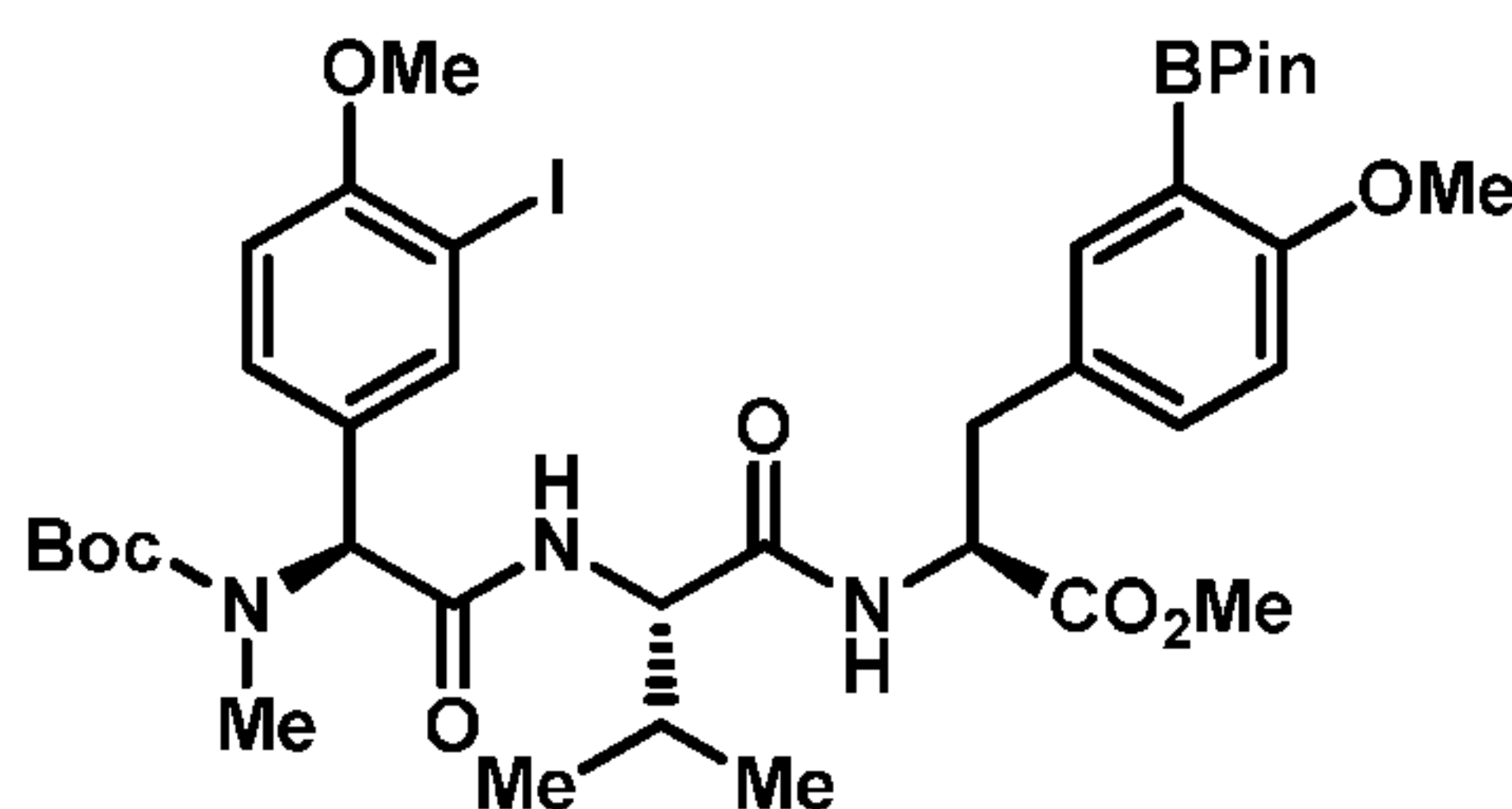
Compound **4.29** was synthesized via general procedure A using compound **4.19** (72% yield). ^1H NMR (CDCl_3 , 400 MHz) δ (ppm) 7.70-7.69 (s, 1H), 7.43-7.37 (m, 1H), 7.24-7.07 (m, 2H), 7.00-6.98 (m, 1H), 6.78-6.67 (m, 3H), 5.66-5.62 (m, 1H), 4.76-4.71 (m, 1H), 4.57-4.51 (m, 1H) 3.86-3.68 (m, 9H), 3.44-3.39 (m, 2H), 3.28-3.18 (m, 3H), 3.06-2.95 (m, 2H), 2.75-2.68 (m, 3H), 1.85-1.71 (m, 2H), 1.62-1.41 (m, 11H) 1.37-1.23 (m, 12H). ^{13}C NMR (CDCl_3 , 400 MHz) δ (ppm) 171.9, 171.0, 169.3, 163.4, 158.0, 140.2, 137.6, 133.2, 130.3, 129.4, 127.2, 110.8, 110.7, 86.1, 83.6, 80.8, 72.8, 62.2, 58.7, 56.5, 55.9, 53.8, 52.7, 52.3, 36.9, 32.0, 30.5, 28.5, 25.3, 25.0, 24.9. MS (ESI) m/z 890.3 ($\text{M} + \text{Na}^+$).

**4.30**

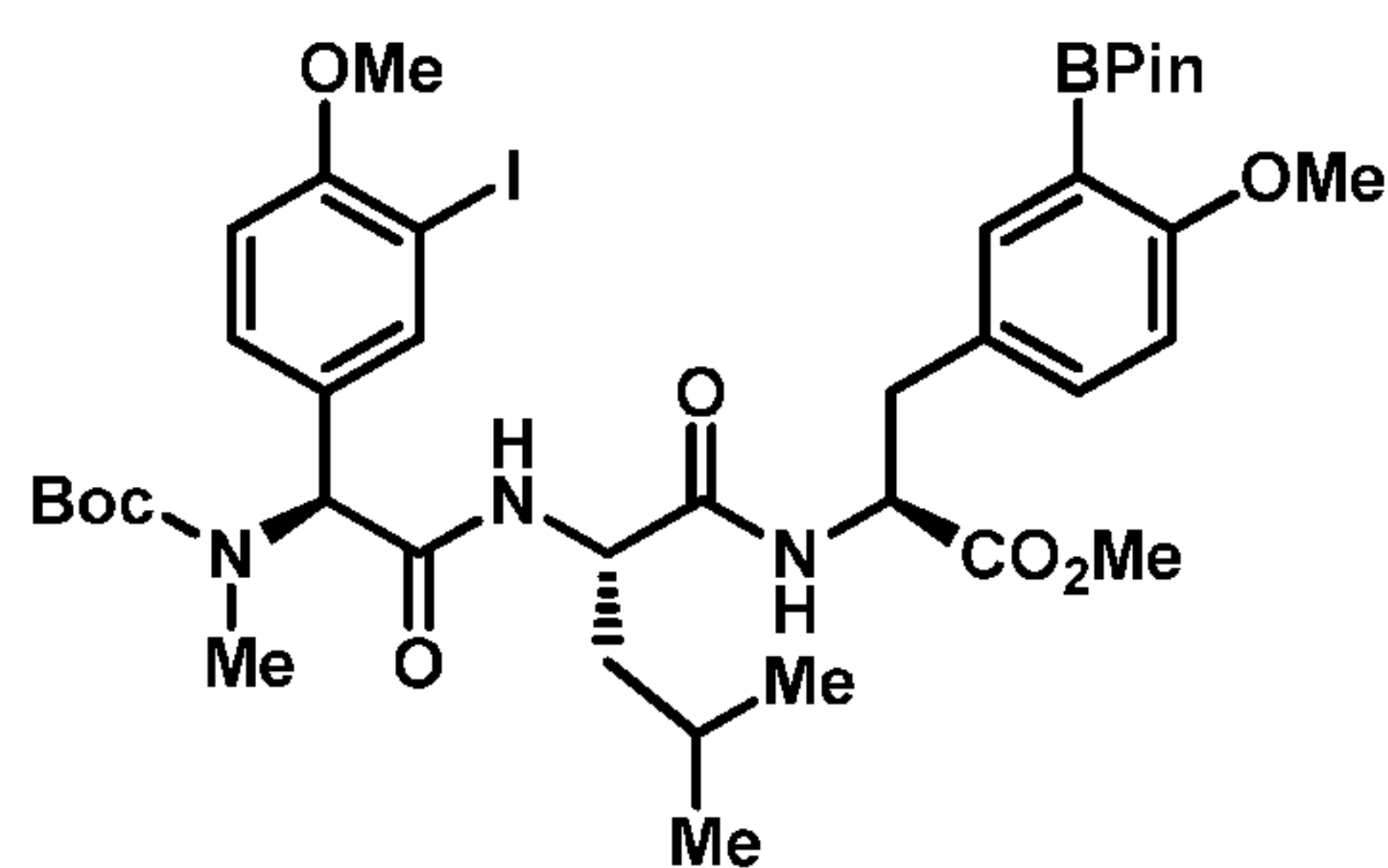
Compound **4.30** was synthesized via general procedure A using compound **4.21** (65% yield). R_f -0.26 (4% MeOH in DCM). ^1H NMR (CDCl_3 , 600 MHz) δ (ppm) 7.74-7.70 (s, 1H), 7.42-7.33 (m, 1H), 7.22-7.16 (m, 1H), 7.11-7.10 (m, 1H), 6.78-6.69 (m, 2H), 6.63-6.53 (m, 1H), 6.42-6.40 (m, 1H), 5.66-5.61 (m, 1H), 4.77-4.74 (m, 1H), 4.49-4.40 (m, 1H) 3.87-3.69 (m, 9H), 3.34-3.26 (m, 5H), 3.06-2.98 (m, 2H), 2.76-2.68 (m, 3H), 2.05-2.03 (m, 1H), 1.91-1.86 (m, 1H), 1.61-1.24 (m, 25H). ^{13}C NMR (CDCl_3 , 600 MHz) δ (ppm) 171.8, 171.0, 169.7, 163.4, 158.1, 140.2, 137.6, 133.3, 130.3, 129.2, 127.0, 110.9, 110.6, 86.2, 83.7, 83.6, 80.9, 72.5, 62.2, 58.6, 56.5, 55.9, 53.7, 53.2, 52.3, 36.9, 32.1, 32.0, 29.0, 28.5, 25.0, 24.9, 24.8, 22.2. MS (ESI) m/z 904.3 ($\text{M} + \text{Na}^+$).

**4.31**

Compound **4.31** was synthesized via general procedure A using compound **4.22** (68% yield). ¹H NMR (MeOD, 600 MHz) δ (ppm) 7.69-7.64 (m, 1H), 7.49-7.46 (m, 1H), 7.31-7.06 (m, 2H), 6.95-6.80 (m, 2H), 5.66-5.56 (m, 1H), 4.87-4.83 (m, 1H), 4.66-4.56 (m, 1H) 3.87-3.68 (m, 9H), 3.14-3.08 (m, 1H), 2.99-2.96 (m, 1H), 2.66-2.43 (m, 5H), 1.49-1.47 (m, 9H), 1.33 (s, 11H). ¹³C NMR (MeOD, 600 MHz) δ (ppm) 173.1 (2C), 173.0, 172.3, 172.1, 171.9, 171.5, 171.3, 171.1, 171.0, 164.9, 164.8, 164.8, 164.7, 159.9, 159.8, 159.7, 141.5, 141.4, 141.3, 141.2, 138.8, 138.7, 138.6, 134.8, 134.8, 132.0, 131.7, 131.7, 130.4, 130.0, 129.3, 129.2, 129.1, 128.3, 126.4, 118.5, 115.0, 112.1 (3C), 111.9, 111.8, 111.7, 111.7, 86.5, 86.4, 86.3, 84.8, 82.0, 63.7, 63.7, 63.2, 57.0, 56.9, 56.0, 55.9, 55.9, 55.9, 52.9, 52.8, 52.8, 52.7, 37.6, 37.5, 28.7, 28.7, 28.6, 25.2, 25.1, 25.1. MS (ESI) m/z 900.3 (M + Na⁺).

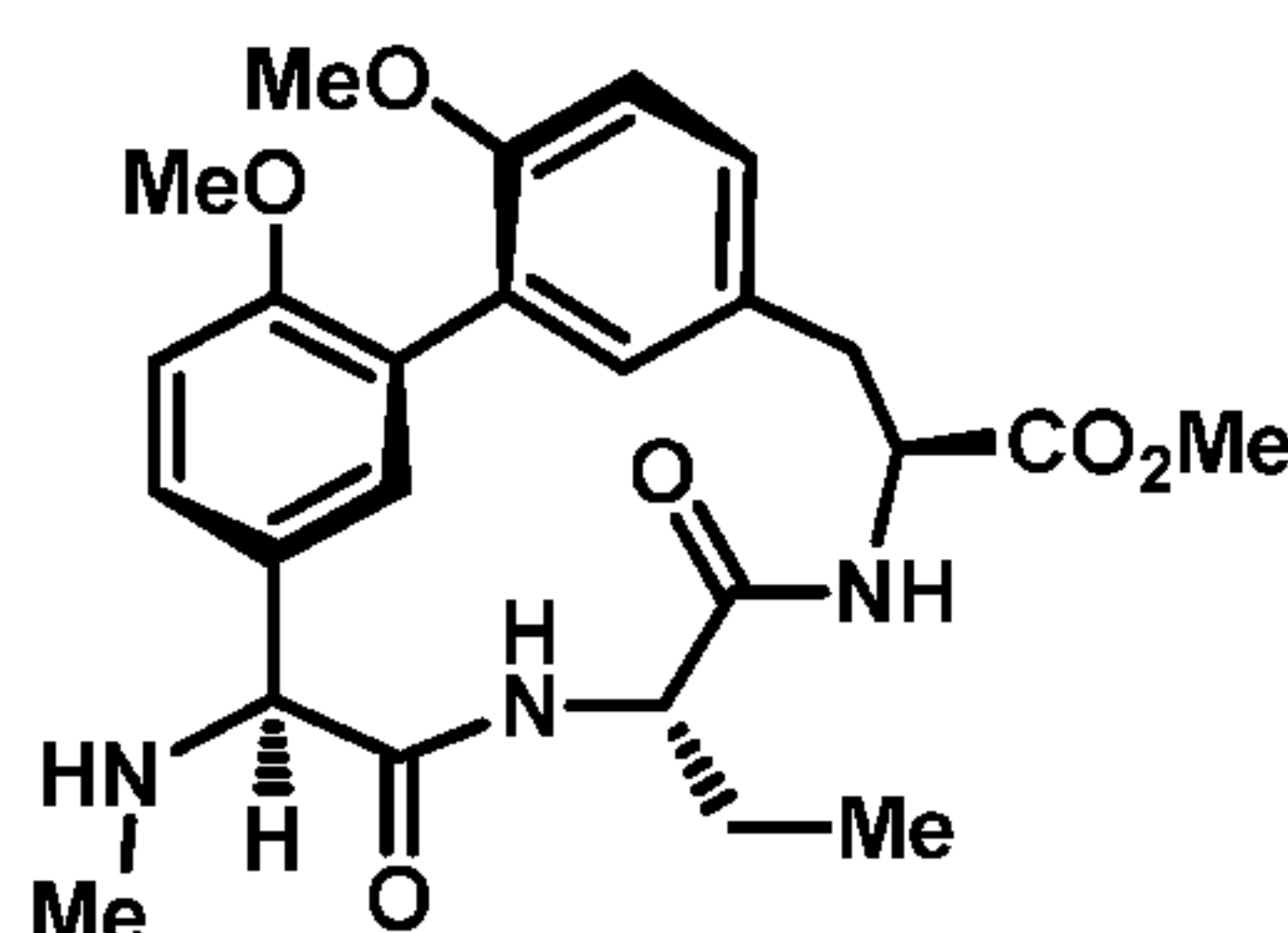
**4.32**

Compound **4.32** was synthesized via general procedure A using compound **4.23** (68% yield). ¹H NMR (CDCl₃, 600 MHz) δ (ppm) ¹³C NMR (CDCl₃, 600 MHz) δ (ppm) 171.8, 171.8, 170.6, 170.5, 170.5, 169.9, 169.6, 163.5, 163.4, 158.8, 158.1, 158.0, 156.1, 140.4, 140.0, 137.7, 137.6, 137.5, 133.4, 133.3, 130.7, 130.3, 130.2, 130.1, 129.2, 129.1, 127.1, 118.0, 114.1, 114.1, 110.8, 110.8, 110.8, 110.6, 86.1, 86.0 (2C), 83.6, 83.6, 83.5, 80.9, 62.5, 58.4, 58.3, 58.3, 56.5 (2C), 55.9, 55.9, 53.7, 53.6, 53.5, 52.4, 52.4, 52.4, 52.3, 36.9, 36.9, 36.8, 30.8, 28.4, 24.9(3C), 24.8, 19.3(3C), 19.2, 17.8. MS (ESI) m/z 860.3 (M + Na⁺).

**4.33**

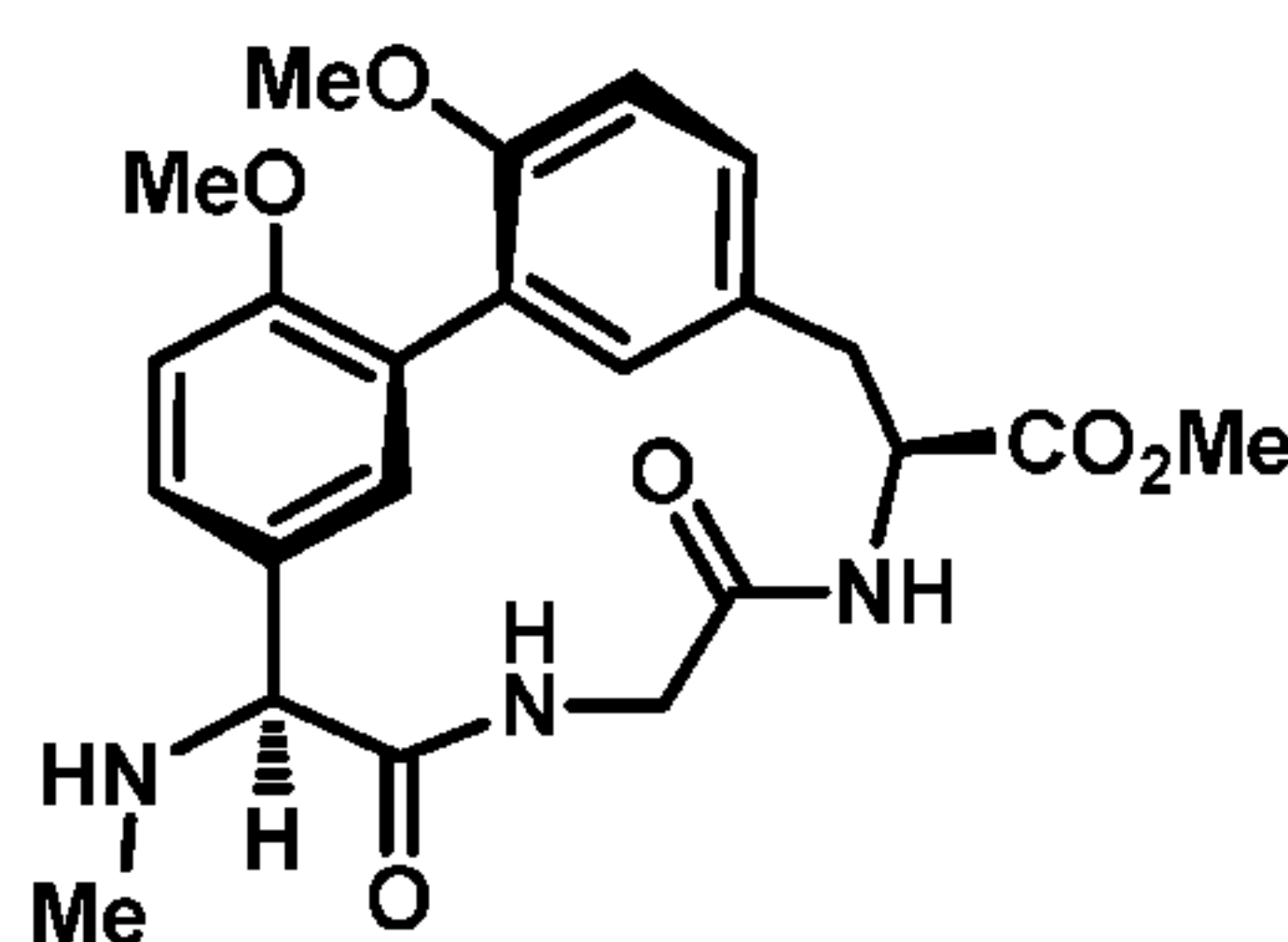
Compound **4.33** was synthesized via general procedure A starting from compound **4.25** (69% yield). R_f -0.41 (4% MeOH in DCM). ^1H NMR (CDCl_3 , 600 MHz) δ (ppm) 7.68 (s, 1H), 7.33-7.31 (m, 1H), 7.20-7.17 (m, 1H), 7.11-7.06 (m, 1H), 6.77-6.59 (m, 3H), 6.30 (d, $J = 7.8$ Hz, 1H), 5.64-5.56 (m, 1H), 4.76-4.72 (m, 1H), 4.53-4.50 (m, 1H), 3.86-3.68 (m, 9H), 3.06-2.97 (m, 2H), 2.72-2.67 (m, 3H), 1.69-1.60 (m, 2H), 1.46-1.45 (m, 10H), 1.32-1.27 (m, 11H), 0.90-0.85 (m, 3H). ^{13}C NMR (CDCl_3 , 600 MHz) δ (ppm) 171.8, 171.4, 169.7, 163.3, 158.0, 140.1, 137.6, 133.3, 130.1, 129.1, 128.6, 127.0, 110.8, 110.5, 86.2, 83.6, 81.0, 80.8, 56.4, 55.8, 53.6, 52.3, 51.7, 40.8, 36.8, 28.4, 25.0, 24.9, 24.8, 24.8, 23.1, 21.8. MS (ESI) m/z 874.3 ($\text{M} + \text{Na}^+$).

General procedure B

**4.34**

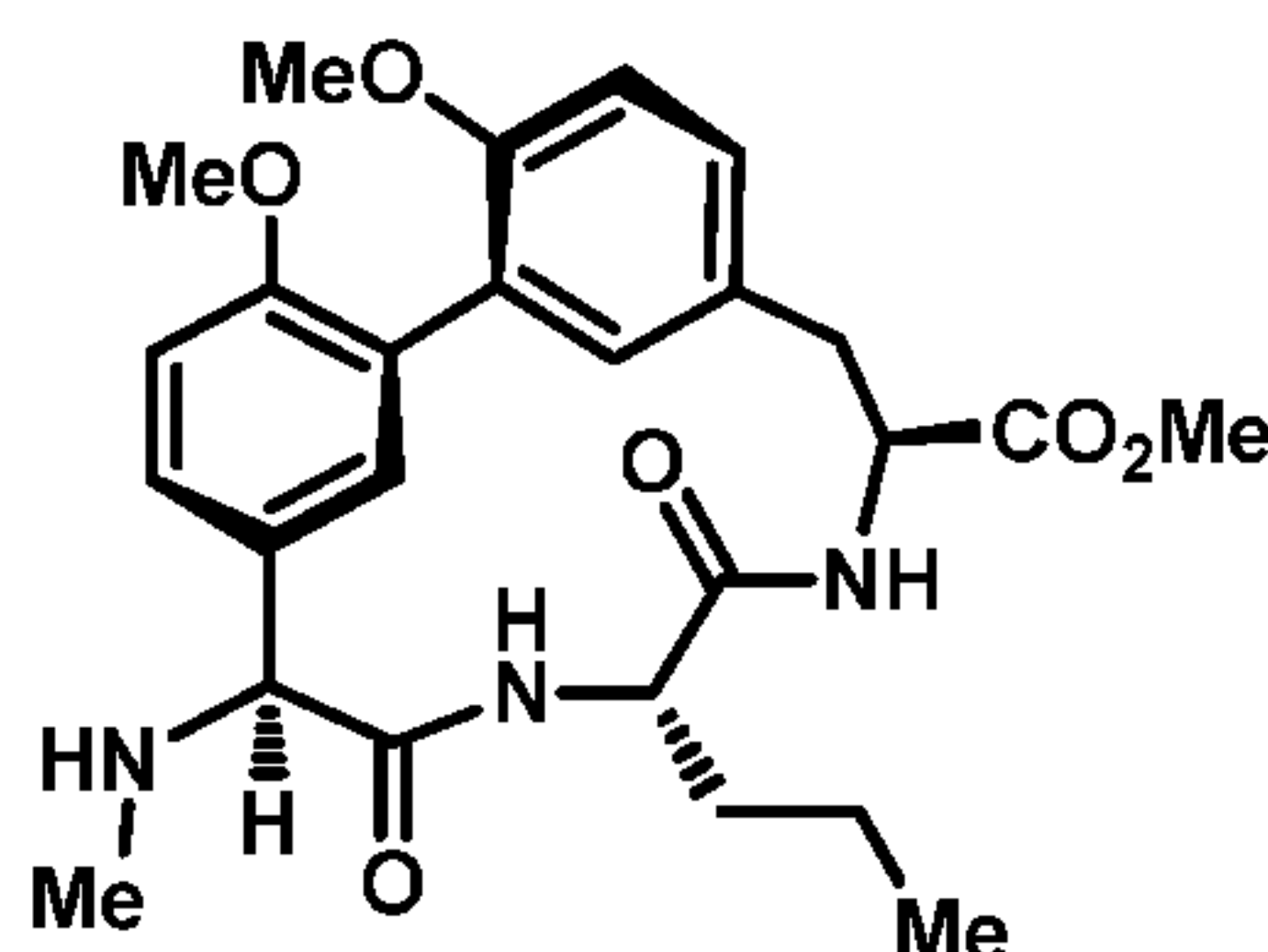
A solution of compound **4.26** (50 mg, 61 μmol , 1 eq) and NaHCO_3 (49 mg, 10 eq) in DMF (1.75 mL) was purged several times via cycling with vacuum and Ar and sealed with a crimped septa. To this solution was added a solution of $\text{PdCl}_2(\text{dppf})$ (9.9 mg, 0.2 eq) in DMF (1.2 mL) that had been sparged with Ar for ~15 minutes via syringe. The resulting mixture was submitted to several more cycles of vacuum and Ar then heated to 80° C. The mixture was cooled to room temperature and water was added. The aqueous phase was extracted with EtOAc 3x then washed with water and brine, dried over sodium sulfate and concentrated. The crude material was subjected to abbreviated column chromatography (4% MeOH in DCM) to remove most of the Pd species then used without further purification. The resulting semi-pure material (16 mg)

was taken up in DCM (1.5 mL) and treated with TFA (0.3 mL). The reaction was monitored via TLC and when starting material was no longer present the volatiles were blown off under a stream of nitrogen. DCM was added and blown off under nitrogen twice more and the crude residue was dissolved EtOAc. The organic layer was washed
5 with saturated NaHCO_3 , dried over sodium sulfate and concentrated. The crude material was purified via pipette column chromatography (7.5% MeOH in DCM) to give the product (7.5 mg, 26% yield). MS (ESI) m/z 470.2 ($M + H^+$).



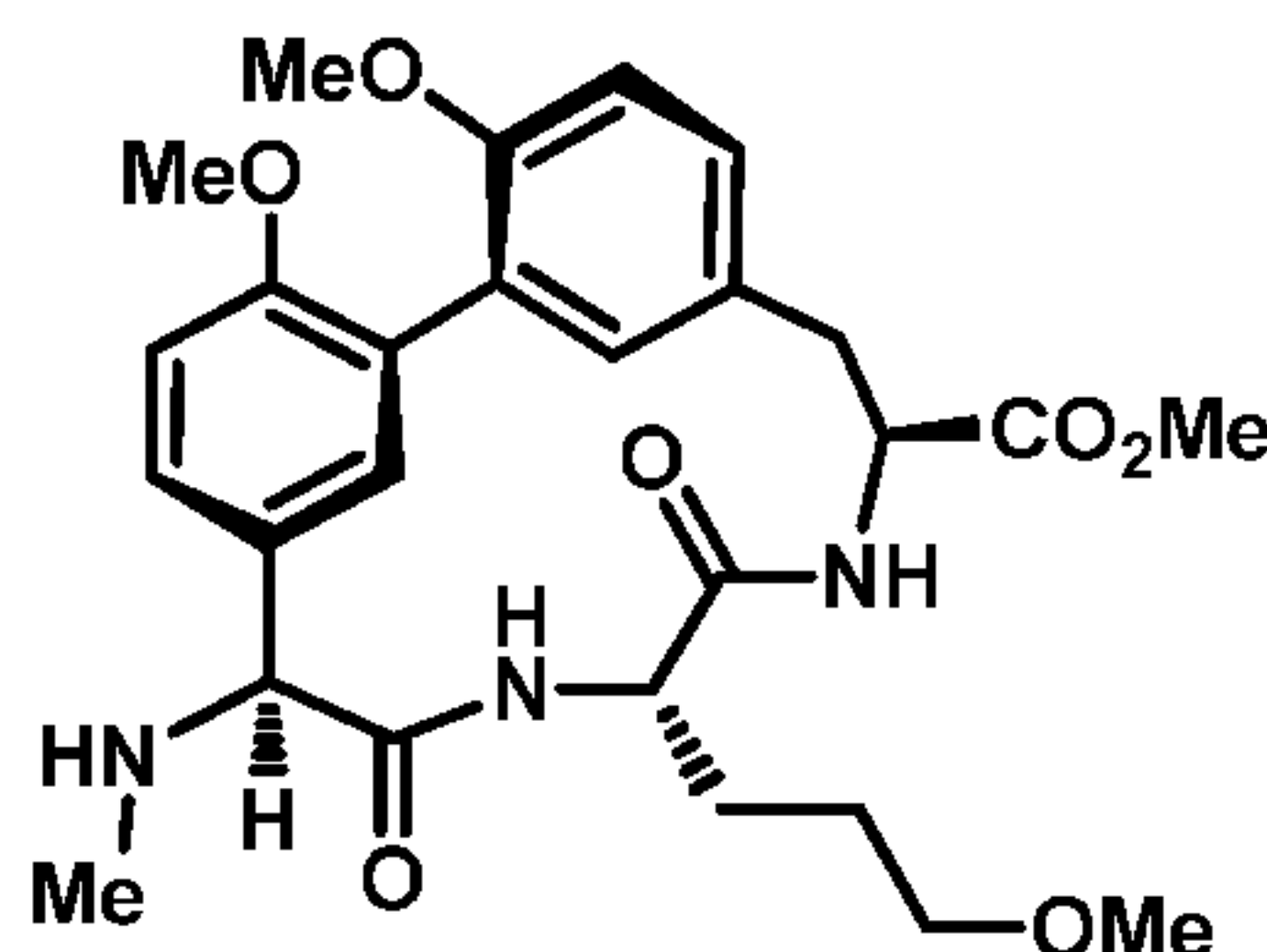
4.35

10 Compound **4.35** was synthesized via general procedure B starting from compound **4.27** (22% yield). MS (ESI) m/z 442.2 ($M + H^+$).



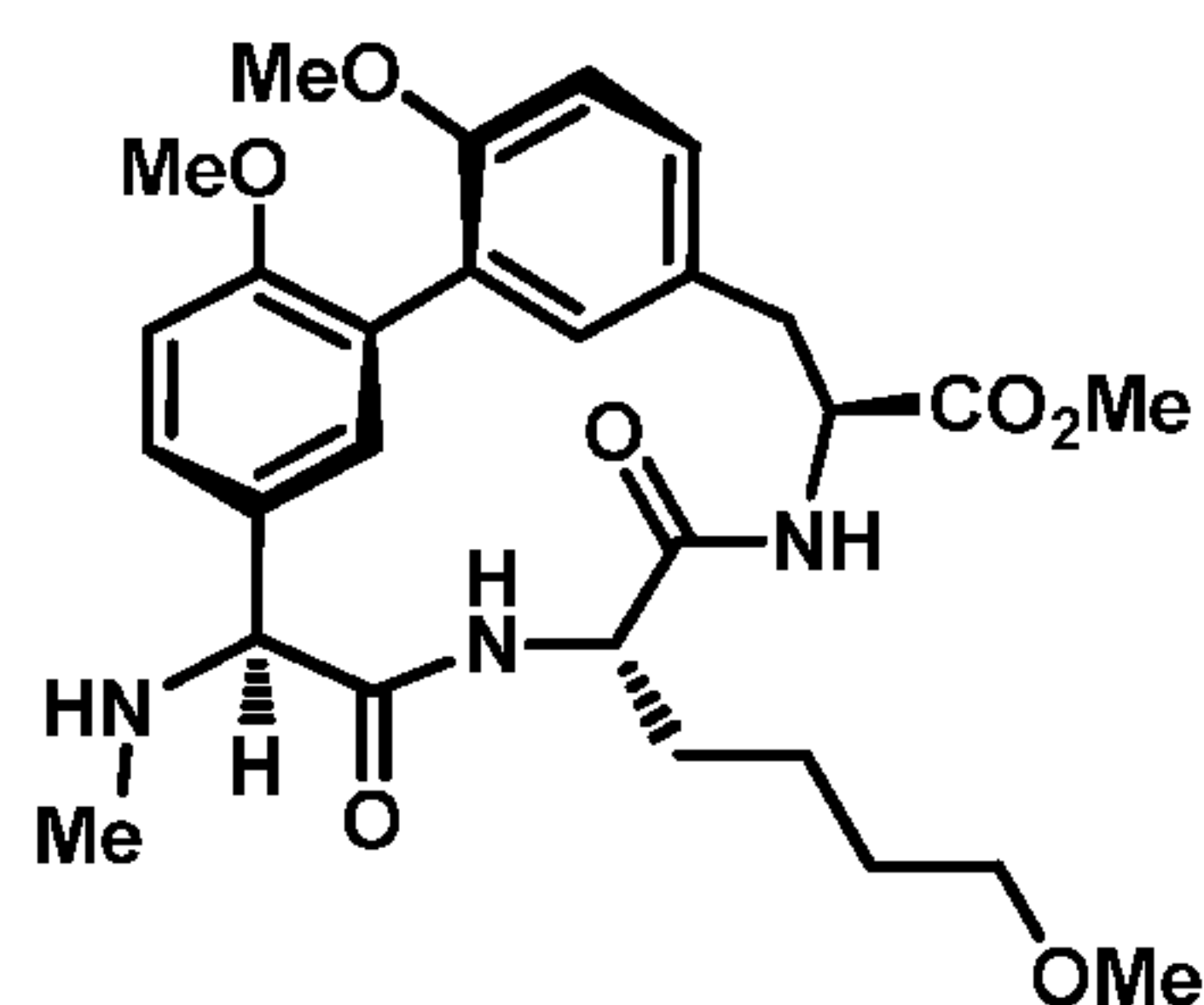
4.36

Compound **4.36** was synthesized via general procedure B starting from
15 compound **4.28** (29% yield). MS (ESI) m/z 484.2 ($M + H^+$).



4.37

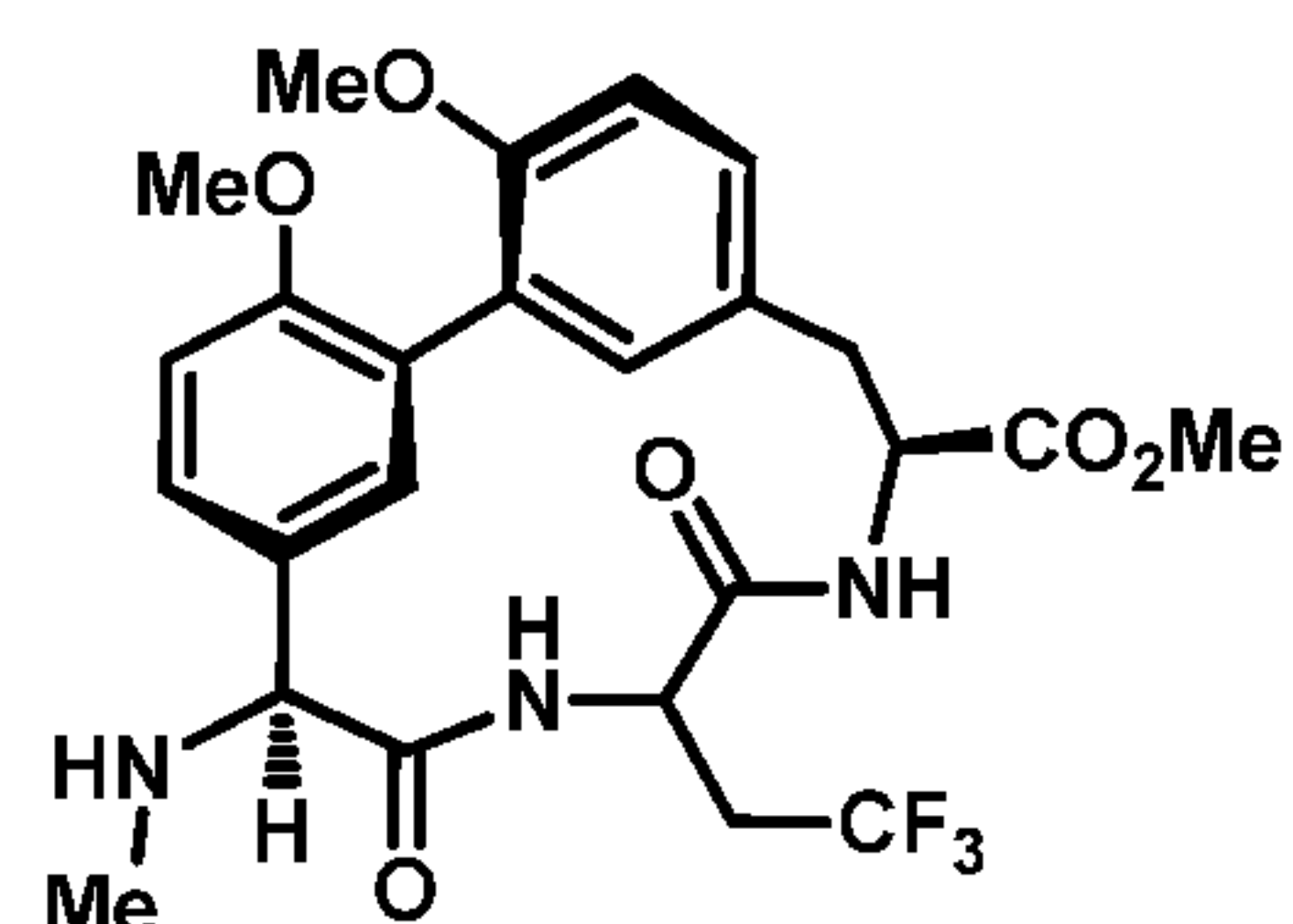
Compound **4.37** was synthesized via general procedure B starting from compound **4.29** (44% yield).



4.38

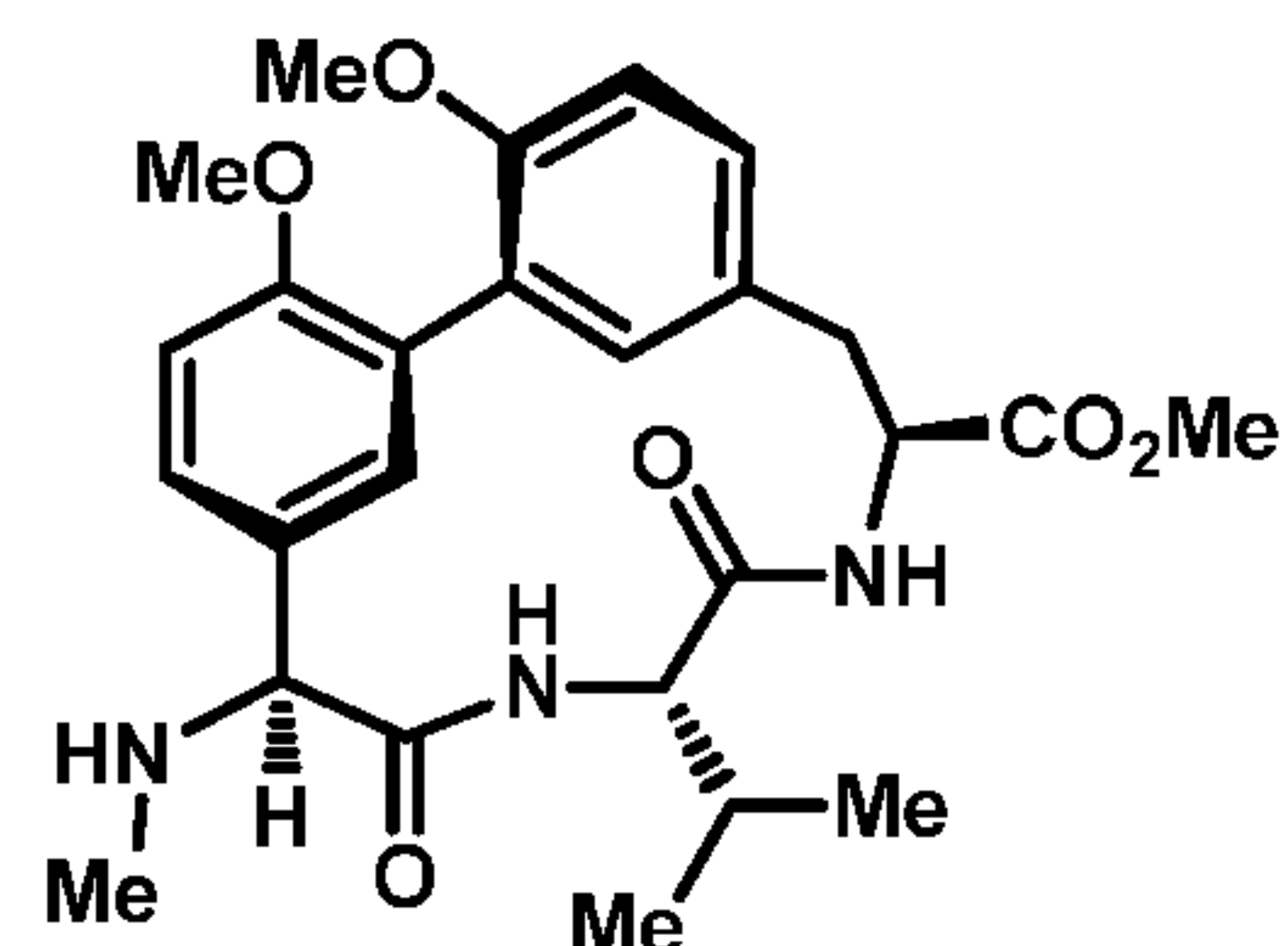
Compound **4.38** was synthesized via general procedure B starting from compound **4.30** (32% yield). MS (ESI) m/z 528.3 ($M + H^+$).

5



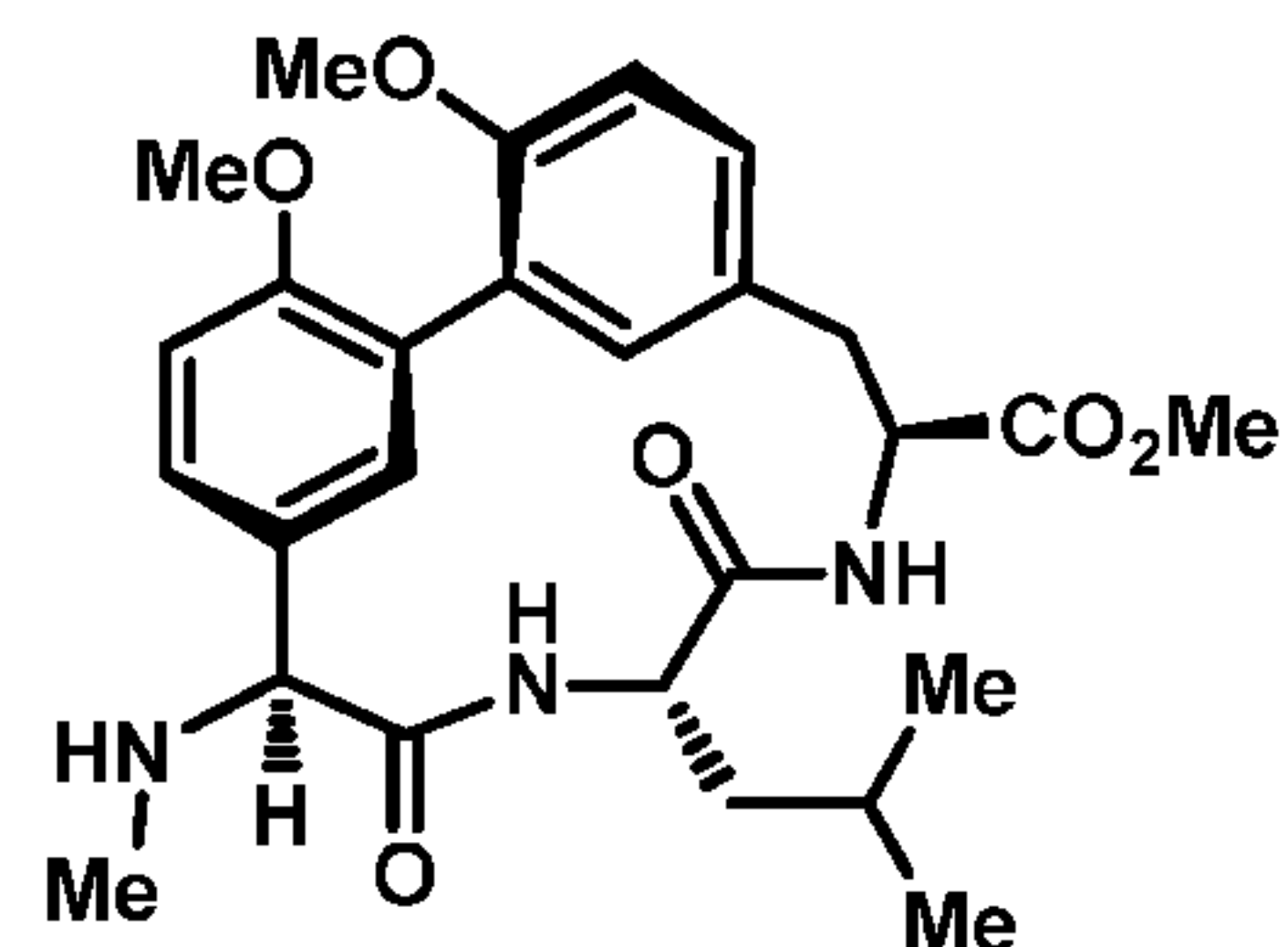
4.39

Compound **4.39** was synthesized via general procedure B starting from compound **4.31** (26% yield). MS (ESI) m/z 524.2 ($M + H^+$).



4.40

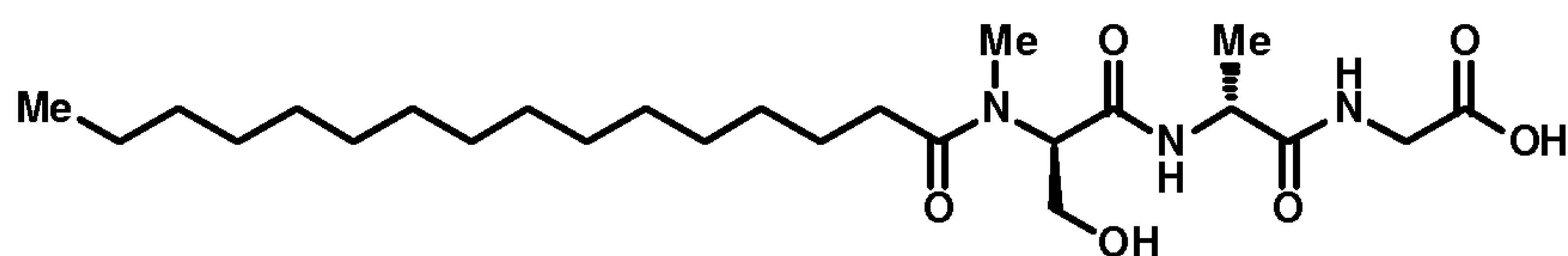
Compound **4.40** was synthesized via general procedure B starting from compound **4.32** (32% yield). MS (ESI) m/z 484.2 ($M + H^+$).



4.41

Compound **4.41** was synthesized via general procedure B starting from compound **4.33** (39% yield). MS (ESI) m/z 498.2 ($M + H^+$).

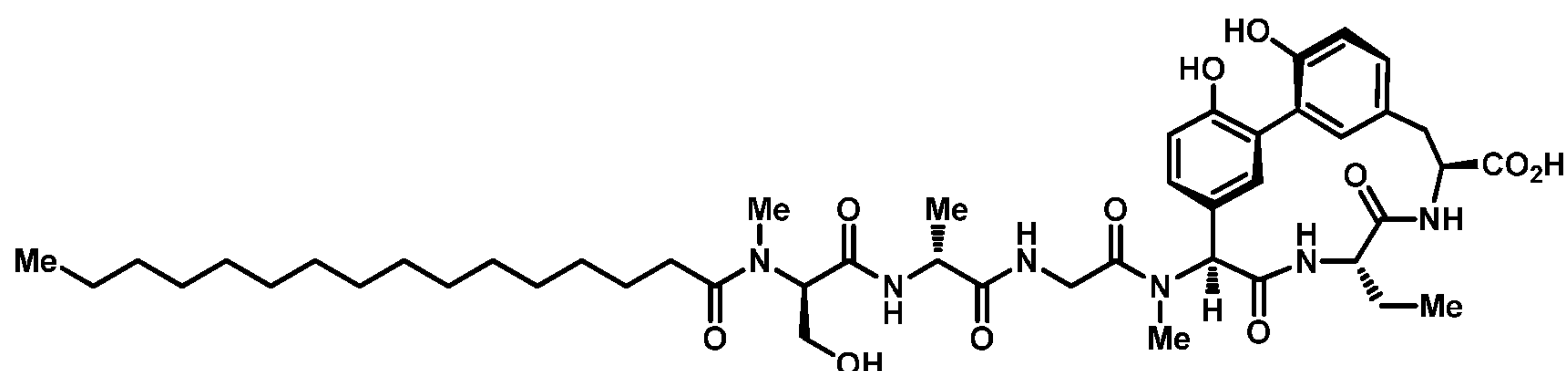
15



4.42

Compound **4.42** was synthesized via standard Fmoc/piperidine solid phase peptide synthesis. Fmoc-Gly-OH was loaded onto chlorotrityl chloride resin with DIEA, then the constituent amino acids, Fmoc-d-Ala-OH and Fmoc-N-Me-d-Ser-OH were coupled to the resin using HCTU/HOBT/DIEA in DMF followed by palmitic acid coupling with HCTU/HOBT/DIEA in DMF and enough DCM to completely dissolve the acid. Cleavage from the resin was achieved using 1% TFA in DCM using protocols detailed in the Novabiochem catalogue. The product was purified via HPLC (linear gradient, 0.66% B per minute, product eluted at 97% B).

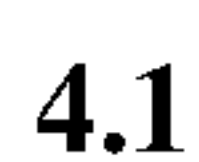
General Procedure C



4.2

To a solution of Compound **4.34** (7.0 mg, 14.9 μ mol) and compound **4.42** (12.8 mg, 1.5 eq) in THF (0.5 mL) at 0° C was added DEPBT (7.0 mg, 1.6 eq) and NaHCO₃ (1.3 mg, 1 eq). The reaction was then allowed to warm to room temperature and stirred overnight. The THF was blown off under a stream of nitrogen and the reaction was dried under vacuum. The crude reaction mixture was taken up in EtOAc, washed 2x with saturated NaHCO₃, then brine, dried over sodium sulfate and concentrated. The crude was purified via pipette column chromatography (3% MeOH in DCM then 4.5% MeOH in DCM) to give the intermediate product. The intermediate product (6.6 mg, 6.4 μ mol, 1 eq) was dissolved in ethanethiol (300 μ L), treated with 1.0 M AlBr₃ in CH₂Br₂ (128 μ L, 20 eq) and heated to 50 °C for 5 hrs. The reaction was allowed to cool to room temperature, quenched by the addition of MeOH and the volatiles were blown off under a stream of nitrogen. The crude was taken up in MeOH and dried twice more to remove lingering ethanethiol then it was dissolved in MeOH centrifuged and purified via HPLC (linear gradient, 0.67% B per minute, product eluted at 82% B) to give the final product

5



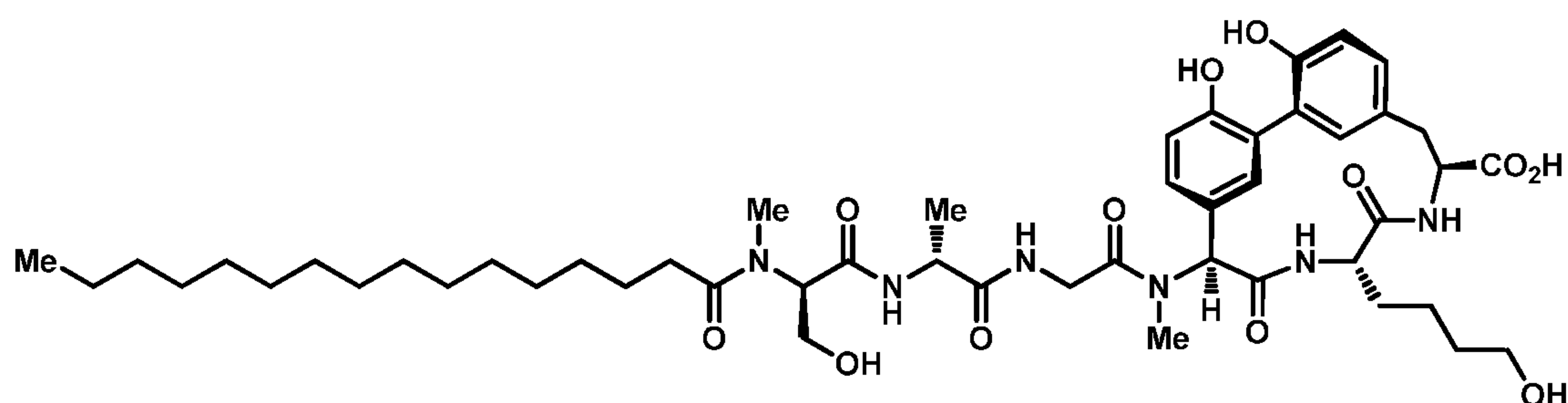
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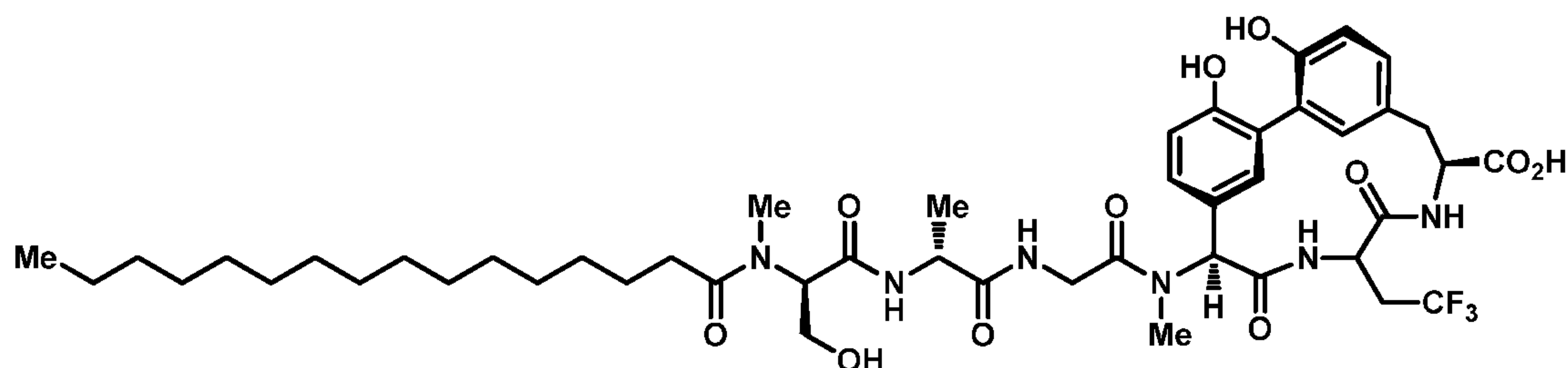


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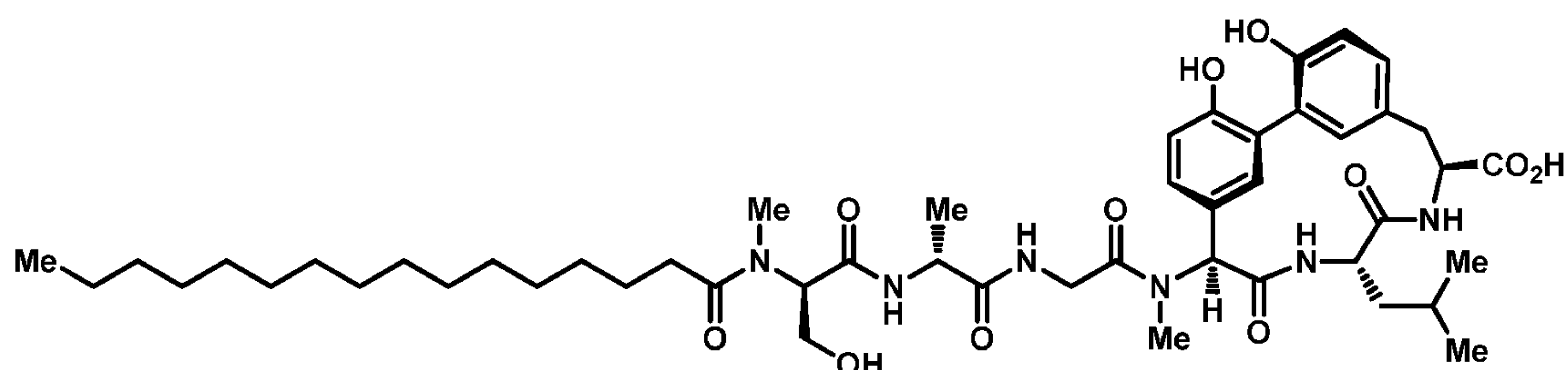
4.7

Compound **4.7** was synthesized via general procedure C starting from compound **4.38** (35% yield). ESI HRMS calcd for $C_{49}H_{74}N_6O_{12}$ $[(M+H)^+]$ 939.5437, found 939.5459.



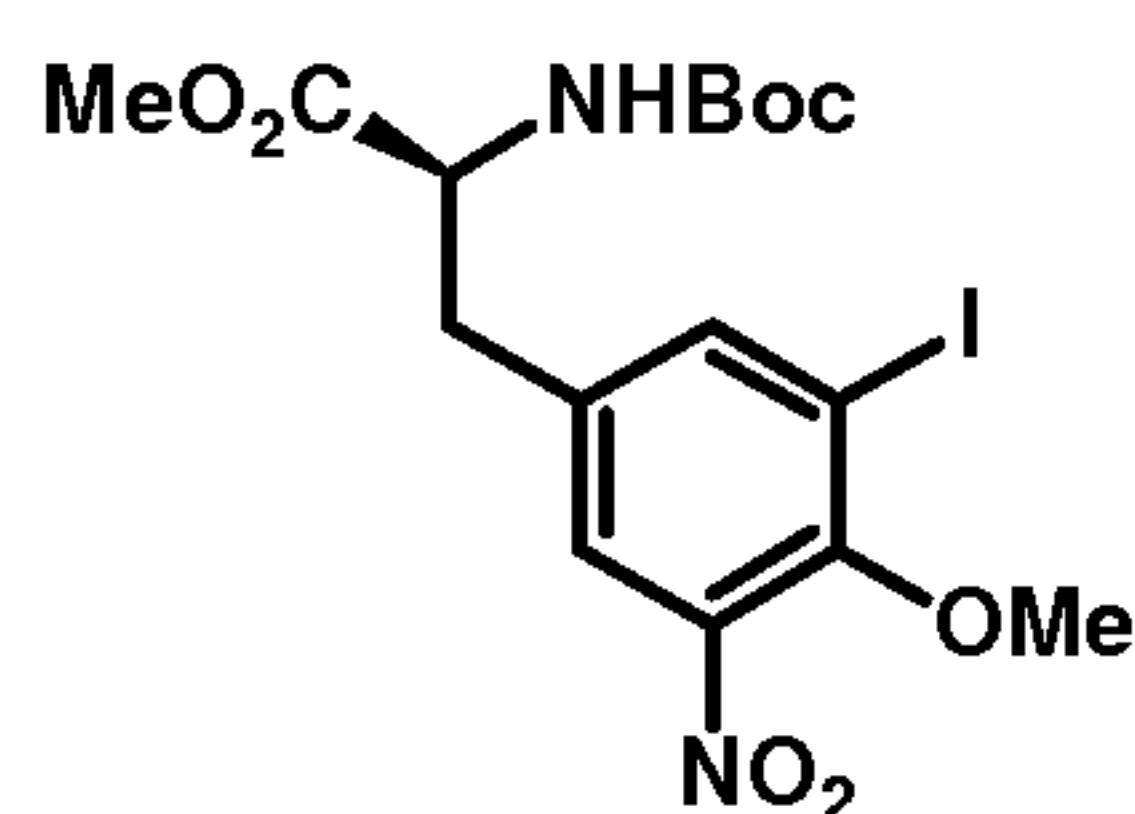
4.8

Compound **4.8** was synthesized via general procedure C starting from compound **4.39** (24% yield). ESI HRMS calcd for $C_{47}H_{67}N_6O_{11}$ $[(M+H)^+]$ 949.4892, found 949.4886.

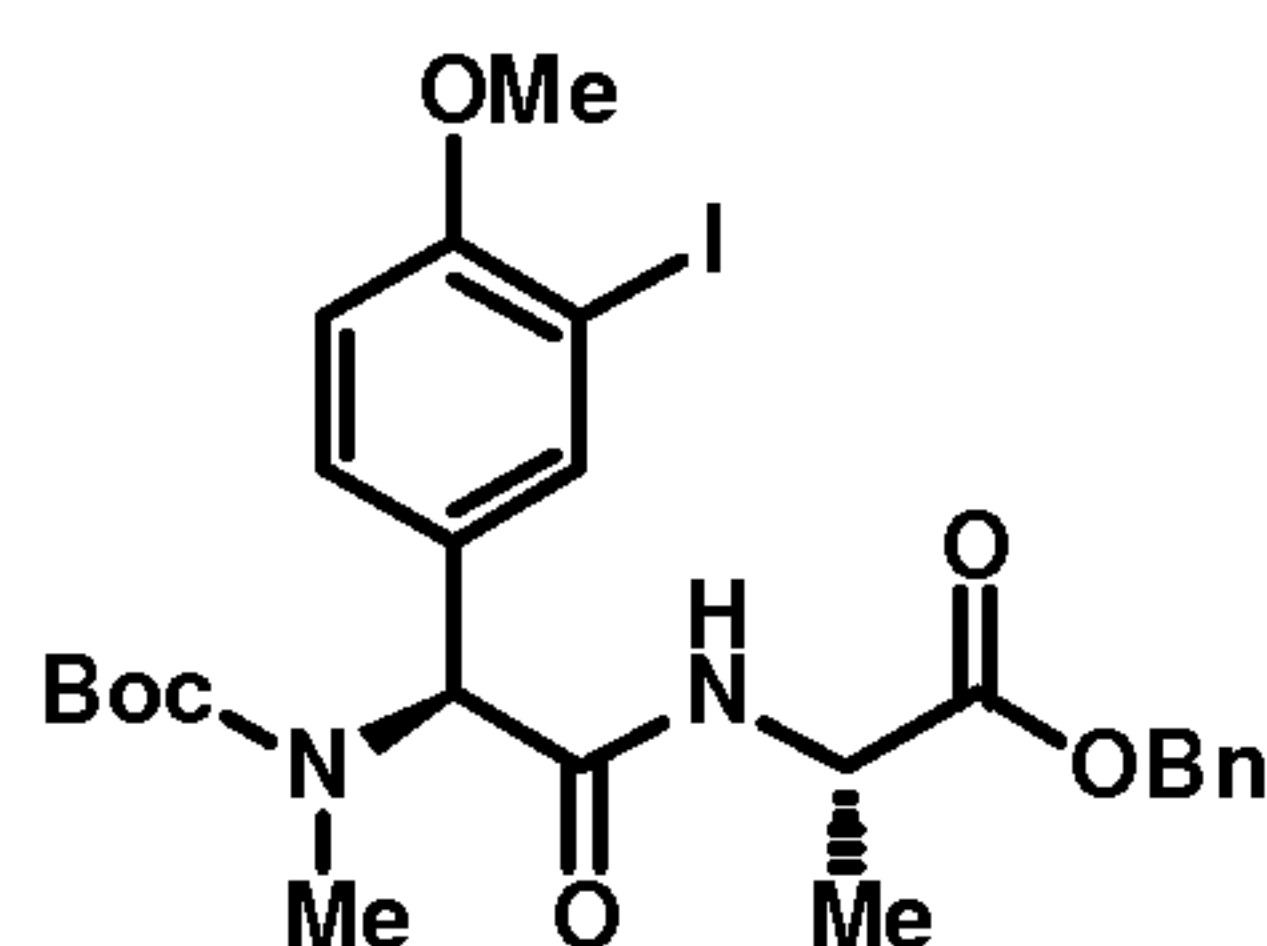


4.10

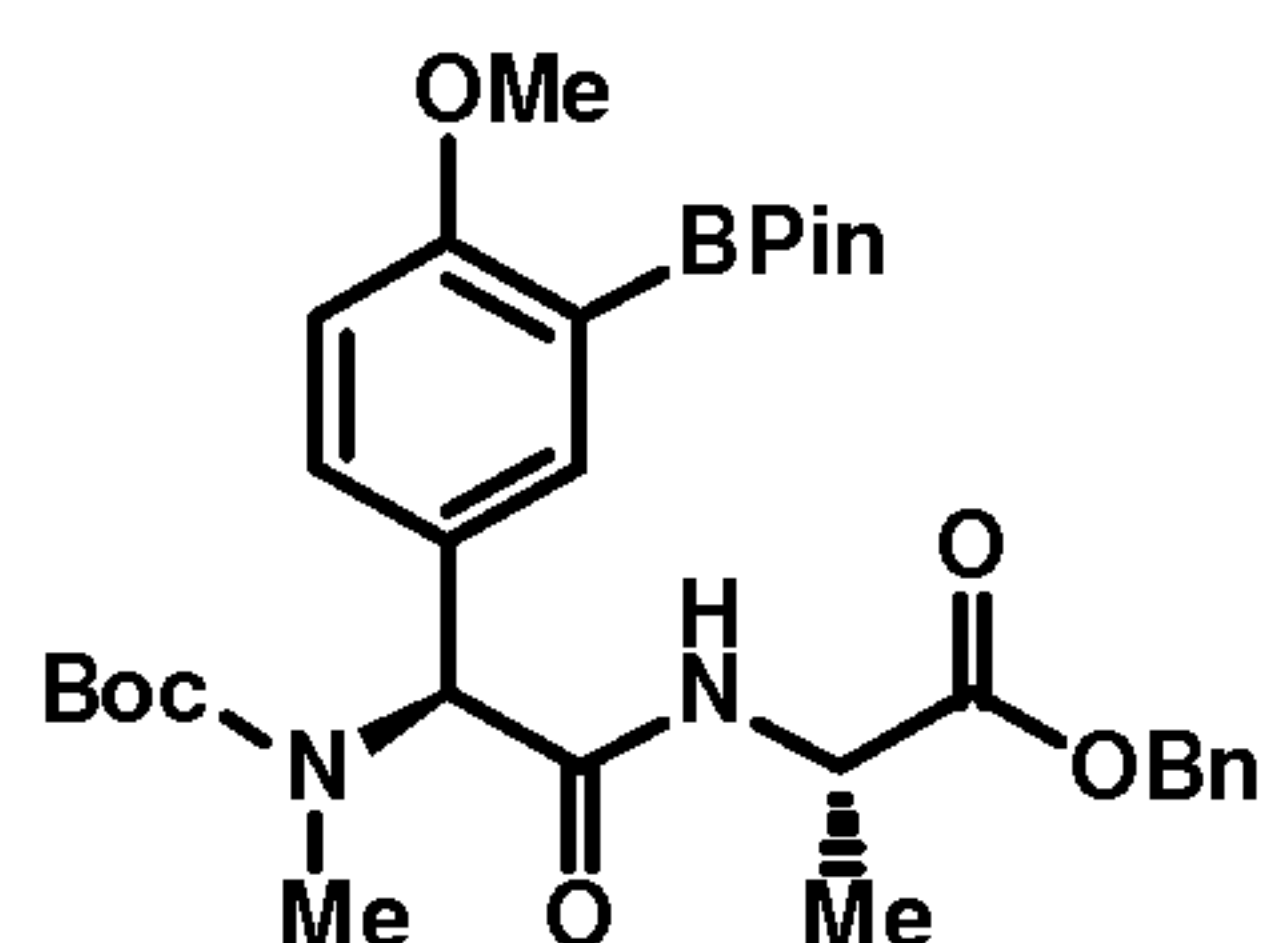
Compound **4.10** was synthesized via general procedure C starting from compound **4.40** (36% yield). ESI HRMS calcd for $C_{49}H_{74}N_6O_{11}$ $[(M+Na)^+]$ 945.5307, found 945.5306.

**5.4**

A solution of 3-nitro-tyrosine (1 g, 4.4 mmol, 1 eq) was dissolved in acetone:H₂O (1:1, 10 mL) and treated with NaHCO₃ (554 mg, 1.5 eq) and Boc₂O (946 μ L, 1 eq) and allowed to stir overnight. The reaction was acidified with 5% citric acid (pH – 3) and extracted 3x with EtOAc then the combined organic fractions were washed with brine, dried over sodium sulfate and concentrated. The crude (1.37 g, 4.2 mmol, 1 eq) was taken up in a 5:2 mixture of DCM:MeOH (56 mL), treated with BTMA-ICl₂ (1.6 g, 1.1 eq) and NaHCO₃ (2.47 g, 7 eq) and allowed to stir overnight. The solid NaHCO₃ was then filtered, the filtrate was concentrated and acidified with 5% citric acid (pH – 3). The aqueous layer was extracted 3x with EtOAc and the combined organic layers were dried over sodium sulfate and concentrated. The crude material (1.89 g, 4.19 mmol, 1 eq) was dissolved in acetone, and treated with K₂CO₃ (2.9 g, 5 eq) and MeI (1.3 mL, 5 eq) and heated to reflux over two days. The reaction mixture was then allowed to cool to room temperature, the reaction was quenched with a small amount of water and the volatiles were evaporated. 5% citric acid (pH – 3) and EtOAc were added then separated and the aqueous layer was extracted 2x with EtOAc. The combined organic layers were washed with brine, dried over sodium sulfate and concentrated. The crude material was purified via column chromatography (0-0.5% MeOH in DCM) to yield compound **5.4** (1.67 g, 82% yield over 3 steps). ¹H NMR (CDCl₃, 500 MHz) δ (ppm) 7.80 (d, *J* = 1.5 Hz, 1H), 7.56 (d, *J* = 1.5 Hz, 1H), 5.12 (d, *J* = 6.5 Hz, 1H), 4.54-4.53 (m, 1H), 3.94 (s, 3H), 3.76 (s, 3H), 3.18 (dd, *J* = 5.0 Hz, *J* = 14.0 Hz, 1H) 2.98 (dd, *J* = 6.5 Hz, *J* = 14.0 Hz, 1H) 1.41 (s, 9H) ¹³C NMR (CDCl₃, 500 MHz) δ (ppm) 171.5, 155.0, 152.1, 144.9, 143.8, 135.1, 126.4, 94.3, 80.5, 62.8, 54.2, 52.8, 37.0, 28.4. MS (ESI) *m/z* 503.0 (M + Na⁺). Compound **5.4** (127 mg, 0.27mmol, 1 eq) was then dissolved in DCM (2.5 mL) and treated with TFA (0.5 mL). When TLC analysis indicated the complete consumption of starting material the volatiles were blown off and the residue was dried under vacuum. The residue was then taken up in EtOAc and saturated NaHCO₃, the aqueous layer was extracted 3x with EtOAc, the combined organic layers were dried over sodium sulfate and concentrated. The resulting compound **5.6** (101 mg) was used without further purification.

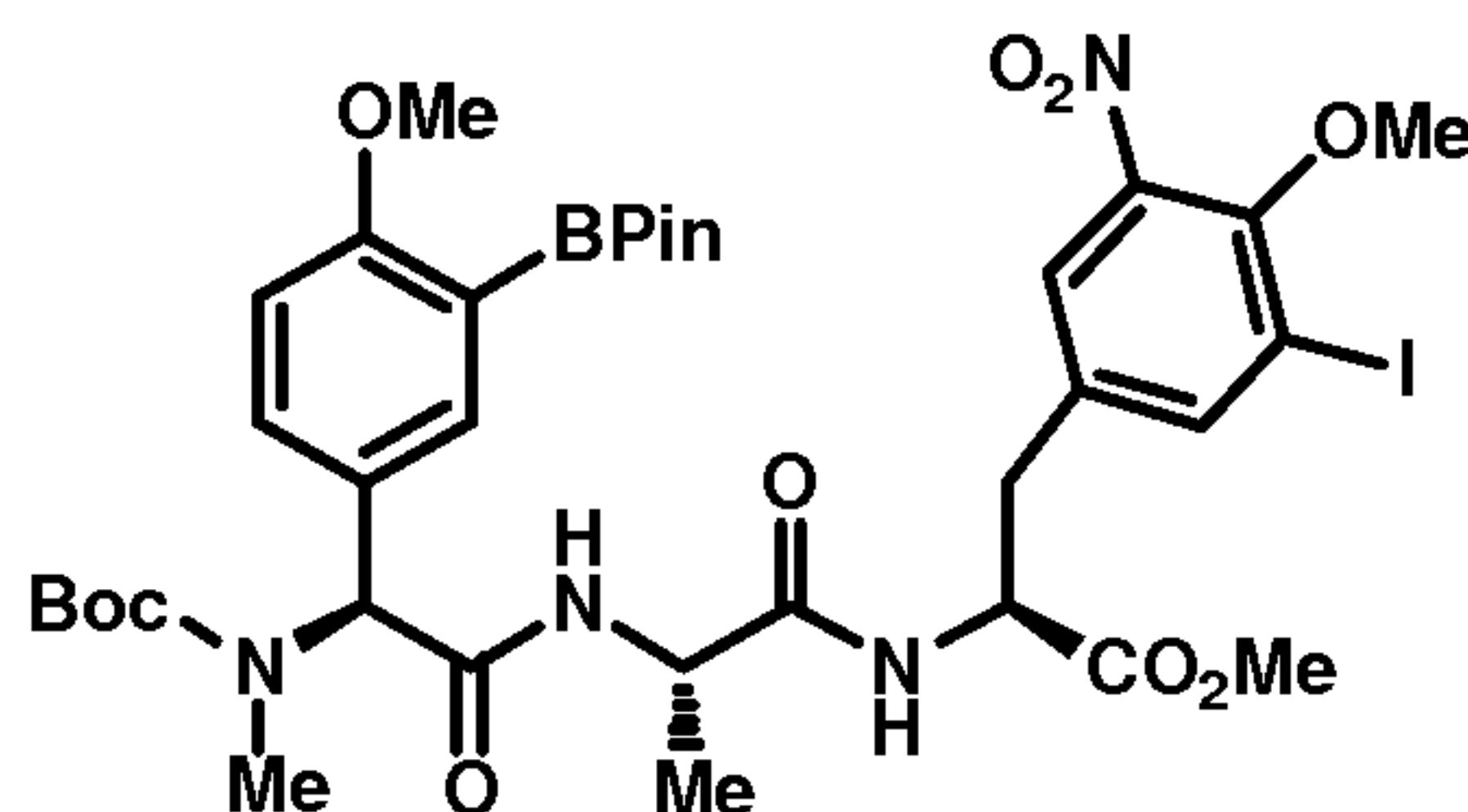
**5.8**

To a solution of compound **5.7** (300 mg, 0.74 mmol, 1 eq) in DMF (7.4 mL) was added sequentially H-Ala-OBn HCl (160 mg, 1 eq), EDC (170 mg, 1.2 eq), HOBt (100 mg, 1 eq) and NaHCO₃ (71 mg, 1.15 eq) and the reaction was allowed to stir overnight. Dilute NaHCO₃ was added and the aqueous phase was extracted 3x with EtOAc. The combined organic layers were washed with 5% citric acid (pH – 3), water and brine then dried over sodium sulfate and concentrated. The crude material (353 mg, 0.62 mmol, 1 eq) was taken up in acetone (6.2 mL) and to this solution was added K₂CO₃ (428 mg, 5 eq) and MeI (386 µL, 10 eq). The mixture was allowed to stir overnight at reflux in a sealed vial then the solvent was evaporated, water was added and the aqueous phase was extracted 3x with EtOAc. The combined organic layers were washed with brine, dried over sodium sulfate and concentrated. The crude material was purified via column chromatography (0.75% MeOH in DCM) to give the product (189 mg, 44% yield over 2 steps). ¹H NMR (CDCl₃, 600 MHz) δ (ppm) 7.80 (s, 1H), 7.37-7.29 (m, 6H), 6.74 (d, *J* = 8.4 Hz, 1H), 6.30 (d, *J* = 7.2 Hz, 1H), 5.74 (br s, 1H), 5.22-5.15 (m, 2H), 4.70-4.66 (m, 1H) 3.87 (s, 3H) 2.70 (s, 3H) 1.48 (s, 9H), 1.44 (d, *J* = 7.2 Hz, 3H). ¹³C NMR (CDCl₃, 600 MHz) δ (ppm) 172.6, 169.3, 158.2, 140.4, 135.4, 130.6, 129.3, 128.8, 128.6, 128.4, 114.2, 110.7, 86.2, 80.9, 67.4, 56.6, 55.4, 53.6, 48.5, 31.7, 28.5, 18.3. MS (ESI) *m/z* 605.1 (M + Na⁺).

**5.9**

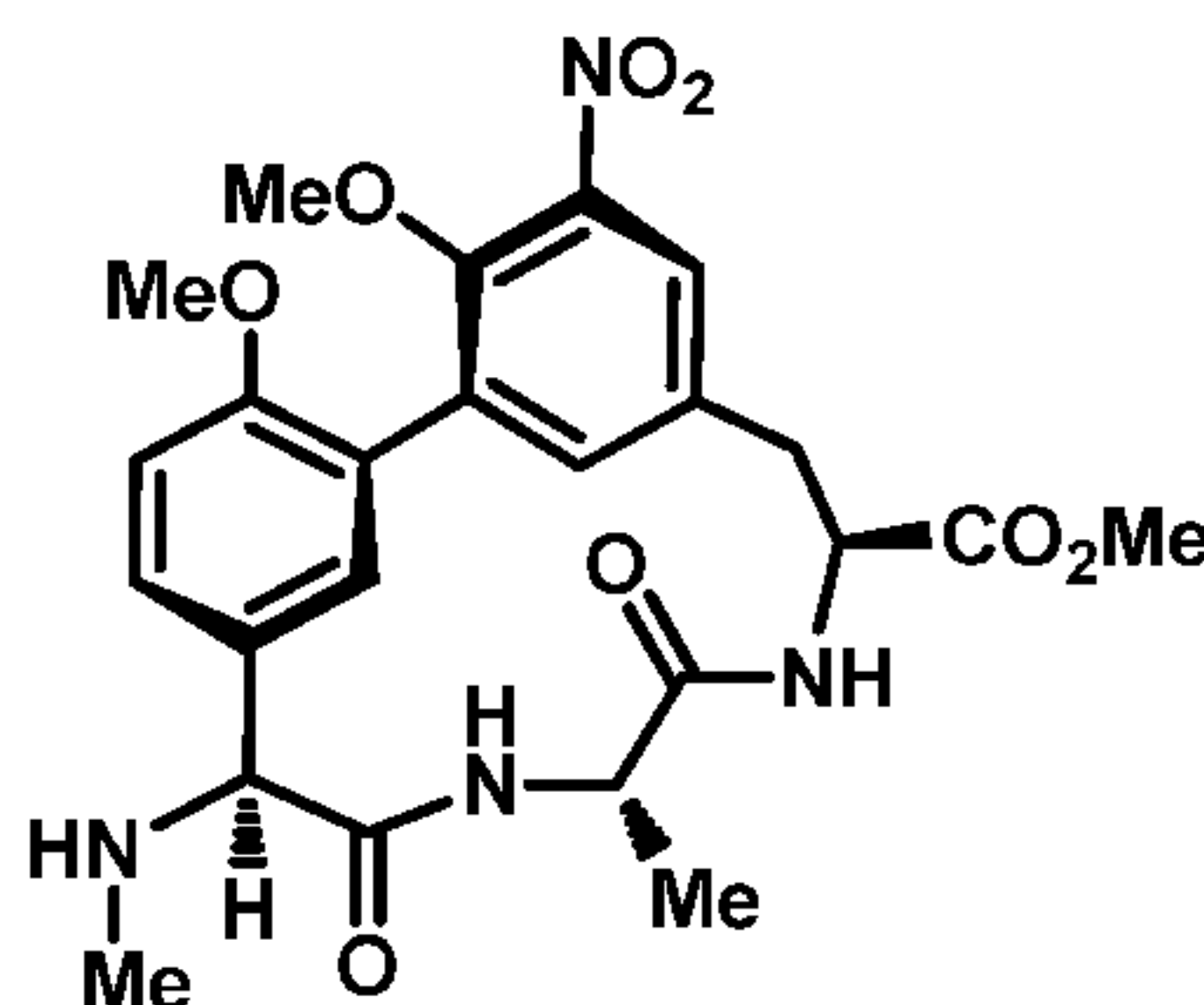
To a solution of compound **5.8** (185 mg, 0.36 mmol, 1 eq) in DMSO (7 mL) under Ar was added sequentially bispinacolatodiboron (95 mg, 1.05 eq), potassium acetate (353 mg, 10 eq) and PdCl₂(dppf) (15 mg, 0.05 eq). The mixture was allowed to stir for 2.5 hrs at 80° C then cooled to room temperature diluted with water and extracted 3x with EtOAc. The combined organic layers were washed with brine dried over sodium

sulfate and concentrated. The crude material was purified by abbreviated (to minimize the time of the compounds exposure to silica) column chromatography (35% EtOAc in Hex) giving compound **5.9** as a mixture of boronic acid and ester (118 mg, 64% yield). NMR spectra showed two sets of overlapping signals in a 3:1 ratio. ¹H NMR (CDCl₃, 600 MHz) δ (ppm) 7.61-7.59 (m, 1H), 7.37-7.31 (m, 5H), 6.81-6.76 (m, 1H), 6.31-6.18 (m, 1H), 5.74 (br, s), 5.20-5.12 (m, 2H), 4.73-4.66 (m, 1H), 3.83-3.80 (m, 3H), 2.68-2.67 (m, 3H) 1.47-1.40 (m, 12H), 1.34-1.33 (m, 9H). MS (ESI) m/z 605.3 (M + Na⁺).



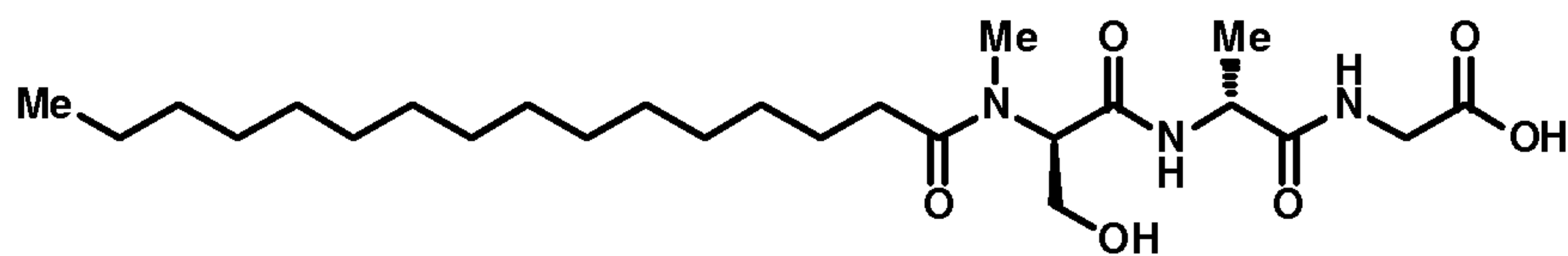
5.11

Compound **5.9** (118 mg, 0.19 mmol, 1 eq) was taken up in 95% EtOH (2 mL), 10% Pd/C (38 mg, 1/3 by weight) was added and the mixture was placed under an atmosphere of H₂. The reaction was allowed to proceed until TLC analysis indicated the complete consumption of starting material. The mixture was then filtered through celite and concentrated to yield compound **5.11**. To a solution of this crude material (94 mg, 0.19 mmol, 1 eq) and compound **5.6** (101 mg, 0.27 mmol, 1.4 eq) in AcCN:DMF (2.2:1, 2mL) was added sequentially HOBt (64 mg, 2.5 eq) and EDC (80 mg, 2.2eq) and the reaction was allowed to stir overnight. Dilute NaHCO_{3(aq)} was then added to the reaction and the aqueous phase was extracted 3x with EtOAc. The combined organic layers were washed with 5% citric acid, water and brine then dried over sodium sulfate and concentrated. The crude material was purified via abbreviated column chromatography (3% MeOH in DCM) to give a semi-pure product (130 mg, 80%). MS (ESI) m/z 877.2 (M + Na⁺).

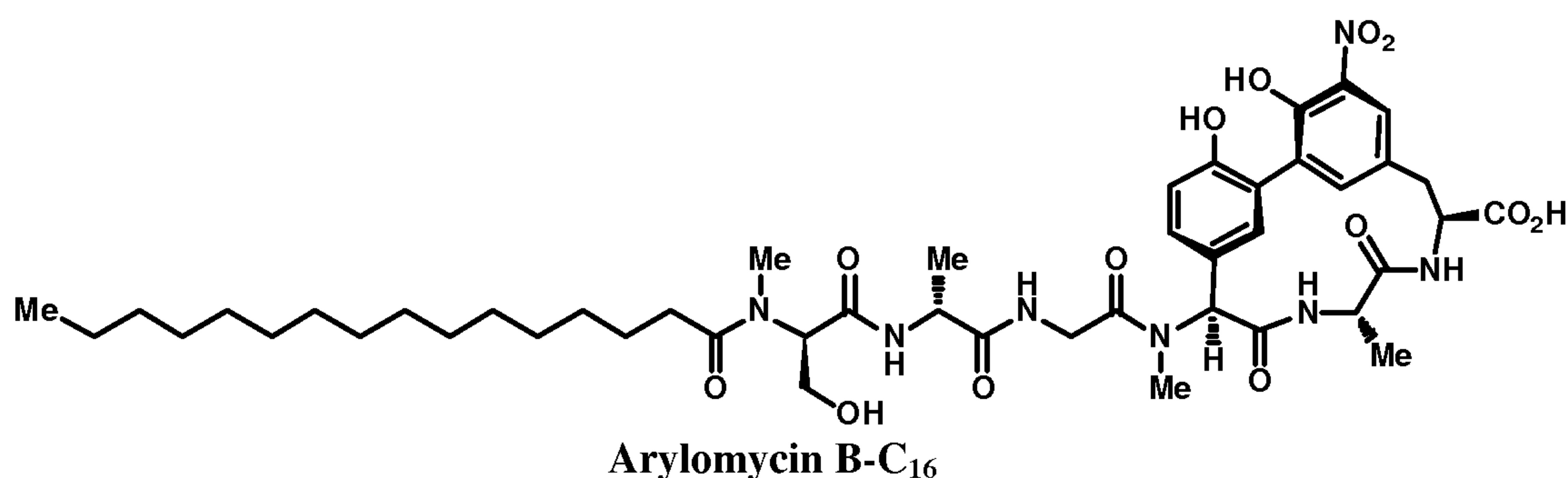


5.12

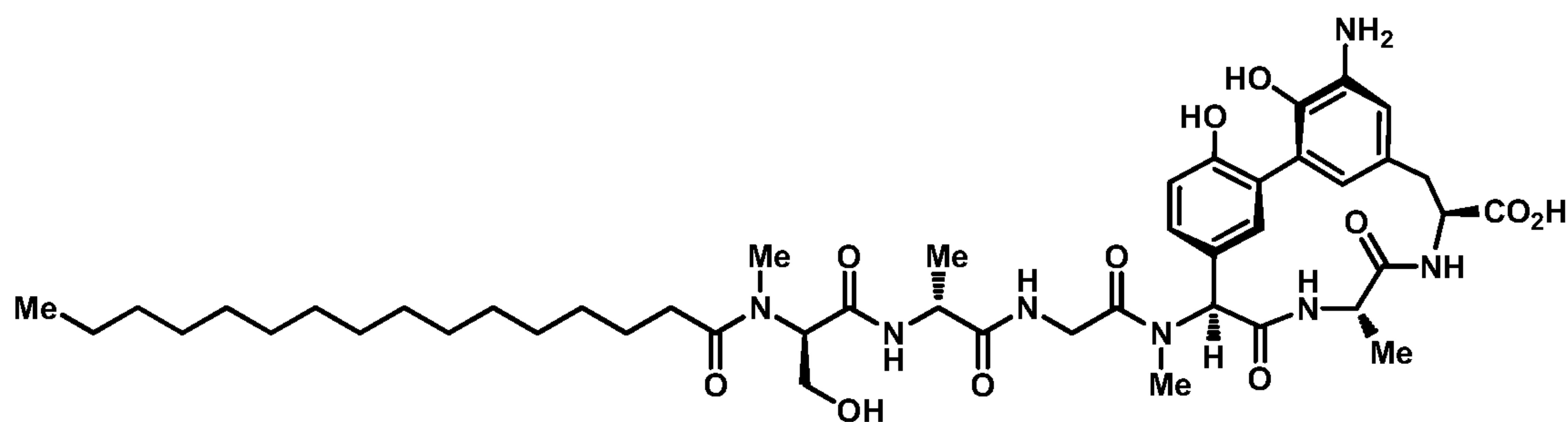
A solution of compound **5.11** (118 mg, 0.14 mol, 1 eq) and NaHCO₃ (118 mg, 10 eq) in DMF (4.2 mL) was purged several times via cycling with vacuum and Ar and sealed with a crimped septa. To this solution was added, via syringe, a solution of PdCl₂(dppf) (23.0 mg, 0.2 eq) in DMF (2.8 mL) that had been sparged with Ar for ~15 minutes. The resulting mixture was submitted to several more cycles of vacuum and Ar then heated to 80° C. The mixture was cooled to room temperature and water was added. The aqueous phase was extracted with EtOAc 3x then washed with water and brine, dried over sodium sulfate and concentrated. The crude material was subjected to abbreviated column chromatography (4% MeOH in DCM) to remove most of the Pd species then used without further purification. The resulting semi-pure material (83 mg) was taken up in DCM (4.0 mL) and treated with TFA (0.8 mL). The reaction was monitored via TLC and when starting material was no longer present the volatiles were blown off under a stream of nitrogen. DCM was added and blown off under nitrogen twice more and the crude residue was dissolved EtOAc. The organic layer was washed with saturated NaHCO₃, dried over sodium sulfate and concentrated. The crude material was purified via pipette column chromatography (9% MeOH in DCM) to give the product (29.7 mg, 42% yield). MS (ESI) m/z 501.1 (M + H⁺).

**5.12**

Compound **5.12** was synthesized via standard Fmoc/piperidine solid phase peptide synthesis. Fmoc-Gly-OH was loaded onto chlorotrityl chloride resin with DIEA, then the constituent amino acids, Fmoc-d-Ala-OH and Fmoc-N-Me-d-Ser-OH were coupled to the resin using HCTU/HOBT/DIEA in DMF followed by palmitic acid coupling with HCTU/HOBT/DIEA in DMF and enough DCM to completely dissolve the acid. Cleavage from the resin was achieved using 1% TFA in DCM using protocols detailed in the Novabiochem catalogue. The product was purified via HPLC (linear gradient, 0.66% B per minute, product eluted at 97% B).



To a solution of Compound **5.12** (29.2 mg, 58.4 μ mol) and compound **5.12** (50 mg, 1.5 eq) in THF (0.5 mL) at 0° C was added DEPBT (28.0 mg, 1.6 eq) and NaHCO₃ (5.0 mg, 1 eq). The reaction was then allowed to warm to room temperature and stirred overnight. The THF was then blown off under a stream of nitrogen and the reaction was dried under vacuum. The crude reaction mixture was taken up in EtOAc, washed 2x with saturated NaHCO₃, then brine, dried over sodium sulfate and concentrated. The crude was purified via column chromatography (3% MeOH in DCM then 4.5% MeOH in DCM) to give the protected arylomycin. The protected arylomycin (10.0 mg, 9.4 μ mol, 1 eq) was dissolved in CHCl₃ (2 mL) treated with ethanethiol (180 μ L, 250 eq) and 1.0 M AlBr₃ in CH₂Br₂ (189 μ L, 20 eq) and stirred in a vial open to air for 6 hrs. The reaction was quenched by the addition of MeOH and the volatiles were blown off under a stream of nitrogen. The crude was taken up in MeOH and dried twice more to remove lingering ethanethiol then it was dissolved in MeOH centrifuged and purified via HPLC (linear gradient, 1.0% B per minute, product eluted at 82% B) to give the product (5.8 mg, 67% yield). ESI HRMS calcd for C₄₇H₇₀N₆O₁₁ [(M+H)⁺] 926.4869, found 926.4873.



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The protected arylomycin (6.3 mg, 6.0 μ mol, 1 eq) was dissolved in ethanethiol (300 μ L) and 1.0 M AlBr₃ in CH₂Br₂ (120 μ L, 20 eq) and stirred in a vial for 5 hrs under Ar. The reaction was quenched by the addition of MeOH and the volatiles were blown off under a stream of nitrogen. The crude was taken up in MeOH and dried twice more

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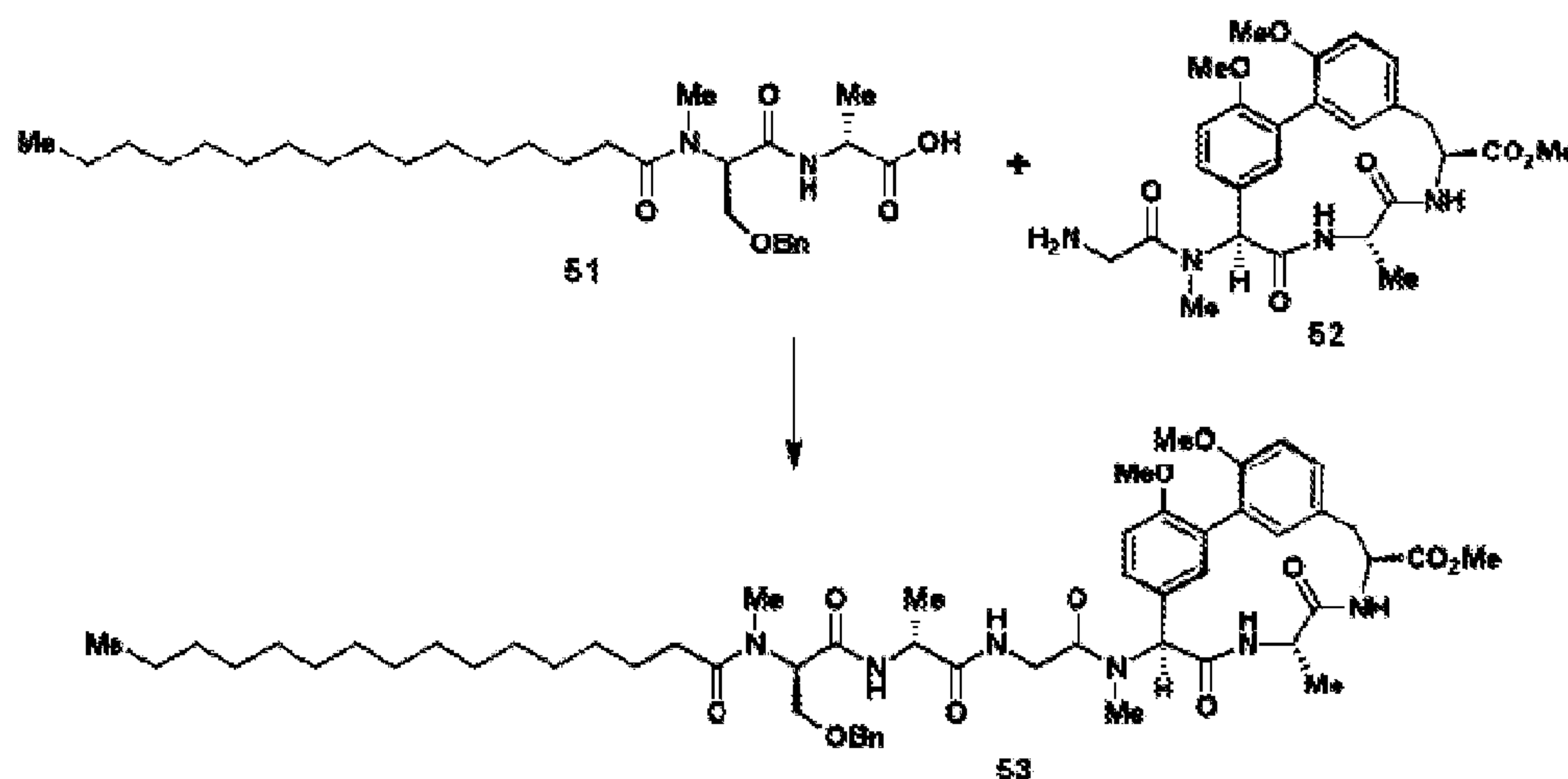
to remove lingering ethanethiol then it was dissolved in MeOH centrifuged and purified via HPLC (linear gradient, 1.0% B per minute, product eluted at 75% B) to give the product (1.0 mg, 19% yield). ESI HRMS calcd for $C_{47}H_{70}N_6O_{11}$ $[(M+H)^+]$ 896.5128, found 896.5123.

5

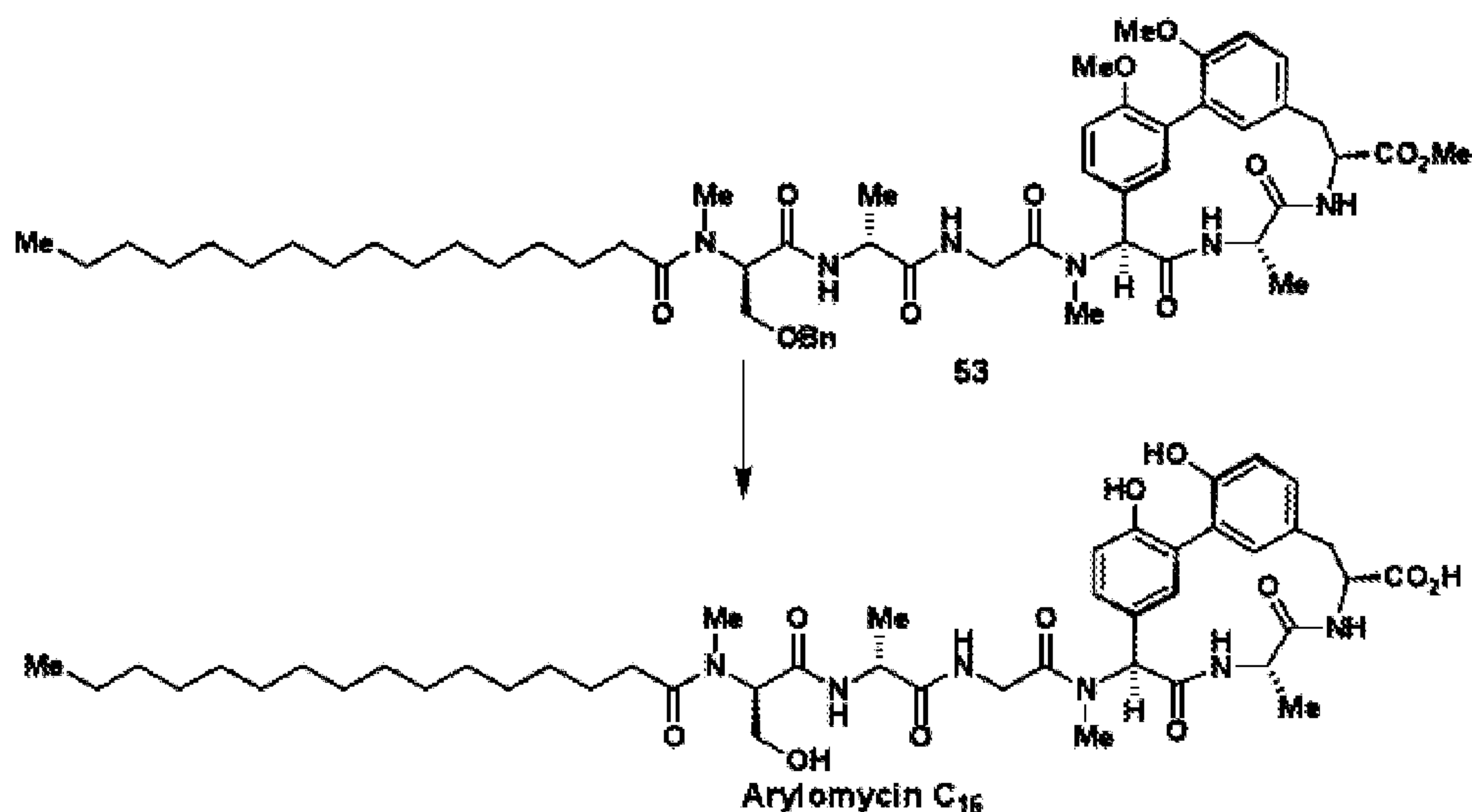
General Procedure D: Macrocycle and Tail Coupling, Example - Arylomycin C16

Compound **52** (80 mg, 0.16 mmol) was taken up in AcCN (7.2 mL) and DMF (3.2 mL) and treated sequentially with HOBt (64 mg, 3 eq), compound **51** (81.3 mg, 1 eq) and EDC (90.3 mg, 3 eq). The reaction was allowed to stir overnight, after which water, saturated $NaHCO_3$, and EtOAc were added, the aqueous phase was extracted 3x with EtOAc and the combined organic layers were washed with 5% citric acid (pH – 3) and brine. The organics were dried over sodium sulfate and concentrated. The crude was purified by column chromatography (5.5% MeOH in DCM) to give the product **53** (72.4 mg, 45% yield).

15

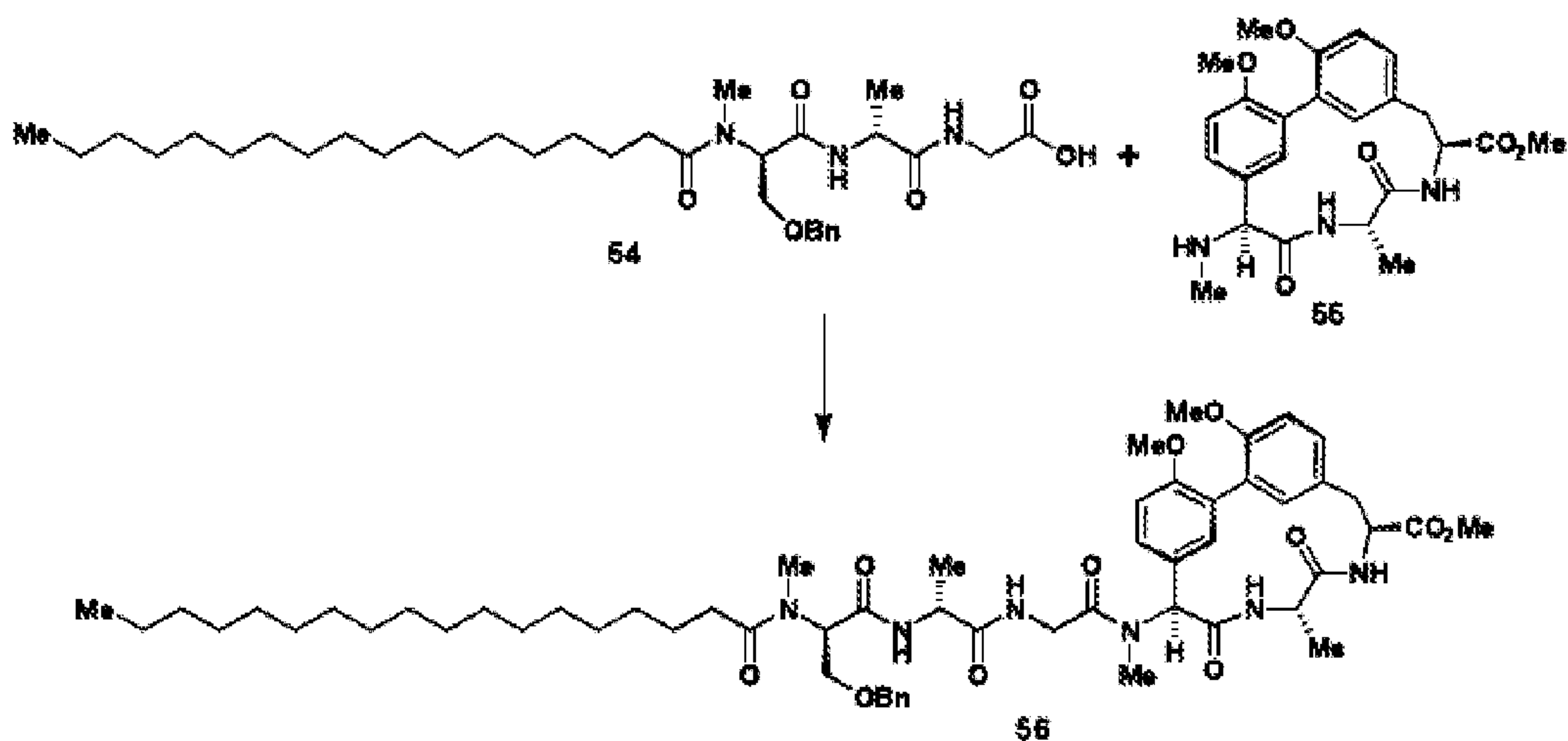


General Procedure E: Global Deprotection, Example- Arylomycin C16



Compound **53** (72.4 mg, 72 μ mol, 1 eq) was dissolved in ethanethiol (2 mL) under Ar and treated with 1.0 M AlBr₃ in CH₂Br₂ (1.79 mL, 25 eq). The reaction vial was sealed and heated to 50 °C and stirred for 4 h. The reaction was cooled to room temperature, MeOH was added (0.5 mL) and the volatiles were blown off under a stream of nitrogen. MeOH was added again and was blown off under a stream of nitrogen and the crude product was dried under vacuum. The crude product was then dissolved in MeOH and purified by HPLC (linear gradient, 0.67% B/ min, product eluted at 80% B) to give Arylomycin C₁₆. (32.6 mg, 51% yield). ESI HRMS calcd for C₄₆H₆₉N₆O₁₁ [(M+H)⁺]: 881.5019, found: 881.5021

General Procedure F: Macrocycle and Tail Coupling Example - Compound 56:



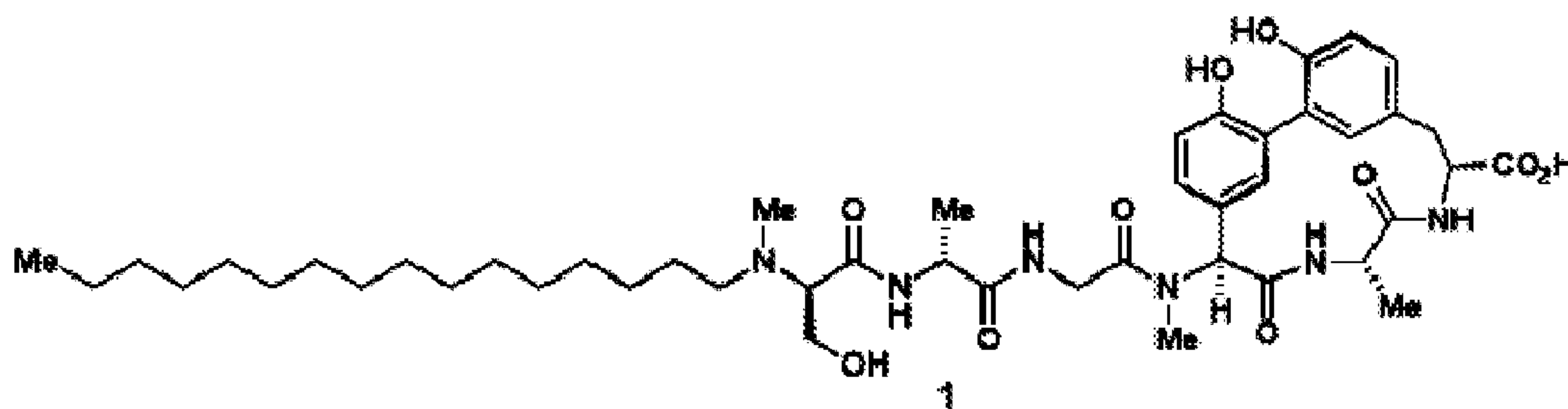
This procedure is based on the conditions previously reported.⁹ Compound **53** (23.5 mg, 52 μ mol, 1 eq) and compound **54** (70 mg, 2.2 eq) were dissolved in THF (2 mL) under Ar and treated with TEA (7 μ L, 1 eq) and DEPBT (39 mg, 2.5 eq). The

reaction was allowed to stir overnight then the volatiles were blown off under a stream of nitrogen, the residue was dried under vacuum, and EtOAc and saturated NaHCO₃ were added. The aqueous layer was extracted, then the organic layer was washed with 0.1N HCl, dried over sodium sulfate and concentrated.

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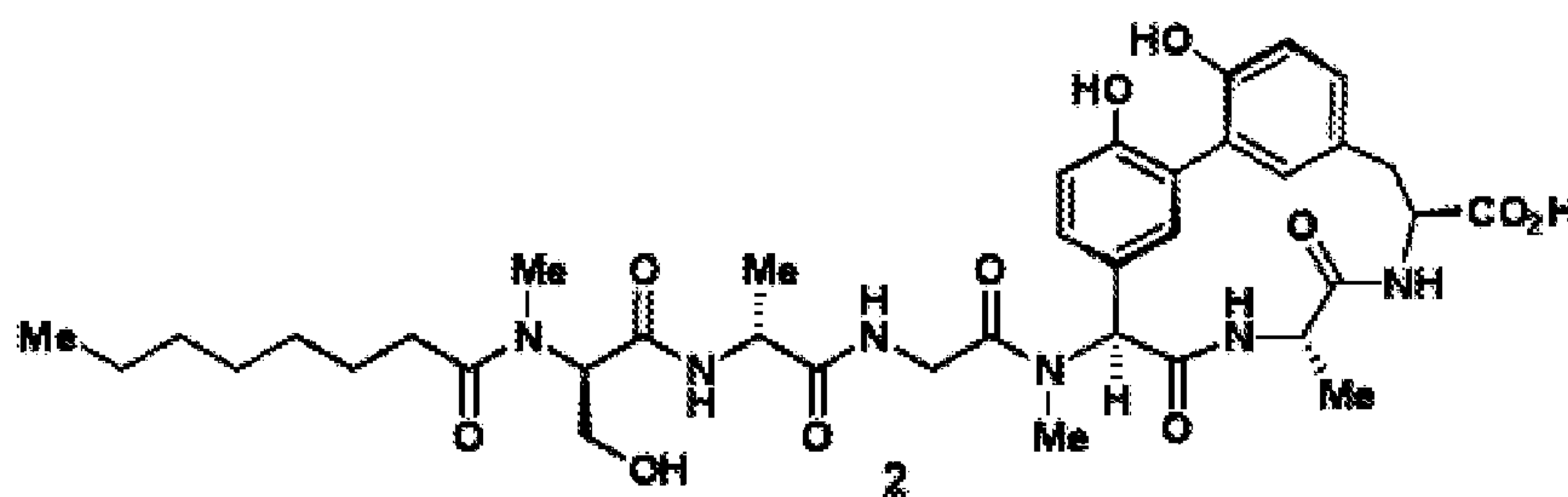
Compound **1** was synthesized using general procedures D and E.

ESI HRMS calcd for C₄₆H₇₀N₆O₁₀ [(M + H)⁺]: 867.5226, found: 867.5207.



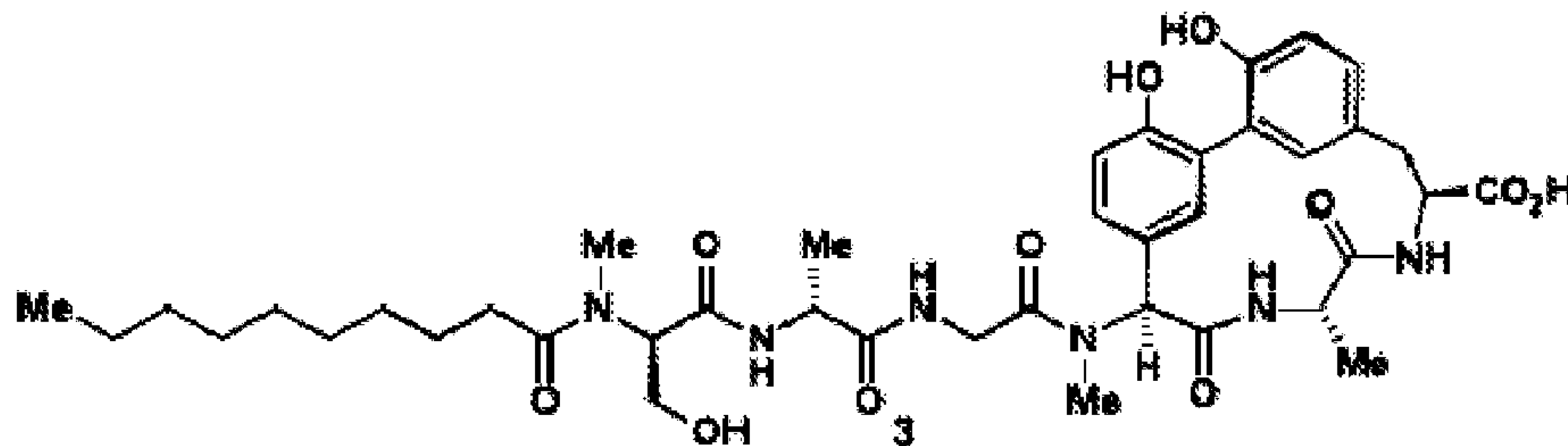
10 Compound **2** was synthesized using general procedures D and E.

ESI HRMS calcd for C₃₈H₅₃N₆O₁₁ [(M + H)⁺]: 769.3767, found: 769.3770.



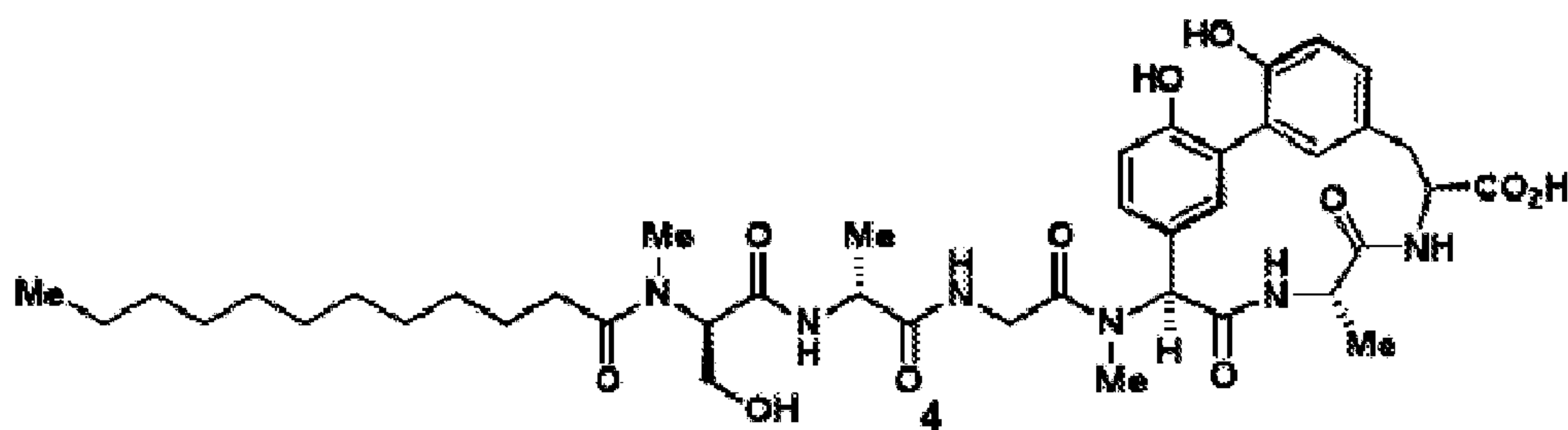
Compound **3** was synthesized using general procedures D and E.

15 ESI HRMS calcd for C₄₀H₅₇N₆O₁₁ [(M + H)⁺]: 797.408, found: 797.4070



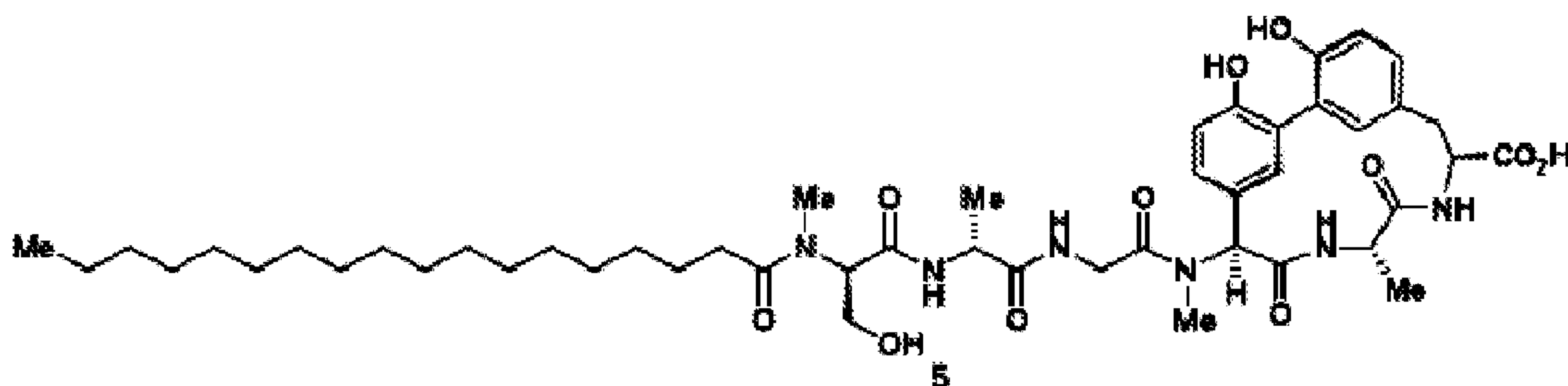
Compound **4** was synthesized using general procedures D and E.

ESI HRMS calcd for C₄₂H₆₁N₆O₁₁ [(M + H)⁺]: 825.4393, found: 825.4386



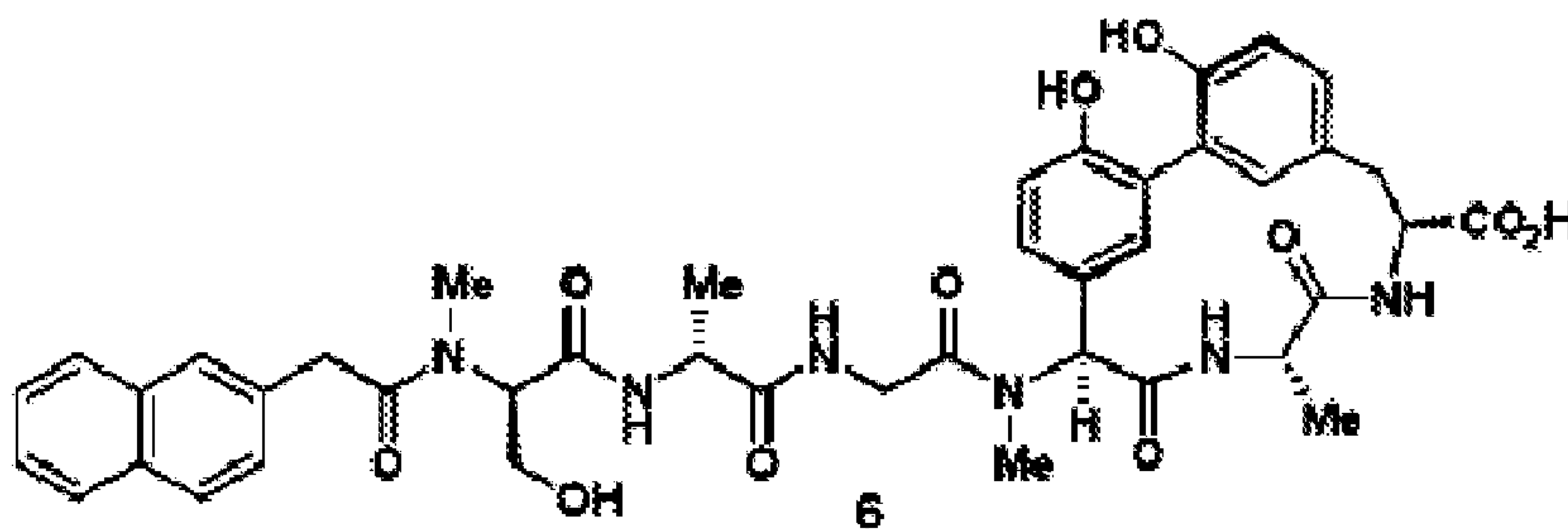
Compound **5** was synthesized as shown above then subjected to general procedure F to give the product (20.6 mg, 58% yield).

ESI HRMS calcd for C₄₈H₇₂N₆O₁₁ [(M + H)⁺]: 909.5332, found: 909.5328.



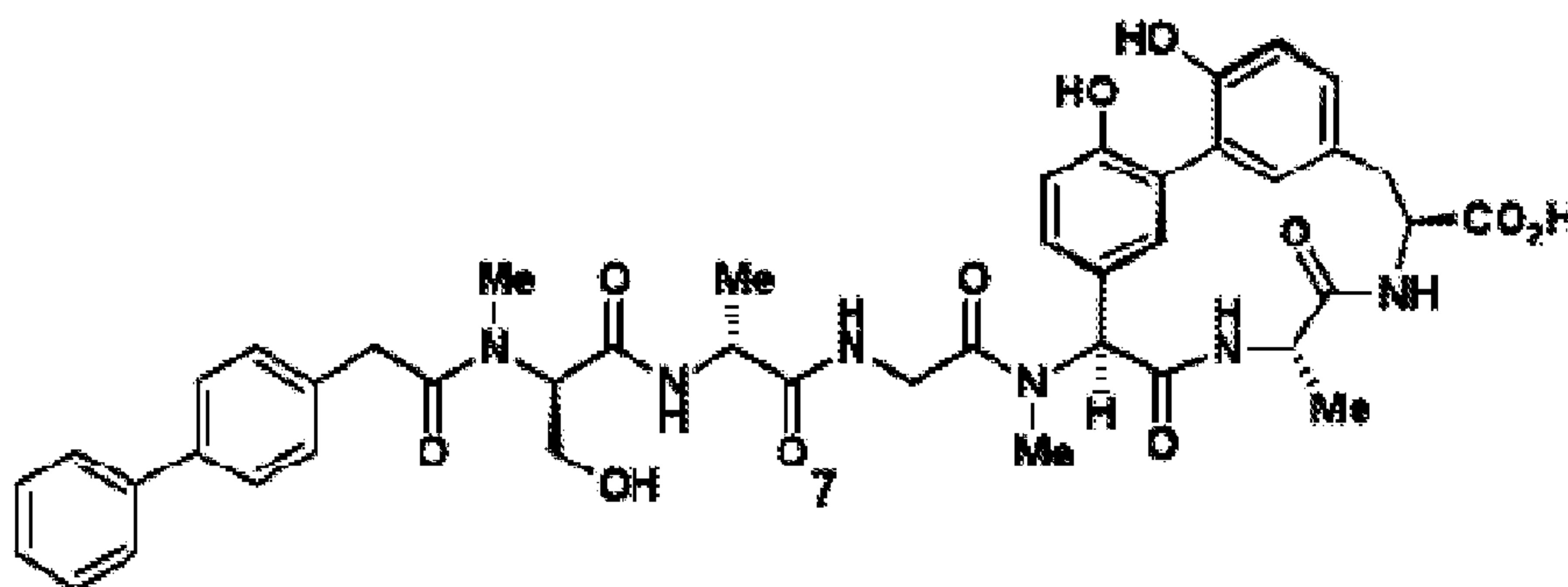
5

Compound **6** was synthesized using general procedures D and E. ESI HRMS calcd for C₄₃H₅₄N₆O₁₁ [(M + H)⁺]: 811.3297, found: 811.3300



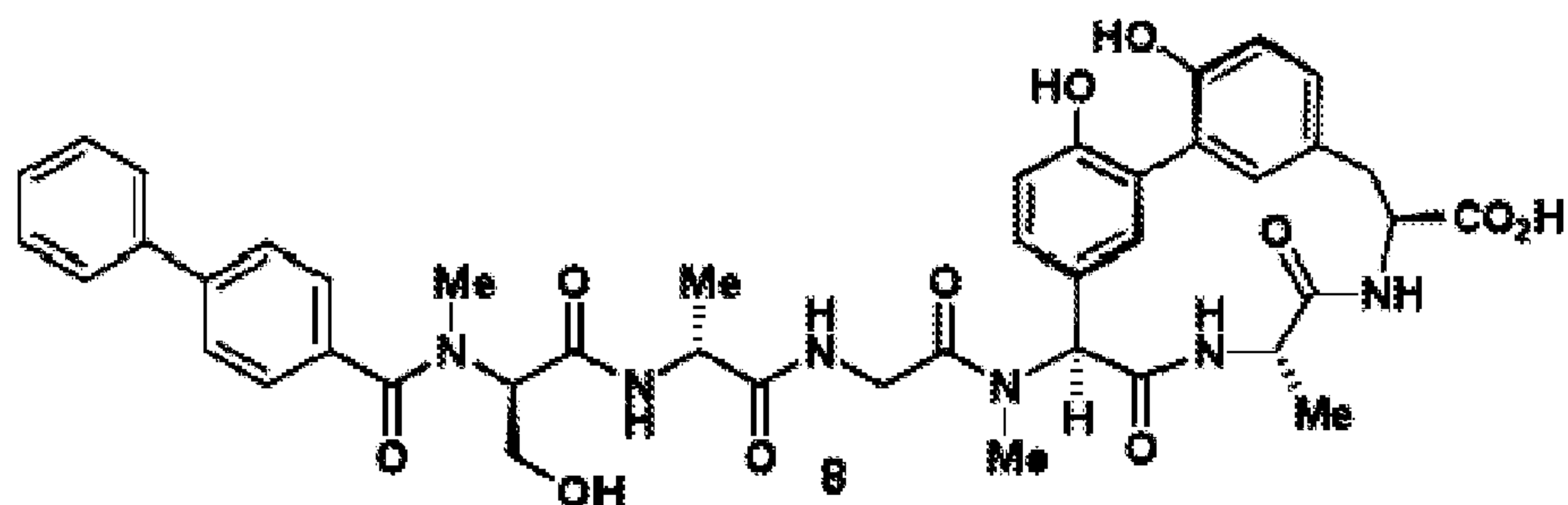
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Compound **7** was synthesized using general procedures D and E. ESI HRMS calcd for C₄₄H₄₈N₆O₁₁ [(M + H)⁺]: 837.3454, found: 837.3443



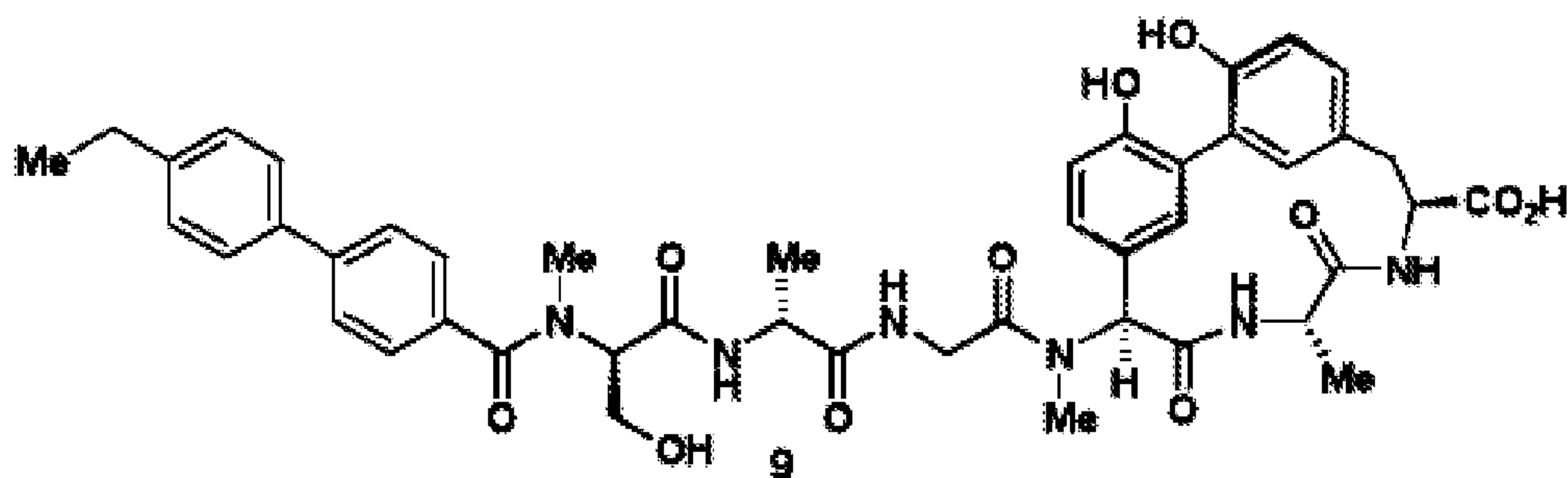
15 Compound **8** was synthesized using general procedures D and E.

ESI HRMS calcd for C₄₃H₄₆N₆O₁₁ [(M + H)⁺]: 823.3297, found: 823.3296



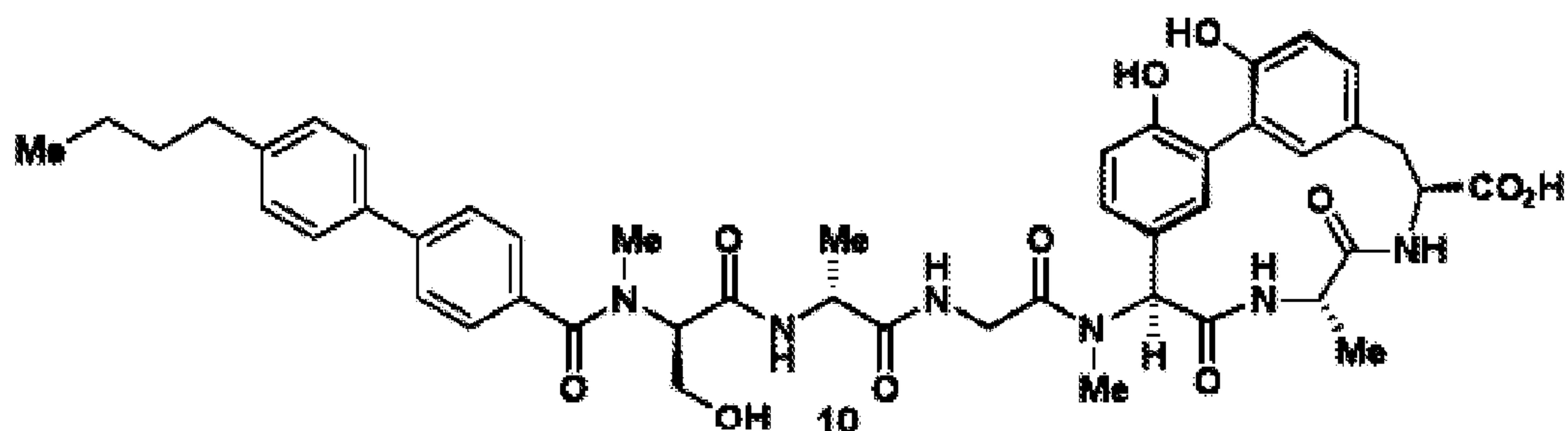
Compound **9** was synthesized using general procedures D and E.

5 ESI HRMS calcd for C₄₅H₅₀N₆O₁₁ [(M + H)⁺]: 851.361, found: 851.359



Compound **10** was synthesized using general procedures D and E.

ESI HRMS calcd for C₄₇H₅₄N₆O₁₁ [(M + H)⁺]: 879.3923, found: 879.3924

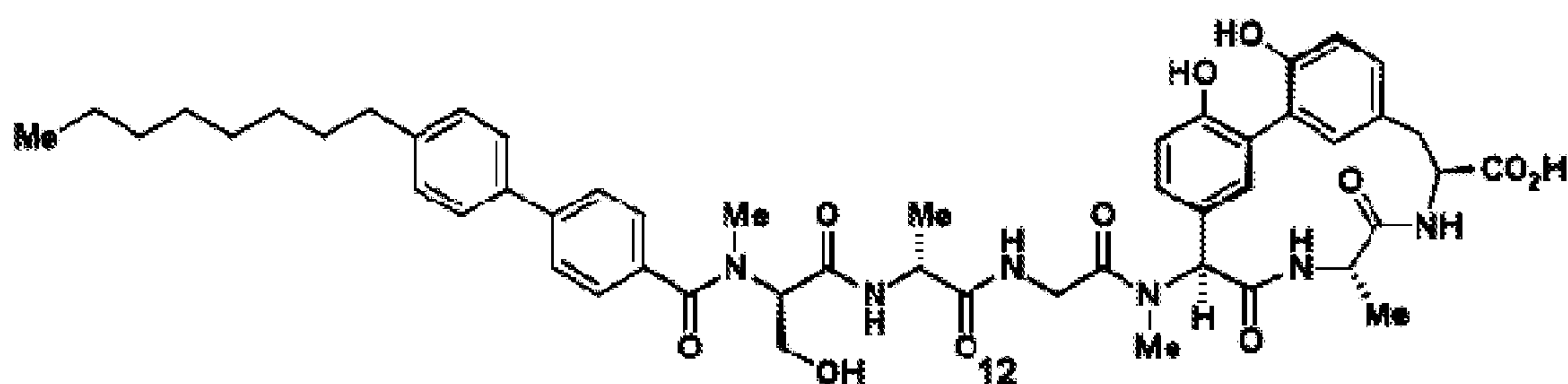


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Compound **11** was synthesized using general procedures D and E.

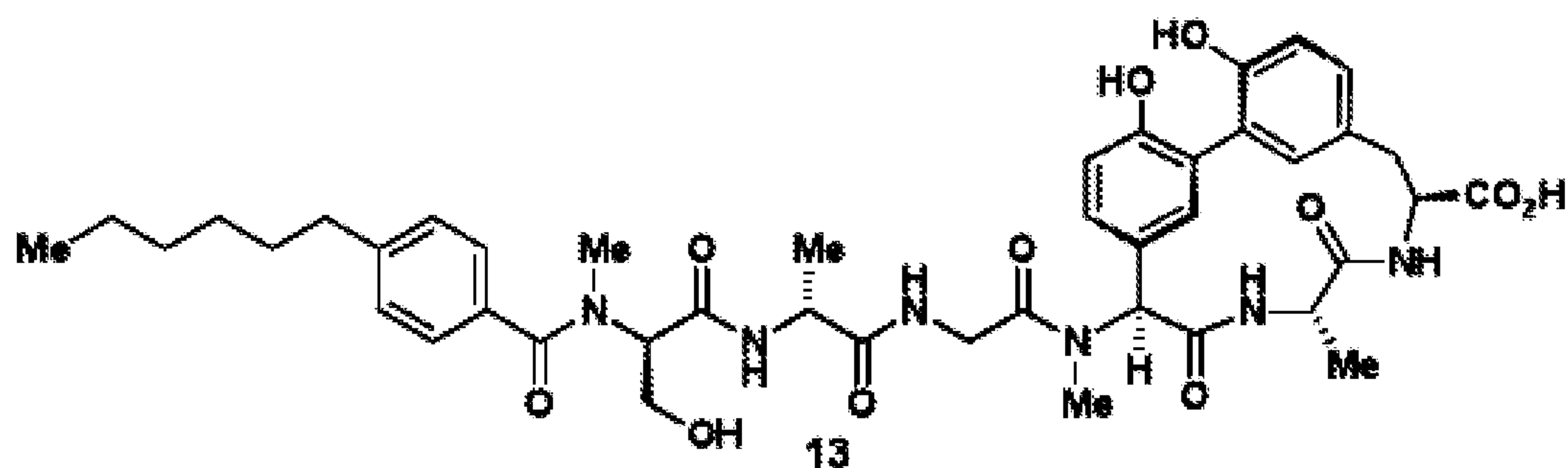
ESI HRMS calcd for C₄₉H₅₈N₆O₁₁ [(M + H)⁺]: 907.4236, found: 907.4246

ESI HRMS calcd for C₅₁H₆₂N₆O₁₁ [(M + H)⁺]: 935.4549, found: 935.4548



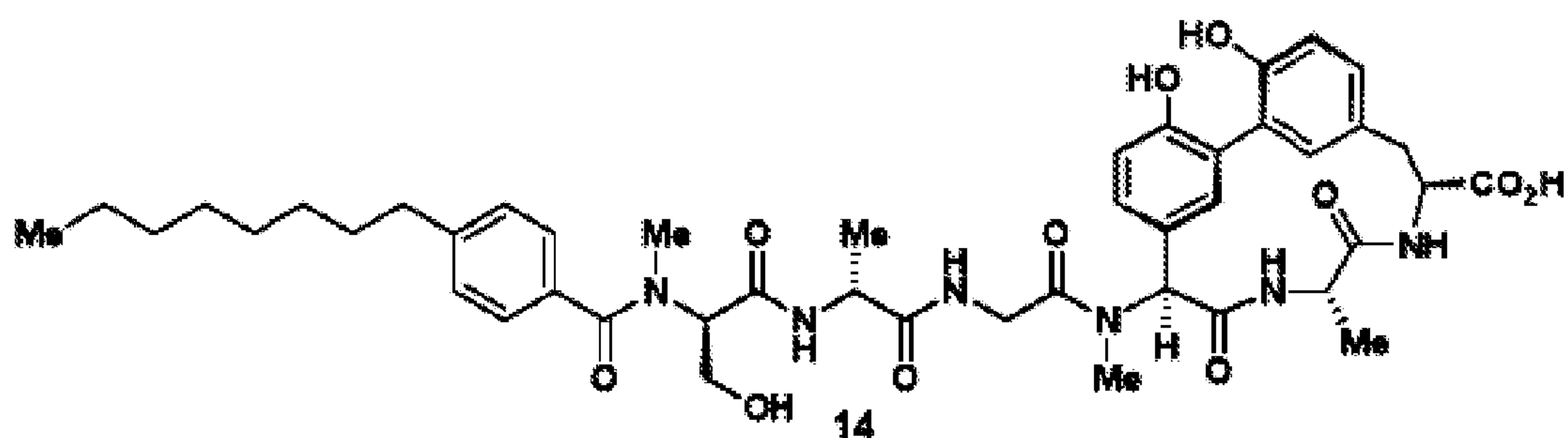
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Compound **13** was synthesized using general procedures D and E. ESI HRMS calcd for C₄₃H₅₄N₆O₁₁ [(M + H)⁺]: 831.3923, found: 831.3917

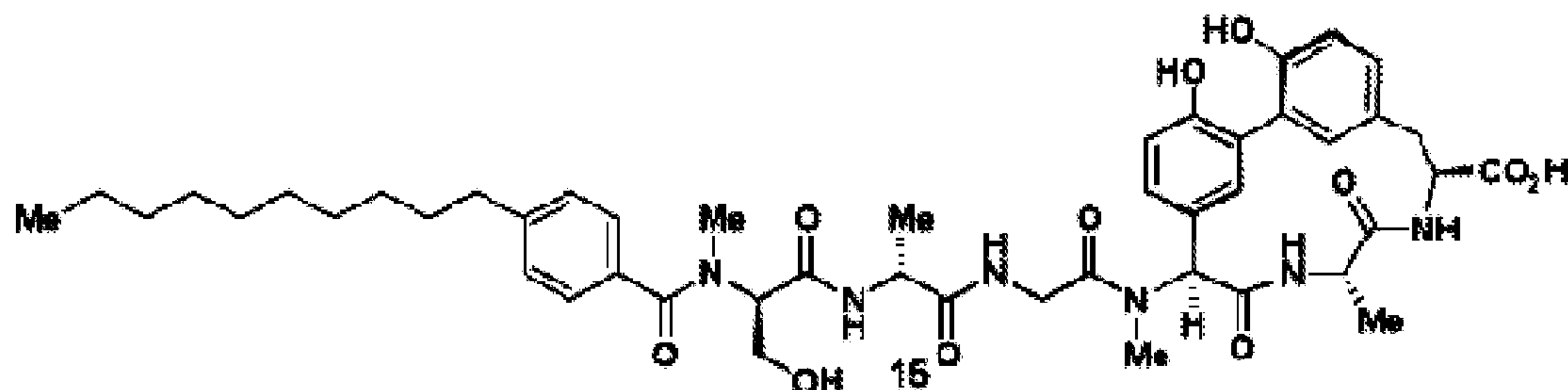
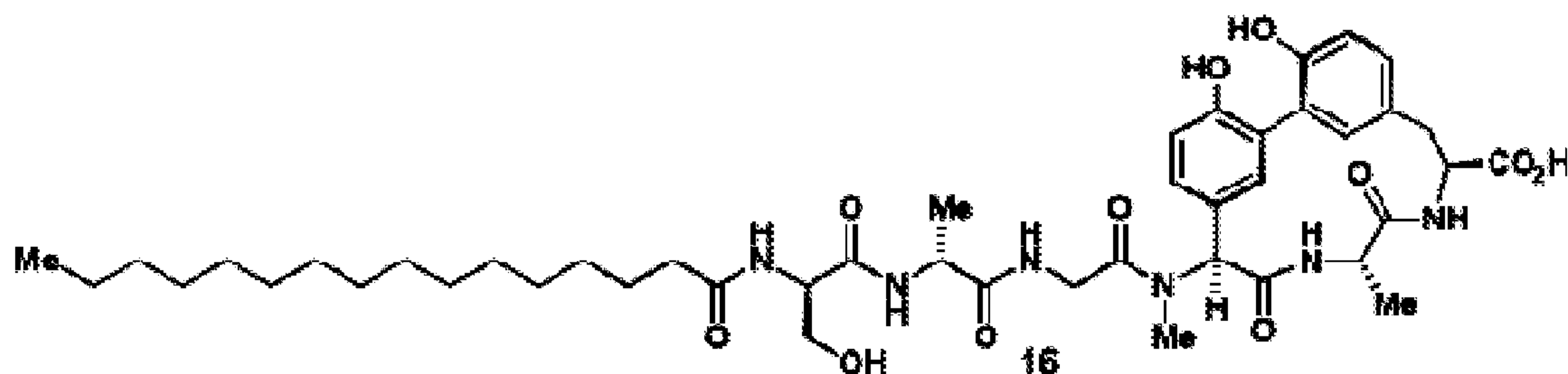


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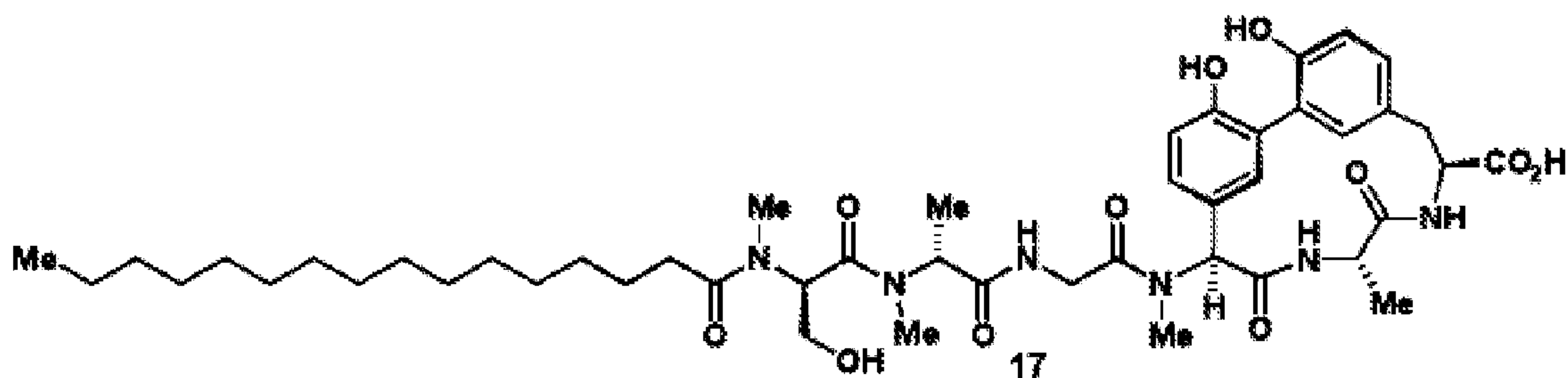
Compound **14** was synthesized using general procedures D and E.

ESI HRMS calcd for C₄₅H₅₈N₆O₁₁ [(M + H)⁺]: 859.4236, found: 859.4231

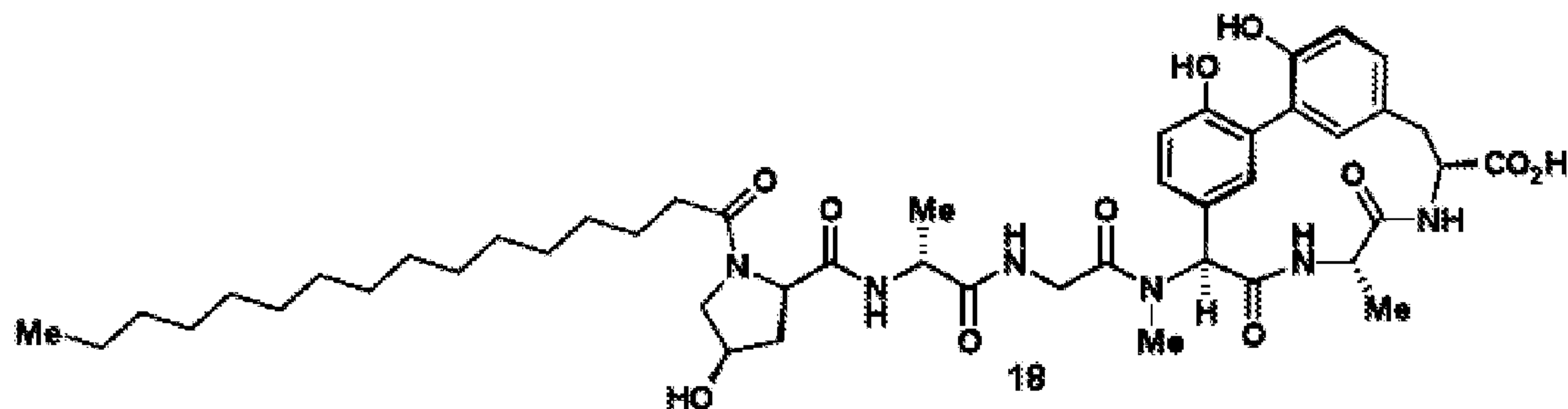
ESI HRMS calcd for C₄₇H₆₂N₆O₁₁ [(M + H)⁺]: 887.4549, found: 887.4539

ESI HRMS calcd for C₄₅H₆₆N₆O₁₁ [(M + H)⁺]: 867.4862, found: 867.4873

10 ESI HRMS calcd for C₄₇H₇₀N₆O₁₀ [(M + H)⁺]: 895.5175, found: 895.5190

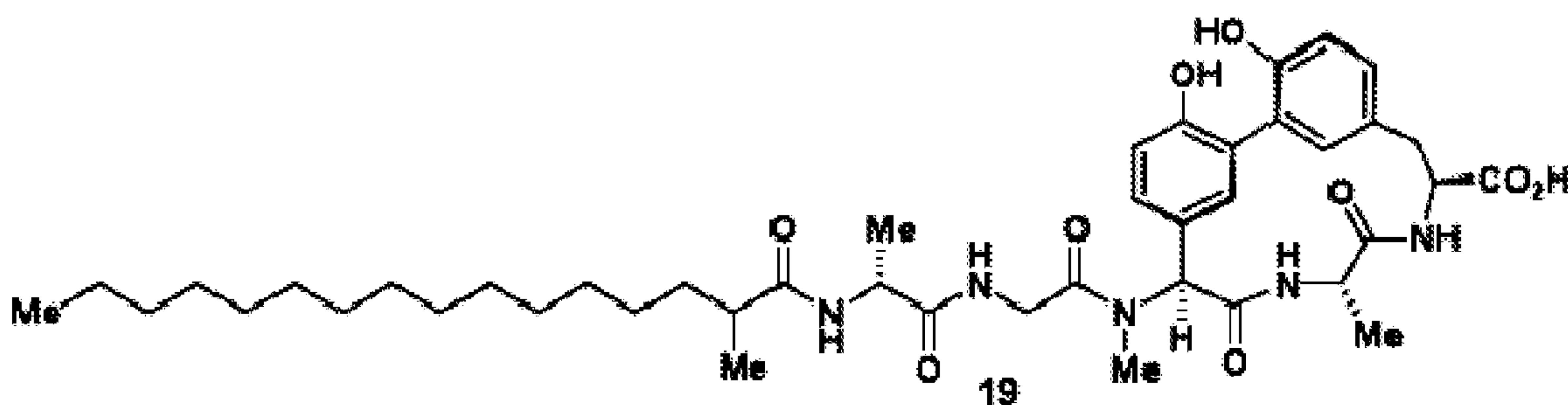


ESI HRMS calcd for C₄₇H₆₈N₆O₁₁ [(M + H)⁺]: 893.5019, found: 893.5014



Diastereomer A of compound **19** was synthesized using general procedures D and E..

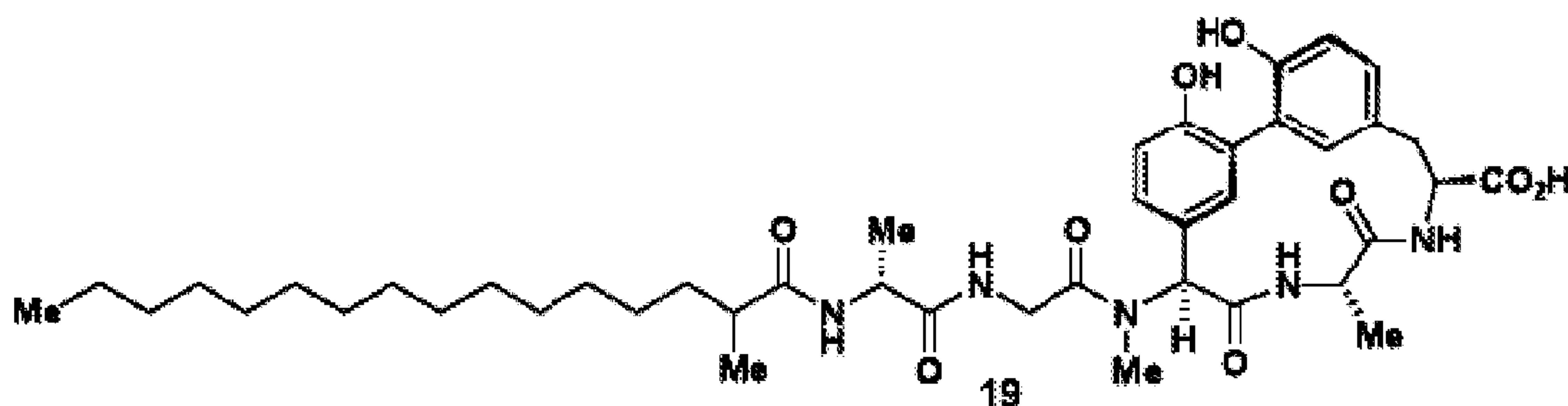
ESI HRMS calcd for C₄₃H₆₃N₅O₉ [(M + H)⁺]: 794.4698, found: 794.4705



5

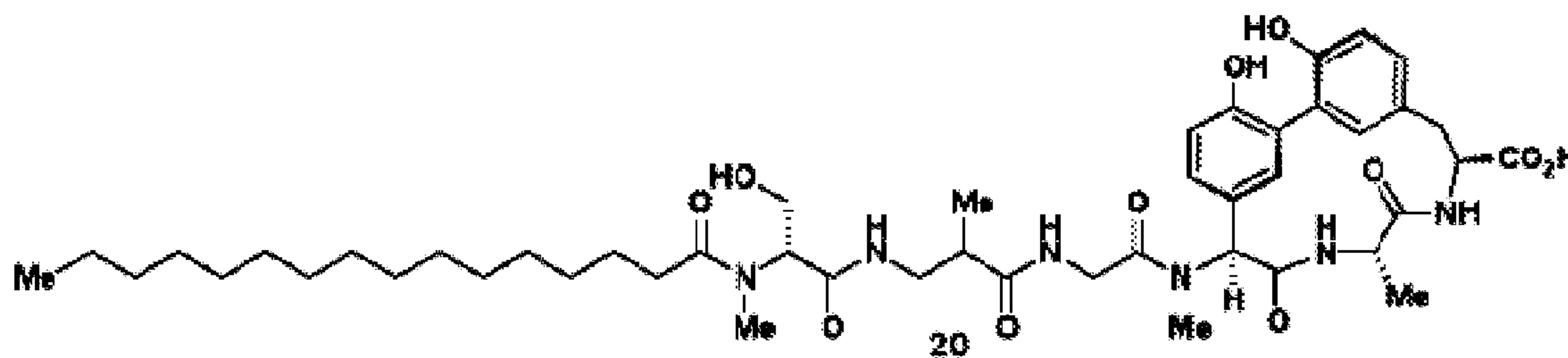
Diastereomer B of compound **19** was synthesized using general procedures D and E.

ESI HRMS calcd for C₄₃H₆₃N₅O₉ [(M + H)⁺]: 794.4698, found: 794.4689



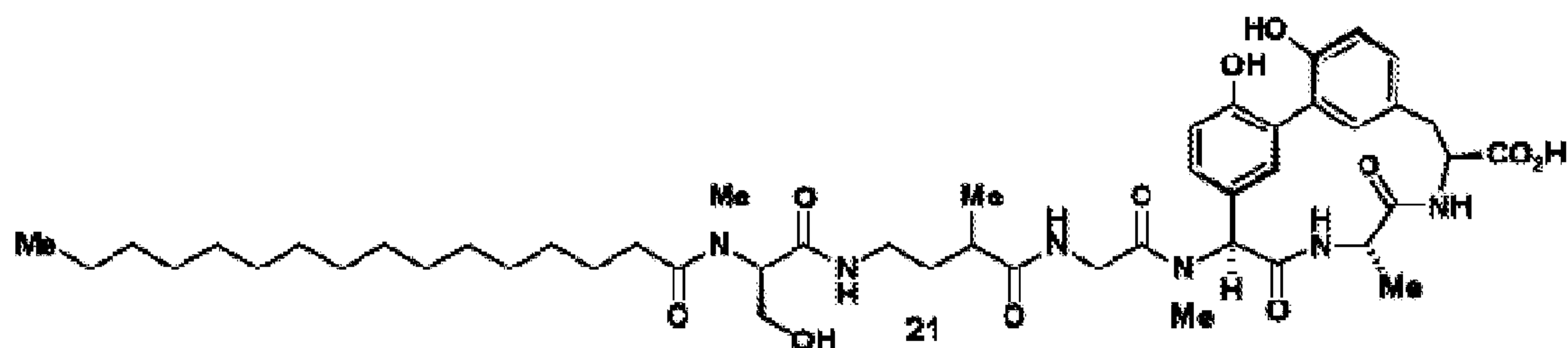
10 Compound **20** was synthesized racemically using general procedures E and F.

ESI HRMS calcd for C₄₇H₇₀N₆O₁₁ [(M + H)⁺]: 895.5175, found: 895.5180



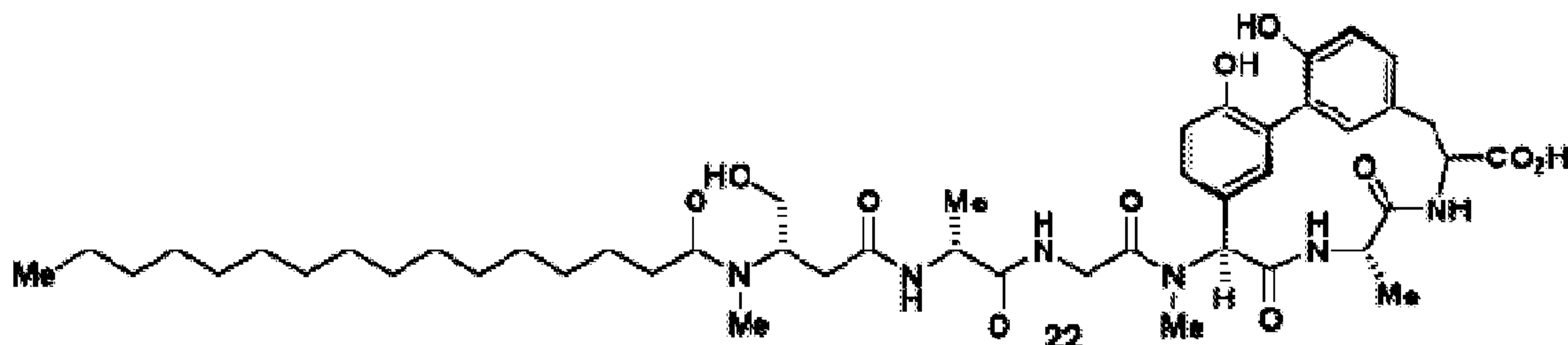
Compound **21** was synthesized racemically using general procedures E and F. ESI

15 HRMS calcd for C₄₈H₇₂N₆O₁₁ [(M + H)⁺]: 909.5332, found: 909.5334



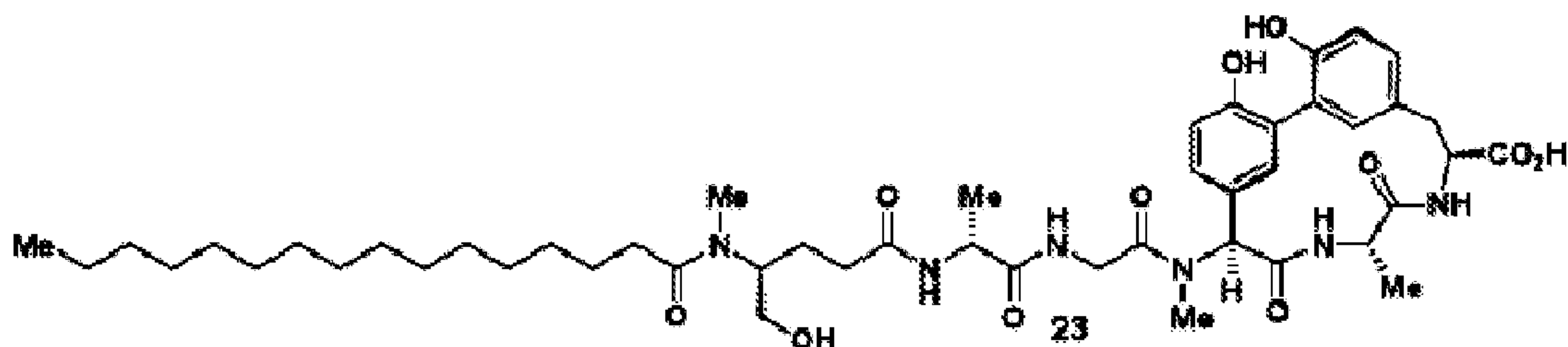
Compound **22** was synthesized using general procedures D and E..

ESI HRMS calcd for C₄₇H₇₀N₆O₁₁ [(M + H)⁺]: 895.5175, found: 895.5178



Compound **23** was synthesized using general procedures D and E.

ESI HRMS calcd for C₄₈H₇₂N₆O₁₁ [(M + H)⁺]: 909.5332, found: 909.5305.



Example 2: Bacteriological Materials and Methods

This Example illustrates procedures for testing and manipulating the response of bacteria to arylomycins.

Strains and Culture Conditions

Standard methods were used to culture bacteria for all experiments and to construct mutant strains. *Escherichia coli* MG1655, *Pseudomonas aeruginosa* PAO1, and *Klebsiella pneumoniae* ATCC 43816 were grown in Luria-Bertani (LB) broth at 37 °C. *Yersinia pestis* Kim+6 was grown in LB broth at 28 °C. *Staphylococcus epidermidis* RP62A, *Staphylococcus haemolyticus*, a clinical isolate obtained from the London Health Services Centre, London, Ontario, Canada, *Staphylococcus aureus* NCTC 8325, and *Corynebacterium efficiens* DSM 44549 were grown in trypticase soy broth (TSB) at 37 °C. *Streptococcus pneumoniae* R800, was grown in Todd Hewitt broth without

shaking at 37 °C. *Streptococcus agalactiae* COH-1 and *Streptococcus pyogenes* M1-5448 were grown in Brain-Heart Infusion (BHI) broth at 37 °C. *Lactobacillus gasseri* ATCC 19992, *Lactobacillus acidophilus* ATCC 4356, and *Lactobacillus plantarum* ATCC 8014 were grown at 37 °C on Man-Rogosa-Sharp agar in a sealed candle jar to provide a CO₂ enriched atmosphere. *Lactococcus Lactis* subsp. *lactis* ATCC 11454 and *Lactococcus Lactis* subsp. *cremoris* ATCC 19257 were grown in Trypticase Soy Yeast broth at 37 °C and 28 °C respectively. *Rhodococcus equi* ATCC 6939 was grown in cation-adjusted Mueller Hinton Broth II (MHBII) at 37 °C. *Rhodococcus opacus* DSM 1069, *Corynebacterium glutamicum* DSM 44475, *Brevibacillus brevis* ATCC 8246, and *Bacillus subtilis* 168 were grown in Mueller Hinton Broth II at 28 °C. *Francisella tularensis* (19 strains including Types A and B) were grown on chocolatzed 9% sheep blood (CHAB) at 37 °C in a BSL level 3 facility. *Clostridia difficile* WAL14572, *Clostridia bolteae* WAL16351, *Clostridia perfringens* WAL 14572, *Bacteroides fragilis* ATCC 25285 and *Prevotella copris* WAL16310 were grown on reinforced clostridial medium (Oxoid CM149) under anaerobic conditions at 37 °C. *Helicobacter pylori* SS1 was grown in BHI broth supplemented with 5% fetal bovine serum in 10% CO₂ at 37 °C. *Chlamydia trachomatis* was propagated and titered in HeLa229 cells grown in Dulbecco's modified Eagle's medium (high glucose; Invitrogen, Carlsbad, CA) as described previously (Lad et al., 2007). All liquid cultures were grown with 275 rpm shaking, and all media was obtained from Difco™.

Selection of Arylomycin Resistant *S. epidermidis* and Sequencing of Signal Peptidase Genes

S. epidermidis (~1 × 10⁹ cfu) were plated on tryptic soy agar (TSA) containing 2 µg/ml arylomycin C16. Resistant colonies visible at 24 hours were re-streaked onto TSA containing 2 µg/ml arylomycin C16 to confirm the resistant phenotype.

Isolation of genomic DNA and sequencing of SPases genes was performed using available procedures. In particular, genomic DNA was obtained by lysing *S. epidermidis* with lysostaphin (Sigma), followed by Proteinase K (Roche) treatment, and heat lysis at 95 °C. Signal peptidase genes were amplified using the primer pairs Se_SpsIB_F/Se_SpsIB_R and Se_SpsI_F/Se_SpsI_R (see Table 10 of Primers, below). Sequencing was performed using primers Se_SpsIB_R and Se_SpsI_F.

Table 10: Primers for Detecting and Synthesizing Bacterial Spase Nucleic Acids

Primer Name	Primer Sequence 5' --> 3'	SEQ ID NO:
Ec_lepB_usNF	TCCCGTTCGCTGGCTGCCTGTG	26
Ec_lepB_CR_Kan	CGGCGGCTTTGTTGAATAAATCGTTAAT GGATGCCGCCAATGCG	27
Ec_lepB_CF_Kan	GAGACACAACGTGGCTTTCCCATTAAT AGCCATCTTCG TTCACG	28
Ec_lepB_dsCR	TTGGTTTCTAGACCAGCGTATTGCCACG GACC	29
EC_lepB_Nconf	TTGGTTTCTAGACTTTATCGACACCCCG G	30
Kan_ICF2	GGTTGTAACACTGGCAGAGC	31
Ec_lepB_QC_P84A_F	CGTTCGTTTATTTATGAAGCGTTCAGATCCCGTCAGGT	32
Ec_lepB_QC_P84A_R	ACCTGACGGGATCTGGAACGCTTCATA AATAAACGAACG	33
Ec_lepB_QC_P84C_F	CGTTCGTTTATTTATGAATGCTTCAGATCCCGTCAGGT	34
Ec_lepB_QC_P84C_R	ACCTGACGGGATCTGGAAGCATTTCATA AATAAACGAACG	35
Ec_lepB_QC_P84D_F	CGTTCGTTTATTTATGAAGATTTCAGATCCCGTCAGGT	36
Ec_lepB_QC_P84D_R	ACCTGACGGGATCTGGAAATCTTCATA AATAAACGAACG	37
Ec_lepB_QC_P84E_F	CGTTCGTTTATTTATGAAGAGTTCAGATCCCGTCAGGT	38
Ec_lepB_QC_P84E_R	ACCTGACGGGATCTGGAACCTTCATA AATAAACGAACG	39
Ec_lepB_QC_P84F_F	CGTTCGTTTATTTATGAATTCTTCAGATCCCGTCAGGT	40
Ec_lepB_QC_P84F_R	ACCTGACGGGATCTGGAAGAATTCATA AATAAACGAACG	41
Ec_lepB_QC_P84G_F	CGTTCGTTTATTTATGAAGGCTTCAGATCCCGTCAGGT	42
Ec_lepB_QC_P84G_R	ACCTGACGGGATCTGGAAGCCTTCATA AATAAACGAACG	43
Ec_lepB_QC_P84H_F	CGTTCGTTTATTTATGAACATTTCAGATCCCGTCAGGT	44
Ec_lepB_QC_P84H_R	ACCTGACGGGATCTGGAAATGTTCATA AATAAACGAACG	45
Ec_lepB_QC_P84I_F	CGTTCGTTTATTTATGAAATCTTCAGATCCCGTCAGGT	46
Ec_lepB_QC_P84I_R	ACCTGACGGGATCTGGAAGATTTCATA AATAAACGAACG	47
Ec_lepB_QC_P84K_F	CGTTCGTTTATTTATGAAAAATTTCAGATCCCGTCAGGT	48
Ec_lepB_QC_P84K_R	ACCTGACGGGATCTGGAATTTTTCATAA ATAAACGAACG	49

Ec_lepB_QC_P84L_F	CGTTCGTTTATTTATGAACTGTTCCAGA TCCCGTCAGGT	50
Ec_lepB_QC_P84L_R	ACCTGACGGGATCTGGAACAGTTCATA AATAAACGAACG	51
Ec_lepB_QC_P84M_F	CGTTCGTTTATTTATGAAATGTTCCAGA TCCCGTCAGGT	52
Ec_lepB_QC_P84M_R	ACCTGACGGGATCTGGAACATTTTCATA AATAAACGAACG	53
Ec_lepB_QC_P84N_F	CGTTCGTTTATTTATGAAAACCTTCCAGA TCCCGTCAGGT	54
Ec_lepB_QC_P84N_R	ACCTGACGGGATCTGGAAGTTTTTCATA AATAAACGAACG	55
Ec_lepB_QC_P84Q_F	CGTTCGTTTATTTATGAACAGTTCAGGA TCCCGTCAGGT	56
Ec_lepB_QC_P84Q_R	ACCTGACGGGATCTGGAACAGTTCATA AATAAACGAACG	57
Ec_lepB_QC_P84R_F	CGTTCGTTTATTTATGAACGGTTCAGGA TCCCGTCAGGT	58
Ec_lepB_QC_P84R_R	ACCTGACGGGATCTGGAACCGTTCATA AATAAACGAACG	59
Ec_lepB_QC_P84S_F	GTGCGTTCGTTTATTTATGAATCGTTCC AGATCCCGTCAGGTTCG	60
Ec_lepB_QC_P84S_R	CGAACCTGACGGGATCTGGAACGATTC ATAAATAAACGAACGCAC	61
Ec_lepB_QC_P84T_F	CGTTCGTTTATTTATGAAACCTTCCAGA TCCCGTCAGGT	62
Ec_lepB_QC_P84T_R	ACCTGACGGGATCTGGAAGGTTTCATA AATAAACGAACG	63
Ec_lepB_QC_P84V_F	CGTTCGTTTATTTATGAAGTGTTCAGGA TCCCGTCAGGT	64
Ec_lepB_QC_P84V_R	ACCTGACGGGATCTGGAACACTTCATA AATAAACGAACG	65
Ec_lepB_QC_P84W_F	CGTTCGTTTATTTATGAATGGTTCAGGA TCCCGTCAGGT	66
Ec_lepB_QC_P84W_R	ACCTGACGGGATCTGGAACCATTCATA AATAAACGAACG	67
Ec_lepB_QC_P84Y_F	CGTTCGTTTATTTATGAATATTTCCAGGA TCCCGTCAGGT	68
Ec_lepB_QC_P84Y_R	ACCTGACGGGATCTGGAAATATTCATA AATAAACGAACG	69
Pa_lepB_usNF3_BamHI	TTGGTTGGATCCTGGTGCTCGACTTCTT CGATCG	70
Pa_lepB_dsCR_SpeI	TTGGTTACTAGTGTCGGACCTCATGTCA GTGTAG	71
Pa_lepB_QC_P84S_F	CGTTCCTTCCTGGTCGAGAGCTTCCAGGA TTCCCTCGGGG	72
Pa_lepB_QC_P84S_R	CCCCGAGGGAATCTGGAAGCTCTCGAC CAGGAAGGAACG	73
Pa_lepB_seqF	GTGGCGATCCAGGCAGCCATC	74

Sa_spsB_usNF_EcoRI	TTGGTTGAATTCGATCTGTAAACGATTG GTGAACAC	75
Sa_spsB_dsCR_EcoRI	TTGGTTGAATTCGTTGCTATAACTACC AACTTCTTGG	76
Sa_spsB_QC_P29S_F	GTAGGTAAATTTATTGTTACGTCATATA CAATTAAAGGTGAATC	77
Sa_spsB_QC_P29S_R	GATTCACCTTTAATTGTATATGACGTAA CAATAAATTTACCTAC	78
Se_spsI_F	CAAGGAAAGCGTGTGTCGTTGTTGTACC	79
Se_spsI_R	CCAATCATTCTTGCTGCAGTAGGTCTAA CG	80
Se_spsIB_F	TGATGGTGATACGATTCCACCGGGAGC	81
Se_spsIB_R	GCATGGCTGTTGACTTTCCTGTACCTGC	82
Ec_lepB_Δ2_75_NF_NcoI	TTGGTTCCATGGTGCGTTCGTTTATTTA TGAAC	83
Ec_lepB_CR_BamHI	TTGGTTGGATCCTGGCATTTAATGGATG CCGCCAATGC	84
Sa_spsIB_NF_KpnI	TTGGTTGGTACCTTGAAAAAAGAAATA TTGGAATGG	85
Sa_spsIB_CR_XhoI	TTGGTTCTCGAGTTAATTTTGTAGTATTTT CAGGATTGAAAT	86

Construction of mutant strains.

E. coli with a kanamycin marked *lepB* gene was constructed using allelic exchange methods described by Cirz et al. (PLoS Biol. 3, e176 (2005)) and the following

5 primers: Ec_lepB_usNF, Ec_lepB_CRKan, Ec_lepB_CF-Kan, Ec_lepB_dsCR, Ec_lepB_Nconf, and Kan_ICF2. The kanamycin marked SPase gene was moved into wild type MG1655 by P1 phage transduction. Point mutations at codon 84 of SPase were introduced by amplifying a pair of overlapping DNA fragments from the cassette used for construction of the wild type cassette using primer pairs

10 Ec_lepB_usNF/Ec_lepB_QC_P83x_R and Ec_lepB_QC_P83x_F/ Ec_lepB_dsCR. Overlapping PCR of the two fragments yielded the complete SPase/kanamycin resistance cassette containing the desired mutation. *P. aeruginosa* mutants were constructed using the allelic exchange plasmid pKNG101 using methods described by Kaniga et al. (Gene 109, 137-141 (1991)) and the primers Pa_lepB_usNF3-BamHI and Pa_lepB_dsCR-SpeI.

15 Point mutations were introduced using overlap PCR as described for *E. coli* with primer pairs Pa_lepB_usNF3-BamHI /Pa_lepB_QC_P84S_R and Pa_lepB_dsCRSpeI/Pa_lepB_QC_P84S_F. *S. aureus* mutants were constructed using the

allelic exchange vector pMAD as described by Arnaud et al. (Appl. Environ. Microbiol. 70, 6887-6891 (2004)) and the primers Sa_spsB_usNF_EcoRI and Sa_spsB_dsCR_EcoRI. Point mutations were introduced using overlap PCR as described for *E. coli* with primer pairs Sa_spsB_usNF_EcoRI/ Sa_spsB_QC_P29S_R and
 5 a_spsB_dsCR_EcoRI/Sa_spsB_QC_P29S_F.

Growth Curves.

For each of the twenty strains of *E. coli*, each harboring one of the twenty amino acids at SPase residue 84, saturated overnight cultures were diluted 100-fold into fresh
 10 LB broth and grown to an OD600nm of 0.4 – 0.6. These cultures were diluted into pre-warmed LB to a final density of OD600nm 0.001 (10⁶ cfu/mL). Growth was measured by plating serial dilutions of the cultures at 30 min. intervals for three hours and counting the resulting colonies. Doubling times were determined from the exponential curve of viable cells versus time. Averages and standard deviations were determined for three
 15 independent growth curves.

***S. aureus* and *S. epidermidis* Competitive Growth Experiments.**

Competitive growth experiments were run in triplicate by diluting equal volumes of saturated *S. epidermidis* SpsIB(WT) and *S. epidermidis* SpsIB(S29P) cultures 2000-
 20 fold into TSB and growing the resulting culture overnight to saturation (~10 doublings). This saturated culture was diluted 1000-fold and grown overnight to saturation an additional three to four times for a total of 40 to 50 doublings. Serial dilutions of each saturated culture were plated onto TSA and onto TSA containing 2 µg/mL arylomycin C16 to quantify the number of total cells and arylomycin C16 resistant cells respectively.
 25 Similar experiments were performed between wild type *S. epidermidis* and the *S. epidermidis* SpsIB(S31P) mutant and between wild type *S. aureus* and the *S. aureus* SpsB(P29S) mutant.

Minimum Inhibitory Concentration (MIC) Experiments

30 With the exception of *C. trachomatis* and *H. pylori*, minimum inhibitory concentrations (MICs) of arylomycin C16 were determined by a modified Clinical and Laboratory Standards Institute (CLSI) micro-broth dilution method in 100 µL of media containing 2-fold dilutions of arylomycin C16. Inocula were formed by resuspending bacteria growing on solid media into the same broth used in the MIC experiment and

diluted a final concentration of 1×10^7 colony forming units/ml. 5ul of this suspension was added wells containing 100ul of media and arylomycin C16. MICs of *E. coli*, *P. aeruginosa*, *K. pneumoniae* and *Y. pestis* were determined in LB. MICs of *S. aureus*, *S. epidermidis*, *S. haemolyticus*, *R. equi*, *R. opacus*, *C. glutamicum*, *C. efficiens*, *B. brevis*,
5 *B. subtilis*, *F. tularensis*, were determined in Cation-adjusted Mueller Hinton broth. MICs of *S. pyogenes*, *S. agalactiae*, and *S. pneumoniae* were determined in Todd Hewitt broth. MICs of both *L. lactis* strains were determined in TSYE broth. MICs of arylomycin C16 for *L. gasseri*, *L. acidophilus*, and *L. plantarum* were determined in cation-adjusted Mueller Hinton broth supplemented with 10% Man-Rogosa-Sharpe broth adjusted to pH
10 6.7 (Klare et al., 2005), and the 96-well plates were incubated a sealed in a jar containing a lit candle to provide a CO₂ enriched atmosphere. MICs of arylomycin for strains of Clostridia and Bacteroidetes were determined using the CLSI approved Wadsworth agar dilution technique. Unless noted otherwise MIC experiments were performed at the optimal growth temperatures of each strain and the MIC determined after 24 hours of
15 growth.

MICs were defined as the lowest arylomycin C16 concentrations yielding no increase in OD_{590nm} above background after 24 hours of incubation. If the MIC breakpoint was uncertain by OD measurement, viable cells were determined by plating serial dilutions, and MIC was defined as the lowest concentration at which less than 5-
20 fold outgrowth occurred by 24 hours. The MIC of arylomycins C16 for *H. pylori* were determined by diluting a culture at $\sim 10^8$ cfu 200-fold into fresh media containing 2-fold dilutions of arylomycin C16. After 24 hours, serial dilutions were plated onto Columbia agar with 5% lysed horse blood and viable cells determined after 5 days of growth. The MIC was defined as the amount of arylomycin C16 required to achieve a 1000-fold
25 decrease in viable cells. To determine MIC of arylomycin C16 for *C. trachomatis*, HeLa 229 cells were grown to 30% confluence, transferred to 12-well plates treated with 2.0 μ g/ml fibronectin, and allowed to adhere overnight. Adherent cells were treated with one infectivity unit of *C. trachomatis* L2 cells (see, Lad et al., J. Bacteriol. 189: 6619-25 (2007)) and with various concentrations of arylomycin C16. After 24 hours cells were
30 fixed with 3% paraformaldehyde and visualized by fluorescence microscopy using monoclonal antibodies to the chlamydial major outer membrane protein (MOMP) provided by L. M. de la Maza. The MIC was defined as the lowest concentration of arylomycin C16 that resulted in no increase in fluorescence relative to background at 24 hours.

The minimal inhibitory concentration (MIC) of each derivative was determined using a standard broth dilution method. Test strains included wild type *S. epidermidis* (strain RP62A), as well as mutant strains of *S. aureus* (strain 8325), *E. coli* (strain MGI655), and *P. aeruginosa* (strain PAGI) that were rendered sensitive to the
 5 arylomycins by mutation of the resistance-conferring Pro to a residue that does not confer resistance (P29S in the *S. aureus* protein, and P84L in the *E. coli*, and *P. aeruginosa* proteins). MICs were also determined with the isogenic wild type strains of *S. aureus*, *E. coli*, and *P. aeruginosa*, as well as an isogenic mutant strain of *S. epidermidis* where the resistance-conferring Pro has been introduced (S29P).

10

Cloning for Protein Expression.

Plasmids for expression of the $\Delta 2$ -75 variant of *E. coli* SPase were constructed by amplifying genomic DNA encoding the $\Delta 2$ -75 variant of WT and (P83S) *E. coli* SPase from the

15 corresponding *E. coli* strains with primers Ec_lepB_ $\Delta 2$ _75_NF_NcoI and Ec_lepB_CR_BamHI and cloning the resulting ORFs into pET15b (Novagen) at the NcoI and BamHI restriction sites, yielding plasmids pET15blepBTrunc and pET15blepBTrunc(P83S). The plasmid pET23-lepB for the expression of full length His6x-tagged *E. coli* SPase protein was kindly provided by Dr. Mark Paetzel (Simon
 20 Fraser University). To express the P83S variant of *E. coli* SPase, the LepB(P83S) mutation was introduced into pET23-lepB using QuikChange site directed mutagenesis (Stratagene) with the primers described above yielding plasmid pET23-lepB(P83S). Plasmids for expression of the His6x-tagged *S. aureus* SPase were constructed by amplifying the genomic DNA encoding SpsB from *S. aureus* NCTC 8325
 25 and the corresponding SpsB(P29S) chromosomal mutant using primers Sa-SPase-KpnI-F and Sa-SPase-XhoI-R and cloning the resulting DNA was into the plasmid pCDF1 (Novagen) at the KpnI and XhoI restriction sites resulting in the addition of an N-terminal His6x-Tag to the *spsB* open reading frame.

30 Protein Expression.

The *E. coli* $\Delta 2$ -75 SPase proteins were expressed in and purified from BL21(DE3) harboring pET15b-lepBTrunc or pET15b-lepBTrunc(P83S) and stored in a manner similar to that described by Paetzel et al. (Proteins 23, 122-125 (1995)). Full length His-

tagged *E. coli* SPase proteins were expressed in BL21(DE3) containing the plasmid pET23-lepB or pET23-lepB(P83S) and purified as described by Klenotic et al. (J. Biol. Chem. 275, 6490-6498 (2000)), with the exception the Q-column step was omitted and that 1% Elugent (Calbiochem) was used in place of Triton X-100 as the detergent while
5 washing and eluting from the Ni-NTA Superflow resin (Qiagen). Full length His-tagged *S. aureus* SPase proteins were expressed in and purified from BL21(DE3) containing the plasmid pCDF1-SaSpsB or pCDF1-SaSpsB(P29S) in a manner analogous to the purification of *Streptococcus pneumoniae* SPase described by Peng et al. (J. Bacteriol. 183, 621-627 (2001)), with the following exceptions. SPase protein was solubilized
10 using 300 mM NaCl, 20 mM Tris pH 8.06, 5 mM imidazole, 10% glycerol, 1% Triton X-100, prior to purification in Ni-NTA Superflow resin and resin bound protein was washed in a similar buffer containing 1% Elugent in place of Triton X-100 prior to protein eluted in wash buffer supplemented with 300mM imidazole. SDS-PAGE followed by Coomassie staining revealed a single band of approximately 21 kD. All
15 protein concentrations were determined by BCA assay.

In Vitro KD Measurements

Construction of expression vectors and the subsequent production of the various SPase variants used in this study are described above. Steady state binding of arylomycin
20 C16 was determined by measuring the previously described increase in arylomycin fluorescence ($\lambda_{ex} = 320$ nm, $\lambda_{em} = 410$ nm) upon binding *E. coli* $\Delta 2-75$ SPase (see, Paetzel et al., J. Biol. Chem. 279, 30781-30790 (2004)). The binding buffer for full length and truncated *E. coli* proteins was as follows: 100 mM NaCl, 20 mM Tris-HCl pH 7.4, 1 mM EDTA, 1% *n*-octyl- β -glucopyranoside (Anatrace). This buffer was
25 supplemented with 10% glycerol for experiments with *S. aureus* SPase protein.

SPase Sequence Analysis

The amino acid sequences of the SPases from *E. coli*, *S. aureus*, *B. fragilis* and *C. efficiens* were concatenated and used as the query sequence in a BLAST against all of the
30 fully sequenced genomes of Bacteroidetes, Actinobacteria, Firmicutes, Proteobacteria, and Chlamydiae/Verrucomicrobia available in the NCBI Microbial Genome Database. The amino acid sequence of BLAST hits with an E-value less than 0.1 were aligned using MUSCLE (Edgar, Nucleic Acids Res. 32, 1792-1797 (2004)), and all sequences lacking the catalytic Ser or Lys residues were removed. Poorly aligned regions were

removed using the “Block Mapping and Gathering using Entropy” program found at <http://mobyli.pasteur.fr/cgi-bin/portal.py>, with Gap Rate Cutoff 0.3 and the Entropy Cutoff of 0.7. Phylogenetic analysis was conducted using PhyML with SPR branch improvement (Guindon and Gascuel, Syst. Biol. 52, 696-704 (2003)). SPases from

5 Gram-positive and Gram-negative organisms were kept separate during alignment and phylogenetic analysis to improve the quality of these analyses.

Also several SPases from the Gram-negative Proteobacteria were removed prior to analysis of SPase phylogeny, since they did not show an obvious relation to any of the other Gram-negative or Grampositive SPases examined. Phylogenetic trees were

10 displayed using the Interactive Tree of Life (Letunic and Bork, Bioinformatics 23, 127-128 (2007)).

Conservation of Residue 29

A single alignment of SPases from all of the Gram-negative and Gram-Positive

15 genomes examined was made using MUSCLE, and poorly aligned regions were removed using “Block

Mapping and Gathering using Entropy” with a gap cutoff of 0.3 and an entropy cutoff of 0.7. The resulting alignment was primarily within the previously described Boxes A-E (Dalbey et al., Protein Sci. 6: 1129-38 (1997)), which are highly conserved across all

20 bacterial SPases. Aligned and trimmed sequences were then grouped by the Phylum of the organisms in which they are found. Each alignment (one for each of the five Phyla) was submitted to the “Score Sequence Conservation” program (Capra and Singh, Bioinformatics 23, 1875-1882 (2007);

<http://compbio.cs.princeton.edu/conservation/score.html>), and the sequence conservation

25 was scored using the Jensen-Shannon divergence method with weighted sequences and a window size of 1. The per residue conservation scores were averaged across the entire alignment, across each set of residues comprising Boxes B-E, and across the regions five amino acids centered on residue 29.

16sRNA Sequence Analysis

Aligned 16sRNA sequences were analyzed were obtained from the Ribosomal Database Project (Cole et al., Nucleic Acids Res. 37, D141-145 (2009)). The “Block Mapping and Gathering using Entropy” program was used with a Gap Rate Cutoff of 0.7 and an Entropy Cutoff of 0.7 to remove poorly aligned regions. Phylogenetic analysis

was performed using PhyML 3.0, with the HKY85 substitution model and SPR tree improvement, and the resulting tree was displayed using the Interactive Tree of Life.

EXAMPLE 3: The Antibiotic Activity of Arylomycins is Masked by SPase Mutations

The Example describes experimental results demonstrating that many strains of bacteria have naturally developed SPase mutations that confer resistance to arylomycins.

Point mutations in SPase confer arylomycin resistance

S. epidermidis is atypical in its sensitivity to the arylomycins (Roberts et al., J. Am. Chem. Soc. 129: 15830-15838 (2007)). To investigate whether *S. epidermidis* lacks specific resistance mechanisms inherent to other bacteria, selection experiments were performed to isolate mutants that were able to grow in the presence of 2 µg/ml arylomycin C16 (8× MIC). Mutants were obtained at a frequency of 4 per 10⁹ viable cells and fell into two phenotypic classes: the majority (~75%) had a 32-fold elevated MIC compared to the wild type strain, and the remainder had a greater than 256-fold elevated MIC. Consistent with this low frequency of resistance, arylomycin resistance was correlated with either of two mutations in SpsIB, one of the two SPases found in *S. epidermidis*. The 32-fold increase in resistance was associated with a Ser to Pro mutation at position 29 (10/11 clones sequenced); while the >256-fold increase in resistance was associated with a Ser to Pro mutation at position 31 (9/11 clones sequenced). None of the resistant mutants in either class exhibited growth defects under the standard laboratory conditions employed (data not shown).

These data indicate that the whole cell antibiotic activity of the arylomycins results from their inhibition of SPase and also that mutations in SPase are the dominant mechanism whereby *S. epidermis* evolves resistance.

To investigate whether naturally resistant bacteria harbor the same mutations that confer resistance in *S. epidermidis*, the amino acid sequences of SPases were examined in the closely related organism *S. aureus*, as well as in the more distantly related Gram-negative organisms *E. coli* and *P. aeruginosa* (Table 11).

Table 11: Resistance to Arylomycin A2 C16

Correlates with Proline at Position -5 and/or -7 in Bacterial SPase*

Bacterial Strain	SPase Type	SPase Alignment	MIC (μg/mL)	SEQ ID NO:
<i>S. epidermidis</i> RP62A	WT	VGKSYSIKGDS	0.25	17
<i>S. epidermidis</i> PAS9001	S29P	VGK P YSIKGDS	8	18
<i>S. epidermidis</i> PAS9002	S31P	VGKSY P IKGDS	>128	19
<i>S. aureus</i> NTCT 8325	WT	VAKPYTVKGDS	>128	20
<i>S. aureus</i> PAS8001	P29S	VAK S YTVKGDS	2	21
<i>E. coli</i> MG1655	WT	IYEPFQIPSGS	>128	22
<i>E. coli</i> PAS0232	P84S	IYE S FQIPSGS	2	23
<i>P. aeruginosa</i> PAO1	WT	LFEPFQIPSGS	>128	24
<i>P. aeruginosa</i> PAS2006	P84S	LFES S FQIPSGS	8	25

*Mutations are shown in boxes (e.g., as **P** or **S**), and the catalytic serine is shown at the C-terminal end of the peptide sequence.

As shown in Table 11, at the position corresponding to the *S. epidermidis* SPase residue 29, Pro is found in the single SPase of *S. aureus*, in the single SPase of *E. coli*, and in one of the two SPases of *P. aeruginosa* (Pro29 in *S. aureus*, Pro84 in *E. coli* and *P. aeruginosa*). However, at the position corresponding to SPase residue 31 in *S. epidermidis*, Pro is not found in any of these *S. aureus*, *E. coli*, and *P. aeruginosa* SPase sequences. Moreover, an *E. coli* strain with Pro at Spase position 31 could not be constructed, suggesting that SPase position 31 mutations are not tolerated in some organisms.

To determine whether the innate arylomycin resistance observed in *E. coli*, *P. aeruginosa*, and *S. aureus* results from the identified Pro residues, mutant strains of these bacteria were constructed in which the Pro was replaced by Ser (the corresponding residue in wild type *S. epidermidis* SpsIB). In each organism, mutation of Pro to Ser conferred a high degree of sensitivity to arylomycin C16 (Table 11). No growth defects

were apparent in the mutant strains (FIG. 2), suggesting that the increased sensitivity does not result from decreased fitness or compromised SPase activity.

The sensitivity of the *E. coli* and *P. aeruginosa* serine mutants to arylomycin C16 indicates that the presence of the Pro residue correlates with arylomycin resistance and
5 that the arylomycins penetrate the formidable outer-membrane of Gram-negative bacteria. Consistent with efficient outer-membrane penetration, experiments demonstrated that permeabilizing these bacteria with polymyxin B nonapeptide had only a negligible effect on the MIC values ($\leq$ 4-fold decrease).

To determine whether the identified Pro is unique in its ability to confer
10 arylomycin resistance, mutant strains of *E. coli* were constructed in which each of the other 19 amino acids was introduced into the *E. coli* SPase at the same position (residue 84). Based on the growth rates observed in arylomycin-free media, most amino acids at this position were well tolerated (FIG. 2), indicating that the nature of the amino acid at residue 84
15 does not generally affect fitness under the conditions employed, although a minor growth defect was observed when Arg, Lys, Glu, and Cys was present at position 84 and a temperature sensitive phenotype was observed when His and Phe were present at position 84. In contrast, when arylomycin C16 was added to the media, the MIC values observed are highly dependent on the identity of the amino acid at residue 84, but Pro
20 was the only amino acid that imparted high-level arylomycin resistance (MIC > 256 μ g/ml) (FIG. 2). All of the other amino acids lead to arylomycin sensitivity (MIC values of $\leq$ 16 μ g/ml), with the hydrophobic amino acids conferring somewhat greater sensitivities.

25 **Resistance-conferring mutations reduce the affinity of arylomycin for SPase**

Based on the previously reported crystal structure of the *E. coli* SPase complex (Paetzel et al., J. Biol. Chem. 279, 30781-30790 (2004)) arylomycin A2 binds in a manner that mimics that proposed for natural peptide substrates, and the resistance-conferring Pro residue (Pro84), is positioned within the *E. coli* SPase substrate binding
30 pocket, but distal to the catalytic residues (FIG. 3A). To test whether the resistance-conferring mutations directly interfere with arylomycin C16 binding *in vitro*, equilibrium binding constants were determined using recombinant SPase enzymes reconstituted in micelles that mimic a lipid bilayer environment. The affinities of arylomycin C16 were measured for a truncated wild type *E. coli* SPase that lacks the N-terminal membrane

helices but that still associates with micelles, and for a P84S variant of this truncated *E. coli* SPase enzyme, (Kuo et al., Arch. Biochem. Biophys. 303, 274-280 (1993)). FIG. 3D shows the binding affinity of arylomycin C16 for the wild type and P84S variants of the soluble N-terminally truncated *E. coli* SPase. Arylomycin C16 bound the truncated wild type protein with a KD of 979 ± 69 nM, which is similar to the value reported for arylomycin A2 (Paetzel et al., Biol. Chem. 279, 30781-30790 (2004)). In contrast, a significantly lower KD of 39 ± 15 nM was observed for the serine-containing P84S variant of this *E. coli* SPase.

To control for artifacts associated with deletion of the N-terminal helices, which might interact with the lipid tail of the inhibitor or help to co-localize the protein and the inhibitor within the membrane-like micellular environment, the affinities of arylomycin C16 for the wild type and P84S variants of a detergent-solubilized full-length *E. coli* SPase were determined (FIG. 3B). While arylomycin C16 bound the full-length proteins with higher affinities than the corresponding soluble fragments, the affinity of arylomycin for the full-length Ser-variant ($KD = 5.7 \pm 1.0$ nM) was again an order-of-magnitude higher than that for the corresponding Pro-variant ($KD = 60 \pm 16$ nM).

Lastly, to characterize a representative Gram-positive SPase, the affinity of arylomycin C16 for the full-length wild type and P29S mutant of *S. aureus* SPase was measured (FIG. 3C). As with the *E. coli* SPase, arylomycin C16 bound the Ser-variant of *S. aureus* SPase an order-of-magnitude more tightly than the Pro-variant, with KD values of 130 ± 53 and 1283 ± 278 nM, respectively. Thus, the Pro residues responsible for resistance in *E. coli* and *S. aureus* appear to act by interfering with arylomycin binding.

Distribution of resistance-conferring residues in nature

To better understand the distribution of this resistance determinant in nature, the phylogenetic relationship of the fully sequenced bacteria from five phyla was determined, as reflected by their 16S rRNA sequences. This phylogeny was then compared to the number of SPases in each organism and to the presence or absence of Pro at the position corresponding to residue 29 in *S. epidermidis* (unless otherwise specified, *S. epidermidis* numbering is used hereafter). In general, Gram-negative bacteria from the Chlamydiae/Verrucomicrobia, Proteobacteria, and Bacteroidetes phyla have a single SPase, and in each phylum, Pro29 is present in the SPases of a subset of organisms (FIG. 5).

Accordingly, almost all of the sequenced α -, β -, γ -Proteobacteria have SPases with Pro29 (115/123, 64/65, and 178/183 of the sequenced organisms, respectively), whereas most of the sequenced δ - and ϵ -Proteobacteria have SPases with Ala29 (32/35 and 27/29, respectively). Similarly, within the Bacteroidetes phylum, each of the sequenced Flavobacteria has one SPase where Pro is always present at position 29, whereas each of the Bacteroidia typically has an SPase with Asn29 and sometimes a second SPase with Ser29. Finally, among the few Chlamydiae/Verrucomicrobia that have been sequenced, each of the Chlamydia has one SPase with Leu29 (7/7), while each of the Verrucomicrobia has at least one SPase with Pro29 (8/8). The phylogeny of the SPase genes themselves largely mirrors that of the 16S rRNA sequences, indicating that relatively little horizontal transfer of SPase genes has occurred and confirming that Pro29 was installed independently into the SPases of these lineages. Interestingly, horizontal gene transfer is responsible for the scattered instances of Proteobacteria that do encode multiple SPases, including the second SPase of *P. aeruginosa* that has at Leu29. These additional SPases are not closely related to any of the sequenced SPases examined in this analysis, and they may not be functionally equivalent to the other Proteobacterial SPases.

In contrast to the Gram-negative bacteria, the Gram-positive Firmicutes and Actinobacteria commonly encode multiple SPases, and comparison of the 16S rRNA and SPase phylogenies indicates that duplication of SPase genes has occurred multiple times in these lineages (FIG. 5). The distribution of Pro29 is also more irregular, which appears to have resulted from reduced conservation leading to the frequent introduction and removal of Pro at this position.

Moreover, the region defined by residues 27-31 appears to be poorly conserved within the Gram-positive SPases relative to the same region in the Gram-negative proteins or to the regions that comprise the core and active site of the protein (Table 12). Table 13 shows the relative conservation of regions of SPase genes from five bacterial phyla as reflected by the average Jensen–Shannon divergence score of the comprising residues (Capra and Singh, Bioinformatics 23, 1875-1882 (2007)). Boxes B-E were defined previously as the conserved regions that form the substrate binding site and active site (Dalbey et al., Protein Sci. 6: 1129-38 (1997)). The rank of residue 29 indicates the degree of conservation at this position relative each the other 137 residues used in the SPase sequence alignment, where 1 indicates the most conserved residue.

Table 12: Conservation of Regions of SPase genes from Five Bacterial Phyla

Bacterial Phyla	Entire Aligned Sequence	Box B	Box C	Box D	Box E	Residues 27-31	Rank Residue 29
Actinobacteria	0.473	0.572	0.464	0.632	0.602	0.416	76/137
Firmicutes	0.431	0.491	0.370	0.626	0.587	0.248	134/137
Bacteroidetes	0.516	0.615	0.529	0.645	0.594	0.431	98/137
Chlamydia/ Verrucomicrobia	0.553	0.681	0.599	0.636	0.616	0.567	47/137
Proteobacteria	0.534	0.629	0.585	0.654	0.664	0.568	30/137

As shown in Table 12, the region defined by residues 27-31 appears to be poorly conserved within the Gram-positive SPases relative to the same region in the Gram-negative proteins. However, Pro29 is particularly common among the SPases of a subset of the Gram-positive bacteria Bacilli, including the genres *Bacillus*, *Listeria*, and *Staphylococcus*. Interestingly, although SPases with Pro29 appear to have been present and maintained during speciation of the *Bacillus* and *Listeria*, the common *Staphylococci* ancestor appears to have had two SPases each with Ser29, as is still the case with *S. epidermidis*. *S. aureus* appears to have deleted one SPase and introduced Pro29 into the other (FIG. 4).

The arylomycins have a broad spectrum of antibiotic activity

To further explore the spectrum of arylomycins and to test the contribution of the Pro29 to arylomycin resistance in a wider range of bacteria, the arylomycin susceptibilities were determined of representative organisms from the above phylogenetic analysis (Table 13). Bacteria from all five phyla were sampled, and when possible important human pathogens were included.

Table 13: Associations between arylomycin C16 sensitivity and SPase genotype(s) among different wild type bacteria

Species	Reside 29	MIC (µg/ml)
<i>Staphylococcus epidermidis</i>	S,S	0.25
<i>Staphylococcus haemolyticus</i>	S,S	2
<i>Rhodococcus opacus</i>	V	2
<i>Corynebacterium glutamicum</i>	M	2
<i>Helicobacter pylori</i>	A	4
<i>Yersinia pestis</i>	P	4
<i>Chlamydia trachomatis</i>	L	6

<i>Francisella tularensis</i>	N	4 -16, >64*
<i>Streptococcus pneumoniae</i>	N	16
<i>Streptococcus pyogenes</i>	A	16
<i>Lactococcus lactis</i>	L	16, >128*
<i>Rhodococcus erythropolis</i>	V,I	16
<i>Corynebacterium efficiens</i>	P	>64
<i>Staphylococcus aureus</i>	P	16-32, >128*
<i>Brevibacillus brevis</i>	P,P,P,P,V	>64
<i>Enterococcus faecalis</i>	P,P,P,S	>64
<i>Bacillus subtilis</i>	P,P,P,D	>128
<i>Streptococcus agalactiae</i>	F,V	>128
<i>Escherichia coli</i>	P	>128
<i>Pseudomonas aeruginosa</i>	P,L	>128
<i>Klebsiella pneumoniae</i>	P	>128
<i>Lactobacillus gasseri</i>	N,N	>128
<i>Lactobacillus acidophilus</i>	N	>128
<i>Lactobacillus plantarum</i>	M,M,V	>128
<i>Clostridium difficile</i>	P,P,P	>16
<i>Clostridium bolteae</i>	N,N,Q	>16
<i>Clostridium perfringens</i>	K,K,K,I	>16
<i>Bacteroides fragilis</i>	S,N	>16
<i>Prevotella copris</i>	N	>16

* Multiple values indicate heterogeneity within different strains of a species, as discussed in the text.

As shown in Table 13, arylomycin C16 is active against the ϵ -Proteobacteria *H. pylori* (whose SPase has Ala29) with an MIC of 4 μ g/ml. Similarly, the intracellular Gram-negative pathogen *C. trachomatis* (Leu29) is eradicated from human HeLa 229
5 cells with an MIC of 6 μ g/ml. Notably, no adverse effects on the human cells were observed up to 20 μ g/ml of arylomycin, the highest concentrations examined.

Francisella tularensis (Asn29) is a potential biological warfare agent and a member of the only genera of γ -Proteobacteria that does not have Pro29. Nineteen clinical isolates of *Francisella tularensis* (Asn29) were examined and it was determined that 8 were
10 inhibited with MICs of 4 to 16 μ g/ml, one with an MIC of 32 μ g/ml, and the remainder with MICs in excess of 64 μ g/ml. *Klebsiella pneumoniae* encodes a single SPase that has Pro29 and is resistant to the arylomycins. Interestingly, although it has a single SPase with a Pro29, *Yersinia pestis*, the causative agent of plague, is sensitive to arylomycin C16.

The Gram-positive Firmicutes *Streptococcus pneumoniae*, *Streptococcus pyogenes*, and *Staphylococcus haemolyticus* are all human pathogens that lack SPases with Pro29. Each of these species is sensitive to arylomycin C16. However, *B. subtilis* and *E. faecalis*,

5 Firmicutes with multiple SPases having Pro29, are resistant. In contrast, the Gram-positive Actinobacteria *Rhodococcus equi* and *Rhodococcus opacus* (Schimana et al., J. Antibiot. (Tokyo) 55, 565-570 (2002)) lack Pro29 and are each sensitive to arylomycin C16. While the actinobacteria *Corynebacterium glutamicum* has a single SPase with Met29 and an arylomycin C16 MIC of 2 µg/ml, the related actinobacteria

10 *Corynebacterium efficiens* has a single SPase with Pro29 and an MIC of 16 µg/ml.

However, while *Lactococcus lactis* spp. *cremonis*, which has one SPase with Leu29, is sensitive to arylomycin C16, the highly related *Lactococcus lactis* spp. *lactii* also has a single SPase with Leu29 and is resistant. Additionally, a variety of other Lactobacillales, and all investigated Clostridia and Bacteriodetes, are resistant to the

15 arylomycins despite the fact that many lack SPases with Pro29 (MIC > 64 µg/ml for the Lactobacillales and > 16 µg/ml for the Clostridia and Bacteriodetes). Finally, a broader survey of *S. aureus* strains revealed that two strains, despite a prediction of arylomycin-resistance because they have SPases with Pro29, are actually arylomycin-sensitive: COL a tetracycline and penicillin resistant strain (MIC = 12µg/ml), and Rosenbach 328, an

20 MRSA strain (Pantosti and Venditti, Eur. Respir. J. 34, 1190-1196 (2009)) (MIC = 25 µg/ml).

Table 14 shows the activity of arylomycin A-C₁₆ and arylomycin B-C₁₆ against *Streptococcus pnemoniae*, *Streptococcus pyogenes*, and *Streptococcus agalactiae*.

25

Table 14

Strain	MIC Arylomycin A-C16 (µg/ml)	MIC Arylomycin B-C16 (µg/ml)
<i>S. pneumoniae</i>	8	16
<i>S. pyogenes</i>	8	4
<i>S. agalactiae</i>	>128	8

Representative SPase Sequences of Arylomycin-Susceptible Bacteria

30 1_Rhodococcus equi ATCC 33707_GI# 296036237_Catalytic Ser
Residue 69 (SEQ ID NO: 106)

VADAPQDPDVTPDETEQEQTGGRSRRRRGKDKKPRSFWREIPILIVVALLLSFLLQTFI
 ARVYLIPSESMETLHGCPGCTGDRIVVEKISYRFGDPKPGDVVFRGPESWSEGYSS
 RSDNVVVRGLQEVSLSLVGVVPPDENDLVKRVIATGGQTVECCDDQGRVLVDGKPLDEPY
 ITMDFPFIPGVQTCDTAVKSGRCFGPVTVPDGHLLWVMGDNRSNSADSRVHVSDEMGTI
 5 PVDNVIGKATFIVLPPGRWGSISSPDIRQQ*

1_Rhodococcus equi ATCC 33707_GI# 296036237_Catalytic Ser
 nucleotides 205-207 (SEQ ID NO: 107)
 GTGGCAGATGCACCGCAGGACCCGGACGTGACGCCGGACGAGACCGAGCAGGAGCAGAC
 10 CGGGGGACGGTCCCGCAGGCGCAGGGGGAAGGACAAGAAACCTCGATCGTTCTGGCGTG
 AGATCCCGATCCTCATCGTCGTCGCCTTGCTGTTGAGTTTCCTGCTGCAGACGTTTCATC
 GCCCGGGTCTACCTCATTCCGTCCGAGTCGATGGAGCCGACGCTGCACGGTTGCCCCGG
 GTGCACCGGTGACCGCATCGTCGTCGAGAAGATCAGTTACCGATTTCGGCGACCCGAAGC
 CCGGCGACGTCGTGGTCTTCCGCGGCCCGGAGTCGTGGTCCGAGGGATATTCGTCGACA
 15 CGCTCGGACAACGTGGTGGTCCGCGGTCTGCAGGAGGTCGGCTCGCTCGTCGGTGTCGT
 GCCGCCGGACGAGAACGATCTCGTCAAACGCGTCATCGCGACGGGTGGGCAGACCGTCG
 AGTGCTGCGACGACCGAGGGCCGTGTCTTGGTCGACGGAAAGCCGCTCGACGAGCCGTAC
 ATCACGATGGACTTCCCTTTTCATCCCCGGCGTGCAGACGTGTGACACCGCCGTGAAGTC
 CGGACGCTGCTTCGGACCCGTCACGGTTCCCGATGGGCACCTGTGGGTGATGGGCGACA
 20 ACCGCAGCAATTCCGCGGATTCGCGGTACCACGTCTCCGACGAGATGCAGGGCACGATT
 CCGGTGGACAATGTGATCGGTAAGGCGACCTTCATCGTCTTCCCCCGGGCCGGTGGGG
 ATCGATCTCGTCTCCCGACATCCGGCAGCAGTGA

2_Rhodococcus opacus B4_GI# 226366004_Catalytic Ser Residue
 25 72 (SEQ ID NO: 108)
 VTDSSKERALSSESETTGDSAATSAVNGGAAETEEKPRSFRLRELPIILILVALVLSFLLQ
 TFVARVYLIPSESMETLHGCGCTGDRIVVEKIGYRFGDPQPGDVIVFRGPDSWSQDF
 VSTRSSNVIRGAQEVSLSLVGLVPPDENDLVKRVIATGGQTVECCDDQGRILVDGQPID
 EPYVVMDFPFVPGSQACDTALKSARCFGPVTVPDGHLLWVMGDNRSNSADSRVHVGDDMQ
 30 GTIPLDNVIGKAVFIALPPSRMGTISSPDIQK*

2_Rhodococcus opacus B4_GI# 226366004_Catalytic Ser
 nucleotides 214-216 (SEQ ID NO: 109)
 GTGACAGATTCTTCGAAGGAGCGGGCATTGTCGTCGGAATCCGAGACCACCGGCGATT
 35 GGCCGCCACCTCCGCAGTGAACGGCGGTGCGGCGGAGACCGAGAAGAAACCCCGCTCCT
 TCCTCCGCGAGTTGCCGATCCTGATCCTGGTCGCGCTCGTCCTGAGTTTCCTGCTGCAG
 ACGTTCGTCGCCCCGCGTGTATCTCATTCCGTCGGAGTCGATGGAACCGACGCTGCACGG
 GTGCGCGGGCTGCACCGGGCGACCGCATCGTGGTTCGAGAAGATCGGCTACCGTTTCGGGG
 ACCCGCAACCCGGTGACGTCATCGTGTTCGCGGGGCCGACTCGTGGTTCACAGGATTTC
 40 GTCTCCACCCGTTCCCTCCAACGTGGTGATCCGCGGTGCGCAGGAAGTCGGTTCCCTCGT
 CGGACTCGTCCCGCCGGACGAGAACGACCTCGTCAAGCGTGTGATCGCCACCGGCGGTC
 AGACCGTCGAATGCTGCGACGACCGAGGGCCGCATCCTGGTGGACGGACAACCGATCGAC
 GAGCCCTACGTCGTCATGGACTTCCCCTTCGTCCCCGGCTCCAGGCCTGCGACACGGC
 GCTGAAGTCGGCGCGCTGCTTCGGTCCCGTCACCGTCCCCGAGGGGCACCTGTGGGTGA
 45 TGGGCGACAACCGCAGCAACTCCGCGGACTCCCGCTACCACGTCGGCGACGACATGCAA
 GGCACCATCCCGCTCGACAACGTGATCGGCAAGGCGGTCTTCATCGCGTTGCCGCCGTC
 GCGAATGGGCACGATCAGTTACCCGATATCCAGGGCAAGTGA

50 3_Corynebacterium diphtheriae NCTC 13129_GI#
 38234095_Catalytic Ser Residue 90 (SEQ ID NO: 110)

MKRSVFSFCMMQQASLGVFHSMAETAARVLKVSSANNETVSPTEGVETHDKEKKQLPWF
 VEIPVVVVVITLLVITLLQTFVGRVYMIPSQSMEPTLHGCAGCTGDRIYVDKLAYRFGEP
 EAGDVVVFAGTESWNTGFTTSRSENPLVRGIQNAAGFVGLVAPDENDLVKRIVATGGQT
 VQCLEGDEGVKVDGKVIDSSYTLMPPAYPVDQTTGSEACGGFYFGPIKVPEGNYFMMGD
 5 NRTNSADSRYPHIGDQYQGTIPKENLKGKVQFKIFPFNRIGAVEDYDIQQ*

3_Corynebacterium diphtheriae NCTC 13129_GI#
 38234095_Catalytic Ser nucleotides 268-270 (SEQ ID NO: 111)
 ATGAAGCGCTCAGTTTTCTCTTTTGTATGATGCAGCAAGCGTCGCTGGGCGTTTTTCA
 10 TTCGATGGCTGAAACAGCTGCTAGAGTTCTCAAAGTGAGTTCAGCTAATAACGAGACTG
 TGTCCCCCACGGAAGGCGTCGAAACGCACGACAAGGAAAAGAAGCAACTGCCATGGTTT
 GTGGAAATCCCTGTCGTCGTAGTGGTGACCCTTCTTGTGATCACCTTGCTTCAAACGTT
 CGTTGGACGGGTCTATATGATCCCAAGTCAGTCAATGGAGCCGACACTTCATGGATGTG
 CAGGGTGTACCGGAGACCGAATTTATGTAGATAAGCTGGCTTATCGTTTTTGGTGAACCA
 15 GAAGCCGGCGACGTTGTAGTTTTTGCAGGTACAGAATCATGGAACACCGGATTTACCAC
 TTCACGGTCAGAAAATCCTCTGGTTTCGTGGAATACAAAATGCGGGTGCTTTCGTGCGAT
 TAGTAGCACCAGACGAAAACGACCTTGTAACGACATCGTAGCAACAGGGGGTCAAACG
 GTGCAGTGCCTTGAAGGCGATGAAGGTGTCAAAGTAGACGGTAAAGTCATCGACTCGTC
 ATATACTCTGATGCCACCAGCGTATCCGGTCGACCAGACCACAGGATCAGAGGCGTGCG
 20 GCGGCTTTTACTTCGGACCTATCAAGGTACCTGAAGGAAATTACTTCATGATGGGCGAT
 AACCGGACAACTCCGCGGATTCTCGTTACCACATTGGTGATCAGTATCAAGGCACCAT
 CCCTAAAGAAAACCTCAAGGGGAAAGTTCAGTTCAAGATTTTCCCATTTAACCGTATTG
 GTGCAGTCGAGGATTACGATATCCAACAGTGA

25 4_Lactococcus lactis subsp. cremoris MG1363_GI#
 125625303_Catalytic Ser Residue 35 (SEQ ID NO: 112)
 MMKFLKEWGLFIFIIAAVLLSRVFIWSLVVVDGHSMDPTLADKERLVIVRRTTKINRFDI
 VVAKENAADGSTKDIVKRVMGPDITKFDHDLTINNKVYPENYLKDYQKQLADGQLE
 KTYGNYPLTKALTDQNRSLFVSLAQSTKAFTTDDSTGNPTFTVKVPDQYFLMGDNRVVS
 30 QDSRAVGSFKRSAIIGEAKLRVWPLNKISFF*

4_Lactococcus lactis subsp. cremoris MG1363_GI#
 125625303_Catalytic Ser nucleotides 103-105 (SEQ ID NO:
 113)
 35 ATGATGAAATTTTTTAAAAGAATGGGGATTATTTATCTTTATAATTGCCGCTGTCCTTCT
 CTCGCGCGTCTTTATTTGGTCACTAGTTGTCGTTGATGGCCATTCAATGGACCCTACTT
 TAGCCGATAAAGAAAGACTTGTAATTGTTAGAACGACAAAAATTAATCGTTTTTGATATT
 GTAGTTGCTAAAGAAAACGCGGCTGATGGTTCAACCAAAGATATTGTCAAACGTGTCGT
 TGGGATGCCTGGGGACACTATAAAATTCGACCATGACCAACTTACTATCAATAATAAGG
 40 TTTATCCAGAAAACCTATCTCAAAGACTATCAAAAACAATTGGCTGATGGTCAATTGGAA
 AAAACTTACGGGAACCTATCCTTTGACAAAAGCATTAACTGATCAAAATCGTAGTTTATT
 TGTAAGCTTAGCTCAGAGCACCAAAGCTTTTACAACGGATAGTACTGGTAATCCAACCT
 TTACAGTCAAAGTCCCTGACGGACAATACTTCTTGATGGGAGATAATCGTGTTGTGTCT
 CAAGATAGCCGAGCAGTTGGAAGTTTCAAACGTTTCAGCGATTATTGGTGAAGCCAAATT
 45 ACGAGTTTGGCCACTCAATAAAATTTCTTTCTTTTAA

5_Corynebacterium glutamicum ATCC 13032_GI#
 19553237_Catalytic Ser Residue 67 (SEQ ID NO: 114)
 VTDFSSASNADDSTQDGRPGRRAGKSKKESKPTPWYIEIPVVVVLTLALIFVLQTFVGR
 50 MYMIPSGSMEPTLHGCCEGCTGDRILVEKVSYYFTDPEPGDVVVFKGTDSDNVGFTTQRS
 DNSVIRGLQNLGSYVGLVAPDENDLVKRIIATGGQTVSCQAGDPGIMVDGKEVDDSYTL

QPAQFPIDETSGSTECGGNYFGPITVPGGNYFMMGDNRTNSMDSRYHLGDQYQGTIPEE
 NIKGKVQAIILPFSRIGGVDDPAIKG*

5_Corynebacterium glutamicum ATCC 13032_GI#
 5 19553237_Catalytic Ser nucleotides 199-201 (SEQ ID NO: 115)
 GTGACTGATTTTTCTAGTGCTTCAAATGCTGACGATTCCACGCAGGACGGTCGTCCTGG
 TCGACGTGCTGGAAAGTCTAAGAAGGAATCGAAGCCAACCTCCGTGGTACATCGAAATTC
 CAGTGGTTGTGGTTTTGACCCTCGCGCTGATTTTCGTGCTCCAGACGTTTGTCTGGACGC
 ATGTACATGATTCCGAGTGGTTCGATGGAACCTACTTTGCACGGATGTGAGGGCTGCAC
 10 GGGTGACCGCATCCTGGTGGAGAAGGTTTCTTACTACTTCACGGATCCAGAGCCGGGCG
 ATGTTGTGGTGTTC AAGGGTACTGATTCCTGGAACGTTGGATTCACTACGCAGCGTTCC
 GATAATTCGGTGATCCGCGGCCTGCAGAACCTGGGTCTTACGTGGGTCTTGTCTGCACC
 TGATGAAAATGACCTGGTCAAGCGCATTATCGCCACCGGCGGTCTCAGACTGTTTCGTGCC
 AAGCCGGTGATCCTGGAATCATGGTTGACGGCAAGGAAGTCGATGACAGCTACACGCTG
 15 CAACCTGCGCAATTCCCCATCGATGAGACCTCCGGTTCACCGAATGCGGCGGCAACTA
 TTTCGGCCCCATCACCGTGCCTGGCGGCAACTACTTCATGATGGGTGACAACCGCACCA
 ACTCCATGGATTCCCGCTACCACCTGGGCGATCAGTACCAAGGAACCATCCCTGAGGAA
 AACATCAAGGGCAAAGTTCAAGCAATTATCCTGCCATTTAGCCGAATCGGTGGCGTCGA
 CGACCCTGCCATCAAAGGCTAG

20 6_Francisella tularensis subsp. holarctica_GI#
 89255957_Catalytic Ser Residue 99 (SEQ ID NO: 116)
 MEILNYILNLSFTFWLLFLTIASGLIYIIDFVFFQKSRLAAYTDELKGLSKKQKRQFYK
 DRGLKAPFIADQARSLFSVFFVFLRLRTFLIGNFLIPTASMTPTLPVGDFIFVNKTAYG
 25 IRAPFTNETLIKVGEPKRGDIVVFHFPVNPVDFVKRVIGLPGDVISYKDKMLTINGKK
 LEYTNCNRDAMNYYNQSLAAGSGDTVCTENLDGVKHEVDWIESIKGTDFENLKVPAGQY
 FVMGDNRDNSEDSRYWGFVPDKDLVGKAKVWMSWDKIDKKVRWDEIGKVF*

6_Francisella tularensis subsp. holarctica_GI#
 30 89255957_Catalytic Ser nucleotides 295-297 (SEQ ID NO: 117)
 ATGGAAATCTTAAACTATATTTTAACTTGAGCTTTACTTTTTGGCTTTTATTCTTAAC
 CATTGCCAGTGGTTTAATTTATATTATTGATTTTGTGTTCTTCCAAAAATCAAGATTAG
 CAGCATATACAGATGAATTAAAAGGTCTTTCTAAGAAGCAAAAACGTCAGTTCTATAAA
 GATAGAGGATTAAAAGCACCTTTTATTGCTGATCAGGCGAGATCTTTATTTAGTGTATT
 35 TTTTGTAGTTTTTCTACTTAGAACCTTCTTGATTGGTAATTTTTTAATTCCAACCTGCAT
 CAATGACACCAACACTTCCAGTTGGTGATTTTATTTTTGTCAATAAACTGCTTATGGT
 ATCAGAGCACCATTTACCAATGAGACTTTAATAAAAGTTGGTGAACCCAAAAGAGGTGA
 TATTGTAGTATTTTCATTTTCCAGTTAATCCTAATGTTGATTTTGTAAAACGAGTGATCG
 GTTTGCCTGGCGATGTAATTTTCGTATAAAGACAAAATGTTGACAATAAATGGTAAAAAA
 40 CTTGAATATACTAATTGTAATCGTGATGCAATGAACTATTATAATCAGTCTTTAGCTGC
 TGGTAGTGGCGATACAGTATGTACGGAAAACCTTGATGGAGTTAAACATGAGGTTGATT
 GGATAGAGTCTATAAAGGGAACCTGATTTTGAACCTTAAAGTCCCAGCAGGTCAATAC
 TTTGTCATGGGAGATAATCGTGATAATAGTGAAGATAGTCGTTATTGGGGTTTTGTACC
 TGACAAAGATCTAGTTGGTAAAGCAAAAGTTGTTTGGATGAGCTGGGATAAGATAGATA
 45 AAAAGGTTCTGCTGGGATGAAATTGGTAAGGTCTTTTAA

7_Campylobacter jejuni RM1221_GI# 57237697_Catalytic Ser
 Residue 38 (SEQ ID NO: 118)
 MEILKKLYKFSQSWTGTVVIVLLVIFFFIQAFVIPSGSMKNTLLVGDFLKVKKFSYGIP
 50 TPHIPWLEIPVLPDFNKGHLIKAQGSQRGDIVVFRNPRNEKEHFVKRCVGTGGDRIVY
 ANKTLYVRMHEGDEFMKEHYPNDLVTGGQIYVKEPYKQKGIHYDPKKDIESDILRFLS

IGDFAMSPTYIKELGNHIGFSGGNAYVFDVPENEYFMMGDNRDYSYDSRFWGSVPYRLI
VGKPFVYFVSWDKDKNVRWERIGRFVDLENDEQYIHDHDDKLS*

7_Campylobacter jejuni RM1221_GI# 57237697_Catalytic Ser
5 nucleotides 112-114 (SEQ ID NO: 119)
ATGGAAATTTTAAAGAAATTATATAAATTTTCACAGTCTTGGACTGGAAGTGTAGTTAT
TGTTCTTTTGGTGATTTTTTTCTTTATAACAAGCTTTTGTTATTCCTTCTGGTTCTATGA
AAAACACCTTATTGGTAGGGGATTTTTTATTTGTTAAAAAATTTAGCTATGGTATCCCA
ACTCCTCATATTCCTTGGTTGGAAATTCCTGTTTTGCCAGATTTCAATAAAGATGGGCA
10 TTGATAAAAGCACAAAGGGTCACAAAGAGGAGATATAGTTGTTTTTAGAAATCCTAGAA
ATGAAAAAGAACACTTTGTAAAGCGTTGTGTAGGCACAGGAGGAGATAGGATAGTTTAT
GCAAATAAAACACTTTATGTAAGAATGCATGAGGGTGATGAATTTATGAAAGAACATTA
TCCGAATGATCTTGTTACTCTTGGAGGGCAAATTTATGTAAAAGAACCTTATAAACAAA
AAGGTATTCATTATGATCCAAAAAAGATATAGAAAGCGATATTTTACGCTTTCTTAGC
15 ATAGGTGATTTTGCTATGTCTCCAACCTTATATTAAAGAACTTGGAAATCATATAGGTTT
TAGCGGCGGAAATGCTTATGTTTTTGATGTGCCTGAAAATGAGTATTTTCATGATGGGTG
ATAATCGCGATTATTCTTATGATAGTCGTTTTTGGGGTTCTGTTTCTTATAGGTTGATA
GTAGGTAAACCTTGGTTTGTATATTTCTCTTGGGATAAAGATAAAAATGTTTCGCTGGGA
AAGGATAGGGCGTTTTGTTGATACCTTGGAAAATGATGAACAATATATCCATGATCATG
20 ATGATGAGGATAAATTAAGCTAA

8_Helicobacter pylori HPAG1_GI# 108562981_Catalytic Ser
Residue 38 (SEQ ID NO: 120)
MKFLRSVYAFCSWVGTVIVLLVIFVFAQAFIIPSRSMVGTLYEGDMLFVKKFSYGIP
25 IPKIPWIELPIMPDKNNHGLIEGDRPKRGEVVVFIPHEKKSYYVKRNFAIGGDEVLF
TNEG FYLHPFESGNDKDYIAKHYPNAMTKEFMGKIFVLNPKYKSKHPGIHYQKDNETHL
MEQLATQGAEANISMQLIQMEGEKVIFYKKINSDEFFMIGDNRDNSSDSRFWGSVAYKNI
VGSPWFVYFSLSLKNSLEMDAENNPCKRYLVRWERMFKSVEGLEKIIKKEKATH*

8_Helicobacter pylori HPAG1_GI# 108562981_Catalytic Ser
nucleotides 112-114 (SEQ ID NO: 121)
ATGAAATTTTTACGCTCTGTTTATGCATTTTGCTCCAGTTGGGTAGGGACGATTGTTAT
TG TGCTGTTGGTTATCTTTTTTGTTGCGCAAGCTTTCATCATTCCTCTCGCTCTATGG
TAGGCACGCTCTATGAGGGCGACATGCTCTTTGTCAAAAAATTTTCTTACGGCATAACC
35 ATTCCTAAAATCCCATGGATTGAGCTTCCTATTATGCCTGATTTTAAAAATAACGGGCA
TTTGATAGAGGGGGATCGCCCTAAGCGCGGCGAAGTGGTCGTATTTATCCCCCCCCATG
AAAAAAAATCTTACTATGTCAAAAGGAATTTTGCCATTGGGGGCGATGAGGTGCTATTC
ACTAATGAGGGGTTTTATTTGCACCTTTTGAGAGCGGCAACGATAAAGATTATATTGC
TAAACATTACCCTAACGCCATGACTAAAGAATTTATGGGTAAAATTTTTGTTTTAAACC
40 CTTATAAAAGTAAGCATCCGGGTATCCATTACCAAAAAGACAATGAAACCTTCCACTTA
ATGGAGCAGTTAGCCACTCAAGGTGCGGAAGCTAATATCAGCATGCAACTCATTCAAAT
GGAGGGCGAAAAGGTGTTTTACAAGAAAATCAATAGCGATGAATTTTTCATGATCGGCG
ATAACAGAGACAATTCTAGCGACTCGCGCTTTTGGGGGAGTGTGGCTTATAAAAACATC
GTGGGTTCGCCATGGTTTGTATTTTTCAGTTTGAAGTTTAAAAAATAGCCTGGAAATGGA
45 TGCAGAAAACAACCCCAAAAAACGCTATTTGGTGCGTTGGGAACGCATGTTTAAAAGCG
TTGAAGGCTTAGAAAAAATCATTAAAAAAGAAAAAGCAACGCATTAA

9_Propionibacterium acnes J139_GI# 282854577_Catalytic Ser
Residue 69 (SEQ ID NO: 122)
50 VADDYRARRAANGDTRDSDDATARGEQASGWQRFRSGAIEVVLIIVVGALIISAVLRGFV
AQM FVIPSKSMQNTLQVGDRVIAVKAADFHRGDVVVFKDTEHWLPAVQDRRSVPGQILE

FVGLLPNKSSNYLIKRVIGMPGDTVACCNVNGQVTVNGKALDERSYLYSENGEMVKPSA
MEFRVTVPRGRMFVLGDHRNASGDSRYHLQDLDPGEYTGAPAFVPLDDVVGPAKAILMP
LNRIEGLGTPNTFRGIPDRSSSAPAKARICVGNTCCPK*

- 5 9_Propionibacterium acnes J139_GI# 282854577_Catalytic Ser
nucleotides 205-207 (SEQ ID NO: 123)
GTGGCGGATGACTACCGGGCGAGGCGGGCTGCAAACGGCGACACCAGGGACTCTGACGA
TGCAACAGCACGTGGGGAACAGGCGTCTGGGTGGCAGCGCTTTCGGTCGGGGGCCATCG
AAGTTGTTCTCATCGTCGTTGGTGCCCTCATCATCTCAGCTGTGCTGCGTGGTTTCGTC
10 GCTCAGATGTTTGTTCATCCCGTCGAAGTCCATGCAAAACACCTTGCAGGTGGGTGACCG
CGTGATCGCGGTGAAAGCCGCCGATTTTCATCGGGGCGACGTCGTCGTGTTCAAAGACA
CCGAACATTGGTTACCTGCTGTTTCCAGGATCGCCGCTCTGTTCCAGGACAGATCCTCGAA
TTCGTCGGGTTGTTGCCTAACAAGAGCTCGAACTACCTCATTAAGCGAGTGATCGGCAT
GCCTGGGGACACCGTTGCCTGCTGCAACGTCAACGGCCAGGTGACCGTCAACGGTAAGG
15 CGCTTGACGAGCGGTCATACCTGTACTCCGAAAATGGTGAAATGGTTAAACCCTCGGCG
ATGGAATTCCGGGTCACTGTTCCCTCGGGGGCGGATGTTTCGTCTTGGGGGACCATCGCAA
TGCCTCGGGTGACTCGCGCTATCACCTCCAAGACCTTGATCCGGGTGAGTATACGGGCG
CTCCTGCGTTTGTGCCGCTCGATGACGTCGTTGGGCCGGCAAAGGCCATTCTTATGCCT
CTCAATCGCATTGAGGGACTGGGGACTCCTAACACTTTCCGGGGAATCCCGGATAGGTC
20 GTCGTCAGCTCCAGCCAAGGCGCGCATCTGCGTCGGTAACACGTGCTGCCCTAAGTGA

- 10_Chlamydia trachomatis 434/Bu_GI# 166154241_Catalytic Ser
Residue 113 (SEQ ID NO: 124)
MTSSYMSRLYSLNKSRRILHSSFRLKSTKMLSHPETQKELQEVLKQLEEAILEDQNRED
25 ASLFAKQAQAIQKRFPKSKLRATFDLIYALTFAAILAFLIRQFWFELYEVPTGSMRPTI
LEQDRILVSKTTFGLRLPFSNRSIGYTPEAITRGELVVFTVGDLPINADTKYFGIIPG
KKRYIKRCMGKPGDTVYFYGGKIYGIDCDGEPIFPQNTENLYHVPYISFDGTPEILTHS
EEQTDVIFNQFHTPCGKISLPQQASYGQFFYKNAWHNDTPYALKDPHNEPVSADLFGI
KNFAMVRILTKKQAALTHVLPSPSLDYLEIAHTPNVSYPHPLRPFETQLIPTIEPMK
30 TLLPLRKEHIHLIRNNLTTSRFTVVDGYAYKYQPAPMNTSGMVRMFALPMPNIPDGCYE
FSKGDVFKINMGGFRTKLKQPHPLTQLSNSQVIDLFNCGISFHTIYIPKNPQYAPFPNR
YAFFNQGNL FVMDSPVFIDSDPALQKFIVSEEEKELQSSSEDKPYIAFIDRGPPPESTEE
FVSFITNFGKIPFGHVLVLGDNC PMSADSRDFGFVPVENLLGSPVGIFWPINRLGLLS
SNITPLSLPGYLVNGLALGAFLYCIGLWYYRKNHRLFP*

- 35 10_Chlamydia trachomatis 434/Bu_GI# 166154241_Catalytic Ser
nucleotides 337-339 (SEQ ID NO: 125)
ATGACGAGCAGTTACATGAGTCGCTTATATTCCTGAATAAGAGTCGTCGCATTCTTCA
TTCTTCCTTTAGATTGCTGAAAAGCACAAAAATGCTCTCTCATCCGGAAACTCAAAAAG
40 AACTACAAGAAGTCTTGAAACAGCTTGAAGAGGCTATTTTGGATCAGAATAGGGAAGAT
GCTTCCCTTTTTGCTAAGCAAGCTCAAGCCATACAAAAAAGATTCCCTAAATCCAACT
CCGAGCTACTTTTGATCTTATCTATGCTTTGACGTTTGCTGCCATTCTTGCTTTTTTTAA
TCCGCCAGTTCTGGTTTGAGCTATATGAAGTTCCTACAGGATCTATGCGGCCTACTATT
CTTGAACAAGATCGTATTCTTGTTTCCAAAACAACATTTGGACTCCGGCTACCTTTTAG
45 TAACAGAAGTATTGGCTATACACCTGAGGCTATCACTCGAGGAGAACTGGTAGTCTTCA
CTGTTGGAGATCTTCCTATCCCTAATGCCGACACTAAGTATTTTGGAAATCATCCCTGGG
AAAAAACGCTATATAAAACGGTG CATGGGTAAACCTGGAGATACCGTATATTTTTATGG
AGGGAAAATTTATGGGATCGATTGCGACGGAGAGCCCATCTTCCCCCAAATAACAGAGA
ATCTCTACCACGTCCCCTATATTTCTTTTGACGGAACTCCAGAAATTCTTACCCATTCA
50 GAAGAGCAAACAGATGTGATCTTTAACCAATTTACACACCTTGTGGAAAGATTTCTCT
CCCTCAACAGGCTTCTTATGGACAATTTTCTATAAGAATGCTTGGCATAATGATACTC

- CCTATGCTTTTAAAAGATCCTCATAATGAGCCTGTTAGCTATGCCGATCTATTCGGAATA
 AAAAATTTTGGCAATGGTTTCGCATCCTTACCAAAAAACAAGCTGCTCTTACTCATGTCCT
 TCCCTCTCCTCTTTTCGGACACCTACCTAGAAATTGCCCACACTCCTAATGTTTCCTATC
 CTCACCCTCACTTACGTCCATTTGAAACACAGCTTATTCCTACTATCGAACCTATGAAA
 5 ACCTTGCTTCCTTTAAGGAAGGAACATATTCATTTGATTCGTAATAACCTCACAACATC
 CCGTTTTACAGTTGTAGATGGATATGCTTACAAGTACCAACCTGCTCCCATGAATACCT
 CAGGCATGGTCAGGATGTTTGCCCTACCTATGCCAAATATTCCTGACGGATGTTATGAA
 TTTTCTAAAGGAGACGTGTTTAAAATCAATATGGGTGGCTTTTCGAACAAAACCTCAAACA
 GCCGCATCCTTTAACGCAATTAAGCAATTCTCAGGTCATTGACTTATTTAATTGCGGCA
 10 TTAGTTTCCACACGATCTATATTCCTAAAAACCCTCAATATGCTCCGTTCCCTAATCGC
 TATGCATTTTTCAATCAAGGGAACCTGTTTCGTTATGGATTCTCCAGTTTTTTATTGATAG
 CGATCCTGCCTTACAGAAATTCATTGTGTCTGAAGAGGAAAAAGAACTTCAATCATCTG
 AAGACAAACCTTACATCGCATTTATTGACAGAGGTCCTCCTCCAGAATCTACAGAGGAA
 TTTGTTTCCTTTATTACTAATTTCCGGTCTTAAAATTCGGGAAGGCCACGTGCTTGTCTT
 15 AGGAGATAATTGTCCTATGAGCGCTGATAGCCGTGATTTTGGTTTTGTTCCCGTTGAAA
 ATCTTTTGGGATCTCCTGTTGGGATCTTCTGGCCTATTAATCGTCTAGGATTGTTATCT
 TCCAATATAACGCCCTTGAGTTTACCTGGCTACCTCGTAAATGGATTGGCTCTAGGAGC
 TTTTCTTTACTGCATAGGATTATGGTACTATCGAAAAAACCATAGGCTATTCCCTTAA
- 20 11_Chlamydomonas reinhardtii C1029_GI# 15618034_Catalytic
 Ser Residue 108 (SEQ ID NO: 126)
 MKQHYSLNKSRLHILRSTYKLLKSKKLAHSPADKKQLQELLEQLLEEAI FEHDQETASDLA
 QQALAFSNRYPNSFGRKTYELIKALLFAGVVAFLVRQFWFELYEVPTGSMRPTILEQDR
 ILVSKTTTFGLHCPFAKKPLAFNPESVTRGGLVFTVVDLPIDADTKYFGLIPGKKRYI
 25 KRCMGRPGDFLYFYGGKIYGLDDAGKRIEFPSVHGLENLVHVPYISFDGTTSSHTEGQK
 TIIDFKQFNQSYGRLIFPQTSMYGQFFDHKEWHQDEPNKLKDPHLSPVSYADLFGMGNY
 AMVRILTEHQARTSHLLPNPGSPTKVYLEICHTANLSYPKPLLRHYEHQLSPA IQPMKT
 LLPLRKEHLHLIRNNLTTSRFIVAQGCAYKYHQFKINTSGIAKAYAILLPKVPDGCY EY
 SKGEAYQIGFGEIRYKLKSSHPLTQLNDKQVIELFNCGINFSSIYNPNVNLQAPLPNRY
 30 AFFNQGNLYIMDSPVFIKNDPTLQKFVTSETEKQEGSSETQPYIAFVDKGLPPEDFKEF
 VEFIHNFGIQVPGKHVVLVDNYPMSADSREFGFVPMENLLGSPLCTFWPIGRMGRLTG
 VSAPTTLSGYLVSGIALATGLSLIGYVYYQKRRRLFPKKEEKNHKK*
- 35 11_Chlamydomonas reinhardtii C1029_GI# 15618034_Catalytic
 Ser nucleotides 322-324 (SEQ ID NO: 127)
 ATGAAACAACACTATTCTCTAAATAAAAGTCGTCATATCCTCCGCAGTACTTATAAGCT
 TTTAAAAAGTAAAAAACTCGCCCATTCCTTGCAGATAAAAAGCAACTGCAAGAACTAC
 TAGAACAACCTAGAAGAGGCTATCTTTGAACATGATCAAGAACTGCAAGCGACTTAGCT
 CAGCAAGCATTAGCATTTTCCAACCGTTATCCTAATTCCTTCGGACGCAAAACCTATGA
 40 GCTTATCAAGGCCCTTCTTTTTGCTGGTGTGTTAGCCTTCTTAGTTTCGGCAATTTTGGT
 TTGAACTTTATGAAGTGCCTACAGGATCCATGAGGCCTACAATTTTAGAACAGGATCGG
 ATTCTTGTATCCAAAACAACATTTGGTCTCCATTGCCCTTTTGCTAAGAAACCACTTGC
 CTTCAATCCTGAATCCGTAACCTCGCGGGGGTCTTGTGTTTTTCACTGTAGGCGACCTCC
 CTATCCCAGATGCTGATACAAAGTACTTCGGATTGATTCCAGGAAAAAAGCGTTACATT
 45 AAACGTTGCATGGGAAGACCTGGGGACTTCTTATATTTCTATGGAGGAAAAAATTTATGG
 TCTTGATGATGCAGGTAAACGCATAGAGTTTCCTTCTGTCCATGGTTTAGAAAACTTAT
 ATCACGTCCCCTATATATCCTTTGATGGCACTACCAGCAGCCATACAGAAGGGCAGAAA
 ACAATTATAGATTTTAAAGCAGTTCAATCAAAGTTATGGTCGGCTGATTTTCCCTCAAAC
 CTCCATGTATGGACAATTCTTTGACCATAAAGAATGGCATCAAGACGAGCCTAATAAAT
 50 TAAAAGATCCTCATCTTTTCGCCAGTCAGCTATGCCGATCTTTTTGGTATGGGTAACTAT
 GCTATGGTGCGCATCTTAACAGAACATCAGGCACGAACATCCCATCTACTTCCGAATCC

AGGAAGTCCAACTAAAGTCTACTTAGAAATTTGCCATACAGCGAACCTTTCCTACCCAA
 AGCCTCTGTTGCGTCACTATGAGCATCAGCTCTCGCCTGCGATTCAACCTATGAAGACT
 TTACTIONCTTTGCGTAAGGAACATTTGCACTTAATTCGGAACAATCTTACTACCTCTCG
 TTTTATTGTTGCTCAAGGATGTGCGTATAAATACCATCAATTCAAGATTAACACTTCAG
 5 GAATTGCCAAAGCCTATGCAATTCTCCTGCCCAAGGTCCCTGATGGTTGTTATGAATAT
 TCTAAAGGCGAAGCGTATCAAATTGGCTTTGGAGAGATTTCGTTATAAGCTAAAATCTTC
 TCACCCCCTTACTCAGCTCAATGATAAGCAAGTGATTGAACTTTTTAACTGCGGGATCA
 ACTTTAGTTCTATTTATAATCCTGTGAATCCGCTGCAAGCACCTTTACCTAACCGTTAT
 GCATTCTTTAACCAAGGGAATCTTTATATCATGGATTCTCCTGTATTTATAAAGAATGA
 10 TCCAACCTCTGCAAAAATTTGTGACTTCTGAAACGGAAAAGCAAGAGGGGTCTTCAGAGA
 CACAACCCTATATAGCTTTTGTGACAAGGGACTCCCTCCAGAAGATTTTAAAGAATTC
 GTGGAGTTTATACATAATTTTGGTATTCAAGTTCCTAAAGGTCATGTTCTCGTCTTGGG
 AGATAACTACCCTATGAGTGCGGATAGTCGAGAATTTGGCTTTGTTCTATGGAAAATC
 TCTTAGGATCTCCTCTATGTACATTCTGGCCTATTGGACGCATGGGACGGTTAACTGGA
 15 GTTTCTGCTCCAACAACACTCTCAGGTTATCTTGTTAGTGGGATAGCATTAGCGACGGG
 TCTCTCTCTCATTGGATATGTCTACTATCAAAAACGACGCAGACTCTTTCCTAAGAAAG
 AGGAGAAAAACCACAAGAAATAA

12_Staphylococcus carnosus subsp. carnosus TM300_GI#
 20 224476066_Catalytic Ser Residue 36 (SEQ ID NO: 128)
 VKKEIKEWIIAIAIALVVLVITNFIKSYTVRGDSMYPTLKDGEKVIIVNMIGFKTGGL
 EKGNVIVFHATKNSDYVKRVIGMPGDSIEYKHDQLVNGKKVKEPYLDYNEKHKSDEI
 TGSFKVKNLPNANGSNTIPKNKLLVLGDNREVSKDSRSFGLIDEDQVVGKVSRLRYWPF
 SFKVNFPDNTKY*

25 12_Staphylococcus carnosus subsp. carnosus TM300_GI#
 224476066_Catalytic Ser nucleotides 106-108 (SEQ ID NO:
 129)
 GTGAAGAAAGAAATTAAAGAGTGGATAATAGCCATAGCAATAGCTTTGGTATTAGTTCT
 30 AGTCATAACAAATTTTATTGCGAAATCATATACGGTTCGTGGTGATTCAATGTATCCAA
 CGCTAAAAGACGGAGAAAAAGTTATCGTTAATATGATTGGATTTAAACTGGCGGTTTA
 GAAAAAGGTAATGTGATTGTATTCCACGCTACTAAAAACAGCGACTACGTTAAACGTGT
 TATCGGTATGCCTGGTGACAGTATTGAATATAAACATGATCAATTGTATGTTAATGGTA
 AAAAAGTGAAAGAACCTTATTTAGATTATAATGAAAAACATAAAAGCTATGATGAAATT
 35 ACAGGTAGCTTTAAAGTGAAAAATTTACCTAATGCAAATGGTTCAAACACAATTCCTAA
 AAACAAACTTCTTGTATTAGGAGATAACCGTGAAGTCAGTAAAGACAGCCGTTTCATTG
 GTTTAATTGATGAAGATCAAGTTGTTGGTAAAGTAAGCTTGCCTTATTGGCCGTTTACA
 TCTTTCAAAGTAACTTTAATCCGGATACAAAATATTAA

40 13_Staphylococcus haemolyticus JCSC1435_GI#
 70726986_Catalytic Ser Residue 36 (SEQ ID NO: 130)
 LKKEIVEWIVAVGLLLVWVMVNFVAKSYTIKGSMDPTLKDGEHVMVNILGYKVGDI
 KKGNVIVFHANQQDDYVKRVIGVPGDNVIYKNDKLYVNGKKINEPYLDYNEKRKQGEYI
 TGSFETKDLLNANPKSNIIPKGKYLVLGDNREVSKDSRAFGGLIDRDQIVGKVSFRFWPF
 45 SEFKFNFPDNEK*

13_Staphylococcus haemolyticus JCSC1435_GI#
 70726986_Catalytic Ser nucleotides 106-108 (SEQ ID NO: 131)
 TTGAAGAAAGAAATAGTTGAATGGATTGTTGCCATAGCGGTAGGTTTATTACTTGTATG
 50 GGTAATGGTTAACTTCGTAGCTAAATCATATACTATAAAAGGCGATTCAATGGATCCAA
 CACTAAAAGATGGCGAACACGTCATGGTTAACATTCTAGGATATAAAGTTGGAGACATA

AAAAAAGGTAATGTAATCGTATTTTCATGCGAATCAACAAGACGATTATGTTAAACGTGT
 CATTGGTGTACCTGGCGATAACGTTATTTATAAAAATGATAAACTATATGTTAATGGTA
 AAAAGATAAATGAACCTTATCTTGATTACAATGAAAAACGTAAACAAGGTGAATATATT
 ACGGGTTCATTTGAAACTAAAGATTTACTAAATGCAAATCCTAAATCAAATATCATACC
 5 AAAAGGTAAATACTTAGTTTTAGGTGATAACAGAGAAGTCAGTAAGGATAGTAGGGCGT
 TTGGTTTAATTGATAGAGATCAAATTGTTGGTAAAGTATCATTTAGATTTTGGCCATTC
 AGTGAATTTAAGTTTAATTTTAATCCAGATAATGAAAAATAA

14_Staphylococcus haemolyticus JCSC1435_GI#
 10 70727661_Catalytic Ser Residue 36 (SEQ ID NO: 132)
 LKKEIIEWIVAIGGALLIVGIVLKFIFGTSYTVSGSSMYPTFQDRNKVIVSKISKTLNHI
 DNGDVVVFHEDAQRDFIKRVIGTPGDKVEYEGDQLYVNDKKVSEPYLDYNKKHKQGGKYL
 TGTFKTSQVNGANGKNKIPKDKYLVLDNRQNSVDSRLAEVGLVDKDQLVGKVVLRYWP
 FNKWEAGFNPGTF*

15 14_Staphylococcus haemolyticus JCSC1435_GI#
 70727661_Catalytic Ser nucleotides 106-108 (SEQ ID NO: 133)
 TTGAAAAAGAGATAATTGAATGGATTGTAGCCATTGGTGGCGCACTCTTAATTGTAGG
 TATTGTATTAAAGTTTATTGGAACATCATAACAGTATCAGGTTTCATCGATGTATCCAA
 20 CTTTCCAAGATAGAAATAAAGTGATAGTTAGTAAGATTTGAAAACATTGAACCACATT
 GATAATGGTGATGTCGTTGTCTTCCATGAAGATGCACAACGTGATTTTATTAAGCGTGT
 GATTGGTACGCCAGGTGATAAAGTTGAGTATGAAGGTGATCAATTATATGTTAATGACA
 AAAAGGTATCAGAGCCTTATTTAGATTATAATAAGAAGCATAAACAAGGTAAGTATTTA
 ACAGGTACATTTAAACAAGCCAAGTGAACGGAGCAAATGGTAAAAATAAAATTCCTAA
 25 AGATAAGTATTTAGTTTTAGGTGATAACAGACAAAATAGTGTAGATAGCCGTTTGGCTG
 AAGTTGGTTTAGTAGATAAAGACCAACTTGTAGGTAAAGTTGTTTTAAGATATTGGCCA
 TTTAATAAATGGGAAGCAGGTTTTAACCCAGGCACATTTTAG

15_Staphylococcus epidermidis ATCC 12228_GI#
 30 27467580_Catalytic Ser Residue 36 (SEQ ID NO: 134)
 LKKEIIEWIVAIAVAIALIAIITKFVGKSYSIKGDSMDPTLKDGERVVVNIIGYKLGGV
 EKGNVIVFHANKKDDYVKRVIGTPGDSVEYKNDTLYVNGKKQSEPYLNYNEKRKQTEYI
 TGSFKTKNLPNANPQSNVIPKGKYLVLGDNREVSKDSRSFGLIDKDQIVGKVSLRYWPF
 SEFKSNFNPNTKN*

35 15_Staphylococcus epidermidis ATCC 12228_GI#
 27467580_Catalytic Ser nucleotides 106-108 (SEQ ID NO: 135)
 TTGAAAAAGAAATTTTAGAGTGGATTGTTGCCATAGCCGTTGCCATTGCACTTATTGC
 CATAATCACTAAATTTGTCGGAATCATATTCTATTAAAGGTGATTCAATGGATCCTA
 40 CATTAAAAGATGGGGAGCGTGTAGTGGTAAATATTATTGGCTATAAATTAGGTGGCGTT
 GAAAAAGGAAATGTCATTGTATTTTCATGCTAATAAAAAAGATGATTATGTTAAAAGAGT
 TATTGGAACCTCCAGGAGATAGTGTGAATATAAAAAATGATACACTCTATGTTAATGGTA
 AAAAGCAATCAGAACCATACTTGAACATAATGAAAAACGTAAAGCAAAGTATATC
 ACAGGTAGTTTCAAACAAAAAATTTACCAAATGCTAATCCTCAATCTAATGTTATTCC
 45 TAAAGGTAAATATTTAGTTTTGGGGGATAACCGTGAGGTAAAGTAAAGATAGTCGTTTCAT
 TCGGTTTAATTGACAAAGACCAAATTGTTGGAAAGGTATCGCTCAGATATTGGCCTTTC
 AGTGAATTTAATCTAACTTTAATCCAAATAACACTAAAAATTAA

16_Staphylococcus epidermidis ATCC 12228_GI#
 50 27469315_Catalytic Ser Residue 36 (SEQ ID NO: 136)

MKKEIIIEWIVAIIVVAIVIVTLVQKFLFASYTVKGASMHPTFENREKVIVSRIAKTLDHI
DTGDVVIFHANAKQDYIKRLIGKPGDSVEYKKDQLYLNGKKVDEPYLSENKKHKVGEYL
TENFKSKDLKGTNGNMKIPSGKYLVLGDNRQNSIDSRMDEVGLLDKNQVVGKVVLRYWP
FNRWGGSFNPGTFPN*

5

16_Staphylococcus epidermidis ATCC 12228_GI#
27469315_Catalytic Ser nucleotides 106-108 (SEQ ID NO: 137)
ATGAAGAAAGAAATAATAGAATGGATTGTAGCCATAATCGTTGCAATTGTTATCGTCAC
ACTTGTGCAAAAGTTTTTATTTGCTTCTTATACAGTCAAAGGAGCGTCTATGCATCCAA
10 CATTGAAAATAGAGAAAAAGTGATAGTAAGTCGTATAGCAAAAACACTTGATCATATT
GATACAGGAGATGTAGTGATTTTTTCATGCTAACGCGAAGCAAGATTATATTAAGCGACT
TATTGGTAAACCAGGTGATTCAGTAGAATATAAAAAAGATCAACTATATTTAAACGGTA
AAAAAGTAGATGAGCCTTATTTAAGTGAAAATAAAAAACATAAAGTTGGAGAATATCTA
ACGGAAAACCTTTAAGTCTAAAGATCTTAAGGGTACGAATGGCAATATGAAAATTCCTAG
15 TGGTAAATACTTGGTTTTAGGTGATAATCGTCAAAACAGTATTGACAGTCGCATGGATG
AAGTAGGTCTTTTAGATAAAAAATCAAGTTGTTGGAAAAGTAGTTTTTGAGATACTGGCCA
TTTAATCGGTGGGGCGGTAGTTTTAATCCTGGAACATTTCTAACTAA

17_Staphylococcus hominis SK119_GI# 228474322_Catalytic Ser
20 Residue 36 (SEQ ID NO: 138)
LKKEITEWIVAIIVGLLLVWLTVVTFVAKSYTIKGDSDPTLKDQGHVMVNILGYKVGNI
KKGNVIVFHANQSDDYVKRVIGVPGDSVTYKKDQLYINGKKVNEPYLDYNEKHKQGEYI
TGSFETKDLLNAHPNSNVIPKNKYLVLDNREVSKDSRAFGGLIDKQQIVGKVSFRFWPL
NNFKFNFPDK*

25

17_Staphylococcus hominis SK119_GI# 228474322_Catalytic Ser
nucleotides 106-108 (SEQ ID NO: 139)
TTGAAAAAGAAATAACAGAATGGATTGTTGCGATAGCTGTAGGTTTATTGCTCGTATG
GCTTGTAGTCACTTTTGTGTCCTTCCATGCTAATCAATCTGATGACTATGTTAAAAGAGT
30 CATTAAAAGATGGGCAACATGTGATGGTTAACATTTTAGGTTATAAGGTAGGAAACATA
AAAAAGGAAATGTTATTGTCTTCCATGCTAATCAATCTGATGACTATGTTAAAAGAGT
AATAGGCGTACCAGGAGATAGTGTGACATATAAAAAAGATCAGCTATATATTAATGGGA
AAAAGGTAAATGAGCCTTACTTAGACTATAATGAAAAACATAAACAAGGAGAGTACATT
ACTGGATCTTTTGAAACTAAGGATCTTCTTAATGCTCATCCTAACTCTAACGTTATTCC
35 TAAAAATAAATACTTAGTATTAGGAGATAACCGTGAAGTTAGTAAAGATAGTAGAGCGT
TTGGATTAATAGATAAACAACAAATCGTCGGTAAAGTATCATTTAGATTTTGGCCATTA
AATAATTTTAAATTTAATTTTAATCCAGATAAGTAG

18_Staphylococcus lugdunensis HKU09-01_GI#
40 289551204_Catalytic Ser Residue 36 (SEQ ID NO: 140)
VKKELTEWLIIVGIIILVILIINFVAKSYTIKGDSDMNPTLKDGDHVLVNIIGYKVGTV
KKGNVIVFHANQKDDYVKRVIGTPGDKVYYRDDQLIINGKKVKEPYLEYNMKRKQGEYI
TGSLDIKDLAGAKHNSNVIPQHKYLVLDNREVSKDSRAFGGLIDEKQIVGKVSLRFWPL
TDFKFNFNPDM*

45

18_Staphylococcus lugdunensis HKU09-01_GI#
289551204_Catalytic Ser nucleotides 106-108 (SEQ ID NO:
141)
GTGAAAAAGGAATTGACAGAATGGTTAATAGCTATAGCGGTAGGTATTATTTTAGTCAT
50 ACTAATCATTATTTTGTAGCGAAATCATATAACCATTAAGGAGACTCAATGAATCCAA
CATTAAAAGATGGCGATCATGTTCTGGTCAATATTATCGGCTATAAAGTAGGCACTGTG

- AAAAAGGGGAATGTCATTGTCTTCCATGCTAACCCAAAAGGATGATTATGTTAAACGCGT
TATAGGCACACCAGGTGACAAAGTATACTATCGAGATGATCAACTTATTATAAACGGAA
AAAAAGTAAAAGAACCTTATCTCGAATAACAATATGAAACGTAAGCAAGGAGAGTATATT
ACTGGATCTTTAGATATAAAAGATTTGGCCGGTGCAAAACATAATTCTAATGTCATACC
5 TCAACATAAATACTCGTGTTAGGAGACAATCGTGAGGTAAGTAAAGATAGCCGTGCTT
TTGGCCTTATCGATGAAAAGCAAATTGTCGGTAAAGTGTCTTTAAGATTTTGGCCATTA
ACTGATTTTAAATTTAATTTTAACCCTGATATGAGCTAA
- 19_Staphylococcus lugdunensis HKU09-01_GI#
10 289551814_Catalytic Ser Residue 36 (SEQ ID NO: 142)
VKKEILEWIVSIAVALIIVGIVVKFIGVTYSVSGDSMYPTFKDREKVVVSKISKTL DHI
DNGDIVVFKEDKDRDFIKRLIGKPGDKVEYKGDQLYVNNKKIDEPYLYNKEHKNGKYL
TGSFKSSDLQNaNGETKIPKDKYLV LGDN RQNSLDSRFPQVGLIDKEQIVGKVVLRFWP
FGEWTTKFNP GTFDK*
- 15 19_Staphylococcus lugdunensis HKU09-01_GI#
289551814_Catalytic Ser nucleotides 106-108 (SEQ ID NO:
143)
GTGAAAAAAGAGATCTTAGAGTGGATTGTGTCTATAGCAGTTGCACTTATCATTGTAGG
20 TATAGTTGTTAAATTTATTGGAGTTACATATTCAGTTTCGGGAGATTCAATGTATCCAA
CATTTAAAGATAGAGAAAAAGTAGTAGTGAGTAAAATTTCCAAAACGTTAGACCATATT
GATAATGGTGATATCGTTGTCTTTAAAGAAGATAAAGATAGAGACTTTATTAAACGTTT
AATTGGTAAACCTGGAGACAAAGTTGAGTATAAAGGTGACCAACTATATGTTAATAATA
AAAAAATTGATGAGCCTTATTTAAAATATAACAAAGAGCATAAAAATGGTAAGTATCTG
25 ACAGGTTCTTTCAAATCGAGTGATTTGCAAAATGCTAATGGTGAGACGAAGATTCCTAA
AGACAAATATTTAGTGTTAGGTGATAATCGTCAAAACAGTTTAGATAGTCGTTTTCCAC
AGGTAGGGCTTATTGATAAAGAACAAATTGTAGGTAAAGTTGTGTTACGTTTCTGGCCA
TTTGGTGAGTGGACAACAAAATTTAATCCTGGAACATTTGATAAGTAA
- 30 20_Streptococcus agalactiae COH1_GI# 77408620_Catalytic Ser
Residue 58 (SEQ ID NO: 144)
MKRQISSDKLSQELDRVITYQKRFWSVIKNTIYILMAVASIAILIAVLWLPVLRIYGHSM
NKTLSAGDVVFTVKGSNFKTG DVVAFYNNKVLVKRVIAESGDWVNIDSQGDVYVNQHK
35 LKEPYVIHKALGNSNIKYPYQVPDKKIFVLGDN RKTSIDSRSTSVGDVSEEQIVGKISF
RIWPLGKISSIN*
- 20_Streptococcus agalactiae COH1_GI# 77408620_Catalytic Ser
nucleotides 172-174 (SEQ ID NO: 145)
40 ATGAAAAGACAGATTAGTTCAGATAAATTATCTCAAGAACTGGATCGCGTAACTTATCA
GAAACGCTTTTGGAGTGTCATTAAAAATACCATATACATCTTGATGGCGGTTGCCTCAA
TAGCCATTTTAATTGCGGTTTTATGGTTGCCTGTATTAAGAATCTACGGACATTCAATG
AATAAGACTTTAAGTGCAGGTGATGTAGTCTTTACAGTAAAAGGTTCAAATTTTAAAC
TGGAGACGTTGTCGCGTTTTACTACAATAAAGGTCCTAGTCAAGCGGGTTATTGCAG
45 AGTCAGGAGACTGGGTAAATATTGATTCTCAAGGGGATGTTTACGTGAATCAACATAAG
TTGAAAGAACCATATGTTATTCATAAAGCACTCGGTAAATAGTAATATAAAATACCCATA
TCAAGTACCTGATAAAAAAATTTTTGTATTAGGAGACAACCGAAAACTTCAATTGATT
CTCGAAGTACTTCTGTAGGAGATGTTTCAGAAGAACAAATTGTAGGTAAATTTCTTTC
AGAATATGGCCTCTAGGTAAGATTAGTAGTATCAATTAA
- 50

21_Streptococcus agalactiae COH1_GI# 77409453_Catalytic Ser
Residue 35 (SEQ ID NO: 146)

MKEFIKEWGVFILILSLFLLSRIFLWQFVKVDGHSMDPTLADKEQLVVLKQTKINRFDI
VVANEEEGGQKKKIVKRVIGMPGDVIKYKNDTLTINNKKTEEPYLKEYTKLFFKKDKLQE
5 KYSYNPLFQDLAQSSSTAFTTDSNGSSEFTTVVPGHYYLVGDDRIVSKDSRAVGSFKKS
TIVGEVKFRFWPIRRFGTIN*

21_Streptococcus agalactiae COH1_GI# 77409453_Catalytic Ser
nucleotides 103-105 (SEQ ID NO: 147)

10 ATGAAAGAATTTATTAAAGAATGGGGTGTCTTTATCCTCATCCTCTCACTTTTTTTTACT
ATCGCGTATCTTTTTATGGCAATTCGTTAAAGTTGACGGACACTCCATGGATCCAACCTT
TAGCTGACAAGGAACAGCTAGTAGTTCTCAAACAAACAAAAATCAATCGATTGATATT
GTAGTGGCTAACGAAGAAGAAGGCGGCCAAAAGAAAAAAATTGTTAAACGTGTCATTGG
TATGCCAGGTGATGTCATCAAATATAAAAATGACACCTTAACCTATTAACAATAAAAAAA
15 CAGAAGAACCTTACCTCAAGGAATATACTAAATTATTTAAAAAGGATAAATTACAGGAA
AAATATTCGTATAACCCACTTTTCCAAGACCTAGCACAAAGCTCTACCGCTTTCACCAC
TGACAGCAATGGCAGCAGCGAATTTACTACTGTGTCGTGCCTAAAGGCCACTACTATCTTG
TTGGTGATGACCGAATTGTCTCTAAAGATAGTCGTGCCGTCGGTTCCTTCAAAAAATCA
ACGATTGTGGGAGAGGTTAAATTCCGCTTCTGGCCAATTCGTGCTTTTGGAACCTATCAA
20 CTAA

22_Streptococcus dysgalactiae subsp. equisimilis
GGs_124_GI# 251783284_Catalytic Ser Residue 35 (SEQ ID NO:
148)

25 MKHFIKEWGPFTLFLILFGLSRLFLWQAVKVDGHSMDPTLAHGERLIVLNQARIDRFDI
VVAREEENGQKKEIVKRVVGMPGDTIAYNDDTLYINGKKTDPEYLVNYLKEFKKDKLQK
TYAYNSLFQQLAETSDAFTTNAEGQTRFEISVPEGEYLLLGGDDRIVSRDSREVGSGFKKE
KLIGEVKARFWPLNKMFLFK*

30 22_Streptococcus dysgalactiae subsp. equisimilis
GGs_124_GI# 251783284_Catalytic Ser nucleotides 103-105
(SEQ ID NO: 149)

ATGAAACATTTTATTAAAGAATGGGGCCCATTTACCCTCTTTCTCATCCTCTTCGGTTT
ATCTCGTCTTTTCTTGTGGCAAGCTGTAAAGTTGATGGCCACTCCATGGACCCTACGT
35 TAGCCCATGGGGAACGTCTCATTGTTTTAAACCAAGCTAGAATTGACCGTTTCGATATT
GTCGTTGCCCGTGAGGAAGAAAATGGGCAGAAAAAAGAAATTGTCAAACGAGTTGTCGG
CATGCCAGGTGATACCATTGCCTACAACGATGATACGCTTTACATTAATGGTAAAAAAA
CAGATGAGCCTTACCTAGTTAACTACCTTAAAGAGTTCAAAAAGGACAAGCTTCAAAAG
ACTTACGCTTACAATAGTCTATTTTCAGCAATTAGCTGAAACATCGGATGCCTTCACCAC
40 TAATGCTGAAGGTCAAACACGTTTTTGAAATCAGTGTACCAGAAGGTGAATACCTCCTTC
TTGGAGATGACCGAATTGTCTCACGCGACAGCCGTGAAGTTGGTAGTTTTTAAAAAAGAA
AAACTTATCGGTGAAGTCAAGGCTCGCTTCTGGCCACTCAATAAAATGACTCTTTTTTAA
GTAA

45 23_Streptococcus mitis B6_GI# 289168569_Catalytic Ser
Residue 38 (SEQ ID NO: 150)

MNSFKNFLKEWGLFLLILSLLALSRIFFWSNVRVEGHSMPTLADGEILFVVKHLPIDR
FDIVVAHEEDGNKDIVKRVIGMPGDTIRYENDKLYINDKETDEPYLADYIKRFKDDKLQ
STYSGKGFEGNKGTFFRSIAEKAQAFTVDVNYNTNFSFTVPEGEYLLLGGDRLVSSDSR
50 HVGTFKAKDITGEAKFRFWPITRIGTF*

- 23_Streptococcus mitis B6_GI# 289168569_Catalytic Ser
nucleotides 112-114 (SEQ ID NO: 151)
ATGAATTCATTTAAAAATTTCTTAAAGAGTGGGGATTGTTCTCCTGATTCTGTCATT
ACTAGCTTTGAGCCGTATCTTTTTTTTGGAGTAATGTCCGCGTAGAAGGGCATTCATGG
5 ATCCGACCCTAGCGGATGGCGAAATTCTCTTCGTTGTCAAACACCTTCCTATTGACCGT
TTTGATATCGTGGTGGCCCATGAGGAAGATGGCAATAAGGACATCGTCAAGCGCGTGAT
TGGAATGCCTGGCGATACTATCCGTTACGAAAACGATAAACTTTACATCAATGATAAAG
AGACGGACGAACCTTACCTAGCTGACTATATCAAACGTTTCAAGGATGACAACTCCAA
AGCACCTACTCAGGCAAGGGCTTTGAAGGAAATAAAGGAACCTTCTTTAGAAAGTATTGC
10 GGAAAAAGCTCAAGCCTTCACAGTTGATGTCAACTATAACACCAACTTTAGCTTTACTG
TTCCAGAAGGAGAATAACCTTCTCCTCGGAGACGACCGCTTGGTTTCTAGCGACAGCCGT
CACGTAGGTACCTTCAAAGCAAAAGATATCACAGGGGAAGCTAAATTCCGCTTCTGGCC
AATCACCCGTATCGGAACATTTTAA
- 15 24_Streptococcus oralis ATCC 35037_GI# 293364826_Catalytic
Ser Residue 38 (SEQ ID NO: 152)
MNSFKTFLKEWGVFFLIILVGLSRIFLWSNVRVEGHSM DPTLADGEVLFVVKHLPIDR
FDIVVAHEEDGNKDIVKRVIGMPGDTIRYENDKLFINGEETNEPYLAEYLNLFKTEKLQ
NTYTGKGFEGNKG VYFRELAQKAQAFTVDVNSNTRFSFTVPQGEYLLL GDDRLVSSDSR
20 HVGTFKASDIKGEAKFRFWPLNRIGTF*
- 24_Streptococcus oralis ATCC 35037_GI# 293364826_Catalytic
Ser nucleotides 112-114 (SEQ ID NO: 153)
ATGAATTCGTTTAAACATTTCTTAAAGAATGGGGAGTTTTCTTCCTGATTATCGCACT
25 GGTCGGTCTTAGCCGCATCTTTCTTTGGAGCAATGTCCGTGTGGAAGGACACTCTATGG
ACCCTACCCTAGCTGACGGAGAAGTTCTCTTCGTTGTAAACACCTCCCAATTGACCGC
TTCGACATCGTGGTTGCGCATGAGGAAGACGGAAATAAAGACATTGTCAAAGGGTTAT
CGGTATGCCTGGTGATAACCATCCGCTACGAAAATGACAACTCTTTATCAACGGTGAAG
AAACGAATGAACCCTACCTAGCTGAGTACCTCAACTTGTTCAAACAGAAAAGTTGCAA
30 AACACCTATACTGGAAAAGGATTTGAAGGCAATAAGGGAGTTTACTTTAGAGAACTTGC
TCAAAAAGCACAAGCCTTTACGGTCGATGTCAATTCCAACACCAGATTCAGCTTTACTG
TCCCTCAAGGCGAATAACCTTCTCCTTGGTGACGATCGTCTAGTCTCTAGCGACAGCCGC
CATGTCGGTACCTTCAAGGCCAGCGATATCAAAGGCGAAGCAAAATTCCGTTTCTGGCC
ACTTAACCGTATCGGAACCTTTTAA
- 35 25_Streptococcus pneumoniae R6_GI# 15902408_Catalytic Ser
Residue 38 (SEQ ID NO: 154)
MNLFKNFLKEWGLFLLILSLLALSRIFFWSNVRVEGHSM DPTLADGEILFVVKHLPIDR
FDIVVAHEEDGNKDIVKRVIGMPGDTIRYENDKLYINDKETDEPYLADYIKRFKDDKLQ
40 STYSGKGFEGNKGTFFRSIAQKAQAFTVDVNYNTNFSFTVPEGEYLLL GDDRLVSSDSR
HVGTFKAKDITGEAKFRFWPITRIGTF*
- 25_Streptococcus pneumoniae R6_GI# 15902408_Catalytic Ser
nucleotides 112-114 (SEQ ID NO: 155)
45 ATGAATTTATTTAAAAATTTCTTAAAGAGTGGGGATTATTCCTCCTGATTCTGTCATT
ACTAGCTTTGAGCCGTATCTTTTTTTTGGAGCAATGTTTCGCGTAGAAGGACATTCCATGG
ATCCGACCCTAGCGGATGGTGAAATCCTCTTTGTTGTAAAGCACCTCCCTATTGACCGT
TTTGATATCGTGGTGGCCCATGAGGAAGATGGCAATAAGGACATCGTCAAGCGCGTGAT
TGGAATGCCTGGCGACACCATTCGTTACGAAAATGATAAACTCTACATCAATGACAAAG
50 AAACGGACGAGCCTTATCTAGCAGACTATATCAAACGCTTCAAGGATGACAACTCCAA
AGCACTTACTCAGGCAAGGGCTTTGAAGGAAATAAAGGAACCTTTCTTTAGAAAGTATCGC

TCAAAAAGCCCAAGCCTTCACAGTTGATGTCAACTACAACACCAACTTTAGCTTTACTG
 TTCCAGAAGGAGAATAACCTTCTCCTCGGAGATGACCGCTTGGTTTCGAGCGACAGCCGC
 CACGTAGGTACCTTCAAAGCAAAAGATATCACAGGGGAAGCTAAATTCCGCTTCTGGCC
 AATCACCCGTATCGGAACATTTTAA

5

26_Streptococcus pyogenes M1 GAS_GI# 15675668_Catalytic Ser
 Residue 35 (SEQ ID NO: 156)

MKQFIKEWGPFTLFLILFGLSRLFLWQAVKVDGHSMDPTLAHGERLIVFNQARIDRFDI
 VVAQEEENGQKKEIVKRVIGLPGDTISYNDDTLYINGKKTVEPYLAEYLKQFKNDKLQK
 10 TYAYNTLFQQLAETSDAFTTNSEGQTRFEMSVPKGEYLLLGDDRIVSRDSREVGSEFKKE
 NLIGEVKARFWPLNKMTVFN*

26_Streptococcus pyogenes M1 GAS_GI# 15675668_Catalytic Ser
 nucleotides 103-105 (SEQ ID NO: 157)

15 ATGAAACAGTTTATTAAAGAATGGGGCCCATTCACCTCTCTTTTAAATTCTCTTTGGTCT
 ATCTCGTCTTTTTTTTGTGGCAGGCTGTAAAGTAGACGGCCATTCTATGGACCCAACTC
 TAGCTCATGGCGAACGCCTTATCGTTTTTAAATCAAGCTAGAATTGATCGCTTTGATATT
 GTAGTTGCTCAGGAAGAAGAAAACGGACAAAAGAAAGAAATCGTAAAAAGAGTTATTGG
 ATTGCCAGGCGATACCATTTCTTATAATGATGACACACTTTATATTAATGGTAAAAAAA
 20 CAGTTGAGCCGTATTTGGCTGAGTATCTAAAACAATTTAAAAACGATAAACTCCAAAAA
 ACTTACGCCTATAATAACCTATTCCAACAGTTAGCAGAAACATCTGATGCTTTTACAAC
 TAATTCTGAGGGACAAACACGCTTTGAGATGAGTGTTCCAAAAGGAGAATACCTTCTTC
 TTGGTGATGATCGTATTGTTTCCAGGGATAGTCGCGAAGTTGGTAGTTTCAAAAAAGAA
 AACCTTATCGGTGAAGTGAAAGCTCGTTTTTGGCCACTCAATAAAATGACCGTTTTTAA
 25 TTAG

SPase Sequences of Arylomycin-Resistant Bacteria

30

1_Escherichia coli str. K-12 substr. MG1655_GI#
 16130493_Catalytic Ser Residues 91 (SEQ ID NO: 158)
 MANMFALILVIATLVTGILWCVDKFFFPKRERQAAAQAAAGDSLDKATLKKVAPKPG
 WLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMPTLLIGDFILVEKFAYGIKDPIYQK
 35 TLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQAC
 ENALPVTYSNVEPSDFVQTFRRNGGEATSGFFEVPKNETKENGIRLSERKETLGDVTH
 RILTVPIAQDQVGMYYQQPGQQLATWIVPPGQYFMMGDNRDNSADSRYWGFVPEANLVG
 RATAIWMSFDKQEGEWPTGLRLSRIGGIH*

40

1_Escherichia coli str. K-12 substr. MG1655_GI#
 16130493_Catalytic Ser nucleotides 271-273 (SEQ ID NO: 159)
 ATGGCGAATATGTTTGCCCTGATTCTGGTGATTGCCACACTGGTGACGGGCATTTTATG
 GTGCGTGATAAATTCTTTTTTCGCACCTAAACGGCGGGAACGTCAGGCAGCGGCGCAGG
 CGGCTGCCGGGGACTCACTGGATAAAGCAACGTTGAAAAAGGTTGCGCCGAAGCCTGGC
 45 TGGCTGGAAACCGGTGCTTCTGTTTTTCCGGTACTGGCTATCGTATTGATTGTGCGTTC
 GTTTATTTATGAACCGTTCAGATCCCGTCAGGTTTCGATGATGCCGACTCTGTTAATTG
 GTGATTTTATTCTGGTAGAGAAGTTTGCTTATGGCATTAAAGATCCTATCTACCAGAAA
 ACGCTGATCGAAACCGGTCATCCGAAACGCGGCGATATCGTGGTCTTTAAATATCCGGA
 AGATCCAAAGCTTGATTACATCAAGCGCGCGGTGGGTTTACCGGGCGATAAAGTCACTT
 50 ACGATCCGGTCTCAAAGAGCTGACGATTCAACCGGGATGCAGTTCCGGCCAGGCGTGT
 GAAACGCGCTGCCGGTCACCTACTCAAACGTGGAACCGAGCGATTTCGTTTCAGACCTT

CTCACGCCGTAATGGTGGGGAAGCGACCAGCGGATTCTTTGAAGTGCCGAAAAACGAAA
 CCAAAGAAAATGGAATTCGTCTTTCCGAGCGTAAAGAGACACTGGGTGATGTGACGCAC
 CGCATTCTGACAGTGCCGATTGCGCAGGATCAGGTGGGGATGTATTACCAGCAGCCAGG
 GCAACAACCTGGCAACCTGGATTGTTCCCTCCGGGACAATACTTCATGATGGGCGACAACC
 5 GCGACAACAGCGCGGACAGCCGTTACTGGGGCTTTGTGCCGGAAGCGAATCTGGTCGGT
 CGGGCAACGGCTATCTGGATGAGCTTCGATAAGCAAGAAGGCGAATGGCCGACTGGTCT
 GCGCTTAAGTCGCATTGGCGGCATCCATTAA

2_Salmonella enterica subsp. enterica serovar Typhi str.
 10 CT18_GI# 16761494_Catalytic Ser Residues 91 (SEQ ID NO:
 160)
 MANMFALILVIATLVTGILWCVDKFVFAPKRRARQAAAQTASGDALDNATLNKVAPKPG
 WLETGASVFPVLAIVLVRSFLYEPFQIPSGSMPTLLIGDFILVEKFAYGIKDPIYQK
 TLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKITYDPVAKEVTIQPGCSSGQAC
 15 ENALPVTYSNVEPSDFVQTFARRNGGEATSGFFEVLNETKENGIRLTERKETLGDVTH
 RILMVPIAQDQLGMYQQPGQPLATWVPPGQYFMMGDNRDNSADSRYWGFVPEANLVG
 KAVAIWMSFDKQEGEWPTGVRLSRIGGIH*

2_Salmonella enterica subsp. enterica serovar Typhi str.
 20 CT18_GI# 16761494_Catalytic Ser nucleotides 271-273 (SEQ ID
 NO: 161)
 ATGGCGAACATGTTTGCCCTGATTCTGGTGATAGCCACACTGGTGACGGGCATTTTATG
 GTGCGTTGATAAGTTTGTTCGCGCCAAAACGTCGGGCGCGCCAGGCTGCCGCGCAAA
 CGGCGTCGGGAGATGCGCTGGATAACGCTACGCTCAATAAAGTGCGCGCCTAAGCCGGGC
 25 TGGCTGGAGACCGGGGCGTCGGTTTTCCCGGTTCTGGCGATCGTTCTGATCGTTTCGTTT
 ATTTCTTTATGAACCTTTTCAGATCCCGTCAGGCTCAATGATGCCGACACTGCTTATCG
 GCGATTTTATTCTGGTGAAAAATTTGCCTACGGCATTAAAGATCCGATCTACCAGAAA
 ACCCTGATTGAAACCGGTCATCCAAAGCGCGGGGATATTGTGGTATTTAAATATCCGGA
 AGATCCTAAGTTAGATTACATCAAACGCGCCGTCGGTTTTGCCGGGCGATAAAATCACTT
 30 ATGATCCGGTTGCGAAAGAGGTGACGATTACGCTGGCTGTAGCTCCGGTCAGGCGTGC
 GAAAATGCGCTGCCGGTTACCTACTCTAACGTTGAGCCGAGCGATTTTGTACAGACCTT
 TGCCCGCCGTAACGGCGGAGAAGCGACCAGCGGTTTTCTTTGAGGTTCCGCTAAACGAGA
 CAAAAGAAAACGGCATTCGCCTGACCGAACGTAAAGAGACGTTAGGCGATGTGACCCAC
 CGCATCCTGATGGTGCCGATAGCCCAGGATCAGTTGGGCATGTATTACCAACAGCCAGG
 35 ACAACCGCTGGCGACCTGGGTTGTACCGCCGGGGCAATATTTTCATGATGGGCGACAACC
 GCGATAACAGCGCGGATAGTCGTTACTGGGGATTTGTTCCGGAAGCGAATCTGGTCGGT
 AAAGCGGTCGCTATCTGGATGAGCTTTGACAAGCAGGAAGGGGAGTGGCCGACAGGCGT
 ACGCCTGAGTCGTATCGGCGGTATTTACTAA

3_Klebsiella pneumoniae subsp. pneumoniae MGH 78578_GI#
 40 152971424_Catalytic Ser Residues 91 (SEQ ID NO: 162)
 MANMFALILVIATLVTGVLWCLDKFIFAPKRRERQAAAQAATGEQLDKKTLKKVGPKPG
 WLETGASVFPVLAIVLVVRSFIYEPFQIPSGSMPTLLIGDFILVEKFAYGIKDPIYQK
 TLIETGHPKRGDIVVFKYPEDPRLDYIKRAVGLPGDKVTYDPVAKQVTIQPGCSSGQAC
 45 GNALPVTYSNVEPSDFVQTFSRNNGGEASSGFWQLPKGETKADGIRLTERQETLGDVTH
 RILMVPIAQDQVGMYYHQSGPLATWIVPPGQYFMMGDNRDNSADSRYWGFVPEANLVG
 KATAIWMSFEKQEGEWPTGVRLSRIGGIH*

3_Klebsiella pneumoniae subsp. pneumoniae MGH 78578_GI#
 50 152971424_Catalytic Ser nucleotides 271-273 (SEQ ID NO:
 163)

ATGGCGAACATGTTTGCCCTGATCCTGGTGATTGCAACCCTGGTGACGGGCGTTTTATG
 GTGCCTGGACAAGTTCATTTTTTGCACCGAAACGTCGTGAACGTCAGGCCGCTGCTCAGG
 CAGCGACCGGGCGAGCAACTGGACAAGAAGACGCTGAAGAAAGTCGGCCCGAAACCGGGC
 TGGCTGGAAACCGGGCGCATCGGTTTTCCCGGTGCTGGCGATCGTTCTGGTGGTACGTTT
 5 ATTTATTTATGAGCCTTTCCAGATCCCTTCAGGTTTCGATGATGCCAACGCTGCTCATCG
 GCGATTTTATTCTGGTGGAGAAATTTGCCTACGGCATTAAAGATCCTATCTACCAGAAA
 ACGCTGATCGAGACCGGCCATCCGAAGCGCGGGCGACATCGTGGTATTTAAATATCCGGA
 AGACCCGCGTCTGGACTACATTAAGCGCGCGGTGGGGTTACCGGGTGATAAGGTCACCT
 ACGATCCGGTTGCCAAACAGGTCACTATTTCAGCCGGGCTGCAGTTCCGGACAGGCCTGC
 10 GGCAACGCGCTGCCGGTGACCTATTCCAACGTGGAGCCGAGCGATTTTGTTCAGACCTT
 CTCCCGCAGCAACGGCGGGCGAAGCGAGCAGCGGTTTCTGGCAGTTGCCGAAGGGCGAAA
 CCAAAGCCGACGGCATTTCGTCTTACCGAGCGTCAGGAGACATTGGGCGACGTGACGCAC
 CGAATTCTGATGGTGCCGATTGCCCAGGATCAGGTTGGGATGTACTACCATCAGTCCGG
 TCTGCCGCTGGCCACCTGGATTGTGCCGCCCGGTGAGTACTTCATGATGGGCGACAACC
 15 GGGATAACAGCGCCGACAGCCGGTACTGGGGCTTTGTGCCGGAAGCCAACCTGGTCGGA
 AAAGCAACCGCTATCTGGATGAGTTTTGAAAAGCAGGAAGGTGAATGGCCGACCGGCGT
 GCGGTTATCGCGCATTGGTGAATTCATTAA

4_Mycobacterium tuberculosis H37Rv_GI# 15610040_Catalytic
 20 Ser Residues 96 (SEQ ID NO: 164)
 VTETTDSPSERQPGPAEPELSSRDPDIAGQVFDAAFPDAAPDADSEGDSKAAKTDEPRP
 AKRSTLREFAVLAVIAVVLVLYVMLTFVARPYLIPSESMEPTLHGCSTCVGDRIMVDKLS
 YRFGSPQPGDVIVFRGPPSWNVGYKSIRSHNVAVRWVQNALSFIGFVPPDENLKVRI
 AVGGQTVQCRSDTGLTVNGRPLKEPYLDPATMMADPSIYPCLGSEFGPVTVPVPPGRVWVM
 25 GDNRTHSADSRAHCPLLCTDDPLPGTVPVANVIGKARLIVWPPSRWGVVRSVNPQQGR*

4_Mycobacterium tuberculosis H37Rv_GI# 15610040_Catalytic
 Ser nucleotides 286-288 (SEQ ID NO: 165)
 GTGACCGAAACCACGGACTCCCCATCGGAGCGCCAGCCGGGTCCGGCAGAGCCGGAGCT
 30 CTCCTCCCGGGACCCGGACATTGCCGGCCAGGTCTTCGACGCAGCCCCGTTTCGACGCAG
 CCCC GGATGCGGACTCCGAAGGCGACTCCAAGGCGGCCAAAACGGACGAGCCGCGGGCCC
 GCGAAGCGATCAACGCTGCGGGAGTTCGCGGTGCTGGCGGTGATTGCTGTGGTGTCTTA
 CTACGTCATGCTGACGTTTGTGCGCGGCCCTTATCTGATTCCGTCGGAATCGATGGAAC
 CCACGTTGCACGGGTGTTTCGACGTGCGTCGGCGACCGCATCATGGTGGACAAACTCAGC
 35 TACCGCTTCGGCTCACCGCAACCTGGCGACGTCATCGTCTTCAGGGGACCGCCGTCGTG
 GAACGTTGGTTACAAGTCGATCCGTTTCGCACAACGTCGCCGTGCGCTGGGTGCAGAACG
 CGTTGTCGTTTCATCGGTTTTCGTGCCTCCCGACGAGAACGACCTGGTCAAGCGTGTCTATC
 GCGGTGCGCGGACAGACGGTTCAATGCCGGTCCGACACCGGCCTGACGGTCAACGGCAG
 GCCACTGAAGGAGCCATACCTGGATCCGGGCCACCATGATGGCCGACCCGTCGATATAACC
 40 CGTGCTTGGGCAGCGAGTTCGGGCGGTCACCGTCCCGCCCCGGGCGTGTCTGGGTGATG
 GGCGACAACCGCACCCATTTCGGCGGATTCCCGCGCTCACTGCCCGTTGCTATGTACTGA
 CGATCCGCTACCGGGGACCGTGCCGGTGGCCAACGTCATCGGTAAGGCCAGGTTGATCG
 TGTGGCCGCGTCGCGTTGGGGTGTGTCGTTTCGGTGAATCCCCAGCAAGGTCGGTAG

5_Yersinia pestis KIM 10_GI# 22123922_Catalytic Ser
 45 Residues 98 (SEQ ID NO: 166)
 MANMFALILAIATLLTGIIWCFERFKWGPARGAKIAAVNAQTAEIKAQTGCAVDNKTILA
 QAAKQPGWIETCASIFPVLALVFIVRSFIYEPFQIPSGSMMPTLLIGDFILVEKFAYGI
 KDPITQTTLIPTGKPNRGDIAVFKYPLDPRLDYIKRVVGLPGDRVIYNPISKEVTVQPS
 50 CNTGTSCDSALAITYSTSEPFVQTFRYSNGESSAGFFPIPLNQAVPDGGVRLRERT

ESLGPVAHHILTVPGRQDPLGSYYQQPDQPLGVWVVPEGHYFMMGDNRDNSADSRFWGF
VPERNLVGKATAIWMSFEKQEGEWPTGVRLSRIGGIH*

5_Yersinia pestis KIM 10_GI# 22123922_Catalytic Ser
5 nucleotides 292-294 (SEQ ID NO: 167)
ATGGCTAACATGTTTGCTTTGATTCTGGCAATAGCAACGCTGTTGACGGGGATTATCTG
GTGCTTCGAGCGGTTTAAATGGGGGCCAGCCCGTCAGGCCAAAATTGCGGCAGTTAATG
CACAAACTGCGGAAATCAAGGCCCAAACCGGGTGTGCCGTAGATAATAAACCTTAGCC
CAAGCTGCAAAGCAACCGGGTTGGATCGAGACATGTGCCTCTATCTTCCCGGTGCTGGC
10 CTGGGTCTTTATCGTGC GTTCGTTTATTTACGAGCCTTTCCAGATCCCTTCTGGTTCGA
TGATGCCAACGCTGCTTATCGGTGATTTTATTTTGGTTGAGAAATTTGCTTATGGGATT
AAAGATCCCATTACTCAGACCACATTAATTCCAACAGGTAAGCCAAACCGCGGTGACAT
TGCGGTGTTTAAATATCCGTTGGATCCACGTTTGGATTATATCAAGCGTGTGGTGGGGC
TGCCGGGGGATCGGGTAATTTATAACCCGATAAGTAAAGAAGTCACGGTACAACCGTCA
15 TGTAATACCGGTACTTCTTGTGATAGTGC GTTGGCCATCACTTACAGCACGTCTGAGCC
AAGTGAGTTTGTGCAGACATTCCGTTATAGCGGTAATGGCGAAAGCTCCGCAGGGTTCT
TCCCAATCCCGCTAAATCAGGCAGTACCTGATGGCGGTGTCCGGTTACGTGAGCGTACT
GAAAGCCTCGGCCCCGGTAGCGCATCACATTCTGACCGTCCCAGGGCGGCAGGATCCGTT
AGGCTCTTATTATCAGCAACCCGATCAACCGTTAGGGGTTTGGGTGGTACCGGAAGGCC
20 ATTACTTTATGATGGGTGATAACCGGGATAACAGTGCAGATAGCCGCTTCTGGGGTTTT
GTACCAGAACGTAATCTGGTAGGTAAGGCTACGGCTATTTGGATGAGTTTTGAAAAGCA
AGAAGGTGAATGGCCAACGGGTGTGCGTTTAAAGCCGAATTGGTGGAATTCACTAA

6_Staphylococcus aureus subsp. aureus COL_GI#
25 57651657_Catalytic Ser Residues 39 (SEQ ID NO: 168)
VSKLKKEILEWIIISIAVAFVILFIVGKFIVTPYTIKGESMDPTLKDGERVAVNIVGYKT
GGLEKGNVVFHANKNDDYVKRVIGVPGDKVEYKNDTLYVNGKKQDEPYLNYNLKHKQG
DYITGTFQVKDLPNANPKSNVIPKGKYLVLGDNREVSKDSRAFG LIDEDQIVGKVSFRF
WPFSEFKHNFNPENTKN*

30 6_Staphylococcus aureus subsp. aureus COL_GI#
57651657_Catalytic Ser nucleotides 115-117 (SEQ ID NO: 169)
GTGTCAAAATTGAAAAAAGAAATATTGGAATGGATTATTTCAATTGCAGTCGCTTTTGT
CATTTTATTTATAGTAGGTAAATTTATTGTTACGCCATATAACAATTAAAGGTGAATCAA
35 TGGATCCAAC TTTGAAAGATGGCGAGCGAGTAGCTGTAAACATTGTTGGATATAAAACA
GGTGGTTTGGAAAAAGGTAATGTAGTTGTCTTCCATGCAAACAAAAATGATGACTATGT
TAAACGTGTCATCGGTGTTCTTGGTGATAAAGTAGAATACAAAAATGATACATTATATG
TCAATGGTAAAAAACAAGATGAACCATATTTAAACTACAATTTAAACATAAACAAGGT
GATTACATTACTGGGACTTTCCAAGTTAAAGATTTACCGAATGCGAATCCTAAATCAAA
40 TGTCATTCCAAAAGGTAAATATTTAGTGCTTGGAGATAATCGTGAAGTAAGTAAAGATA
GCCGTGCGTTTGGCCTCATTGATGAAGACCAAATTGTTGGTAAAGTTTCATTTAGGTTC
TGGCCATTTAGTGAATTTAAACATAATTTCAATCCTGAAAATACTAAAAATTAA

7_Vibrio cholerae O1 biovar El Tor str. N16961_GI#
45 15642458_Catalytic Ser Residues 90 (SEQ ID NO: 170)
MANTFSLILVIVTLVTGIVWTLEKLVWAKKRQKQAH LQAQTPDMPASALDKVVAQPWW
IENSVSIFPVIAFVLVLR SFIYEPFQIPSGSMPTLLVGDFILVEKYAYGLKDPVWRTQ
LVETGKPERGDIVVFKYPVNPEIDYIKRVVGMPGDTVRY SAGKELCIQH QGESECAVVK
LSNVQESEFYQNEIPLIQLNEQLGKVEHNILVNPLSIDNVANYRPRSGVNEWVVPQGHY
50 FVMGDNRDNSADSRFWGFVPEQNLVGKAVAIWISFEFERAEDSVLPRWIPTGVRFNRVG
GIH*

- 7_Vibrio cholerae O1 biovar El Tor str. N16961_GI#
15642458_Catalytic Ser nucleotides 268-270 (SEQ ID NO: 171)
ATGGCGAACACATTCTCACTGATTTTGGTGATCGTAACTCTGGTCACCGGTATCGTCTG
5 GAACTGGAAAAGCTGGTGTGGGCGAAAAAACGCCAACAGAAACAAGCTCATTTACAGG
CGCAAACGCCCCGATATGCCAGCCTCAGCGCTGGATAAAGTCGTGGCTCAGCCGTGGTGG
ATTGAAAACAGTGTCTCGATTTTCCCTGTTATTGCTTTTGTGCTGGTACTGCGCTCGTT
CATTTATGAACCGTTCCAAATTCCATCCGGTTCGATGATGCCGACTCTGCTGGTCGGGG
ATTTTATTCTGGTTGAGAAATACGCTTACGGCTTGAAAGATCCTGTATGGCGCACTCAG
10 TTAGTGGAACGGGTAAACCTGAGCGTGGTGATATTGTGGTGTTCAAATACCCAGTGAA
CCCTGAGATCGACTACATCAAACGTGTGGTGGGGATGCCCCGAGATAACCGTACGTTACA
GCGCAGGTAAAGAGCTGTGTATTACGACCAAGGCGAGAGCGAATGCCAAGCAGTTAAA
CTCTCTAACGTGCAAGAGAGCGAGTTTTACCAAATGAGATCCCCCTGATCCAGCTGAA
CGAACAGCTAGGTAAGGTTGAGCACAATATTTTGGTTAACCCATTGAGCATTGATAACG
15 TGGCGAATTATCGCCCCACGCAGTGGCGTGAATGAATGGGTTGTACCACAAGGGCACTAT
TTTGTGATGGGTGATAACCGTGACAACAGTGCTGACAGCCGTTTCTGGGGCTTTGTGCC
AGAGCAGAATCTGGTCGGAAAAGCTGTGGCTATCTGGATCAGTTTCGAGTTTGAACGCG
CTGAAGACAGCGTACTTCCACGCTGGATTCTACCGGAGTACGATTCAATCGTGTTGGT
GGGATCCACTAA
20
- 8_Haemophilus influenzae 86-028NP_GI# 68248566_Catalytic
Ser Residues 115 (SEQ ID NO: 172)
MSNLEFFVILLAVGFGVWKVLDYFQLPNTFSILLILTLALSGVLWCYHRFVVLPRHRQV
ARAEQRSGKTLSEEEKAKIEPISEASEFLSSLFPVLAVVFLVRSFLFEPFQIPSGSMES
25 TLRVGDFLVVNKYAYGVKDPIFQNTIIEGEKPKQRGDVIVFKAPQQALIRTGLGATRAAF
AENLALSSKDNMSGVDYIKRIVGKGGDRIIFDVEQKTLKIVYGKDGKPCFVDCETKAFF
YTQNPTNPAFPNELELTEKGDVTHNVLIGEYRRYSDFEFPQEGMQTAEWLVPEGQYFV
MGDHRDHSDDSRFWGFFVPEKNIVGKATYIWMSLEKEANEWPTGFRFDRFFTAIK*
- 30 8_Haemophilus influenzae 86-028NP_GI# 68248566_Catalytic
Ser nucleotides 343-345 (SEQ ID NO: 173)
ATGTCAAATTTATTTTTTTGTGATTTTATTGGCTGTCGGCTTTGGTGTGTGGAAAGTTTT
AGATTATTTTCAGTTGCCAAATACTTTTAGTATTTTGTACTAATTTTGACCGCACTTT
CTGGCGTATTATGGTGTATCATCGTTTTGTGGTGCTGCCAAAACGTCATCGTCAAGTG
35 GCACGTGCAGAACAAACGTTCTGGTAAAACCTTAAGTGAGGAAGAAAAAGCCAAAATTGA
ACCGATTTCTGAGGCTTCAGAATTTTTGTCTTCACTTTTTCTGTGCTTGCAGTGGTAT
TTTTGGTTCGTTCTTTTTTTGTTTGAACCGTTTCAAATTCCCTCTGGCTCAATGGAGTCC
ACTTTACGCGTTGGCGATTTTTTTAGTTGTGAATAAATATGCTTATGGTGTGAAAGATCC
GATTTTCCAAAACACCATTATTGAGGGCGAAAAACCAACAGTGGCGATGTGATTGTGT
40 TTAAAGCACCACAACAAGCGTTAATTCGTAAGTCTTGGGGCTACTCGAGCGGCTTTT
GCAGAAAATTTAGCGTTAAGTTCAAAGATAATATGTCTGGTGTGGATTATATTAAGCG
TATTGTTGAAAGGGCGGAGATCGCATCATTTTTTGATGTGGAACAAAAACATTAAAAA
TTGTATATGGCAAAGATGGTAAACCTTGTGAAGTTGATTGCGAAACCAAGGCGTTTGAA
TATACACAAAATCCAACAAATCCTGCTTTTCCGAATGAATTAGAATTGACTGAAAAAGG
45 CGATGTAACACATAACGTGTTAATTGGTGAGTATCGTCGTTATTCAGACCTTGAATTTT
TCCCACAAGAGGGAATGCAAACCTGCGAATGGCTTGTGCCAGAGGGGCAGTATTTTGTG
ATGGGGGATCATCGCGATCACAGCGATGACAGTCGTTTTTGGGGCTTTGTGCCTGAAAA
AAATATTGTGGGGAAAGCCACTTATATTTGGATGAGCTTAGAAAAAGAAGCGAATGAAT
GGCCAACAGGTTTCCGTTTTGATCGCTTCTTTACAGCAATAAAATAA
50

- 9_Pseudomonas aeruginosa PA01_GI# 15595965_Catalytic Ser
Residues 90 (SEQ ID NO: 174)
MTLNFPLLLVIAVAVCGALALVDLVLFAPRRRRAAISSYEGQVNEPDPAVLEKLNKEPLL
VEYGKSFFPVLFIVLVLRSLVEPFQIPSGSMKPTLEVGDFFILVNKFAYGIRLPVLDTK
5 VIPIGDPQRGDVMVFRYPSEPNINIKRVVGLPGDTVRYTKEKRLYVNGELVAEKLVE
EPGTLGSVTLYQEKLGQAEHLIRKEMSRYRIEPDRQWTIPAGHYFMMGDNRDNSNDSRY
WNDPKIPKDLLGMVPDRNIVGKAFAVWMSWDPKMSNLPNFSRVGVH*
- 9_Pseudomonas aeruginosa PA01_GI# 15595965_Catalytic Ser
10 nucleotides 268-270 (SEQ ID NO: 175)
ATGACACTCAATTTCCCGTTGTTGCTGGTCATCGCCGTGGCTGTATGCGGCGCCCTGGC
CCTGGTCGACCTGGTGCTGTTTCGCGCCGCGTCGGCGGGCCGCGATCTCTTCCTACGAAG
GGCAGGTGAACGAGCCCGATCCGGCAGTGCTGGAGAAGCTCAACAAGGAACCGCTGCTG
GTGGAGTACGGCAAGTCGTTCTTCCCGGTGCTGTTTCATCGTGCTGGTGCTGCGTTCCTT
15 CCTGGTCGAGCCGTTCCAGATTCCCTCGGGGTCGATGAAACCTACCCTCGAGGTCGGCG
ATTTTCATCCTGGTCAACAAGTTCGCCTACGGTATCCGCCTGCCGGTGCTGGACACCAAG
GTGATCCCGATCGGTGATCCGCAGCGCGGCGATGTCATGGTGTTCCGCTATCCCAGCGA
ACCGAACATCAACTACATCAAGCGCGTGGTCGGCCTGCCCCGGCGACACCGTGCGCTACA
CCAAGGAAAAGCGCCTGTACGTCAACGGCGAGCTGGTGCGGAGAACTGGTCGGCGAG
20 GAACCGGGCACCTGGGCAGCGTGACCCTGTACCAGGAGAAGCTGGGCCAGGCCGAGCA
CCTGATCCGCAAGGAAATGAGCCGCTATCGCATCGAGCCCGACCGCCAGTGGACCATTC
CCGCCGGCCACTACTTCATGATGGGCGACAACCGCGACAACCTCCAACGACAGCCGCTAC
TGGAACGATCCGAAGATCCCCAAGGATCTGCTGGGCATGGTTCCGGACCGCAATATCGT
CGGCAAGGCCTTCGCCGTGTGGATGAGCTGGCCCGATCCGAAGATGAGCAACCTGCCGA
25 ACTTCTCCCGGGTCGGCGTGATTCACTGA
- 10_Acinetobacter baumannii ATCC 19606_GI#
260556580_Catalytic Ser Residues 72 (SEQ ID NO: 176)
VDFDFNLILVPVTLILFAVWLLDKLVFKQRANKGRENENFVITWAYDFWPVLAVVLVLR
30 SFLYEPFNIPSDSMVPTLETGDFILVNKFDYGVRLPIVNKKVIDVGEPKRGDVIVFRYP
PQPTISYIKRVIGLPGDHIVYDHGQLIINGQKIPKVPTQFSREKDALDTPTSIYHKETI
GDHTFTMRELEGVNVARQAPFINYVDNGKYANQDGLYWEVTVPKGHYFAMGDNRDQSAD
SRFWGFVPEENLTGRAFYVWMHKEPGFHLPSFNRNGKID*
- 10_Acinetobacter baumannii ATCC 19606_GI#
260556580_Catalytic Ser nucleotides 214-216 (SEQ ID NO:
177)
GTGGATTTTGATTTTAATTTAATTCTTGTTCTGTTACGCTGATTTTATTTGCAGTGTG
GTTGCTAGATAAGCTTGTTTTTTAAACAGCGTGCAAATAAAGGGCGAGAGAACGAAAATT
40 TTGTTATTACATGGGCCTATGACTTTTGGCCGGTTTTAGCTGTTGTGCTTGTACTTCGC
TCATTTCTTTATGAACCATTTAATATTCCATCAGACTCTATGGTTCCGACCTTAGAGAC
TGGCGATTTTATTTTAGTTAATAAATTTGACTATGGTGTCCGTTTACCTATCGTCAATA
AAAAAGTGATTGATGTCGGTGAACCGAAACGTGGTGATGTCATTGTATTCCGTTATCCA
CCACAACCTACTATTAGTTATATTAAACGTGTAATTGGCTTACCTGGTGACCATATTGT
45 TTATGATCATGGACAATTGATTATTAATGGTCAAAAAATTCTAAAGTACCAACACAGT
TTAGTCGCGAAAAAGATGCTTTAGATACACCAACTTCTATTTATCATAAAGAAACAATT
GGTGATCATACTTTTACGATGCGTGAGCTTGAAGGCGTAAATGTTGCGCGTCAGGCGCC
ATTTATCAACTATGTTGATAATGGTAAATATGCAAACCAAGACGGTTTATATTGGGAAG
TAACAGTTCCGAAAGGACATTACTTTGCAATGGGGGATAACCGTGATCAAAGTGCTGAC
50 AGTCGTTTCTGGGGCTTCGTACCTGAAGAAAATTTAACAGGCCGAGCTTTCTATGTCTG

GATGCATAAAGAACCTGGTTTCCACCTGCCAAGCTTTAACCGAAATGGGAAAATAGATT
AA

11_Bacillus anthracis str. Ames_GI# 30263049_Catalytic Ser
5 Residues 40 (SEQ ID NO: 178)

MKENTKKELFSWAKTIGFTLVLIAIIRGVLFPSLVQGESMMPTLENNERVLVNKIGYS
ISGLERFDIIVFHGKEGYDLVKRVIGLPDIVEYKNDVLYVNGKAMEEPYLKEFKEKAA
GRVLTPDFTLEQITGKTKVPEGQVFVLGDNREVSKDGRMFGFISEDEIVGKGQAVFWPL
KQVRAL*

10

11_Bacillus anthracis str. Ames_GI# 30263049_Catalytic Ser
nucleotides 118-120 (SEQ ID NO: 179)

ATGAAGGAAAATACGAAGAAAGAATTATTCTCATGGGCGAAAACGATAGGATTTACCCCT
TGTATTAATCGCAATTATTCGCGGTGTTTTATTTACACCGTCATTAGTACAAGGCGAAT
15 CGATGATGCCGACTTTAGAAAATAACGAACGAGTTCTCGTCAATAAGATTGGTTATAGT
ATAAGTGGATTAGAACGCTTTGATATTATCGTTTTCCATGGAAAAGAAGGATATGATTT
AGTAAAACGAGTAATTGGTTTACCAGGCGATACAGTTGAGTATAAAAATGATGTTTTAT
ATGTAAACGGCAAAGCGATGGAAGAACCATATTTAAAAGAGTTTAAAGAAAAAGCAGCA
GGTCGTGTATTAACTCCAGACTTTACGTTAGAACAAATTACAGGAAAAACGAAAGTGCC
20 AGAAGGCCAAGTGTTTGTATTAGGTGATAATCGTGAAGTTTCTAAAGACGGTCGTATGT
TTGGATTTATTTTCAGAAGATGAAATTGTCGGAAAAGGACAAGCTGTTTTCTGGCCGTTG
AAACAAGTAAGAGCGCTATAA

12_Neisseria meningitidis MC58_GI# 15676663_Catalytic Ser
25 Residues 123 (SEQ ID NO: 180)

MNTMLMSGAAAALLAGIILYFKSDKKRQENGEWSSGLEAYAYILTAVGVFAALSLFMSFT
AVFLIFVVLCGTAWGVYKYRLKTHPEISESSHFGDYFGSFFPTVLVLFLIRSFIAEPFQ
IPSSSMRPGLIKGDFILVGKFSYGLRVPVLNNIFIPTGKIERGDVVVFNYPLQPEMTYI
KRIVGIPGDVVEYRDKILTVNGKPTSDIPDGTYRYPDDTDPSEIHNTDMFRSGLDGKSF
30 NILKKEGQPAVSLPVLGKYTSDIMSENGYSIEQSGLEHCQYADDGSGFVCKVPEGRYFA
MGDNRDNSADSRYWGFVDDKLVVGKAMFILMNFDFGRSGTAIR*

12_Neisseria meningitidis MC58_GI# 15676663_Catalytic Ser
nucleotides 367-369 (SEQ ID NO: 181)

35 ATGAACACAATGCTAATGTCGGGCGCGGCTGCCGCGCTGCTTGCCGGCATCATCCTTTA
TTTCAAAAGCGACAAGAAGCGGCAGGAAAACGGGGAATGGAGTTCCGGCCTTGAATACG
CCTATATCCTGACAGCGGTCGGCGTGTTTGCCGCTTTGTCCCTGTTTATGAGCTTTACC
GCCGTTTTCTGATTTTTCGTTGTATTGTGCGGTACGGCTTGGGGGGTATATAAATACCG
CCTGAAGACTCATCCCGAAATCTCGGAAAGCAGCCACTTCGGCGATTATTTTCGGCAGTT
40 TCTTCCCTACCGTTTTTGGTATTGTTCCCTCATCCGGTCGTTTATCGCCGAACCGTTCCAA
ATCCCGTCCAGCTCGATGCGCCCGGGCCTGATCAAGGGCGATTTTCATTTTGGTTCGGCAA
ATTTTCCTACGGCCTGCGCGTACCCGTTTTTAAACAATATATTTATTCCTACAGGCAAAA
TCGAACGGGGCGATGTCGTTGTTTTTAATTATCCTCTGCAGCCGGAGATGACCTACATC
AAGCGTATTGTCGGCATTCCGGGCGATGTGGTTCGAATATCGGGATAAGATTTTGACGGT
45 AAATGGCAAACCCACTTCCGACATTCCCTGACGGCACATAACCGTTATCCCGACGACACCG
ACCCTTCCGAAATCCACAACACGGATATGTTCCGCAGCGGTCTAGACGGCAAATCCTTC
AATATTCTGAAAAAAGAAGGACAGCCTGCCGTTTCCCTGCCCGTATTGGGCAAATATAC
CTCCGATATTATGTCTGAAAACGGATATTCCATAGAGCAAAGCGGTTTGGAACTGACC
AATATGCCGACGACGGCAGCGGTTTCGTGTGCAAAGTTCCCGAAGGACGCTATTTTCGCT
50 ATGGGCGACAACCGCGACAACAGTGCCGATTCGCGCTACTGGGGATTTGTGGATGACAA

GCTGGTTGTCGGCAAGGCAATGTTTCATTTTGATGAACTTCGGCGATTTCGGCAGGTCCG
GTACGGCAATCCGTTAG

13_Bacillus anthracis str. Ames_GI# 30263037_Catalytic Ser
5 Residues 35 (SEQ ID NO: 182)

MKQEIKRGWGKYILFVFLVVAHSHFTLCKVEGKSMQPTLYEEDYVFNKAAVHFSDLE
HGEIVIIKEEDESKEYVVKRVIGLPDGINITNGSVYVNDKKQEEPYNKDLFNNTQVFY
NFQKTKIPPKNLFLVMGDNRELSRDSRNLGYIEEDNIIGKVEFVYYPFSKMKIIE*

10 13_Bacillus anthracis str. Ames_GI# 30263037_Catalytic Ser
nucleotides 103-105 (SEQ ID NO: 183)

ATGAAACAGGAGATTAAAAGAGGTTGGGGGAAATATATACTCTTCGTGTTTGTGTTTGGT
AGTAGCTTATCATTCTTTTACTTTTATGTAAAGTGGAAGGGAAATCAATGCAACCGACTT
TATATGAAGAAGACTACGTATTTGTAAATAAAGCAGCAGTACATTTTTCCGATTTAGAG
15 CATGGAGAAATTGTCATTATAAAGGAAGAGGATGAATCGAAATATTATGTAAAACGAGT
AATAGGACTTCCTGGTGACGTAATTAACATAACGAATGGATCTGTATATGTAAATGATA
AAAAACAAGAAGAACCGTATACAAATAAAGATTTATTCAATAATACGCAAGTGTTTTAT
AACTTTCAAAGACAAAAATCCCACCAAATAAATTATTTGTAAATGGGAGATAATCGTGA
ACTTAGTAGAGATAGTCGAAACGGTTTAGGATATATTGAAGAAGATAATATAATAGGCA
20 AAGTGGAATTTGTATATTATCCTTTTTTCAAAAATGAAGATCATAGAATAA

14_Streptococcus mutans UA159_GI# 24380230_Catalytic Ser
Residues 35 (SEQ ID NO: 184)

25 MKRFLKEWGLFLVIIIFALLLPRLFIFWFPVQVDGHSMDPTLANGEHLIVVRTTSIKHFDI
VVAAEGNKNIVKRVIGMPGDTITYENDMLSINGKKVNETYLKQYKDKFAKDKLQKTYAY
NQYFQELASQSTAFTTDEQGNASFTIKVPGKRYLLLGDDRIVSKDSRHVGTFAKNKIVG
EVKFRFWPLNAIRFISNK*

14_Streptococcus mutans UA159_GI# 24380230_Catalytic Ser
30 nucleotides 103-105 (SEQ ID NO: 185)

ATGAAAAGATTTTTTAAAAGAATGGGGCCTTTTCTTGGTCATCATTTTTCGCATTGCTACT
CCCGCGTCTCTTTATCTGGTTTCCTGTCCAAGTAGATGGACATTCAATGGATCCTACCT
TAGCCAATGGGGAGCATCTCATTTGTCGTCAGGACAACCTTCTATCAAACATTTTGACATT
GTTGTTGCTGCTGAAGGCAATAAAAATATTGTCAAACGTGTGATTGGCATGCCCGGTGA
35 TACCATTACCTATGAAAATGATATGCTTTCTATTAATGGGAAAAAAGTCAATGAAACTT
ATCTCAAGCAATACAAGGATAAATTTGCCAAGGACAACTCCAAAAGACTTATGCCTAC
AATCAGTATTTCCAAGAATTAGCCTCACAATCAACAGCTTTCACAACAGACGAACAAGG
AAACGCCAGCTTTACGATTAAAGTACCAAAGGACGTTACCTGCTTTTAGGTGATGATC
GCATTGTCTCTAAAGACAGCCGCCATGTTGGAACTTTTGCTAAGAATAAAATTGTTGGT
40 GAAGTTAAATTCCGCTTTTGGCCTTTAAACGCTATTCGTTTCATTTCAAATAAATAA

15_Shigella flexneri 2a str. 301_GI# 24113910_Catalytic Ser
Residues 91 (SEQ ID NO: 186)

45 MANMFALILVIATLVTGILWCVDKFFFPKRRERQAAAQAAAGDSLDKATLKKVAPKPG
WLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMPTLLIGDFILVEKFAYGIKDPIYQK
TLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQAC
ENALPVTYSNVEPSDFVQTFSSRNGGEATSGFFEVPKNETKENGIRLSERKETLGDVTH
RILTVPIAQDQVGMYYQQPGQQLATWIVPPGQYFMMGDNDRNSADSRYWGFVPEANLVG
RATAIWMSFDKQEGEWPTGVRLSRIGGIH*

50

- 15_Shigella flexneri 2a str. 301_GI# 24113910_Catalytic Ser
nucleotides 271-273 (SEQ ID NO: 187)
ATGGCGAATATGTTTGCCCTGATTCTGGTGATTGCCACACTGGTGACGGGCATTTTATG
GTGCGTGGATAAAATTTCTTTTTCGCACCTAAACGGCGGGAACGTCAGGCAGCGGCGCAGG
5 CGGCTGCCGGTGACTCACTGGATAAAGCAACGTTGAAAAAGGTTGCACCGAAGCCTGGC
TGGCTGGAAACCGGAGCTTCTGTTTTTCCGGTGCTGGCTATCGTATTGATTGTACGTTT
GTTTATTTATGAACCGTTCCAGATCCCGTCAGGTTTCGATGATGCCGACTCTGTTAATCG
GTGATTTTATTCTGGTAGAGAAGTTTGCTTATGGCATTAAAGATCCTATCTACCAGAAA
ACGCTGATCGAAACCGGTCATCCGAAACGCGGCGATATCGTGGTCTTTAAATATCCGGA
10 AGATCCAAAGCTTGATTACATCAAGCGCGCGGTGGGTTTACCGGGCGATAAAGTCACTT
ACGATCCGGTCTCAAAAGAGCTGACGATTCAACCGGGATGCAGTTCCGGCCAGGCGTGT
GAAAACGCGCTGCCGGTCACCTACTCAAACGTGGAACCGAGCGATTTTCGTTTCAGACCTT
CTCACGCCGTAATGGTGGGGAAGCGACCAGCGGATTCTTTGAAGTGCCGAAAAACGAAA
CCAAAGAAAATGGAATTCGTCTTTCCGAGCGTAAAGAGACACTGGGTGATGTGACGCAC
15 CGAATTCTGACAGTGCCGATTGCGCAGGACCAGGTGGGGATGTATTACCAGCAGCCAGG
GCAACAACCTGGCAACCTGGATTGTTCCGCCGGGACAATACTTCATGATGGGCGACAACC
GCGACAACAGCGCGGACAGCCGTTACTGGGGCTTTGTGCCTGAAGCGAATCTGGTCGGT
CGGGCCACGGCTATCTGGATGAGCTTCGATAAGCAAGAAGGCGAATGGCCGACTGGTGT
GCGCTTAAGTCGCATTGGCGGCATCCATTAA
20
- 16_Citrobacter koseri ATCC BAA-895_GI# 157144497_Catalytic
Ser Residues 91 (SEQ ID NO: 188)
MANMFALILVIATLVTGILWCVDKFIFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPG
WLETGASVFPVLAIVLVRSFIYEPFQIPSGSMPTLLIGDFILVEKFAYGIKDPIYQK
25 TLIETGHPKRGDIVVFKYPEDPRLDYIKRAVGLPGDKVTYDPVAKEVTVQPGCRSGQAC
ENALPVTYSDVQPSDFVQTFARRNGGEASSGFFEVLNETKDNGIRLAERKETLGDVTH
RILTVPIAQDQAGMYRQPGQQLATWIVPPGQYFMMGDNRDNSADSRYWGFVPEANLVG
KATAIWMSFDKQEGEWPTGVRLSRIGGIH*
- 30 16_Citrobacter koseri ATCC BAA-895_GI# 157144497_Catalytic
Ser nucleotides 271-273 (SEQ ID NO: 189)
ATGGCGAATATGTTTGCCCTGATTCTGGTGATTGCCACACTGGTGACGGGCATTTTATG
GTGCGTTGATAAAATTTATCTTTCGCGCCAAAACGTCGGGAACGTCAGGCAGCGGCACAGG
CCGCTGCGGGTGATTCACTGGATAAAGCCACGTTGAAAAAAGTGGCGCCTAAGCCGGGC
35 TGGCTGGAAACAGGGGCTTCGGTTTTTCCGGTACTGGCGATTGTGCTGGTGGTGGCTC
ATTTATCTATGAACCTTTCCAGATCCCGTCGGGTTTCGATGATGCCGACGCTGTTAATCG
GTGACTTTATTCTGGTGGAGAAATTCGCCTATGGAATTAAAGATCCGATTTACCAGAAA
ACGTTGATTGAAACGGGTCATCCGAAACGCGGTGATATCGTGGTCTTTAAATACCCGGA
AGATCCGCGCCTGGACTACATTAAACGCGCTGTTCGGCCTGCCGGGTGACAAAGTGACGT
40 ACGATCCGGTAGCCAAAGAGGTTACTGTACAGCCAGGATGCCGTTCCGGTCAGGCGTGT
GAAAACGCGCTGCCGGTGACTTACTCTGACGTTTCAGCCAGCGATTTTCGTGCAGACCTT
TGCCCGCCGTAATGGGGGAGAAGCCAGCAGTGGGTTCTTCGAAGTGCCGTTAAACGAAA
CGAAAGATAACGGCATTCGTCTGGCGGAGCGTAAAGAGACGCTGGGAGACGTAACCCAC
CGTATTCTGACCGTACCGATCGCGCAGGATCAGGCGGGGATGTATTACCGTCAGCCGGG
45 GCAGCAACTGGCGACCTGGATCGTACCGCCAGGACAATACTTCATGATGGGTGATAACC
GCGATAACAGCGCGGACAGCCGTTACTGGGGATTTGTACCGGAAGCGAATCTGGTTGGT
AAAGCGACCGCGATCTGGATGAGTTTCGACAAACAGGAAGGTGAATGGCCGACCGGCGT
ACGCTTAAGCCGTATTGGTGGGATCCATTAA

- 17_Bordetella pertussis Tohama I_GI# 33593416_Catalytic Ser
Residues 101 (SEQ ID NO: 190)
MSWNFALILFVLLVITGVIWGLDLALFRKRERRAQAAAAQVDAAGITDAEQAGRERRE
AIDAARRAPWWIEYAVSFFPVILFVFLRSFVVEPFHIPSGSMLPTLQSGDLILVNKFS
5 YGIRLPIIDRKIIETGSLERGDVVVFRYPVDTDVDYIKRIVGLPGDQVAYLDKKLYING
KLVPHERDGDYFEPDRVSYIAQYKEKLGEVEHKILLDEQKIQDFGPIWKFPSIQNCQYA
RNGVRCTVPPGHYFAMGDNRDNSADSRYWGFVPDGNIVGKAFFVWMNFSDLRIGRFH*
- 17_Bordetella pertussis Tohama I_GI# 33593416_Catalytic Ser
nucleotides 301-303 (SEQ ID NO: 191)
ATGAGTTGGAACTTTGCCCTGATACTTTTTGTACTGCTGGTGATTACCGGCGTTATCTG
GGGATTGGATCTGGCGCTGTTTCGCAAGCGACGCGAACGGCGGGCCCAGGCGGCGGCCG
CGCAAGTGGACGCCGCCGGCATCACGGATGCCGAGCAGGCCGGCCGCGAGCGGCGCGAG
GCCATCGACGCGGCGCGCCGCGCGCCCTGGTGGATCGAGTATGCGGTCAGCTTCTTCCC
15 GGTGATCCTGTTCGTGTTTCGTGCTGCGCTCGTTTCGTGGTCGAGCCGTTTCACATTCCGT
CGGGGTCCATGCTGCCCCACGCTGCAATCGGGCGACCTGATCCTGGTGAACAAGTTCAGC
TACGGCATCCGCCTGCCCATCATCGATCGCAAGATCATCGAGACGGGCTCGCTGGAGCG
TGGCGACGTGGTGGTGTTCGCTACCCGGTCGATACGGATGTCGACTACATCAAGCGCA
TCGTGGGTCTGCCGGGCGACCAGGTGGCCTACCTGGACAAGAAGCTGTACATCAACGGA
20 AAATTGGTGCCGCATGAACGCGACGGGGATTATTTTCGAGCCCGATCGCGTGTCTTATAT
TGCGCAATACAAGGAAAAACTGGGCGAAGTGGAGCATAAGATCCTGCTTGATGAGCAGA
AAATACAGGATTTTCGGCCCCATCTGGAAATTTCCCAGTATCCAGAACTGCCAGTACGCC
CGCAACGGCGTGCGCTGTACCGTCCCCCCCCGGCCATTATTTTCGCCATGGGAGACAACCG
TGACAATAGTGCGGACAGCCGCTACTGGGGATTTCGTGCCAGACGGTAATATCGTGGGGA
25 AGGCATTTTTTTGTCTGGATGAACTTCAGCGATTTGAGCCGCATTGGCCGCTTCCATTGA
- 18_Clostridium difficile 630_GI# 126698930_Catalytic Ser
Residues 37 (SEQ ID NO: 192)
MSVKKEIFDWIKSIAMAIVLAFVILQFIIPSIVSGESMYPTLDDKDYLILNRISYKVGK
30 PEKGDIVVFKTNLVDGETGKKKDLIKRVIATEGDRIKISNSKVYVNGKLLNEPYIHNNY
TSGDIDTVVPKGKLFAMGDNRENSNDSRFPDVG MVDEDEV LGKVMVRLPLDNIGKVD*
- 18_Clostridium difficile 630_GI# 126698930_Catalytic Ser
nucleotides 109-111 (SEQ ID NO: 193)
ATGAGTGTTAAAAAAGAAATATTTGATTGGATTAAAGTCAATAGCTATGGCTATTGTACT
TGCATTTGTAATTCTACAATTTATAATACCTTCTATTGTAAGTGGAGAATCAATGTATC
CTACTTTAGATGATAAAGATTATCTGATTTTAAATAGGATATCATAACAAGTTGGTAAA
CCTGAAAAAGGCGATATTGTAGTTTTTTAAACCAATTTAGTTGATGGAGAAACAGGAAA
GAAAAAAGACTTAATAAAAAGAGTTATAGCTACTGAAGGTGACAGAATAAAAATATCAA
40 ATTCTAAAGTGTATGTAAATGGAAAATTATTAAATGAACCATATATACACAATAACTAT
ACTTCTGGAGATATAGATACTGTTGTTCCAAAAGGTAAACTATTTGCAATGGGAGATAA
TAGAGAAAATAGTAATGATAGTAGATTCCCTGATGTAGGTATGGTTGATGAAGATGAAG
TTCTTGGTAAGGTTATGGTGAGACTATTACCTCTTGATAATATTGGGAAAGTAGACTAA
- 19_Clostridium difficile 630_GI# 126698133_Catalytic Ser
Residues 39 (SEQ ID NO: 194)
VGEAVKKEVVEWIKVIVIALVLAFAITRFIVPTIVKGESMYPTLVERDYLIVNRIAYKV
GEPKYKDIIIVFKTDLTEENGKKKDLVKRVIGVPGDHVKIQDSKVYVNDKLLDETSYIHN
NRTDGDIDIVVPEGKLFAMGDNREKSLDSRYDEVGLVDEHTILGKVLVRLYPFSKIGTI
50 D*

- 19_Clostridium difficile 630_GI# 126698133_Catalytic Ser
nucleotides 115-117 (SEQ ID NO: 195)
GTGGGTGAAGCAGTTAAAAAAGAAGTTGTAGAATGGATAAAAAGTGATTGTCATAGCTCT
TGTTTTGGCATTGCAATAACTCGTTTTATAGTGCCAACAATAGTCAAAGGAGAATCAA
5 TGTATCCTACATTAGTTGAACGTGATTATTTGATAGTTAACAGAATTGCGTACAAGGTA
GGAGAGCCAAAATACAAAGATATAATAGTATTCAAACCGACTTAACAGAGGAAAATGG
AAAGAAAAAAGATTTAGTAAAAAGAGTTATCGGGGTTCTGGTGACCATGTAAAAATAC
AAGACTCCAAGGTATATGTAAATGATAAGTTGTTAGATGAGACTTCCTATATACATAAT
AATCGTACTGATGGAGATATTGATATCGTAGTTCCAGAAGGAAAATTATTTGCAATGGG
10 AGATAATAGAGAAAAAAGTTTAGATAGTAGATACGATGAGGTTGGATTGGTCGACGAGC
ATACCATTTTAGGAAAGGTTCTAGTCAGATTGTATCCATTTTCTAAGATAGGAACTATT
GACTAA
- 20_Clostridium difficile 630_GI# 126698134_Catalytic Ser
15 Residues 39 (SEQ ID NO: 196)
MNETIKEEIVEWIKIIITALLFFAFIITRFIKPTLVNGESMYPTLKSHDYLVANRMTYKL
SEPKCGDIMIFKTDLLQENGRKKELVKRVIGVPGDHLKIKDSKVYINGKLLNEVSYIHD
NYTEGDIDMVIPKGKVFAMGDNREVSLDSRYKEVGLVDEENIKGKVILRVFPFTDIGIF
E*
20
- 20_Clostridium difficile 630_GI# 126698134_Catalytic Ser
nucleotides 115-117 (SEQ ID NO: 197)
ATGAATGAACTATTAAAGAAGAGATTGTAGAGTGGATAAAAATAATTATTACTGCACT
TTTTTTTGCATTTATTATAACTCGTTTTATAAAACCAACATTAGTAAATGGAGAATCAA
25 TGTACCCAACACTTAAATCACATGATTATTTGGTAGCAAACAGGATGACATATAAGTTA
TCAGAACCAAAATGTGGAGATATAATGATATTTAAGACTGATTTATTACAAGAGAATGG
AAGGAAAAAAGAGCTTGTA AAAAGGGTTATAGGTGTTCTGGTGACCATCTAAAAATTA
AGGATTCTAAGGTTTATATAAATGGTAAGTTATTAAATGAAGTTTCATATATACATGAT
AATTATACTGAAGGCGATATTGATATGGTGATTCCTAAGGGAAAAGTATTTGCGATGGG
30 AGACAATAGAGAAGTTAGTTTAGACAGTAGATATAAAGAAGTGGGATTAGTAGATGAAG
AAAATATTAAAGGAAAAGTTATTTTAAGAGTATTTCTTTTACAGATATAGGTATTTTT
GAGTAG
- 21_Enterococcus faecalis V583_GI# 29377531_Catalytic Ser
35 Residues 35 (SEQ ID NO: 198)
MSSLKRLVQLVLLVAVLLIRHYVFS PAAVNGSSMEPTLHNNDRLWVTSIKKPQRFDI
IAFPSPRNGQRVAKRLIGLPGETVEYRDDTLYINGVSLSE DYLASAKRNVSKNENYTQD
FTLETLEATQSLTVPEGMYFVLGDNRP RSDDSR YFGFVKQASVEGVLTFRYYPLDKIGF
P*
40
- 21_Enterococcus faecalis V583_GI# 29377531_Catalytic Ser
nucleotides 103-105 (SEQ ID NO: 199)
ATGTCCTCATTATTAAAACGATTGGTTCAGTTGGTTTTGTTAGTCGTCGCTGTCTTGCT
GATTCGACACTATGTTTTCTCCCCTGCTGCGGTGAACGGCTCTTCAATGGAACCAACAC
45 TTCATAACAACGACCGTTTATGGGTGACCTCGATTAAAAAACCACAGCGCTTTGATATT
ATCGCTTTCCCTAGTCCTCGCAACGGCCAACGAGTAGCCAAACGTTTAATTGGTTTACC
TGGCGAAACAGTCGAGTATCGCGATGATACCCTTTATATTAATGGTGTATCACTCAGTG
AAGATTACTTAGCAAGTGCTAAACGAAATGTCTCTAAAAATGAAAATTATACCCAAGAT
TTTACGCTAGAGACCTTAGAAGCCACCCAATCCCTGACCGTTCCAGAAGGCATGTATTT
50 TGTCTTGGGGGATAATCGCCCGCGCTCAGACGACAGTCGTTATTTTGGCTTTGTAAAC

AAGCGAGTGTGGAAGGTGTTTTGACTTTTCGTTATTATCCATTAGATAAAATTGGCTTT
CCATAA

22_Enterococcus faecalis V583_GI# 29375442_Catalytic Ser
5 Residues 101 (SEQ ID NO: 200)
MRTIRHIKRAFLKQKLPATYQLKKQKANTAMEYILLEQTDNHQSIRGPKRKMTAEIEIKKK
RQAYQKKQRVQVVKFFMPAILFAIFVFFFVLKTSSYPPIAGQSMKPTLNAGERVLVQRTK
QVARYDVIAFKAPLASKGTYVKRIIGVPGDRIWVNEGKLYLSEEPISDNEALPENASR
FDLSEEEAAQLRLFQKIPAGHYFVLGDNRTHSSDSRTFGFVEIQAIEGIVVFKMAPFKE
10 IGKVK*

22_Enterococcus faecalis V583_GI# 29375442_Catalytic Ser
nucleotides 301-303 (SEQ ID NO: 201)
ATGCGAACAATTTCGCCACATTAAGCGCGCCTTCTTGAAGCAAAAGTTGCCTGCGACATA
15 TCAGCTAAAAAAGCAAAAGGCTAACACAGCAATGGAATATTTGCTTGAGCAAACAGATA
ACCATCAATCAATAAGAGGACCGAAAAGAAAAATGACCGCTGAAGAGATTAAAAAAAAG
CGGCAAGCCTACCAAAAGAAACAACGCGTCCAAGTCGTTAAATTTTTTATGCCAGCTAT
TCTTTTCGCCATTTTTTGTGTTCTTTTTTGTGTTAAAGACATCTAGCTACCCAATTGCTG
GGCAATCCATGAAGCCGACACTTAACGCAGGGGAACGAGTCTTAGTACAACGGACGAAG
20 CAAGTAGCAAGGTACGATGTGATTGCATTTAAAGCACCGCTAGCTAGCAAAGGTACGTA
CGTCAAGCGAATCATCGGGGTTCTTGGTGATCGAATTTGGGTAAACGAGGGAAAACCTTT
ATCTTTTCAGAAGAACCTATAGCAAGCGATAATGAGGCACTGCCTGAGAATGCCAGTCGT
TTTGACTTATCAGAAGAAGCGGCAGCCCAACTTCGCCTGTTTCAGAAGATTCCAGCTGG
TCATTACTTTGTCTTAGGGGACAATCGTACGCATTCAAGTGATAGTCGTACGTTCCGGCT
25 TTGTCGAGATACAAGCGATTGAAGGAATCGTGGTATTTAAAATGGCGCCGTTTAAGGAA
ATAGGGAAAGTAAAATAA

23_Enterococcus faecalis V583_GI# 29375687_Catalytic Ser
Residues 39 (SEQ ID NO: 202)
30 MSLKSKELIKTVVFFACLALGLFLLRQFVFTPVVVRGHSMDPTLADGERVITLKNTEIN
RFDIITFPAPDEPDKNYIKRVIGLPGDTIAYKDDTLYINGKEVDEPYLDEFKKALTDGQ
PLTGDFSLKEKVPADSYFVLGDNRRNSKDGRVIGFIHKKDILGEVKFVMWPF SRFGPIP
EVSKQ*

23_Enterococcus faecalis V583_GI# 29375687_Catalytic Ser
nucleotides 115-117 (SEQ ID NO: 203)
ATGAGTTTGAAATCAAAAGAATTAATTAACAGTCGTCTTTTTTGCCTGTTTAGCTTT
GGGTCTGTTTTTACTGAGACAATTTGTATTTACGCCTGTCGTAGTGAGAGGTCATTCAA
TGGATCCAACGTTAGCAGATGGTGAACGGGTAATTACGTTAAAAAACACAGAAATTAAT
40 CGTTTCGATATTATTACTTTCCAGCGCCAGATGAACCAGATAAAAATTATATTAAACG
TGTGATTGGTTTACCTGGAGATACAATTGCGTACAAGGATGATACGTTGTACATCAATG
GAAAAGAAGTTGACGAACCCTATTTAGATGAATTTAAAAAGCCTTAACAGATGGTCAA
CCTTTGACAGGCGATTTTTTCATTAAAAGAAAAAGTACCAGCAGATAGCTACTTTGTTTT
AGGTGATAATCGACGGAATTCAAAAGACGGTCGTGTCATTGGTTTTATTCATAAAAAAG
45 ATATTTTGGGTGAAGTGAAATTTGTGATGTGGCCATTCTCACGGTTTGGTCCAATACCA
GAAGTGTCAAAACAATAA

24_Enterococcus faecalis V583_GI# 29376232_Catalytic Ser
Residues 42 (SEQ ID NO: 204)
50 LKKKR DYVGYLMYFLKILVPAIVAVFILRGFFLIPVRVDGHSMQKTLNQGDMIVMEKFS
AIKRFDVVVFKTDTGSILIKRVIGLPGEAVRYENDQLYVNNQPIAEPYLTKNRKKDHET

MPYTTNFDSKELLMQEKLKPKDSYFVLGDNRRMSKDSRSFGAIHADQILGKAQFVYYPLT
HMKIIPK*

24_Enterococcus faecalis V583_GI# 29376232_Catalytic Ser
5 nucleotides 124-126 (SEQ ID NO: 205)
TTGAAGAAGAAACGTGATTATGTTGGGTATTTAATGTACTTTCTGAAAATTTTAGTACC
AGCAATCGTAGCCGTTTTTTATTTTAAGAGGATTTTTCTGATTCCTGTTTCGGGTGGATG
GCCATTCTATGCAAAAAACCTTGAATCAAGGAGATATGATTGTGATGGAAAAATTCTCC
GCCATTAAACGGTTTGTATGTGGTGGTCTTTAAAACAGATACAGGATCGATTCTGATTAA
10 ACGTGTGATTGGTTTACCAGGAGAAGCTGTGCGTTACGAAAACGATCAATTATATGTCA
ATAATCAGCCAATCGCTGAACCGTATTTAACTAAAAACAGAAAAAAGATCATGAAACG
ATGCCTTACACTACGAATTTTGTATTCAAAGAATTGTTAATGCAAGAAAAATTACCTAA
AGATAGCTATTTTGTGCTTGGTGATAATCGCCGTATGTCCAAAGACAGCCGTTCTTTTG
GTGCAATACATGCAGATCAAATCTTAGGGAAAGCACAAATTTGTTTATTACCCACTCACT
15 CATATGAAGATCATTCTCTAAATAA

25_Listeria monocytogenes str. 4b F2365_GI#
46907497_Catalytic Ser Residues 49 (SEQ ID NO: 206)
MTDQYDKKPKKSGAHQLLSWVLVIVAALAIALVIRNFVVAPVKVEGTSMVPTYQDGDR
20 IFIEKISKPDREFDIIVFDEPPMIGSGEHFIKRVIGLPGDKIAFKNGELYLNGKRKVENY
LPEGTLTLWNPDPQTQKPPIADYTLEDMTGESTVPGKGLFVLGDNRRGGSSDSRVFGFIDD
SMVNGTVIQFGK*

25_Listeria monocytogenes str. 4b F2365_GI#
25 46907497_Catalytic Ser nucleotides 145-147 (SEQ ID NO: 207)
ATGACAGATCAATATGACAAAAAGCCCAAGAAAAAAGCGGGGCGCACCAATTATTAAG
CTGGGTGCTAGTTATCGTTGCAGCGCTTGCAATTGCACTTGTGATTCGTAACTTTGTAG
TTGCACCAGTAAAAGTAGAAGGAACATCTATGGTTCCAACATATCAAGATGGCGATAGA
ATTTTCATTGAAAAAATTTCCAAGCCTGATCGTTTCGACATTATCGTGTTTGATGAACC
30 TCCAATGATTGGTTCAGGAGAGCATTTTCATCAAGCGAGTGATTGGTTTGCCGGGAGATA
AAATAGCATTTAAAAACGGTGAATTATATTTAAATGGAAAACGAAAAGTAGAAAATTAC
TTGCCAGAAGGAACATTAACCCCTTTGGAATCCAGATCCAACGCAAAAACCATACATAGC
GGATTATACGCTGGAGGATATGACAGGCGAAAGTACTGTTCCGAAAGGGAAACTATTTG
TACTTGGAGATAATCGCGGCGGGAGTTCAGATAGTCGCGTTTTTCGGATTTATTGATGAT
35 TCCATGGTAAACGGTACAGTGATACAATTTGGAAAATAA

26_Listeria monocytogenes str. 4b F2365_GI#
46907496_Catalytic Ser Residues 42 (SEQ ID NO: 208)
MKSENKFFSGAFGWIKIILIALILAFGIRYFLISPVTVNGKSMDPTLHDGEHLFINKVS
40 DPKRFDIIVFPAPDEENAEYIKRVIGLPGDKVEYKEDQLYINGKKYDEPYLDSEKEALK
NGYLTDAEGDPNFTMADIPNSDGSALTVPKGELFVLGDNRRQVSKDSRYIGFISQDTVLG
KVISFGKSLER*

26_Listeria monocytogenes str. 4b F2365_GI#
45 46907496_Catalytic Ser nucleotides 124-126 (SEQ ID NO: 209)
ATGAAAAGTGAAAACAAATTTTTTTCTGGGGCATTGATGGATAAAAATAATTCTCAT
CGCGCTTATACTTGCTTTTGGTATTCGCTATTTTTTAATTTCTCCAGTTACTGTTAATG
GGAAATCAATGGACCCAACACTTCATGATGGGGAACATTTATTTATTAACAAGGTATCA
GATCCGAAGCGTTTTGACATTATTGTATTTCTGCGCCTGATGAGGAAAATGCAGAGTA
50 CATTAAACGCGTCATTGGCCTTCCAGGAGATAAAGTGGAGTACAAAGAAGATCAACTTT
ATATTAATGGAAAAAATATGATGAACCTTATTTAGATTCAGAAAAAGAAGCTCTAAAA

AACGGTTATTTAACCACTGATGCAGAAGGCGATCCTAATTTTACGATGGCAGACATTCC
AAACTCTGACGGCTCTCTCACTGTCCCTAAAGGAGAACTTTTTGTTTTAGGAGATAATC
GTCAAGTAAGTAAAGATAGTCGCTACATTGGCTTTATATCACAGGATAACCGTGCTTGGA
AAAGTAATTTTCATTTGGAAAATCCTTAGAACGTTAA

5

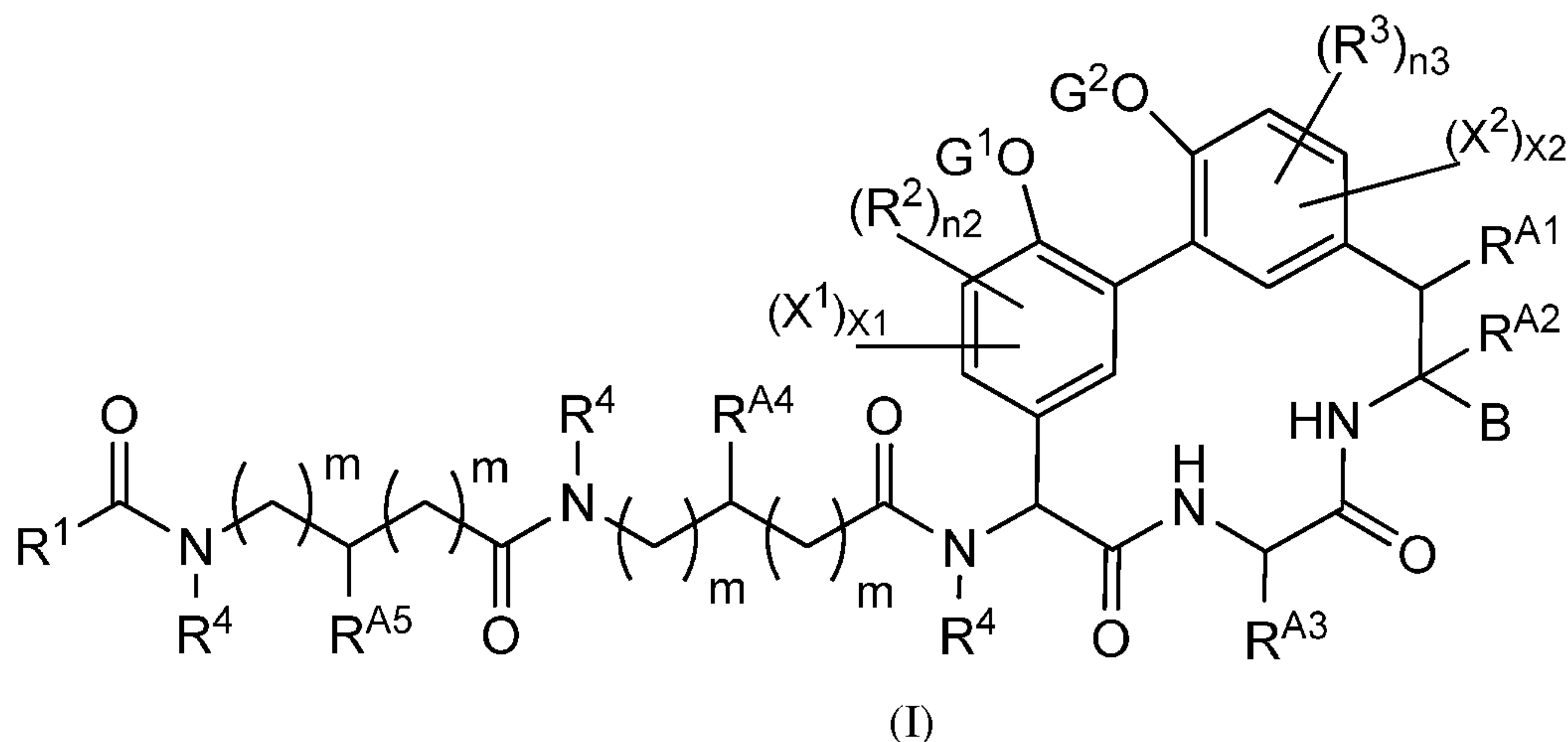
27_Listeria monocytogenes str. 4b F2365_GI#
46907498_Catalytic Ser Residues 40 (SEQ ID NO: 210)
LKEKNLKR LWSWIWA AVLA VLI AVIIRFYLFVPILVDGISMMPTLHSDDRVIINRFGNV
DRFDVIVFRES DGKEYIKRVIGLP GDTVEYKEDQLYINGKKYNEPYLD TYKEKLKDGYL
10 TDDYSSKDQLDGGKIPKDTYFVLGDNRRASKDSRIIGPIPF SKVLGTT PICYWP IEDAK
LID*

27_Listeria monocytogenes str. 4b F2365_GI#
46907498_Catalytic Ser nucleotides 118-120 (SEQ ID NO: 211)
15 TTGAAGGAGAAGAATTTAAAACGGTTATGGTCATGGATTTGGGCGGCTGTTCTAGCAGT
GTTAATAGCTGTTATAATCCGTTTTTTATTTATTTGTCCCTATTCTCGTCGATGGGATAT
CAATGATGCCTACACTTCATAGCGATGACCGTGTAATTATAAATCGCTTCGGAAATGTA
GATCGTTTTCGATGTGATTGTTTTCCGAGAATCAGATGGAAAAGAATACATCAAGCGAGT
GATCGGTTTGCCGGGTGATACAGTAGAATACAAAGAAGACCAACTTTACATCAATGGTA
20 AAAAGTATAATGAACCATATTTGGATACTTACAAAGAAAAGTTAAAAGATGGCTATTTA
ACAGATGATTACAGTTTCGAAAGATCAACTAGATGGTGGCAA AATTCCAAAAGATACTTA
TTTTGTTTTAGGTGACAATCGAAGAGCAAGCAAAGACAGTCGGATAATTGGGCCAATTC
CATTTAGCAAGGTGTTAGGAACAACACCGATTTGTTACTGGCCGATTGAAGATGCCAAA
CTTATAGATTAG

25

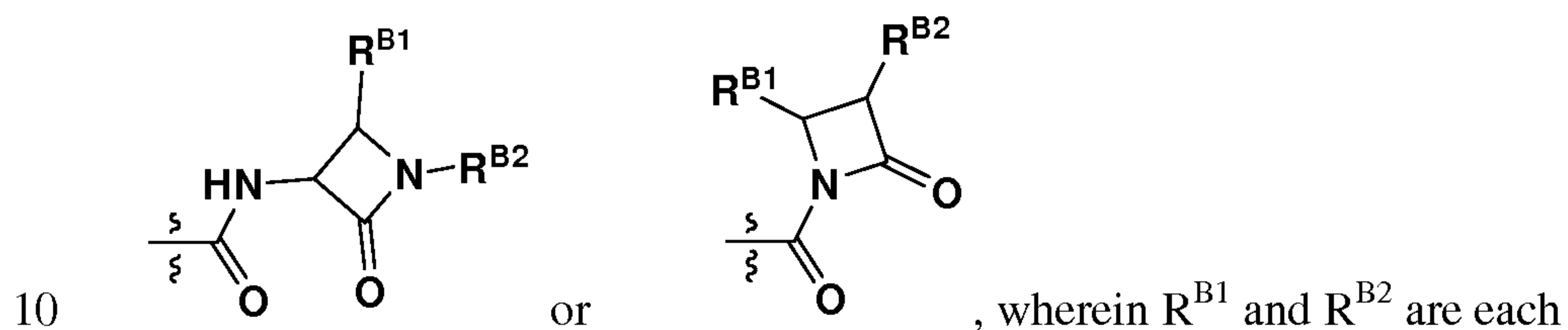
Embodiments of the Invention

1. A compound of formula (I)



wherein

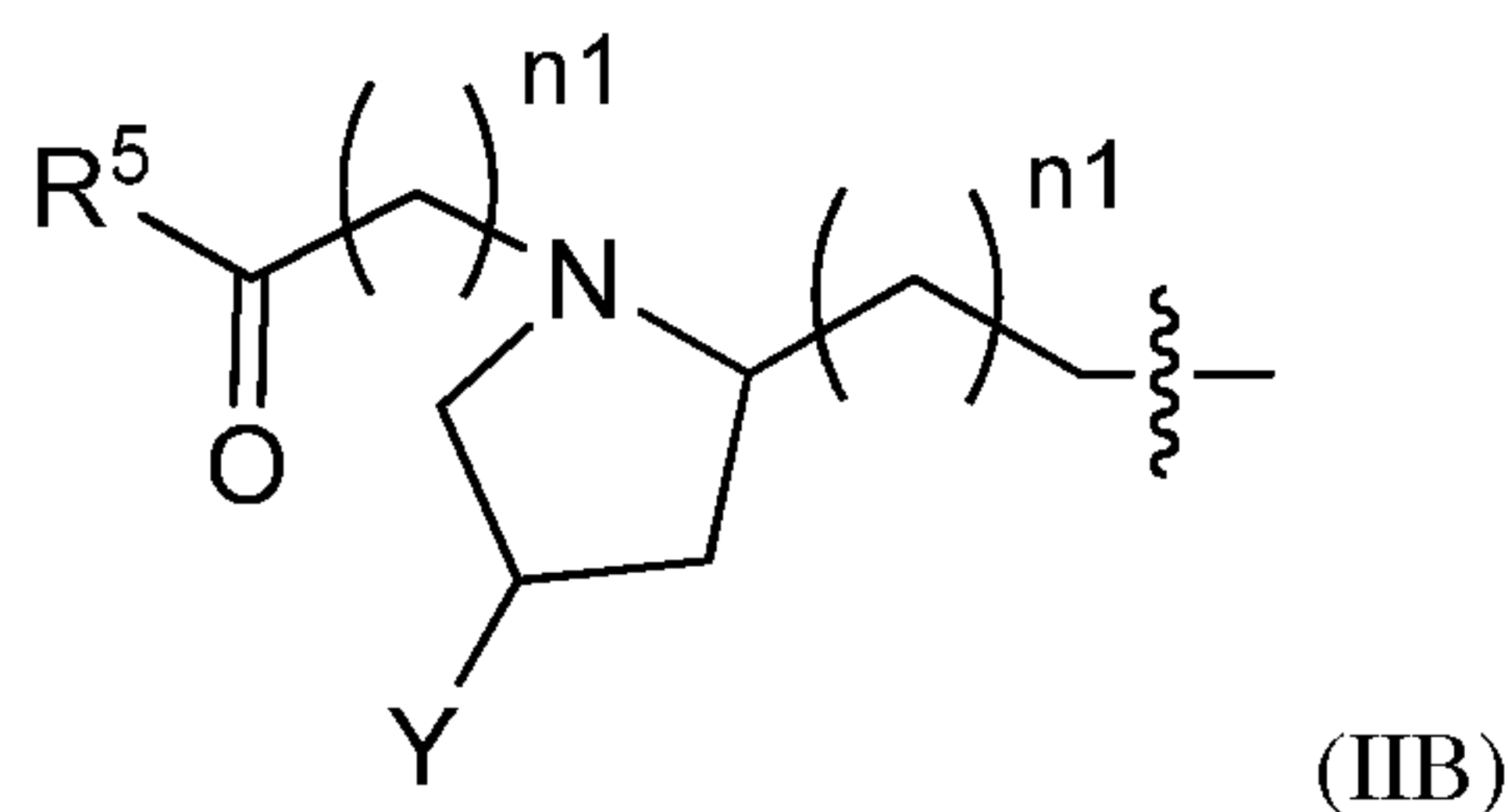
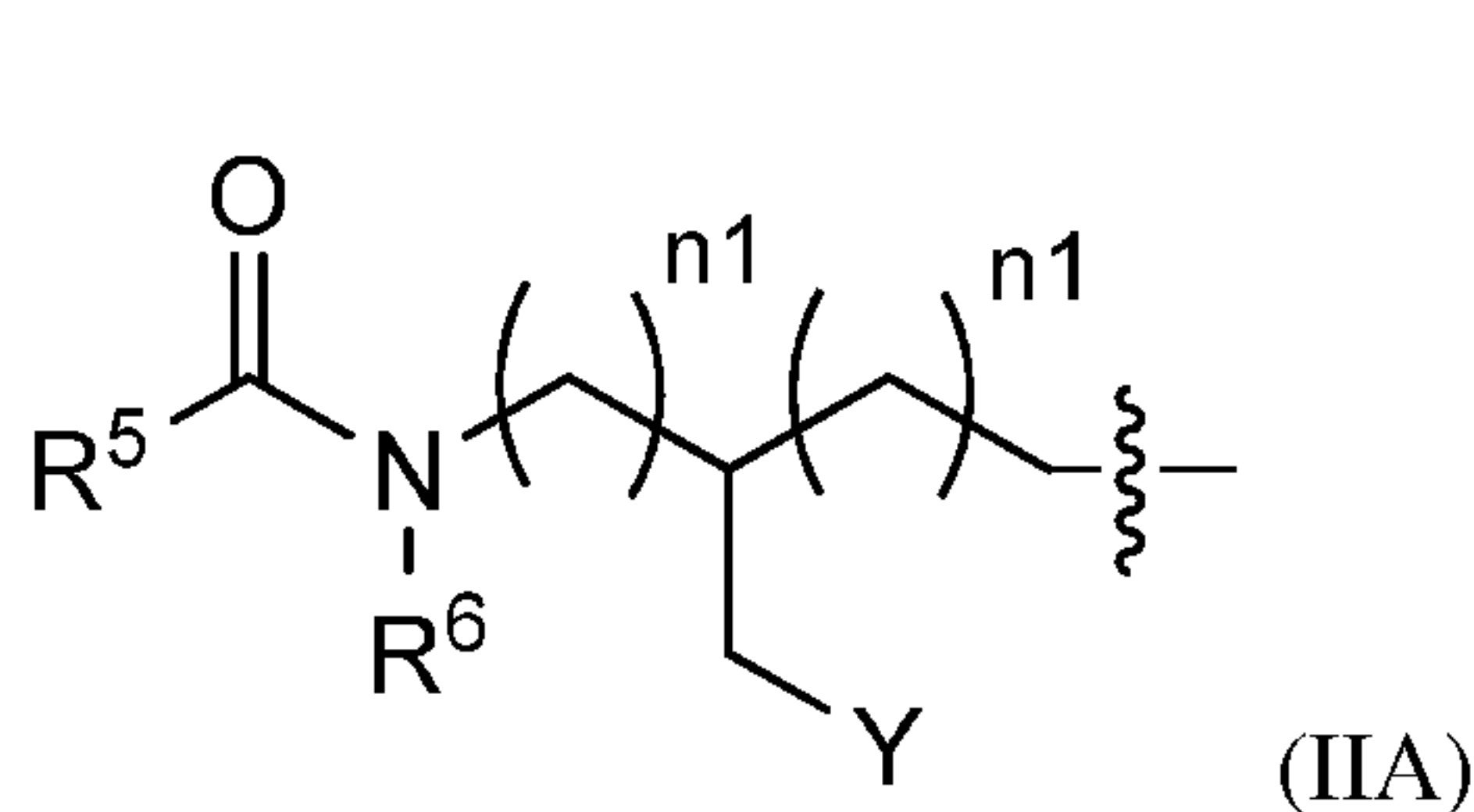
B is CO₂H, CH₂CO₂H, C(=O)NHCH₂C(=O)H, CH₂C(=O)H, C(=O)NHCH₂B(OR^B)₂ or C(=O)NHCH₂P(=O)(OR^B)₂ wherein R^B is H or (C₁-C₆)alkyl, or B is a group of formula

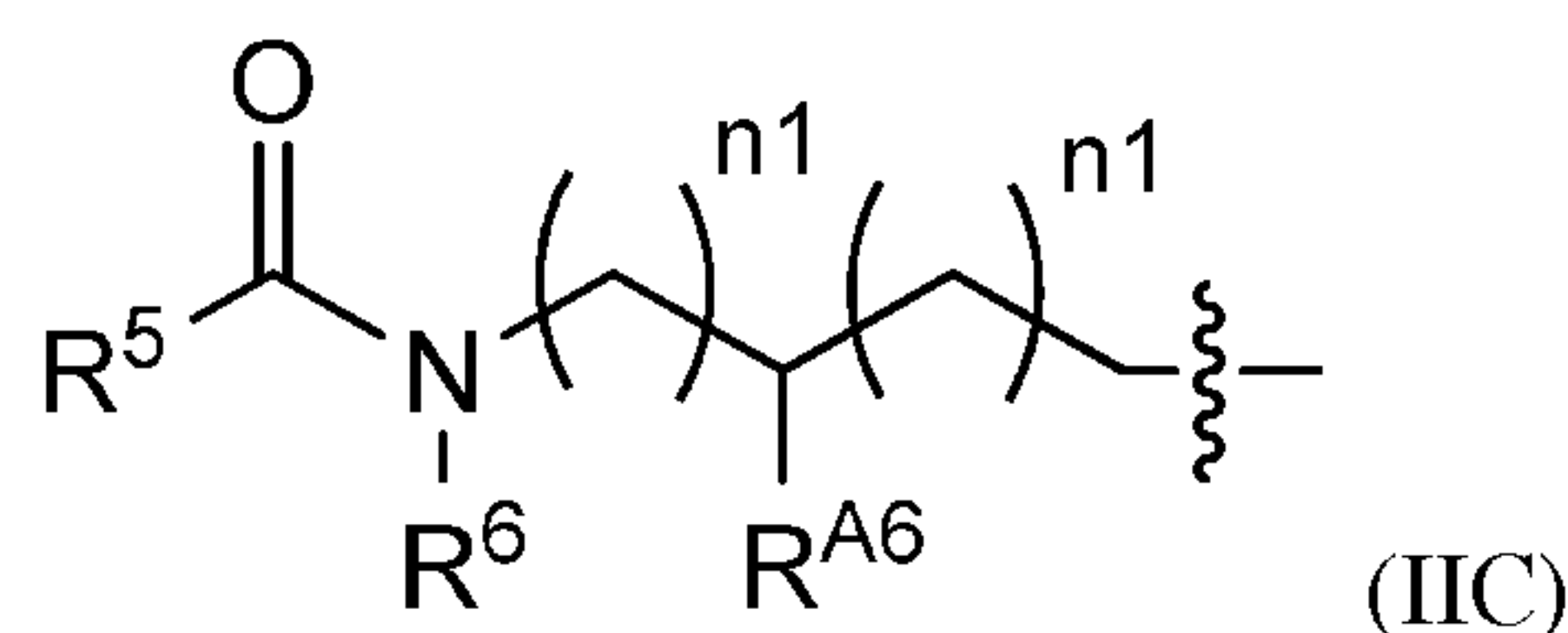


independently H, (C₁-C₆) alkyl, (C₃-C₆) cycloalkyl, OR^C, C(=O)NR^C₂, O C(=O)NR^C₂, C(=O)OR^C, OC(=O)OR^C, nitro, trifluoromethyl, trifluoromethoxy, (C₁-C₆)alkoxy, (C₁-C₆)thioalkoxy, NR^C₂, 5-7 membered heterocyclyl or 5-7 membered heteroaryl, or (C₆-C₁₀) aryl; R^C is independently at each occurrence H or (C₁-C₆) alkyl, and a wavy line indicates a point of attachment of B to a carbon of formula (I) bearing B;

15

R¹ comprises a group of formula (IIA) or (IIB) or (IIC)

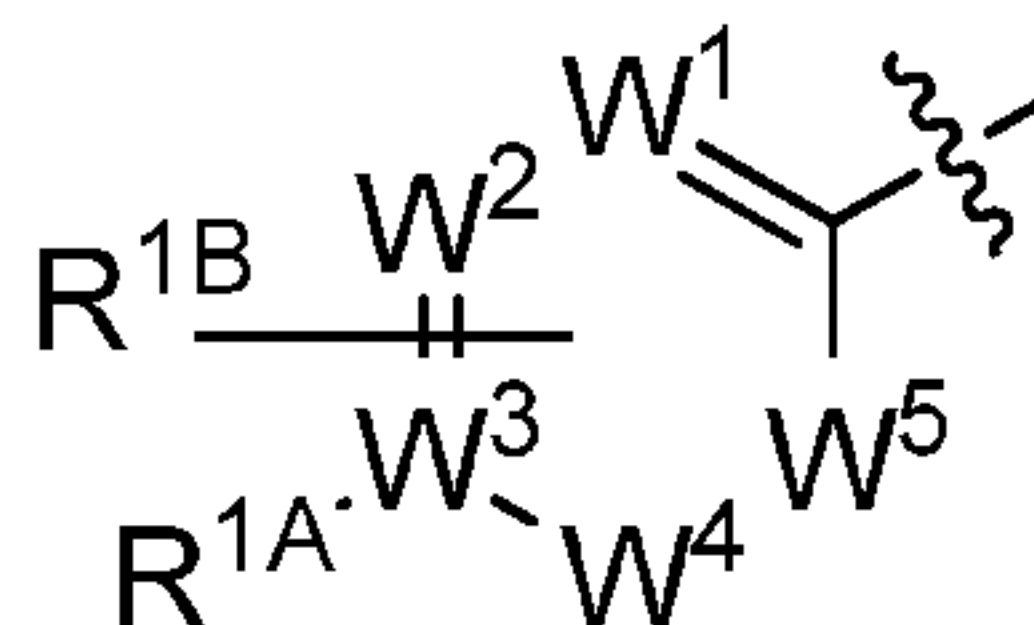




wherein each m is independently 0, 1, or 2, n_1 is independently at each occurrence 0, 1, or 2; Y is $(CH_2)_{0-2}H$, $(CH_2)_{0-2}OH$, or $(CH_2)_{0-2}OC(=O)(C_1-C_6)alkyl$; R^{A6} is hydrogen, $(C_1-C_6)alkyl$, $(C_3-C_7)cycloalkyl$, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or $(C_6-C_{10}) aryl$, wherein any alkyl, cycloalkyl, heterocyclyl, aryl or heteroaryl may be substituted with 1 to 3 substituents, wherein each substituent is independently selected from the group consisting of halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, cyano, trifluoromethyl, trifluoromethoxy, 5- to 7- membered heterocyclyl, $(C_1-C_6)alkoxy$, $(C_1-C_6)alkyl$, $(C_3-C_7)cycloalkyl$, (C_1-C_6) -mono- or di-alkylamino, $(C_1-C_6)alkoxycarbonyl$, $(C_1-C_6)alkylhydroxycarbonyl$, $(C_1-C_6)alkylaminocarbonyl$, $(C_1-C_6)alkylsulfonylamino$, and $(C_6-C_{10})-arylsulfonylamino$; and a wavy line indicates a point of attachment of R^1 to an atom of formula (I) bearing R^1 ; and

R^5 is a linear or branched alkyl chain of about 1-22 carbon atoms, bonded to the carbonyl carbon to which it is attached directly or by an O or NR, to provide an amide, carbamate, or urea linkage respectively; optionally comprising within the chain or at a chain terminus, any of the following groups:

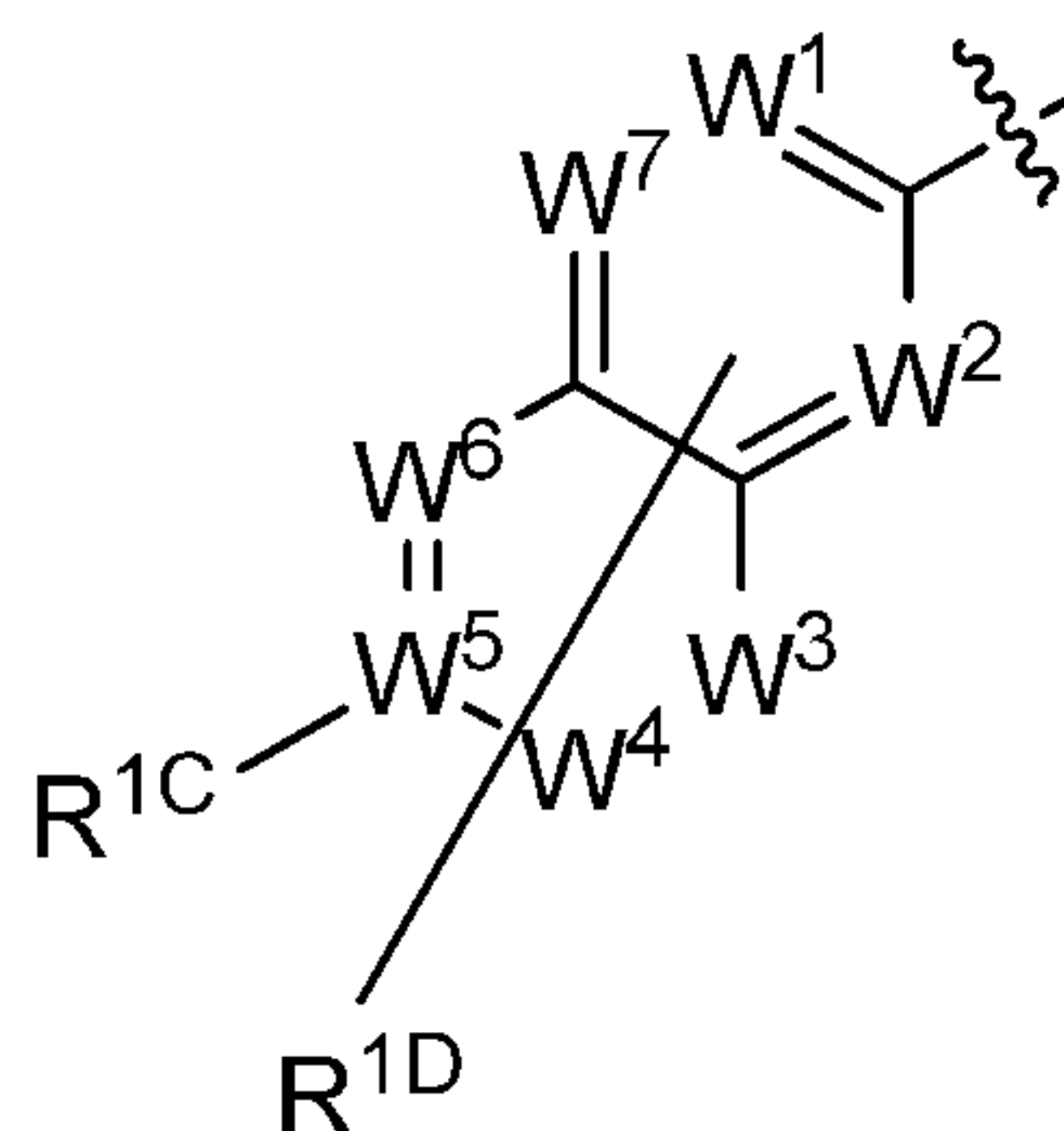
(A)



wherein W^1 , W^2 , W^3 , W^4 and W^5 are each independently C or N, provided that no more than two of W^1 , W^2 , W^3 , W^4 and W^5 are N; provided that when R^{1A} or R^{1B} is non-hydrogen, any W atom to which the R^{1A} or R^{1B} is respectively bonded is C, wherein there can be one or more R^{1B} bonded to the ring bearing the W atoms; R^{1A} is hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, cyano, (C_1-C_6) -thioether, fluoroalkoxy, (C_1-C_6) -alkyl, (C_1-C_6) -alkoxy, (C_1-C_6) -mono- or di-alkylamino, (C_1-C_6) -alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or $(C_6-C_{10}) aryl$; R^{1B} is hydrogen, alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C_1-C_6) -thioalkyl, fluoroalkoxy, cyano, (C_1-C_6) -alkyl, (C_1-C_6) -alkoxy, (C_1-C_6) -alkylamino, (C_1-C_6) -alkyl, 5- to 7-

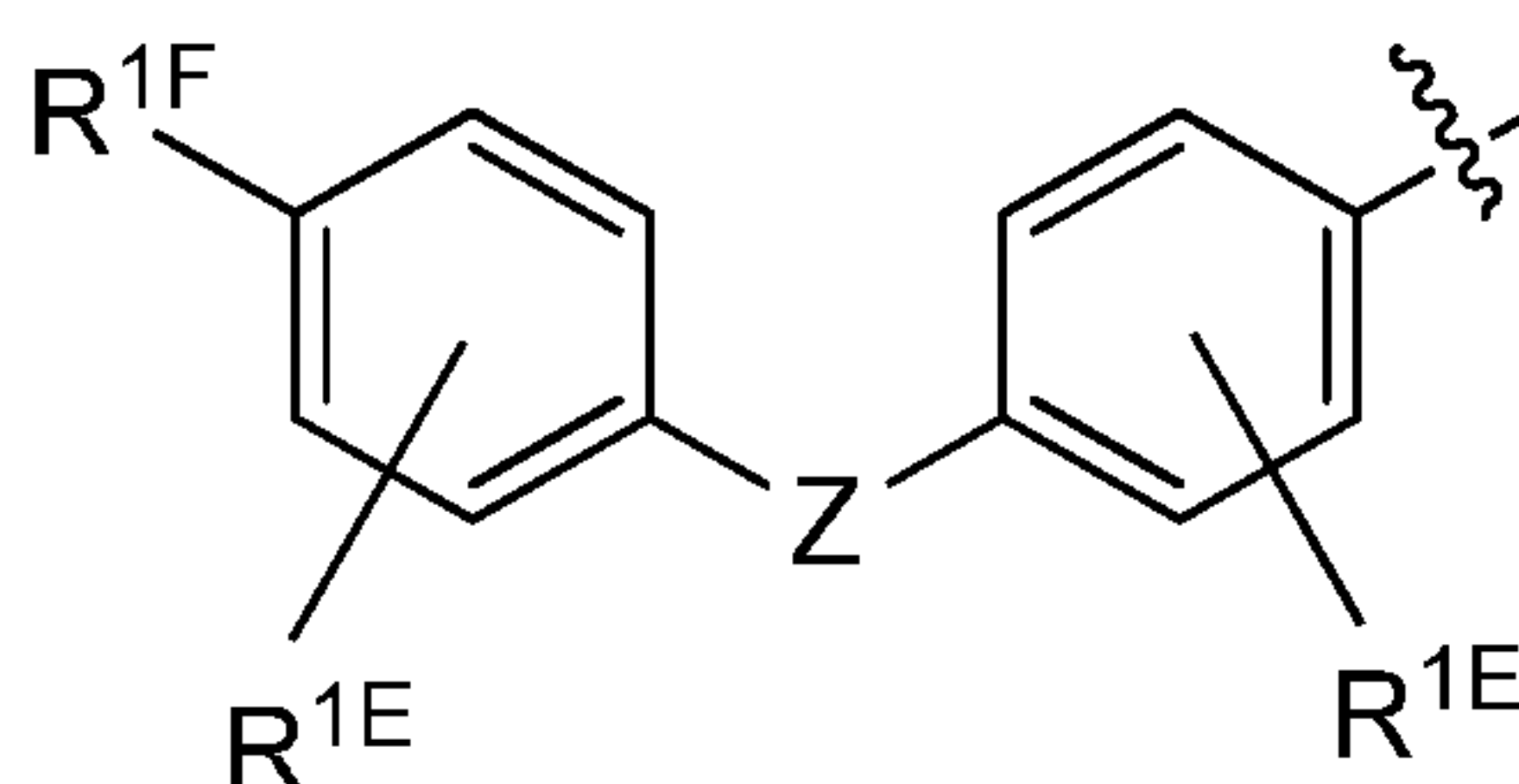
membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1A} or R^{1B} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁- C₆)-alkyl, (C₁- C₆)-alkoxy, (C₁- C₆)-alkylamino, (C₁- C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl groups; wherein a wavy line indicates a point of attachment;

(B)



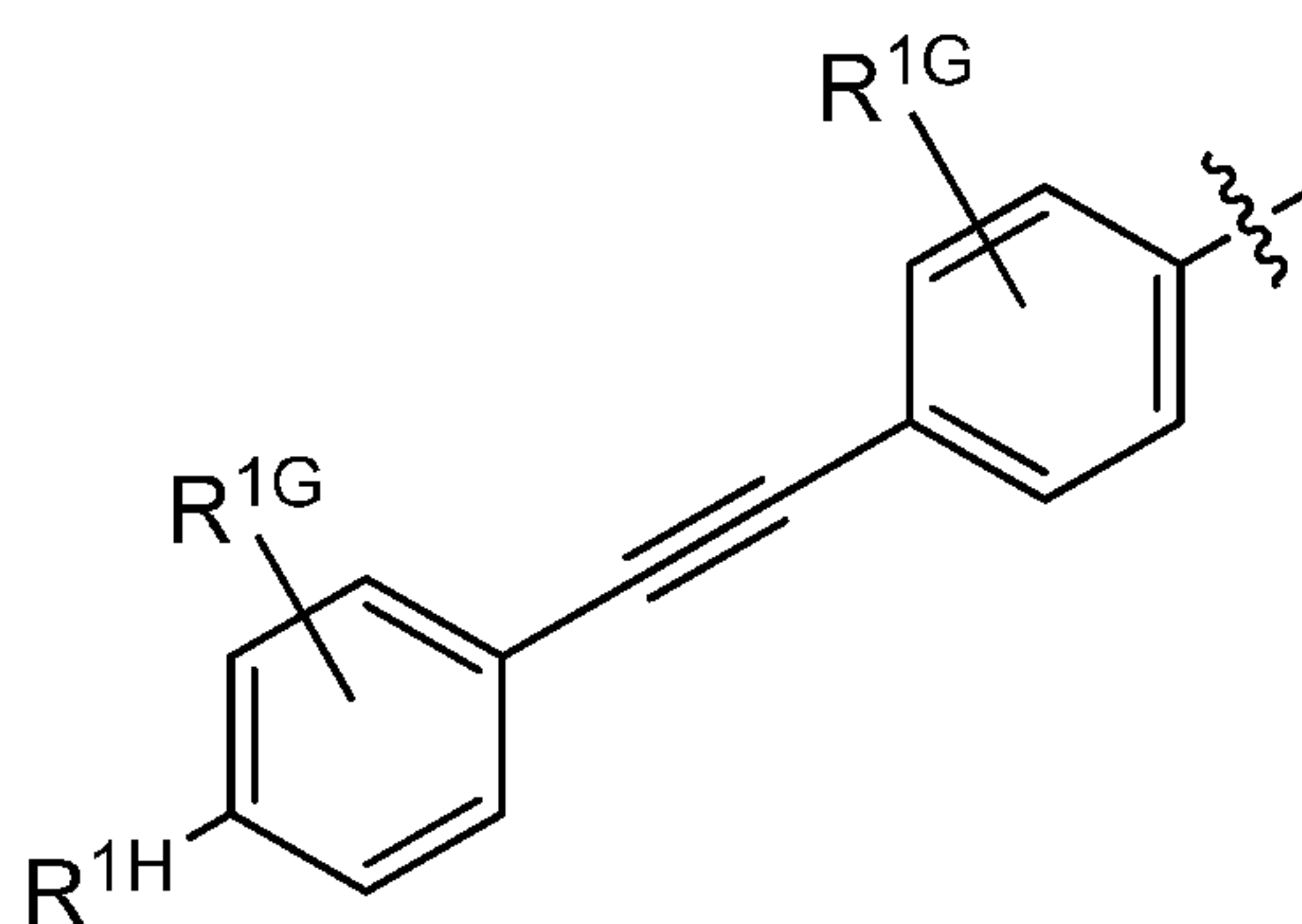
wherein W¹, W², W³, W⁴, W⁵, W⁶, and W⁷ are each independently C or N, provided that no more than three of W¹, W², W³, W⁴, W⁵, W⁶, and W⁷ are N; provided that when R^{1C} or R^{1D} is non-hydrogen, any W atom to which the R^{1C} or R^{1D} is respectively bonded is C, wherein either ring can bear one or more R^{1D}; R^{1C} is hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1D} is hydrogen, alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1C} or R^{1D} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁- C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment;

(C)



wherein Z is O, S, NH or CH₂; R^{1E} at each occurrence is independently hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1F} is hydrogen or alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1E} or R^{1F} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment; or

(D)



wherein R^{1G} at each occurrence is independently hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1H} is hydrogen or alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7-

membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1G} or R^{1H} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment;

R² and R³ are each independently nitro, halo, cyano, hydroxy, glycosyloxy, amino, (C₁-C₄)alkoxy, (C₁-C₄)acyloxy, or (C₁-C₄)alkyl, wherein any carbon atom can be unsubstituted or substituted with J, wherein n² and n³ are independently 0, 1, 2, or 3; or wherein two R² groups taken together, and/or two R³ groups taken together, can comprise fused cycloalkyl, aryl, heterocyclyl, or heteroaryl ring or rings, any of which is substituted with 0-3 J;

R⁴ and R⁶ are each independently at every occurrence hydrogen, (C₁-C₆)alkyl, (C₃-C₇)cycloalkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl, wherein any alkyl, cycloalkyl, heterocyclyl, aryl or heteroaryl can be substituted with 1 to 3 J;

R^{A1}, R^{A2}, R^{A3}, R^{A4}, R^{A5} are independently at each occurrence hydrogen, (C₁-C₆)alkyl, (C₃-C₇)cycloalkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl, wherein any alkyl, cycloalkyl, heterocyclyl, aryl or heteroaryl can be substituted with 1 to 3 J;

J is halogen, R', OR', CN, CF₃, OCF₃, O, S, C(O), S(O), methylenedioxy, ethylenedioxy, (CH₂)_{0-p}N(R')₂, (CH₂)_{0-p}SR', (CH₂)_{0-p}S(O)R', (CH₂)_{0-p}S(O)₂R', (CH₂)_{0-p}S(O)₂N(R')₂, (CH₂)_{0-p}SO₃R', (CH₂)_{0-p}C(O)R', (CH₂)_{0-p}C(O)CH₂C(O)R', (CH₂)_{0-p}C(S)R', (CH₂)_{0-p}C(O)OR', (CH₂)_{0-p}OC(O)R', (CH₂)_{0-p}C(O)N(R')₂, (CH₂)_{0-p}OC(O)N(R')₂, (CH₂)_{0-p}C(S)N(R')₂, (CH₂)_{0-p}NH-C(O)R', (CH₂)_{0-p}N(R')N(R')C(O)R', (CH₂)_{0-p}N(R')N(R')C(O)OR', (CH₂)_{0-p}N(R')N(R')CON(R')₂, (CH₂)_{0-p}N(R')SO₂R', (CH₂)_{0-p}N(R')SO₂N(R')₂, (CH₂)_{0-p}N(R')C(O)OR', (CH₂)_{0-p}N(R')C(O)R', (CH₂)_{0-p}N(R')C(S)R', (CH₂)_{0-p}N(R')C(O)N(R')₂, (CH₂)_{0-p}N(R')C(S)N(R')₂, (CH₂)_{0-p}N(COR')COR', (CH₂)_{0-p}N(OR')R', (CH₂)_{0-p}C(=NH)N(R')₂, (CH₂)_{0-p}C(O)N(OR')R', or (CH₂)_{0-p}C(=NOR')R'; wherein p is about 4,

each R' is independently at each occurrence hydrogen, (C₁-C₁₂)-alkyl, (C₂-C₁₂)-alkenyl, (C₂-C₁₂)-alkynyl, (C₃-C₁₀)-cycloalkyl, (C₃-C₁₀)-cycloalkenyl, [(C₃-C₁₀)cycloalkyl or (C₃-C₁₀)-cycloalkenyl]-[(C₁-C₁₂)-alkyl or (C₂-C₁₂)-alkenyl or (C₂-C₁₂)-

alkynyl], (C₆-C₁₀)-aryl, (C₆-C₁₀)-aryl-[(C₁-C₁₂)-alkyl or (C₂-C₁₂)-alkenyl or (C₂-C₁₂)-alkynyl], mono- or bicyclic 3-10 membered heterocyclyl, mono- or bicyclic 3-10 membered heterocyclyl-[(C₁-C₁₂)-alkyl or (C₂-C₁₂)-alkenyl or (C₂-C₁₂)-alkynyl], mono- or bicyclic 5-10 membered heteroaryl, or mono- or bicyclic 5-10 membered heteroaryl-
 5 [(C₁-C₁₂)-alkyl or (C₂-C₁₂)-alkenyl or (C₂-C₁₂)-alkynyl], wherein R' is substituted with 0-3 substituents selected independently from J;

or, when two R' are bound to a nitrogen atom or to two adjacent nitrogen atoms, the two R' groups together with the nitrogen atom or atoms to which they are bound can form a 3- to 8-membered monocyclic heterocyclic ring, or an 8- to 20-membered,
 10 bicyclic or tricyclic, heterocyclic ring system, wherein any ring or ring system can further contain 1-3 additional heteroatoms selected from the group consisting of N, NR', O, S, S(O) and S(O)₂, wherein each ring is substituted with 0-3 substituents selected independently from J;

wherein, in any bicyclic or tricyclic ring system, each ring is linearly fused,
 15 bridged, or spirocyclic, wherein each ring is either aromatic or nonaromatic, wherein each ring can be fused to a (C₆-C₁₀)aryl, mono- or bicyclic 5-10 membered heteroaryl, (C₃-C₁₀)cycloalkyl or mono- or bicyclic 3-10 membered heterocyclyl;

G¹ and G² are each independently a hydrogen or a glycosyl residue, or a group cleavable under physiological conditions to provide a compound of formula (I) wherein
 20 G¹ or G² respectively is hydrogen;

(X¹)_{X1} and (X²)_{X2} each signify that 0, 1, or 2 ring atoms of each respective ring can be nitrogen, provided that where a non-hydrogen substituent is bonded, X¹ or X², respectively, is C;

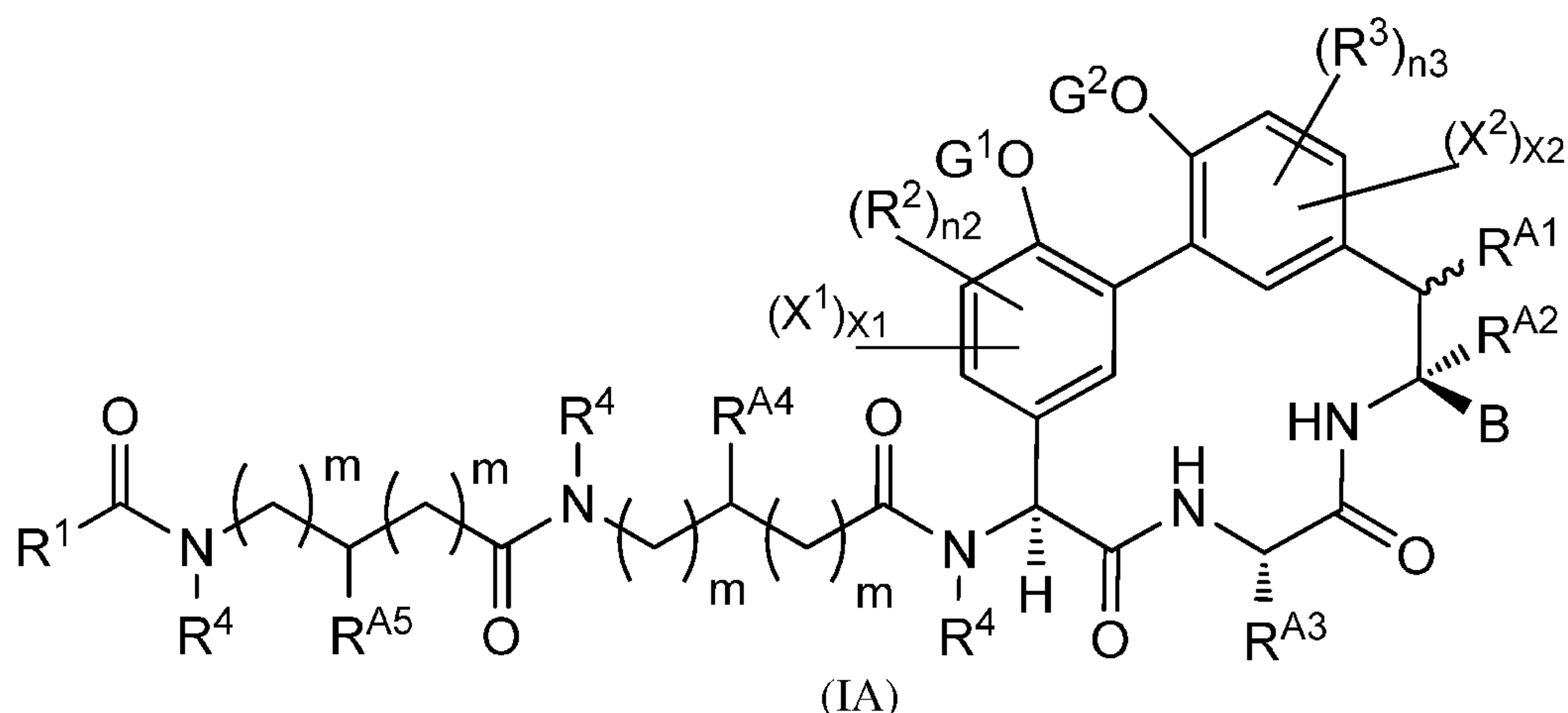
provided that when G¹ is a 6-deoxyhexopyranosyl residue, G² is H, R¹ is of
 25 formula (IIA), R² is hydrogen or hydroxy, R³ is hydrogen, R^{A1} and R^{A2} and R^{A4} are H, R^{A3} and R^{A5} are methyl, and B is CO₂H, or when G¹ and G² are H, R¹ is of formula (IIA), R² is hydrogen, R³ is hydrogen or nitro, R^{A1} and R^{A2} and R^{A4} are H, R^{A3} and R^{A5} are methyl, and B is CO₂H, then R⁵ is not unsubstituted (C₁₀-C₁₆)-alkyl;

or a salt thereof.

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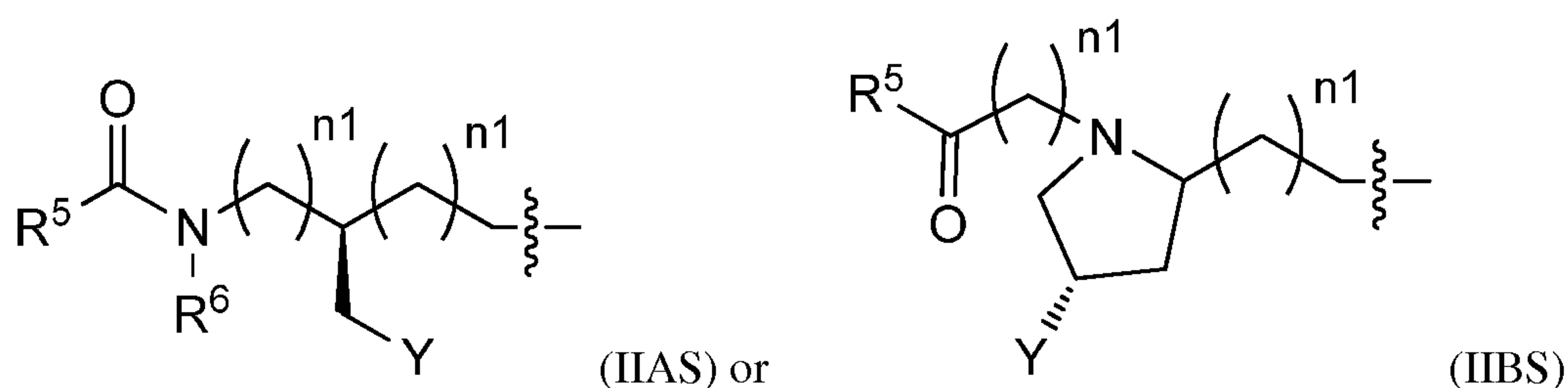
2. The compound of formula I of embodiment 1 wherein when G¹ is a H or a 6-deoxyhexopyranosyl residue, G² is H, R¹ is of formula (IIA), R² is hydrogen or hydroxy, R³ is hydrogen or nitro, R^{A1} and R^{A2} and R^{A4} are H, R^{A3} and R^{A5} are methyl, and B is CO₂H, then R⁵ is not unsubstituted (C₁-C₂₂)alkyl.

3. The compound of embodiment 1 or 2 wherein the compound is of formula (IA)



- 5 wherein R^1 , R^2 , R^3 , R^4 , R^5 , R^6 , R^{A1} , R^{A2} , R^{A3} , R^{A4} , R^{A5} , R^B , R^{B1} , R^{B2} , and R^C , and m , n , n^2 , n^3 , p , B , G^1 , G^2 , $(X^1)_{x1}$, $(X^2)_{x2}$, and Y , are as defined in embodiment 1 and a wavy line indicates a point of attachment of R^1 to an atom bonded to R^1 in formula (IA); or a salt thereof.

- 10 4. The compound of any one embodiments 1-3 wherein R^1 is a group of formula (IIAS) or (IIBS)



wherein n^1 , n^2 , p , R^5 , R^6 , and Y , are as defined in embodiment 1 and a wavy line indicates a point of attachment of R^1 to an atom bonded to R^1 in formula (I);

- 15 or a salt thereof.

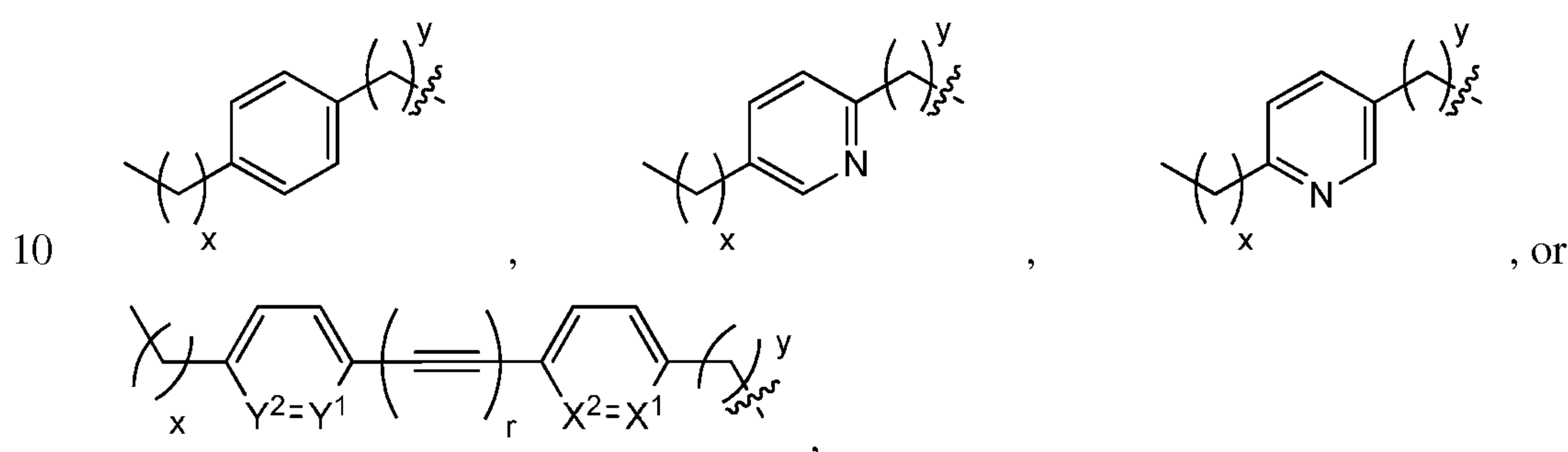
5. The compound of embodiment 1 or 2 wherein R^5 is a (C_1-C_{22}) linear or branched alkyl.

- 20 6. The compound of embodiment 1 or 2 wherein R^5 is a (C_1-C_{22}) linear or branched alkyl comprising one or more of groups (A), (B), (C), or (D), of embodiment 1.

7. The compound of embodiment 3 or 4 wherein R^5 is a (C_1-C_{22}) linear or branched alkyl.

8. The compound of embodiment 3 or 4 wherein R^5 is a (C_1-C_{22}) linear or branched alkyl, comprising one or more of groups (A), (B), (C), or (D), of embodiment 1.

9. The compound of any one of embodiments 1-4 wherein R^5 is any of the following groups

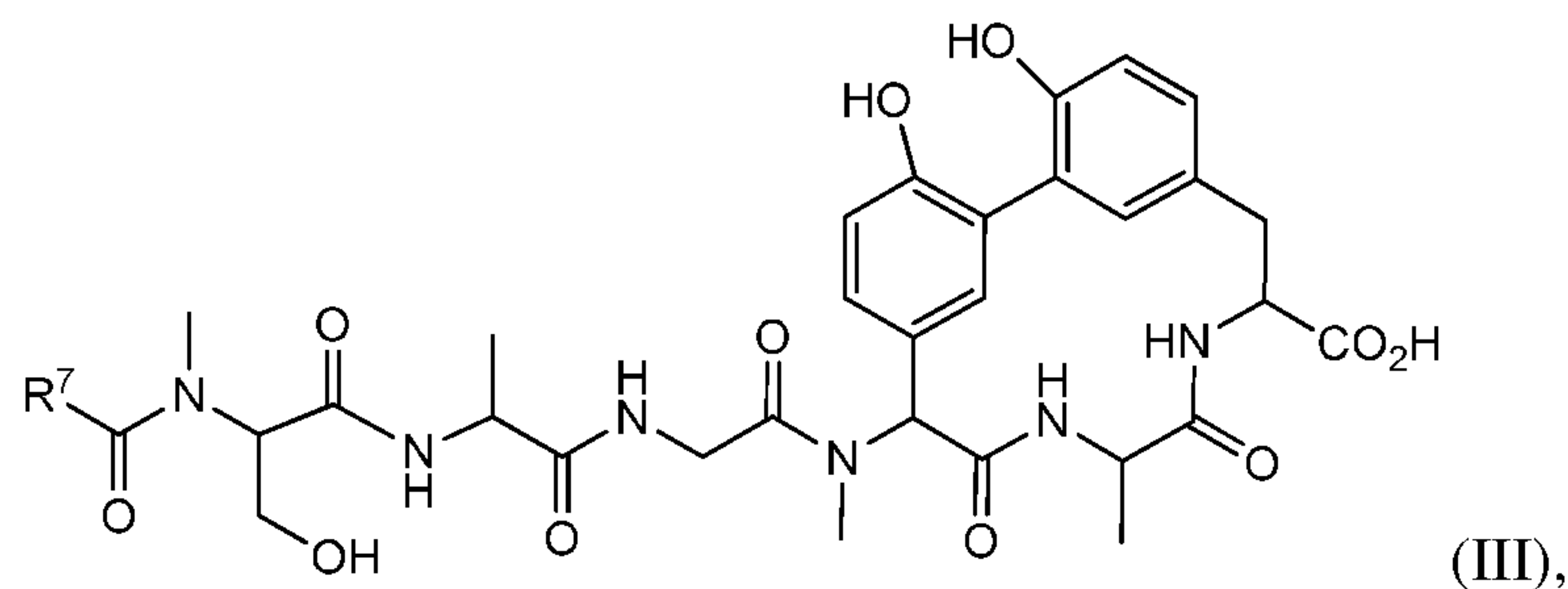


15 wherein x is 0-14, y is 0-14, provided that $x + y \leq 22$, and X^1 , X^2 , Y^1 and Y^2 are each independently C or N, provided that no more than one of X^1 and X^2 , and no more than one of Y^1 and Y^2 , is N, wherein a wavy line indicates a point of attachment of R^5 to an atom bonded to R^5 in formula (IIA), (IIB), or (IIC).

10. The compound of any one of embodiments 1-4 wherein R^5 is any of the following: methyl, ethyl, (C_3-C_{22}) -n-alkyl, (C_3-C_{22}) -isoalkyl, (C_4-C_{22}) -anteisoalkyl, naphthyl, (C_2-C_{10}) naphthyl, naphthylmethyl, (C_2-C_{10}) naphthylmethyl, biphenyl, (C_2-C_{10}) alkylbiphenyl, biphenylmethyl, (C_2-C_{10}) alkylbiphenylmethyl, (C_4-C_{12}) phenyl, (C_4-C_{12}) benzyl, (C_2-C_{10}) -1,2-diphenylethynyl, or (Z)- or (E)- (C_2-C_{10}) -1,2-diphenylethenyl, wherein a wavy line indicates a point of attachment of R^5 to an atom bonded to R^5 in formula (IIA), (IIB), or (IIC).

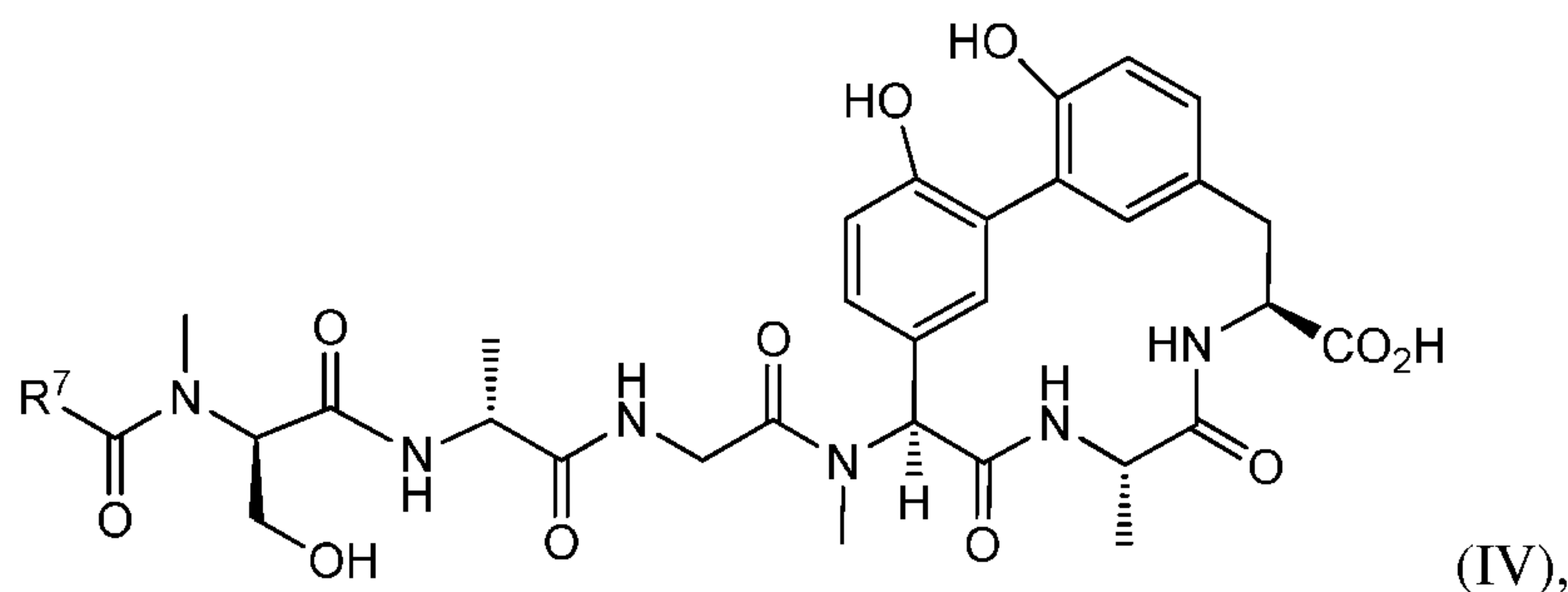
25 11. The compound of embodiment 1 wherein ring bearing one or more X^1 or X^2 , respectively, is a phenyl, pyridyl, pyrazinyl, pyrimidyl, or pyridazinyl. optionally wherein R^2 and R^3 are both hydrogen.

12. The compound of any of embodiments 1-4 wherein at least one of R^2 and R^3 is hydrogen.
- 13 The compound of any of embodiments 1-4 wherein at least one of R^2 and R^3 is
 5 nitro, halo, cyano, hydroxy, glycosyloxy, amino, (C_1-C_4) alkoxy, or (C_1-C_4) alkyl, and n^2 or n^3 respectively, or both, is 1.
14. The compound of any one of embodiments 1-4 wherein both G are hydrogen.
- 10 15. The compound of any one of embodiments 1-4 wherein any of R^{A1} , R^{A2} and R^{A4} are hydrogen, any of R^{A3} and R^{A5} are methyl, or any combination thereof.
16. The compound of any one of embodiments 1-4 wherein R^{A3} is hydrogen, methyl, ethyl, n-propyl, isopropyl, n-butyl, isobutyl, 3-hydroxypropyl, 4-hydroxybutyl, or 2,2,2-
 15 trifluoroethyl.
17. The compound of any one of embodiments 1-4 wherein all of R^4 and R^6 are independently selected hydrogen or methyl.
- 20 18. The compound of embodiment 1 wherein the compound is any of the following compounds of formula (III)



- wherein R^7 is (C_8-C_{18}) -n-alkyl, (C_8-C_{18}) -isoalkyl, (C_8-C_{18}) -anteisoalkyl, any of which includes a group (A), (B), (C), (D), or (E) of embodiment 1; or is 2-naphthyl, 6-
 25 (C_2-C_{10}) -2-naphthyl, 2-naphthylmethyl, 6- (C_2-C_{10}) -2-naphthylmethyl, 4-biphenyl, 4-biphenylmethyl, 4'- (C_2-C_{10}) alkyl-4-biphenyl, 4'- (C_2-C_{10}) alkyl-4-biphenylmethyl, p- (C_4-C_{12}) phenyl, p- (C_4-C_{12}) benzyl, or 4'- (C_2-C_{10}) -1,2-diphenylethynyl;
 or a salt thereof.

19. The compound of embodiment 3 wherein the compound is any of the following compounds of formula (IV)



herein R^7 is (C₈-C₁₈)-n-alkyl, (C₈-C₁₈)-isoalkyl, (C₈-C₁₈)-anteisoalkyl, any of
 5 which includes a group (A), (B), (C), (D), or (E) of embodiment 1; or is 2-naphthyl, 6-(C₂-C₁₀)-2-naphthyl, 2-naphthylmethyl, 6-(C₂-C₁₀)-2-naphthylmethyl, 4-biphenyl, 4-biphenylmethyl, 4'-(C₂-C₁₀)-4-biphenyl, 4'-(C₂-C₁₀)-4-biphenylmethyl, p-(C₄-C₁₂)-phenyl, p-(C₄-C₁₂)-benzyl, or 4'-(C₂-C₁₀)-1,2-diphenylethynyl;
 or a salt thereof.

10

20. A compound comprising a hydrate, solvate, prodrug, or metabolite of a compound of any one of embodiments 1-19.

21. A pharmaceutical composition comprising the compound of any one of
 15 embodiments 1-20 and a pharmaceutically acceptable excipient.

22. Use of a compound of any one of embodiments 1-20 for preparation of a medicament for treatment of a bacterial infection in a patient.

20 23. A method of treatment of a bacterial infection in an animal, comprising administering an effective amount of a compound of any one of embodiments 1-20 to the animal at a frequency and for a duration sufficient to provide a beneficial effect to the animal.

25 24. The method of embodiment 23 wherein a causative bacterial species of the bacterial infection is of a genotype resistant to treatment with arylomycin A2.

25. The method of embodiment 23, wherein the bacterial infection is an infection involving *Corynebacterium diphtheriae*, *Corynebacterium glutamicum*, *Campylobacter*

- jejuni*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Francisella tularensis*, *Helicobacter pylori*, *Lactococcus lactis* subsp. *cremoris*, *Lactococcus lactis* subsp. *lactis*, *Propionibacterium acnes*, *Rhodococcus equi*, *Rhodococcus opacus*, *Staphylococcus capitis*, *Staphylococcus caprae*, *Staphylococcus carnosus*, *Staphylococcus cohnii*,
5 *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus hominis* subsp. *hominis*, *Staphylococcus hominis* subsp. *novobiosepticus*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*, *Streptococcus dysgalactiae*, *Streptococcus mitis*, *Streptococcus oralis*, *Streptococcus pyogenes*, *Streptococcus pneumoniae*, and/or *Yersinia pestis*.
- 10
26. The method of any of embodiments 23-25, wherein the bacterial infection is an infection involving a gram negative bacteria.
27. A method of treating a bacterial infection in an animal that includes
15 administering arylomycin A and/or arylomycin B and/or a compound of any of embodiments 1-20 to the animal, wherein the infection involves a microbial species that expresses a signal peptidase without a proline residue within 10 amino acids N-terminal to the signal peptidase catalytic serine.
- 20 28. The method of embodiment 27, wherein the bacterial species encodes or expresses an SPase enzyme without a proline residue 5 to 7 amino acids N-terminal to the SPase catalytic serine.
29. The method of embodiment 27 or 28, wherein the bacterial infection is an
25 infection involving *Corynebacterium diphtheriae*, *Corynebacterium glutamicum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Francisella tularensis*, *Helicobacter pylori*, *Lactococcus lactis* subsp. *cremoris*, *Lactococcus lactis* subsp. *lactis*, *Propionibacterium acnes*, *Rhodococcus equi*, *Staphylococcus carnosus*, *Staphylococcus cohnii*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*,
30 *Staphylococcus hominis* subsp. *hominis*, *Staphylococcus hominis* subsp. *novobiosepticus*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*, *Streptococcus dysgalactiae*, *Streptococcus mitis*, *Streptococcus oralis*, *Streptococcus pyogenes*, and/or *Streptococcus pneumoniae*.

30. The method of any of embodiments 27-29, wherein the bacterial infection is an infection involving a gram negative bacteria.
31. The method of any of embodiments 27-30, wherein administering comprises
5 topical administration.
32. A method of treating a bacterial infection in an animal comprising administering to the animal any one or any combination of the compounds of any of embodiments 1-20, wherein the bacterial infection comprises an infection by a bacteria that encodes or
10 expresses an SPase enzyme that has a proline within about 10 amino acids N-terminal to the SPase catalytic serine.
33. The method of embodiment 32, wherein the bacteria encodes or expresses an SPase enzyme that does not have a proline 5 to 7 amino acids N-terminal to the SPase catalytic
15 serine.
34. The method of embodiment 32 or 33, wherein the bacterial infection involves *Staphylococcus capitis*, *Staphylococcus caprae* and/or *Yersinia pestis*.
- 20 35. A method of treating a bacterial infection in an animal comprising administering to the animal arylomycin A or arylomycin B, wherein the microbial infection is an infection involving *Corynebacterium diphtheriae*, *Corynebacterium glutamicum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Francisella tularensis*, *Helicobacter pylori*, *Lactococcus lactis* subsp. *cremoris*, *Lactococcus lactis* subsp. *lactis*, *Propionibacterium acnes*, *Rhodococcus equi*, *Staphylococcus capitis*, *Staphylococcus caprae*, *Staphylococcus carnosus*, *Staphylococcus cohnii*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus hominis* subsp. *hominis*, *Staphylococcus hominis* subsp. *novobioceticus*, *Staphylococcus lugdunensis*,
25 *Streptococcus agalactiae*, *Streptococcus dysgalactiae*, *Streptococcus mitis*, *Streptococcus oralis*, *Streptococcus pyogenes*, *Streptococcus pneumoniae*, and/or *Yersinia pestis*.
- 30 36. The method of embodiment 35, wherein administering comprises topical
35 administration.

37. The method of any of embodiments 23-36 further comprising administering a second therapeutic agent.
38. The method of embodiment 37, wherein the second therapeutic agent is a non-arylomycin antibiotic.
39. The method of embodiment 38, wherein the non-arylomycin antibiotic is an aminoglycoside antibiotic, fluoroquinolone antibiotic, penicillin antibiotic, cephalosporin antibiotic, macrolide antibiotic, glycopeptide antibiotic, rifampicin, chloramphenicol, fluoramphenicol, colistin, mupirocin, bacitracin, daptomycin, or linezolid.
40. A method of detecting whether a test sample contains a bacterium sensitive to an arylomycin antibiotic comprising detecting whether a bacterial signal peptidase is present in the test sample, wherein the bacterial signal peptidase does not have a proline within about 10 amino acids N-terminal to the bacterial signal peptidase's catalytic serine.
41. The method of embodiment 40, further comprising detecting whether a test sample contains *Yersinia pestis*.
42. The method of embodiment 40, wherein the bacterial signal peptidase nucleic acid or the bacterial signal peptidase polypeptide is detected.
43. The method of any of embodiments 40-42, further comprising contacting the test sample with an anti-signal peptidase antibody and detecting whether the antibody forms a complex with a bacterial signal peptidase in the test sample.
44. The method of embodiment 43, wherein the antibody selectively binds to a signal peptidase that does not contain a proline with about 10 amino acids N-terminal to the bacterial signal peptidase's catalytic serine.
45. The method of any of embodiments 40-44, further comprising contacting the test sample with an anti-signal peptidase antibody that selectively binds to a signal peptidase that does contain a proline with about 10 amino acids N-terminal to the bacterial signal

peptidase catalytic serine and detecting whether the antibody forms a complex with a bacterial signal peptidase in the test sample.

46. The method of embodiment 40-42, further comprising contacting a nucleic acid
5 isolated from the test sample with a probe or primer that selectively hybridizes to a DNA encoding a bacterial signal peptidase that does not contain a proline with about 10 amino acids N-terminal to the bacterial signal peptidase's catalytic serine.

47. The method of embodiment 46, wherein the probe or the primer hybridizes to the
10 DNA under stringent hybridization conditions.

48. The method of embodiment 46 or 47, wherein the probe or primer hybridizes to the signal peptidase DNA encoding a region comprising about 4 to about 15 amino acids of the bacterial signal peptidase that includes the catalytic serine.

15 49. The method of embodiment 40-42, 46-48, wherein detecting comprises nucleic acid amplification, nucleic acid sequencing, or single nucleotide polymorphism detection.

50. The method of any of embodiments 40-49, wherein the signal peptidase does not
20 have a proline seven amino acids N-terminal to the bacterial signal peptidase' catalytic serine.

51. The method of any of embodiments 40-50, wherein the signal peptidase does not
25 have a proline five amino acids N-terminal to the bacterial signal peptidase' catalytic serine.

52. The method of any of embodiments 40-51, wherein the bacterium is a *Eubacteria*, and/or the antibody selectively binds to the signal peptidase from a selected species of *Eubacteria* and/or the probe or primer selectively hybridizes to a DNA encoding a signal
30 peptidase from a selected species of *Eubacteria*.

53. A bacterium genetically engineered to encode and/or express a signal peptidase with a proline at 5 to 7 amino acids N-terminal to the signal peptidase's catalytic serine, wherein the bacterium is selected from the group consisting of *Corynebacterium*

diphtheriae, *Corynebacterium glutamicum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Francisella tularensis*, *Helicobacter pylori*, *Lactococcus lactis* subsp. *cremoris*, *Lactococcus lactis* subsp. *lactis*, *Propionibacterium acnes*, *Rhodococcus equi*, *Rhodococcus opacus*, *Staphylococcus carnosus*,
 5 *Staphylococcus cohnii*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*,
Staphylococcus hominis, *Staphylococcus hominis* subsp. *hominis*, *Staphylococcus hominis* subsp. *novobiosepticus*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*,
Streptococcus dysgalactiae, *Streptococcus mitis*, *Streptococcus oralis*, *Streptococcus pyogenes*, and *Streptococcus pneumoniae*.

10

54. A bacterium genetically engineered to encode and/or express a signal peptidase without a proline at 5 to 7 amino acids N-terminal to the signal peptidase's catalytic serine, wherein the bacterium is *Escherichia coli*, *Klebsiella pneumoniae*, *Salmonella enterica*, *Vibrio cholera*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, *Neisseria meningitidis*, *Haemophilus influenza*, *Citrobacter koseri*, *Shigella flexneri*, *Bordetella pertussis*, *Mycobacterium tuberculosis*, *Staphylococcus aureus*, *Bacillus anthracis*,
 15 *Streptococcus mutans*, *Clostridium difficile*, *Enterococcus faecalis* and/or *Listeria monocytogenes*.

20

55. A mutant signal peptidase with a *Corynebacterium diphtheriae*, *Corynebacterium glutamicum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Francisella tularensis*, *Helicobacter pylori*, *Lactococcus lactis* subsp. *cremoris*, *Lactococcus lactis* subsp. *lactis*, *Propionibacterium acnes*, *Rhodococcus equi*, *Rhodococcus opacus*, *Staphylococcus carnosus*, *Staphylococcus cohnii*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus hominis* subsp. *hominis*, *Staphylococcus hominis* subsp. *novobiosepticus*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*, *Streptococcus dysgalactiae*, *Streptococcus mitis*,
 25 *Streptococcus oralis*, *Streptococcus pyogenes*, or *Streptococcus pneumoniae* signal peptidase amino acid sequence that is modified to have a proline substitution at a
 30 position 5 or at a position 7 amino acids N-terminal to the signal peptidase's catalytic serine.

56. A mutant signal peptidase with a *Escherichia coli*, *Klebsiella pneumoniae*, *Salmonella enterica*, *Vibrio cholera*, *Pseudomonas aeruginosa*, *Acinetobacter*

baumanii, *Neisseria meningitides*, *Haemophilus influenza*, *Citrobacter koseri*, *Shigella flexneri*, *Bordetella pertussis*, *Mycobacterium tuberculosis*, *Staphylococcus aureus*, *Bacillus anthracis*, *Streptococcus mutans*, *Clostridium difficile*, *Enterococcus faecalis* or *Listeria monocytogenes* signal peptidase amino acid sequence that is modified by replacement of a proline with a selected amino acid, wherein the proline was at 5 to 7 amino acids N-terminal to the signal peptidase's catalytic serine.

57. The mutant signal peptidase of embodiment 56, wherein the selected amino acid is a serine.

58. A method of identifying an antibiotic effective for treating a bacterial infection involving an arylomycin-resistant bacterial species, comprising contacting the arylomycin-resistant bacteria with a test agent and observing whether the test agent inhibits growth of the arylomycin-resistant bacteria, wherein the arylomycin-resistant bacteria encodes or expresses a signal peptidase enzyme that has a proline residue 5 to 7 amino acids N-terminal to the signal peptidase catalytic serine.

59. A method of identifying a compound that has antibiotic activity against bacteria comprising contacting a culture of bacteria with the test compound and identifying whether the test compound inhibits growth of the bacteria, wherein the bacteria in the culture expresses a modified SPase that has a natural bacterial SPase amino acid sequence modified at position -5 to -7 relative to the catalytic serine by substitution or replacement of an amino acid at that position.

60. The method of embodiment 59, wherein an amino acid at position -5 and/or at position -7 relative to the catalytic serine is replaced with a proline.

61. The method of embodiment 59, wherein the amino acid at position -5 and/or at position -7 relative to the catalytic serine is a proline replaced by a selected amino acid.

62. The method of embodiment 61, wherein the selected amino acid is a serine.

63. The method of embodiments 58 to 62, wherein the test compound that inhibits the growth of the bacteria has antibiotic activity.

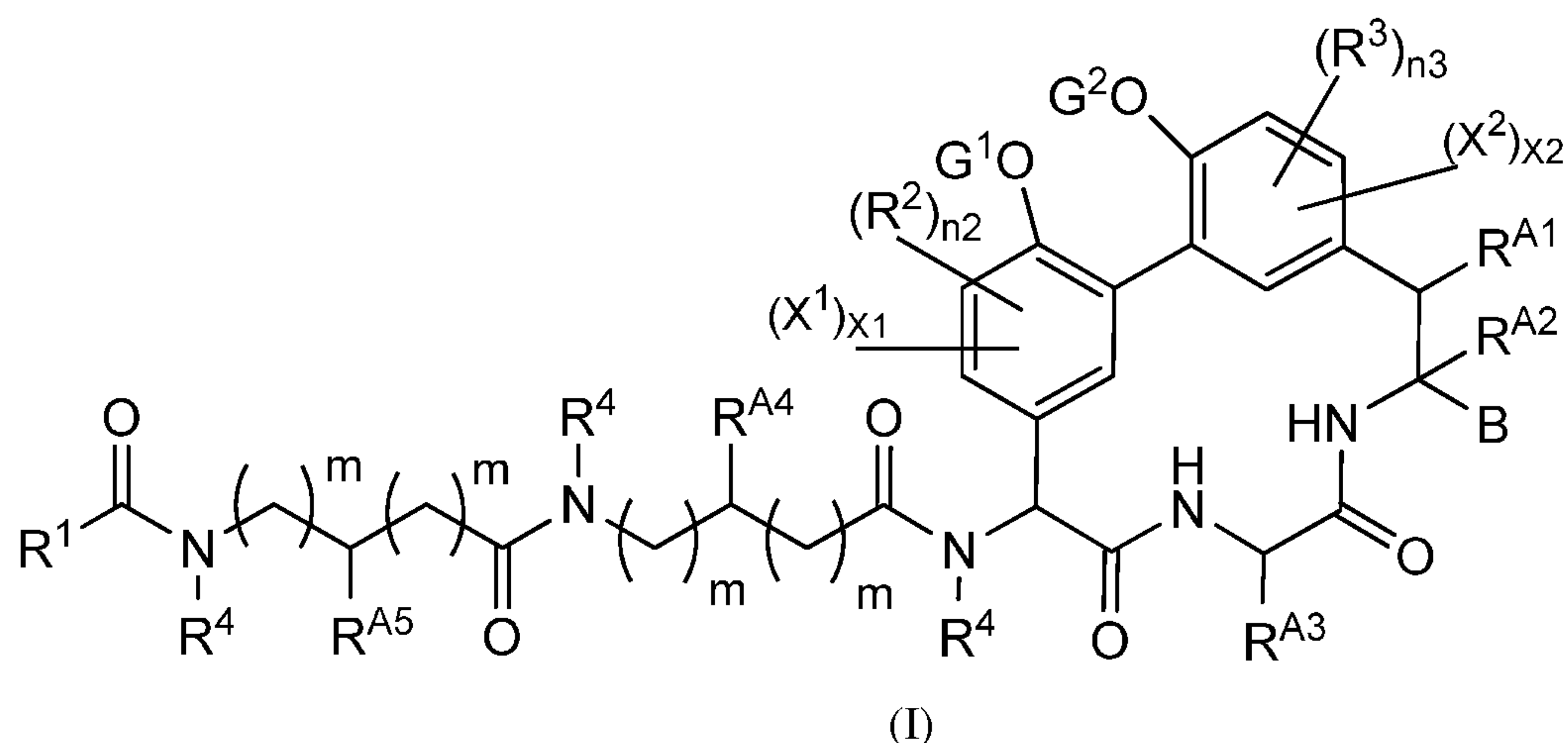
All patents and publications referred to herein are incorporated by reference herein to the same extent as if each individual publication was specifically and individually indicated to be incorporated by reference in its entirety.

5 The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments and optional
10 features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the appended claims.

CLAIMS

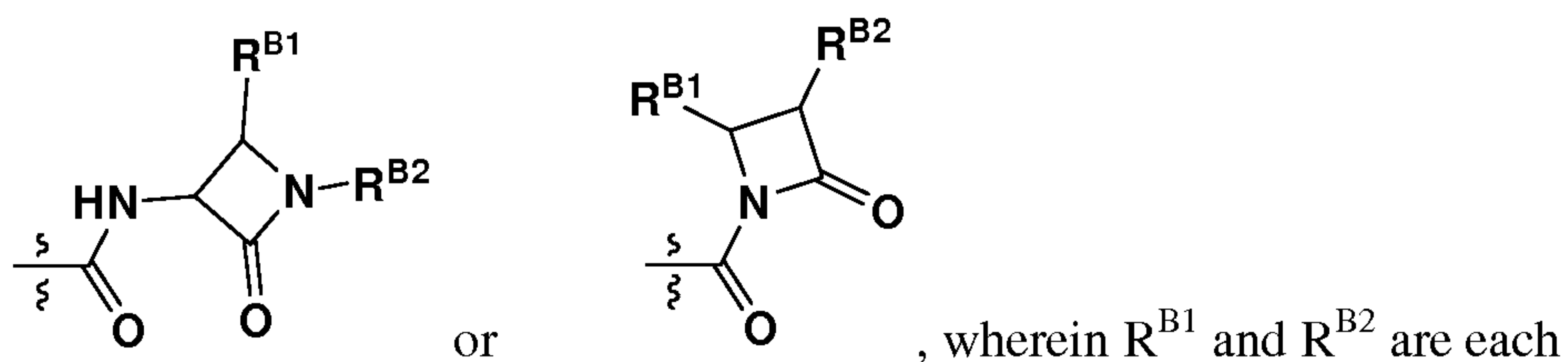
What is claimed is:

1. A compound of formula (I)



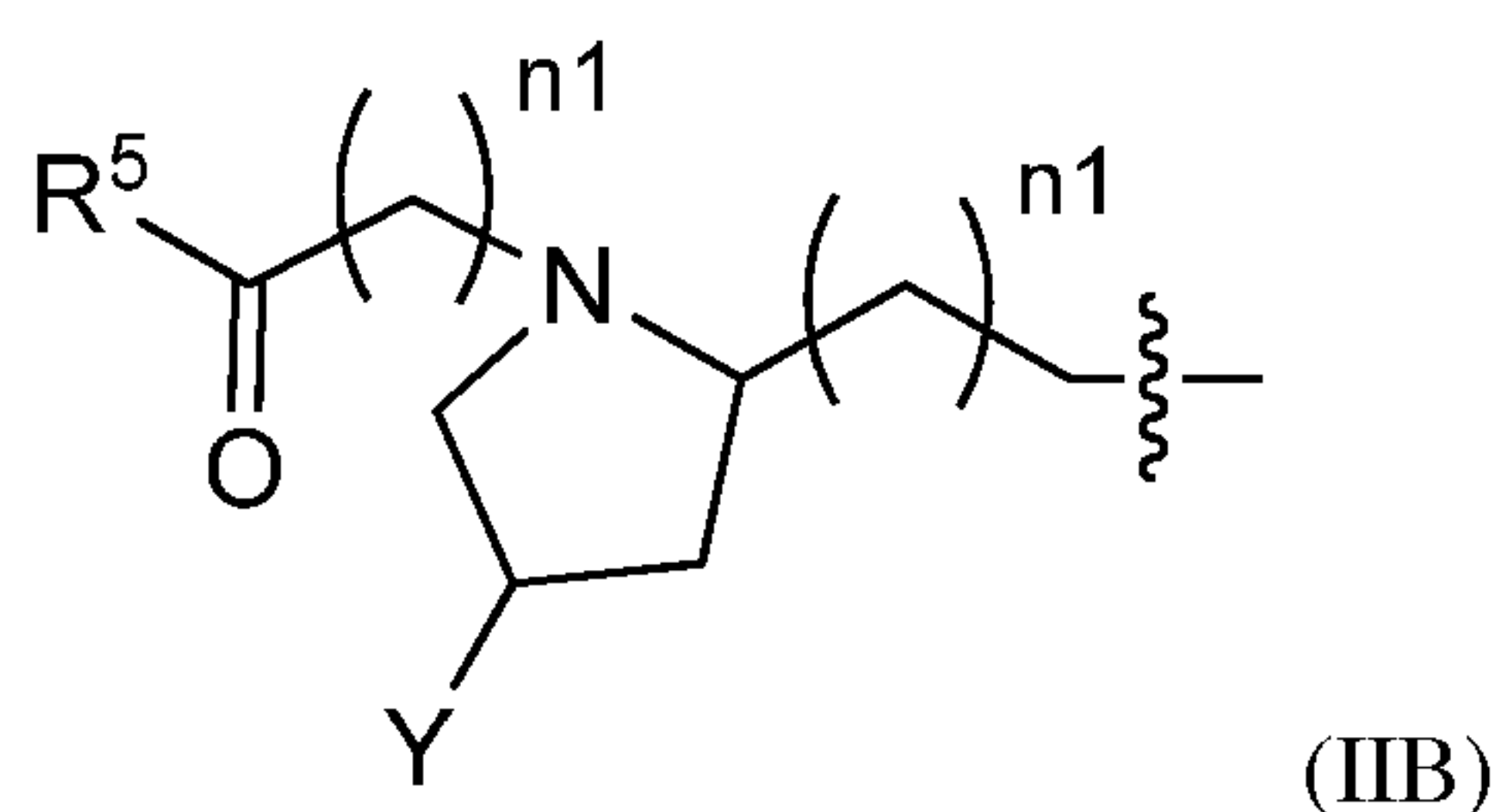
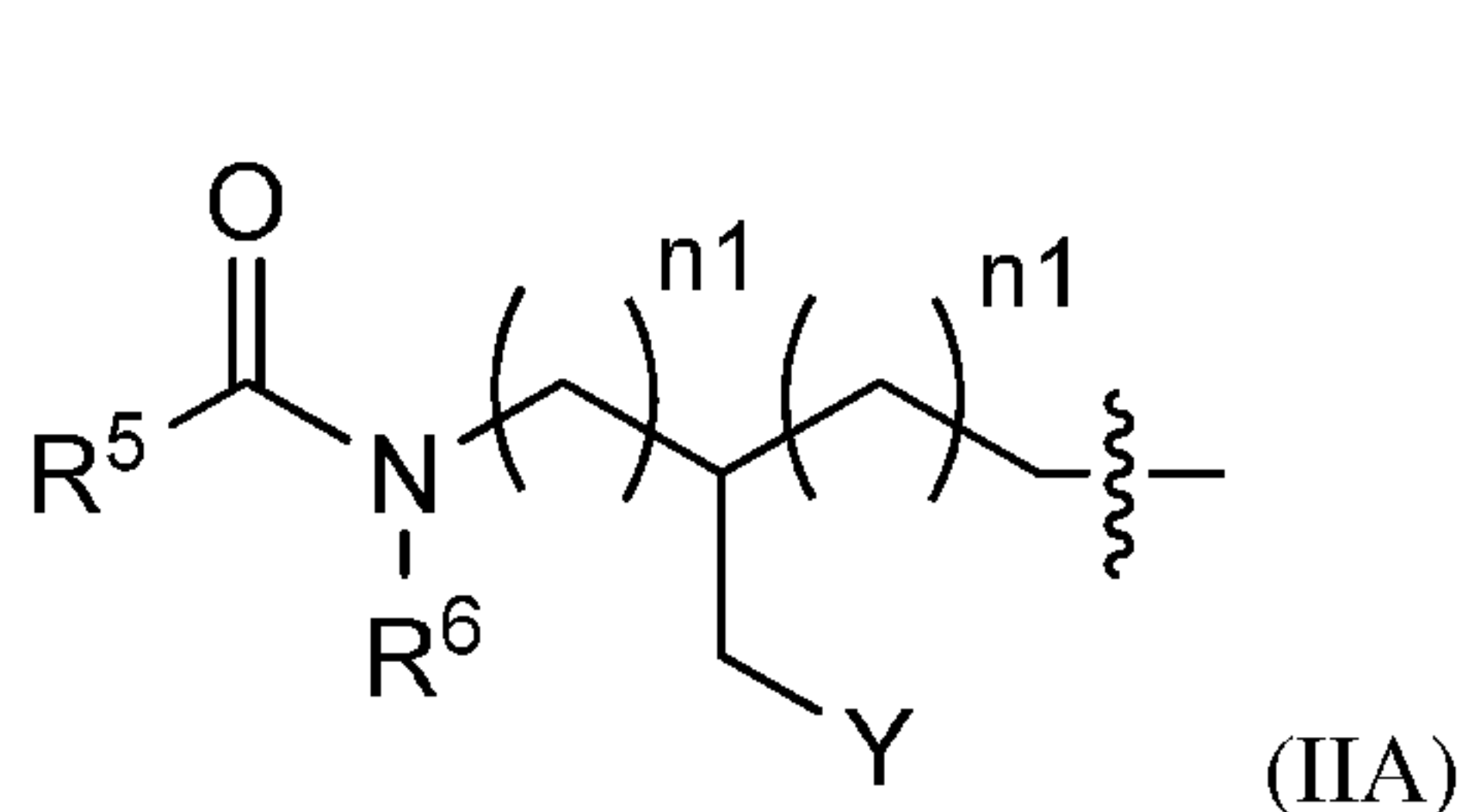
wherein

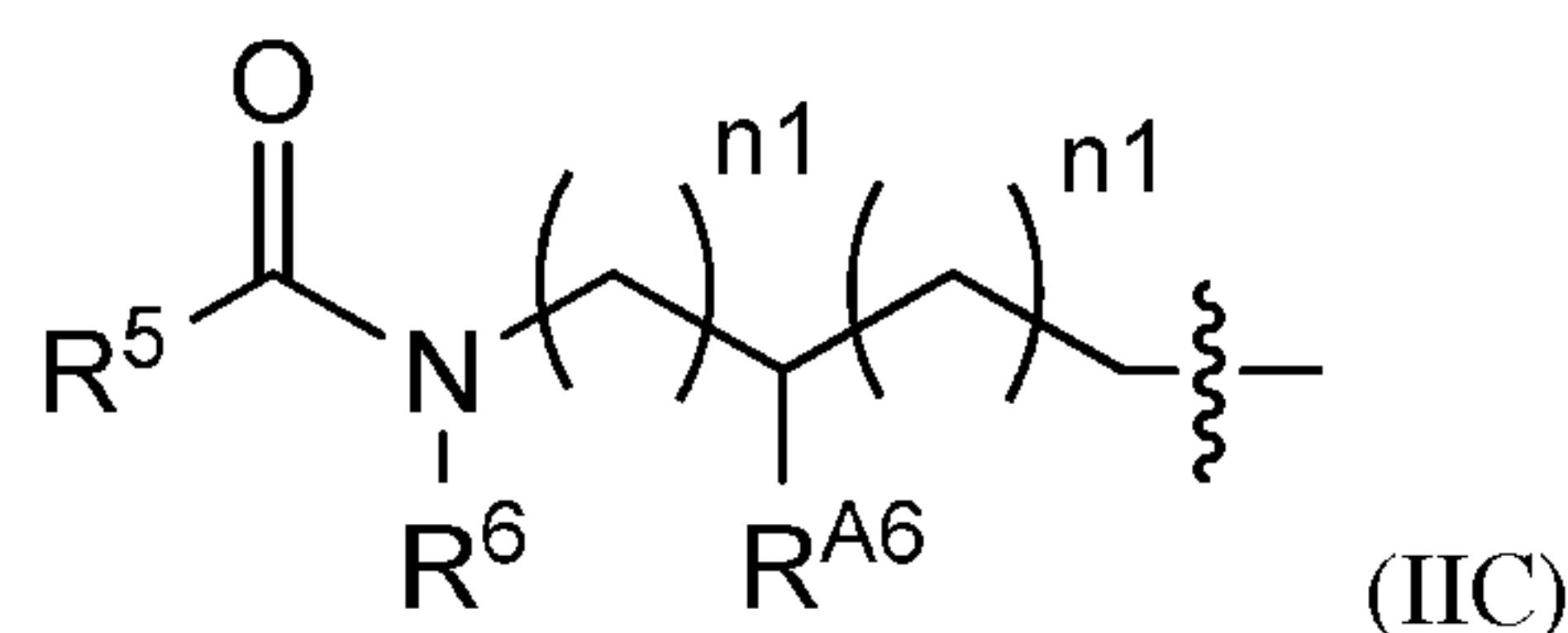
B is CO_2H , $\text{CH}_2\text{CO}_2\text{H}$, $\text{C}(=\text{O})\text{NHCH}_2\text{C}(=\text{O})\text{H}$, $\text{CH}_2\text{C}(=\text{O})\text{H}$, $\text{C}(=\text{O})\text{NHCH}_2\text{B}(\text{OR}^{\text{B}})_2$ or $\text{C}(=\text{O})\text{NHCH}_2\text{P}(=\text{O})(\text{OR}^{\text{B}})_2$ wherein R^{B} is H or $(\text{C}_1\text{-C}_6)\text{alkyl}$, or B is a group of formula



independently H, $(\text{C}_1\text{-C}_6)$ alkyl, $(\text{C}_3\text{-C}_6)$ cycloalkyl, OR^{C} , $\text{C}(=\text{O})\text{NR}^{\text{C}}_2$, $\text{O C}(=\text{O})\text{NR}^{\text{C}}_2$, $\text{C}(=\text{O})\text{OR}^{\text{C}}$, $\text{OC}(=\text{O})\text{OR}^{\text{C}}$, nitro, trifluoromethyl, trifluoromethoxy, $(\text{C}_1\text{-C}_6)\text{alkoxy}$, $(\text{C}_1\text{-C}_6)\text{thioalkoxy}$, NR^{C}_2 , 5-7 membered heterocyclyl or 5-7 membered heteroaryl, or $(\text{C}_6\text{-C}_{10})$ aryl; R^{C} is independently at each occurrence H or $(\text{C}_1\text{-C}_6)$ alkyl, and a wavy line indicates a point of attachment of B to a carbon of formula (I) bearing B;

R^1 comprises a group of formula (IIA) or (IIB) or (IIC)

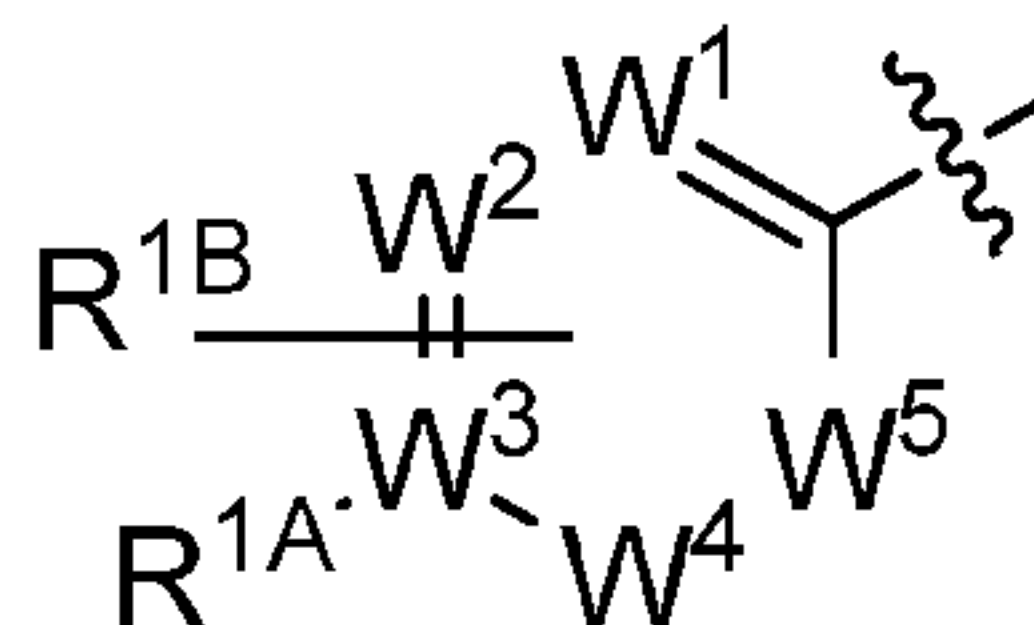




wherein each m is independently 0, 1, or 2, n_1 is independently at each occurrence 0, 1, or 2; Y is $(CH_2)_{0-2}H$, $(CH_2)_{0-2}OH$, or $(CH_2)_{0-2}OC(=O)(C_1-C_6)alkyl$; R^{A6} is hydrogen, $(C_1-C_6)alkyl$, $(C_3-C_7)cycloalkyl$, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or $(C_6-C_{10}) aryl$, wherein any alkyl, cycloalkyl, heterocyclyl, aryl or heteroaryl may be substituted with 1 to 3 substituents, wherein each substituent is independently selected from the group consisting of halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, cyano, trifluoromethyl, trifluoromethoxy, 5- to 7- membered heterocyclyl, $(C_1-C_6)alkoxy$, $(C_1-C_6)alkyl$, $(C_3-C_7)cycloalkyl$, (C_1-C_6) -mono- or di-alkylamino, $(C_1-C_6)alkoxycarbonyl$, $(C_1-C_6)alkylhydroxycarbonyl$, $(C_1-C_6)alkylaminocarbonyl$, $(C_1-C_6)alkylsulfonylamino$, and (C_6-C_{10}) -arylsulfonylamino; and a wavy line indicates a point of attachment of R^1 to an atom of formula (I) bearing R^1 ; and

R^5 is a linear or branched alkyl chain of about 1-22 carbon atoms, bonded to the carbonyl carbon to which it is attached directly or by an O or NR, to provide an amide, carbamate, or urea linkage respectively; optionally comprising within the chain or at a chain terminus, any of the following groups:

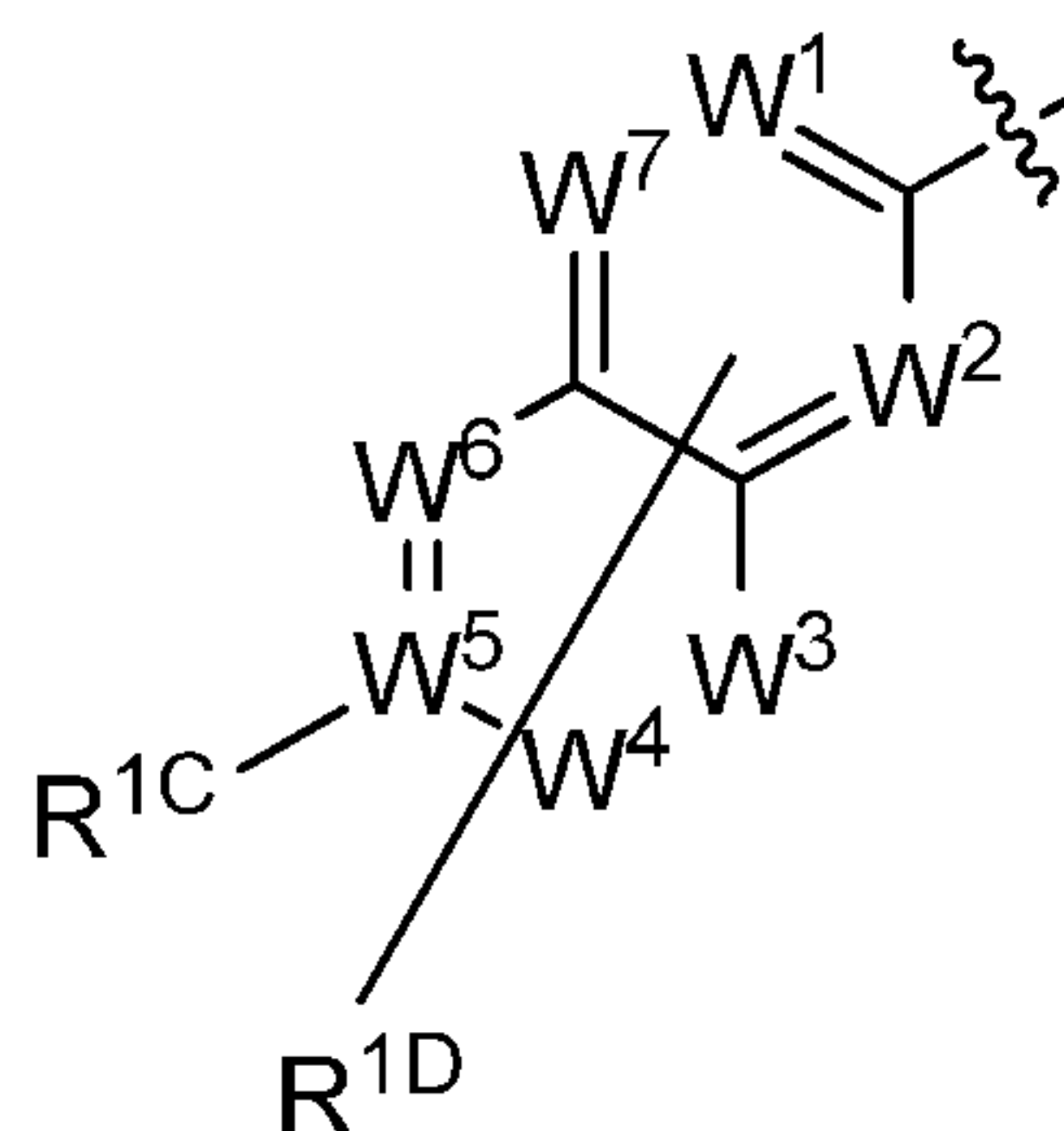
(A)



wherein W^1 , W^2 , W^3 , W^4 and W^5 are each independently C or N, provided that no more than two of W^1 , W^2 , W^3 , W^4 and W^5 are N; provided that when R^{1A} or R^{1B} is non-hydrogen, any W atom to which the R^{1A} or R^{1B} is respectively bonded is C, wherein there can be one or more R^{1B} bonded to the ring bearing the W atoms; R^{1A} is hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, cyano, (C_1-C_6) -thioether, fluoroalkoxy, (C_1-C_6) -alkyl, (C_1-C_6) -alkoxy, (C_1-C_6) -mono- or di-alkylamino, (C_1-C_6) -alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or $(C_6-C_{10}) aryl$; R^{1B} is hydrogen, alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C_1-C_6) -thioalkyl, fluoroalkoxy, cyano, (C_1-C_6) -alkyl, (C_1-C_6) -alkoxy, (C_1-C_6) -alkylamino, (C_1-C_6) -alkyl, 5- to 7-

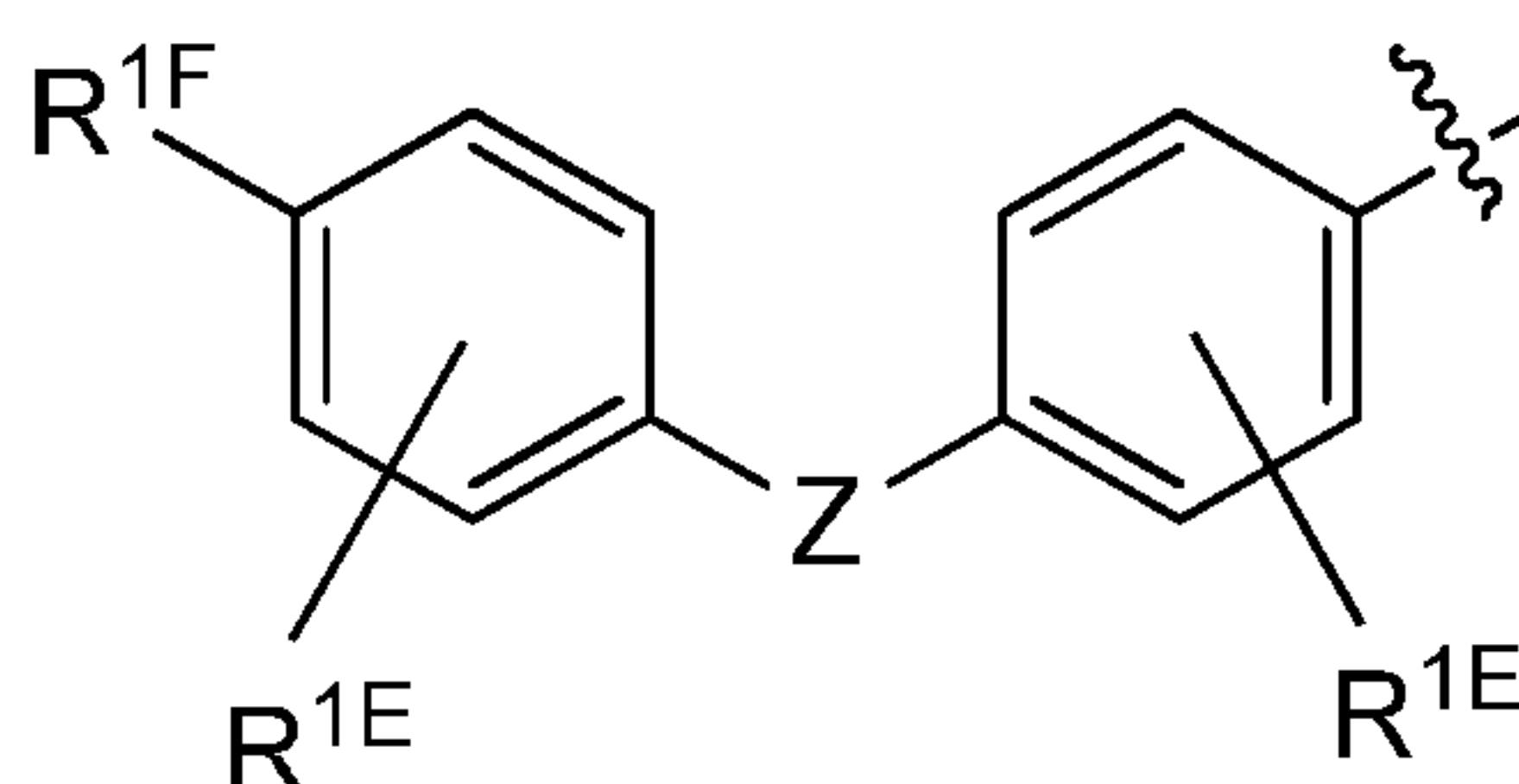
membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1A} or R^{1B} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl groups; wherein a wavy line indicates a point of attachment;

(B)



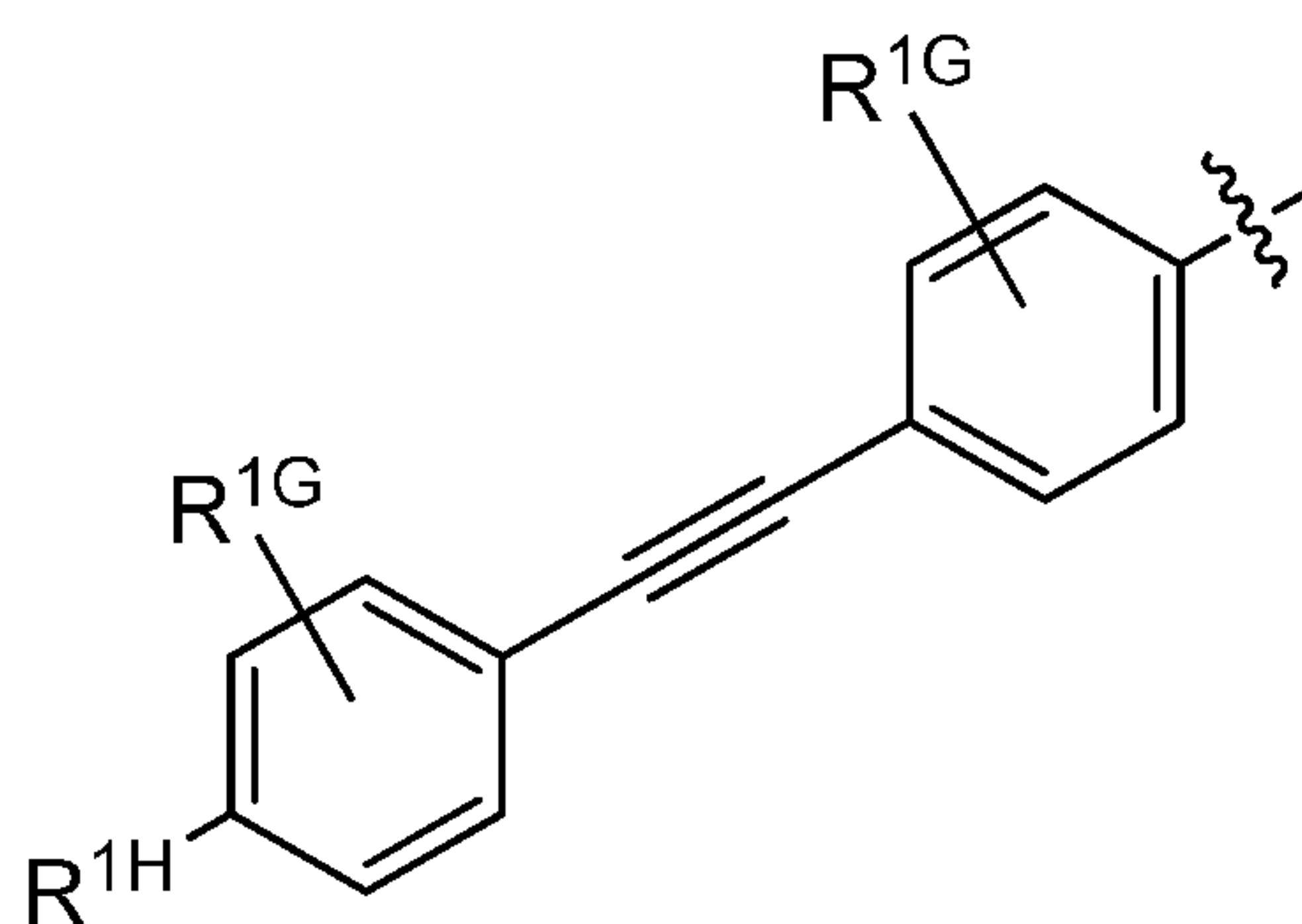
wherein W¹, W², W³, W⁴, W⁵, W⁶, and W⁷ are each independently C or N, provided that no more than three of W¹, W², W³, W⁴, W⁵, W⁶, and W⁷ are N; provided that when R^{1C} or R^{1D} is non-hydrogen, any W atom to which the R^{1C} or R^{1D} is respectively bonded is C, wherein either ring can bear one or more R^{1D}; R^{1C} is hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1D} is hydrogen, alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1C} or R^{1D} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment;

(C)



wherein Z is O, S, NH or CH₂; R^{1E} at each occurrence is independently hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1F} is hydrogen or alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1E} or R^{1F} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment; or

(D)



wherein R^{1G} at each occurrence is independently hydrogen, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; R^{1H} is hydrogen or alkyl, halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)-thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7-

membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein any R^{1G} or R^{1H} can be further substituted with one to three (C₁-C₁₂)-alkyl or -alkoxy groups, which can further bear halogen, amino, hydroxyl, aminocarbonyl, hydroxycarbonyl, nitro, fluoroalkyl, (C₁-C₆)thioalkyl, fluoroalkoxy, cyano, (C₁-C₆)-alkyl, (C₁-C₆)-alkoxy, (C₁-C₆)-mono- or di-alkylamino, (C₁-C₆)-alkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl; wherein a wavy line indicates a point of attachment;

R² and R³ are each independently nitro, halo, cyano, hydroxy, glycosyloxy, amino, (C₁-C₄)alkoxy, (C₁-C₄)acyloxy, or (C₁-C₄)alkyl, wherein any carbon atom can be unsubstituted or substituted with J, wherein n² and n³ are independently 0, 1, 2, or 3; or wherein two R² groups taken together, and/or two R³ groups taken together, can comprise fused cycloalkyl, aryl, heterocyclyl, or heteroaryl ring or rings, any of which is substituted with 0-3 J;

R⁴ and R⁶ are each independently at every occurrence hydrogen, (C₁-C₆)alkyl, (C₃-C₇)cycloalkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl, wherein any alkyl, cycloalkyl, heterocyclyl, aryl or heteroaryl can be substituted with 1 to 3 J;

R^{A1}, R^{A2}, R^{A3}, R^{A4}, R^{A5} are independently at each occurrence hydrogen, (C₁-C₆)alkyl, (C₃-C₇)cycloalkyl, 5- to 7- membered heteroaryl, 5- to 7- membered heterocyclyl, or (C₆-C₁₀) aryl, wherein any alkyl, cycloalkyl, heterocyclyl, aryl or heteroaryl can be substituted with 1 to 3 J;

J is halogen, R', OR', CN, CF₃, OCF₃, O, S, C(O), S(O), methylenedioxy, ethylenedioxy, (CH₂)_{0-p}N(R')₂, (CH₂)_{0-p}SR', (CH₂)_{0-p}S(O)R', (CH₂)_{0-p}S(O)₂R', (CH₂)_{0-p}S(O)₂N(R')₂, (CH₂)_{0-p}SO₃R', (CH₂)_{0-p}C(O)R', (CH₂)_{0-p}C(O)CH₂C(O)R', (CH₂)_{0-p}C(S)R', (CH₂)_{0-p}C(O)OR', (CH₂)_{0-p}OC(O)R', (CH₂)_{0-p}C(O)N(R')₂, (CH₂)_{0-p}OC(O)N(R')₂, (CH₂)_{0-p}C(S)N(R')₂, (CH₂)_{0-p}NH-C(O)R', (CH₂)_{0-p}N(R')N(R')C(O)R', (CH₂)_{0-p}N(R')N(R')C(O)OR', (CH₂)_{0-p}N(R')N(R')CON(R')₂, (CH₂)_{0-p}N(R')SO₂R', (CH₂)_{0-p}N(R')SO₂N(R')₂, (CH₂)_{0-p}N(R')C(O)OR', (CH₂)_{0-p}N(R')C(O)R', (CH₂)_{0-p}N(R')C(S)R', (CH₂)_{0-p}N(R')C(O)N(R')₂, (CH₂)_{0-p}N(R')C(S)N(R')₂, (CH₂)_{0-p}N(COR')COR', (CH₂)_{0-p}N(OR')R', (CH₂)_{0-p}C(=NH)N(R')₂, (CH₂)_{0-p}C(O)N(OR')R', or (CH₂)_{0-p}C(=NOR')R'; wherein p is about 4,

each R' is independently at each occurrence hydrogen, (C₁-C₁₂)-alkyl, (C₂-C₁₂)-alkenyl, (C₂-C₁₂)-alkynyl, (C₃-C₁₀)-cycloalkyl, (C₃-C₁₀)-cycloalkenyl, [(C₃-C₁₀)cycloalkyl or (C₃-C₁₀)-cycloalkenyl]-[(C₁-C₁₂)-alkyl or (C₂-C₁₂)-alkenyl or (C₂-C₁₂)-

alkynyl], (C₆-C₁₀)-aryl, (C₆-C₁₀)-aryl-[(C₁-C₁₂)-alkyl or (C₂-C₁₂)-alkenyl or (C₂-C₁₂)-alkynyl], mono- or bicyclic 3-10 membered heterocyclyl, mono- or bicyclic 3-10 membered heterocyclyl-[(C₁-C₁₂)-alkyl or (C₂-C₁₂)-alkenyl or (C₂-C₁₂)-alkynyl], mono- or bicyclic 5-10 membered heteroaryl, or mono- or bicyclic 5-10 membered heteroaryl-[(C₁-C₁₂)-alkyl or (C₂-C₁₂)-alkenyl or (C₂-C₁₂)-alkynyl], wherein R' is substituted with 0-3 substituents selected independently from J;

or, when two R' are bound to a nitrogen atom or to two adjacent nitrogen atoms, the two R' groups together with the nitrogen atom or atoms to which they are bound can form a 3- to 8-membered monocyclic heterocyclic ring, or an 8- to 20-membered, bicyclic or tricyclic, heterocyclic ring system, wherein any ring or ring system can further contain 1-3 additional heteroatoms selected from the group consisting of N, NR', O, S, S(O) and S(O)₂, wherein each ring is substituted with 0-3 substituents selected independently from J;

wherein, in any bicyclic or tricyclic ring system, each ring is linearly fused, bridged, or spirocyclic, wherein each ring is either aromatic or nonaromatic, wherein each ring can be fused to a (C₆-C₁₀)aryl, mono- or bicyclic 5-10 membered heteroaryl, (C₃-C₁₀)cycloalkyl or mono- or bicyclic 3-10 membered heterocyclyl;

G¹ and G² are each independently a hydrogen or a glycosyl residue, or a group cleavable under physiological conditions to provide a compound of formula (I) wherein G¹ or G² respectively is hydrogen;

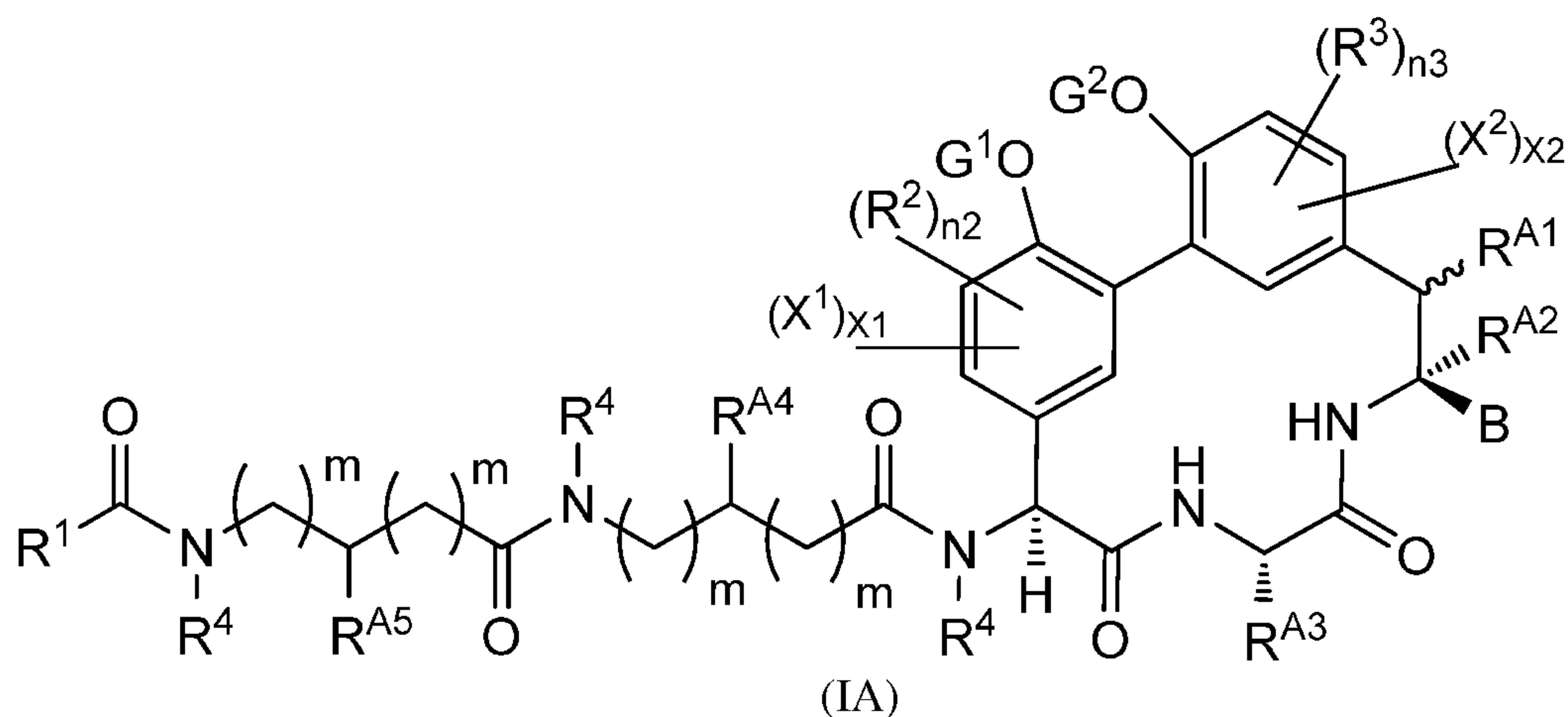
(X¹)_{X1} and (X²)_{X2} each signify that 0, 1, or 2 ring atoms of each respective ring can be nitrogen, provided that where a non-hydrogen substituent is bonded, X¹ or X², respectively, is C;

provided that when G¹ is a 6-deoxyhexopyranosyl residue, G² is H, R¹ is of formula (IIA), R² is hydrogen or hydroxy, R³ is hydrogen, R^{A1} and R^{A2} and R^{A4} are H, R^{A3} and R^{A5} are methyl, and B is CO₂H, or when G¹ and G² are H, R¹ is of formula (IIA), R² is hydrogen, R³ is hydrogen or nitro, R^{A1} and R^{A2} and R^{A4} are H, R^{A3} and R^{A5} are methyl, and B is CO₂H, then R⁵ is not unsubstituted (C₁₀-C₁₆)-alkyl;

or a salt thereof.

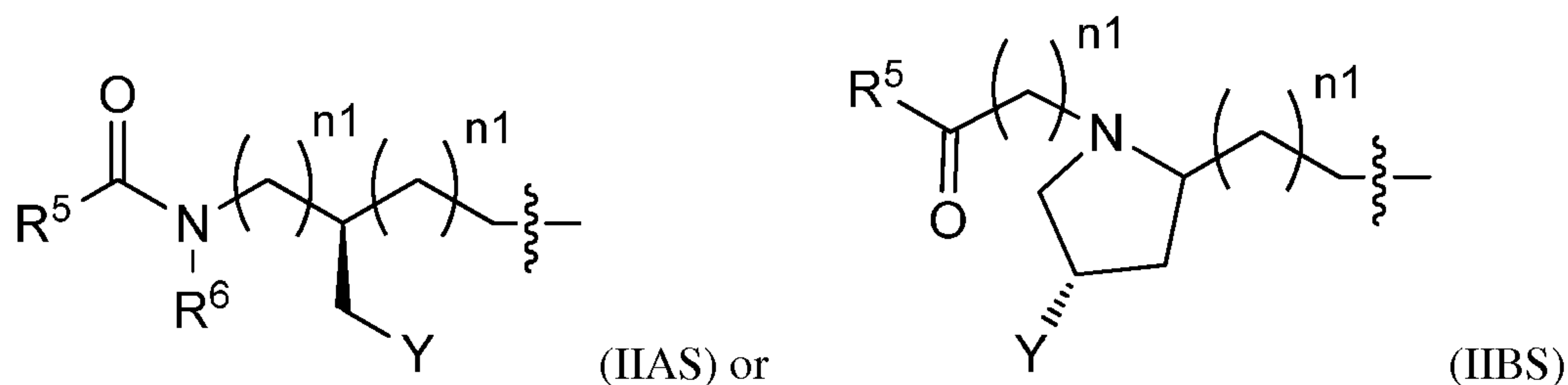
2. The compound of formula I of claim 1 wherein when G¹ is a H or a 6-deoxyhexopyranosyl residue, G² is H, R¹ is of formula (IIA), R² is hydrogen or hydroxy, R³ is hydrogen or nitro, R^{A1} and R^{A2} and R^{A4} are H, R^{A3} and R^{A5} are methyl, and B is CO₂H, then R⁵ is not unsubstituted (C₁-C₂₂)alkyl.

3. The compound of claim 1 wherein the compound is of formula (IA)



- wherein R^1 , R^2 , R^3 , R^4 , R^5 , R^6 , R^{A1} , R^{A2} , R^{A3} , R^{A4} , R^{A5} , R^B , R^{B1} , R^{B2} , and R^C , and m , n , n^2 , n^3 , p , B , G^1 , G^2 , $(X^1)_{x1}$, $(X^2)_{x2}$, and Y , are as defined in claim 1 and a wavy line indicates a point of attachment of R^1 to an atom bonded to R^1 in formula (IA);
or a salt thereof.

4. The compound of claim 1 wherein R^1 is a group of formula (IIAS) or (IIBS)

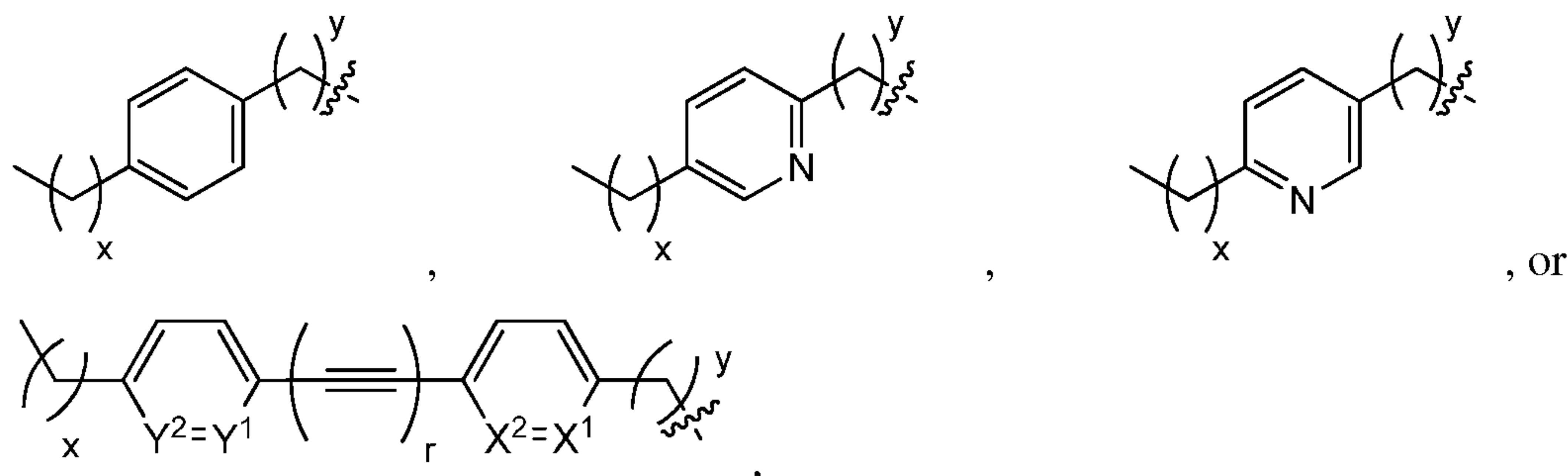


- wherein n^1 , n^2 , p , R^5 , R^6 , and Y , are as defined in claim 1 and a wavy line indicates a point of attachment of R^1 to an atom bonded to R^1 in formula (I);
or a salt thereof.

5. The compound of claim 1 wherein R^5 is a (C_1-C_{22}) linear or branched alkyl.
6. The compound of claim 1 wherein R^5 is a (C_1-C_{22}) linear or branched alkyl comprising one or more of groups (A), (B), (C), or (D), of claim 1.
7. The compound of claim 3 or 4 wherein R^5 is a (C_1-C_{22}) linear or branched alkyl.

8. The compound of claim 3 or 4 wherein R^5 is a (C_1 - C_{22}) linear or branched alkyl, comprising one or more of groups (A), (B), (C), or (D), of claim 1.

9. The compound of claim 1 wherein R^5 is any of the following groups



wherein x is 0-14, y is 0-14, provided that $x + y \leq 22$, and X^1 , X^2 , Y^1 and Y^2 are each independently C or N, provided that no more than one of X^1 and X^2 , and no more than one of Y^1 and Y^2 , is N, wherein a wavy line indicates a point of attachment of R^5 to an atom bonded to R^5 in formula (IIA), (IIB), or (IIC).

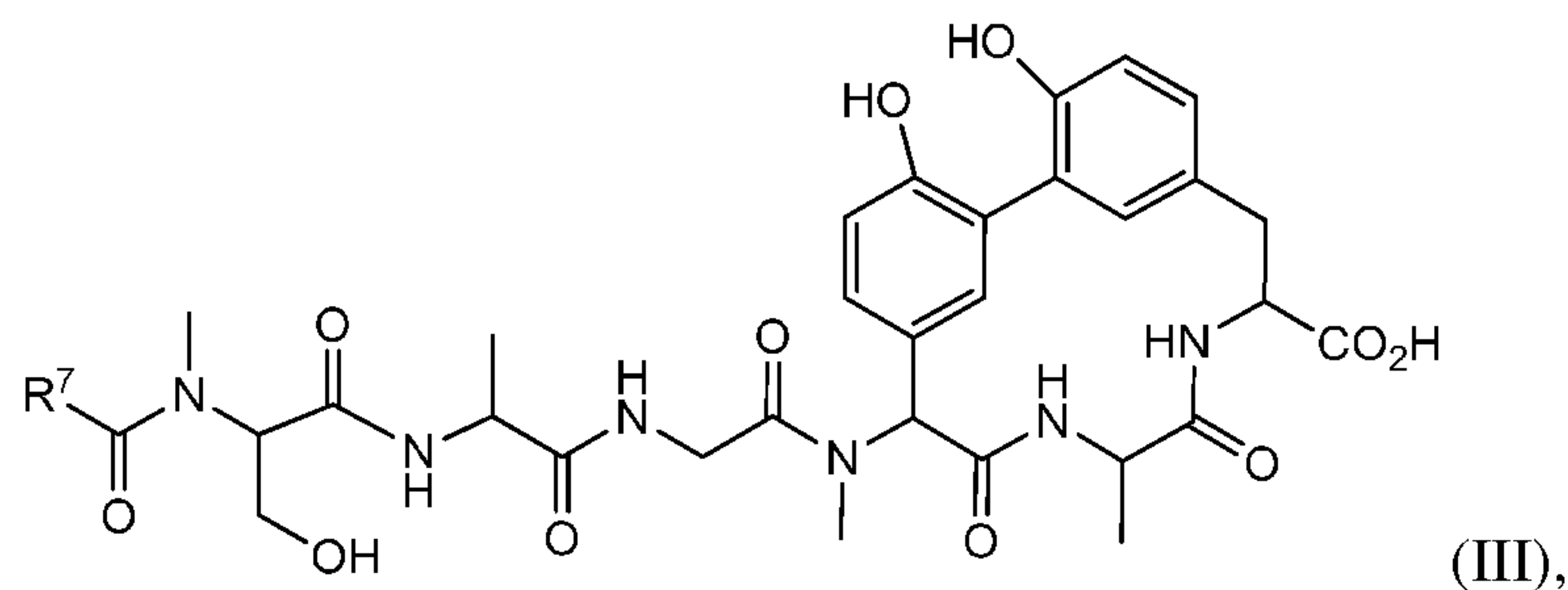
10. The compound of claim 1 wherein R^5 is any of the following: methyl, ethyl, (C_3 - C_{22})-n-alkyl, (C_3 - C_{22})-isoalkyl, (C_4 - C_{22})-anteisoalkyl, naphthyl, (C_2 - C_{10}) naphthyl, naphthylmethyl, (C_2 - C_{10}) naphthylmethyl, biphenyl, (C_2 - C_{10})alkylbiphenyl, biphenylmethyl, (C_2 - C_{10})alkylbiphenylmethyl, (C_4 - C_{12})phenyl, (C_4 - C_{12})benzyl, (C_2 - C_{10})-1,2-diphenylethynyl, or (Z)- or (E)-(C_2 - C_{10})-1,2-diphenylethenyl, wherein a wavy line indicates a point of attachment of R^5 to an atom bonded to R^5 in formula (IIA), (IIB), or (IIC).

11. The compound of claim 1 wherein ring bearing one or more X^1 or X^2 , respectively, is a phenyl, pyridyl, pyrazinyl, pyrimidyl, or pyridazinyl. optionally wherein R^2 and R^3 are both hydrogen.

12. The compound of claim 1 wherein at least one of R^2 and R^3 is hydrogen.

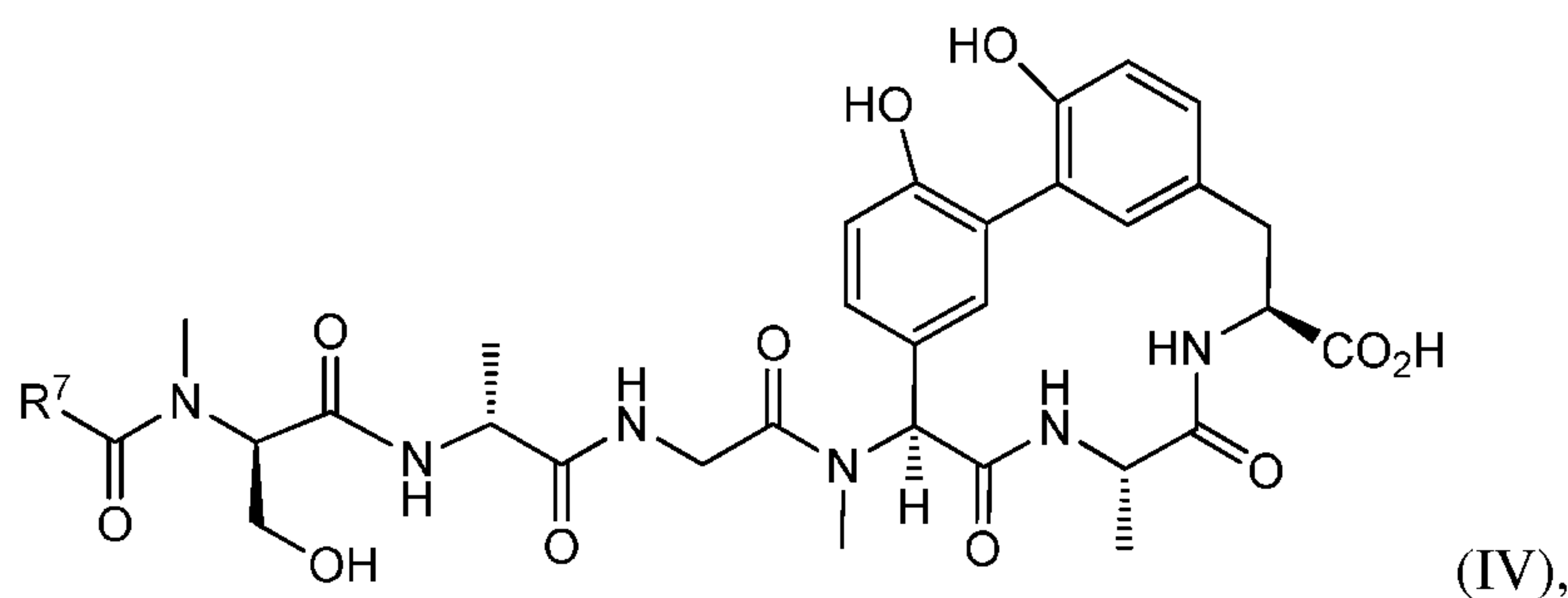
13. The compound of claim 1 wherein at least one of R^2 and R^3 is nitro, halo, cyano, hydroxy, glycosyloxy, amino, (C_1 - C_4)alkoxy, or (C_1 - C_4)alkyl, and n^2 or n^3 respectively, or both, is 1.

14. The compound of claim 1 wherein both G are hydrogen.
15. The compound of claim 1 wherein any of R^{A1} , R^{A2} and R^{A4} are hydrogen, any of R^{A3} and R^{A5} are methyl, or any combination thereof.
16. The compound of claim 1 wherein R^{A3} is hydrogen, methyl, ethyl, n-propyl, isopropyl, n-butyl, isobutyl, 3-hydroxypropyl, 4-hydroxybutyl, or 2,2,2-trifluoroethyl.
17. The compound of claim 1 wherein all of R^4 and R^6 are independently selected hydrogen or methyl.
18. The compound of claim 1 wherein the compound is any of the following compounds of formula (III)



wherein R^7 is (C₈-C₁₈)-n-alkyl, (C₈-C₁₈)-isoalkyl, (C₈-C₁₈)-anteisoalkyl, any of which includes a group (A), (B), (C), (D), or (E) of claim 1; or is 2-naphthyl, 6-(C₂-C₁₀)-2-naphthyl, 2-naphthylmethyl, 6-(C₂-C₁₀)-2-naphthylmethyl, 4-biphenyl, 4-biphenylmethyl, 4'-(C₂-C₁₀)alkyl-4-biphenyl, 4'-(C₂-C₁₀)alkyl-4-biphenylmethyl, p-(C₄-C₁₂)phenyl, p-(C₄-C₁₂)benzyl, or 4'-(C₂-C₁₀)-1,2-diphenylethynyl;
or a salt thereof.

19. The compound of claim 3 wherein the compound is any of the following compounds of formula (IV)



herein R^7 is (C₈-C₁₈)-n-alkyl, (C₈-C₁₈)-isoalkyl, (C₈-C₁₈)-anteisoalkyl, any of which includes a group (A), (B), (C), (D), or (E) of claim 1; or is 2-naphthyl, 6-(C₂-C₁₀)-2-naphthyl, 2-naphthylmethyl, 6-(C₂-C₁₀)-2-naphthylmethyl, 4-biphenyl, 4-biphenylmethyl, 4'-(C₂-C₁₀)alkyl-4-biphenyl, 4'-(C₂-C₁₀)alkyl-4-biphenylmethyl, p-(C₄-C₁₂)phenyl, p-(C₄-C₁₂)benzyl, or 4'-(C₂-C₁₀)-1,2-diphenylethynyl;

or a salt thereof.

20. A compound comprising a hydrate, solvate, prodrug, or metabolite of a compound of claim 1.
21. A pharmaceutical composition comprising the compound of claim 1 and a pharmaceutically acceptable excipient.
22. Use of a compound of claim 1 for preparation of a medicament for treatment of a bacterial infection in a patient.
23. A method of treatment of a bacterial infection in an animal, comprising administering an effective amount of a compound of claim 1 to the animal at a frequency and for a duration sufficient to provide a beneficial effect to the animal.
24. The method of claim 23 wherein a causative bacterial species of the bacterial infection is of a genotype resistant to treatment with arylomycin A2.
25. The method of claim 23, wherein the bacterial infection is an infection involving *Corynebacterium diphtheriae*, *Corynebacterium glutamicum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Francisella tularensis*, *Helicobacter pylori*, *Lactococcus lactis* subsp. *cremoris*, *Lactococcus lactis* subsp. *lactis*, *Propionibacterium acnes*, *Rhodococcus equi*, *Rhodococcus opacus*, *Staphylococcus*

capitis, *Staphylococcus caprae*, *Staphylococcus carnosus*, *Staphylococcus cohnii*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus hominis subsp. hominis*, *Staphylococcus hominis subsp. novobiosepticus*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*, *Streptococcus dysgalactiae*, *Streptococcus mitis*, *Streptococcus oralis*, *Streptococcus pyogenes*, *Streptococcus pneumoniae*, and/or *Yersinia pestis*.

26. The method of claim 23, wherein the bacterial infection is an infection involving a gram negative bacteria.

27. A method of treating a bacterial infection in an animal that includes administering arylomycin A and/or arylomycin B and/or a compound of claim 1 to the animal, wherein the infection involves a microbial species that expresses a signal peptidase without a proline residue within 10 amino acids N-terminal to the signal peptidase catalytic serine.

28. The method of claim 27, wherein the bacterial species encodes or expresses an SPase enzyme without a proline residue 5 to 7 amino acids N-terminal to the SPase catalytic serine.

29. The method of claim 27, wherein the bacterial infection is an infection involving *Corynebacterium diphtheriae*, *Corynebacterium glutamicum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Francisella tularensis*, *Helicobacter pylori*, *Lactococcus lactis subsp. cremoris*, *Lactococcus lactis subsp. lactis*, *Propionibacterium acnes*, *Rhodococcus equi*, *Staphylococcus carnosus*, *Staphylococcus cohnii*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus hominis subsp. hominis*, *Staphylococcus hominis subsp. novobiosepticus*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*, *Streptococcus dysgalactiae*, *Streptococcus mitis*, *Streptococcus oralis*, *Streptococcus pyogenes*, and/or *Streptococcus pneumoniae*.

30. The method of claim 27, wherein the bacterial infection is an infection involving a gram negative bacteria.

31. The method of claim 27, wherein administering comprises topical administration.

32. A method of treating a bacterial infection in an animal comprising administering to the animal any one or any combination of the compounds of claim 1, wherein the bacterial infection comprises an infection by a bacteria that encodes or expresses an SPase enzyme that has a proline within about 10 amino acids N-terminal to the SPase catalytic serine.

33. The method of claim 32, wherein the bacteria encodes or expresses an SPase enzyme that does not have a proline 5 to 7 amino acids N-terminal to the SPase catalytic serine.

34. The method of claim 32, wherein the bacterial infection involves *Staphylococcus capitis*, *Staphylococcus caprae* and/or *Yersinia pestis*.

35. A method of treating a bacterial infection in an animal comprising administering to the animal arylomycin A or arylomycin B, wherein the microbial infection is an infection involving *Corynebacterium diphtheriae*, *Corynebacterium glutamicum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Francisella tularensis*, *Helicobacter pylori*, *Lactococcus lactis* subsp. *cremoris*, *Lactococcus lactis* subsp. *lactis*, *Propionibacterium acnes*, *Rhodococcus equi*, *Staphylococcus capitis*, *Staphylococcus caprae*, *Staphylococcus carnosus*, *Staphylococcus cohnii*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus hominis* subsp. *hominis*, *Staphylococcus hominis* subsp. *novobiosepticus*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*, *Streptococcus dysgalactiae*, *Streptococcus mitis*, *Streptococcus oralis*, *Streptococcus pyogenes*, *Streptococcus pneumoniae*, and/or *Yersinia pestis*.

36. The method of claim 35, wherein administering comprises topical administration.

37. The method of claim 23 or 35 further comprising administering a second therapeutic agent.

38. The method of claim 37, wherein the second therapeutic agent is a non-arylomycin antibiotic.

39. The method of claim 38, wherein the non-arylomycin antibiotic is an aminoglycoside antibiotic, fluoroquinolone antibiotic, penicillin antibiotic, cephalosporin antibiotic, macrolide antibiotic, glycopeptide antibiotic, rifampicin, chloramphenicol, fluoramphenicol, colistin, mupirocin, bacitracin, daptomycin, or linezolid.
40. A method of detecting whether a test sample contains a bacterium sensitive to an arylomycin antibiotic comprising detecting whether a bacterial signal peptidase is present in the test sample, wherein the bacterial signal peptidase does not have a proline within about 10 amino acids N-terminal to the bacterial signal peptidase's catalytic serine.
41. The method of claim 40, further comprising detecting whether a test sample contains *Yersinia pestis*.
42. The method of claim 40, wherein the bacterial signal peptidase nucleic acid or the bacterial signal peptidase polypeptide is detected.
43. The method of claim 40, further comprising contacting the test sample with an anti-signal peptidase antibody and detecting whether the antibody forms a complex with a bacterial signal peptidase in the test sample.
44. The method of claim 43, wherein the antibody selectively binds to a signal peptidase that does not contain a proline with about 10 amino acids N-terminal to the bacterial signal peptidase's catalytic serine.
45. The method of claim 40, further comprising contacting the test sample with an anti-signal peptidase antibody that selectively binds to a signal peptidase that does contain a proline with about 10 amino acids N-terminal to the bacterial signal peptidase catalytic serine and detecting whether the antibody forms a complex with a bacterial signal peptidase in the test sample.
46. The method of claim 40, further comprising contacting a nucleic acid isolated from the test sample with a probe or primer that selectively hybridizes to a DNA

encoding a bacterial signal peptidase that does not contain a proline with about 10 amino acids N-terminal to the bacterial signal peptidase's catalytic serine.

47. The method of claim 46, wherein the probe or the primer hybridizes to the DNA under stringent hybridization conditions.

48. The method of claim 46, wherein the probe or primer hybridizes to the signal peptidase DNA encoding a region comprising about 4 to about 15 amino acids of the bacterial signal peptidase that includes the catalytic serine.

49. The method of claim 40, wherein detecting comprises nucleic acid amplification, nucleic acid sequencing, or single nucleotide polymorphism detection.

50. The method of claim 40, wherein the signal peptidase does not have a proline seven amino acids N-terminal to the bacterial signal peptidase' catalytic serine.

51. The method of claim 40, wherein the signal peptidase does not have a proline five amino acids N-terminal to the bacterial signal peptidase' catalytic serine.

52. The method of claim 40, wherein the bacterium is a *Eubacteria*, and/or the antibody selectively binds to the signal peptidase from a selected species of *Eubacteria* and/or the probe or primer selectively hybridizes to a DNA encoding a signal peptidase from a selected species of *Eubacteria*.

53. A bacterium genetically engineered to encode and/or express a signal peptidase with a proline at 5 to 7 amino acids N-terminal to the signal peptidase's catalytic serine, wherein the bacterium is selected from the group consisting of *Corynebacterium diphtheriae*, *Corynebacterium glutamicum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Francisella tularensis*, *Helicobacter pylori*, *Lactococcus lactis* subsp. *cremoris*, *Lactococcus lactis* subsp. *lactis*, *Propionibacterium acnes*, *Rhodococcus equi*, *Rhodococcus opacus*, *Staphylococcus carnosus*, *Staphylococcus cohnii*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus hominis* subsp. *hominis*, *Staphylococcus hominis* subsp. *novobiosepticus*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*,

Streptococcus dysgalactiae, *Streptococcus mitis*, *Streptococcus oralis*, *Streptococcus pyogenes*, and *Streptococcus pneumoniae*.

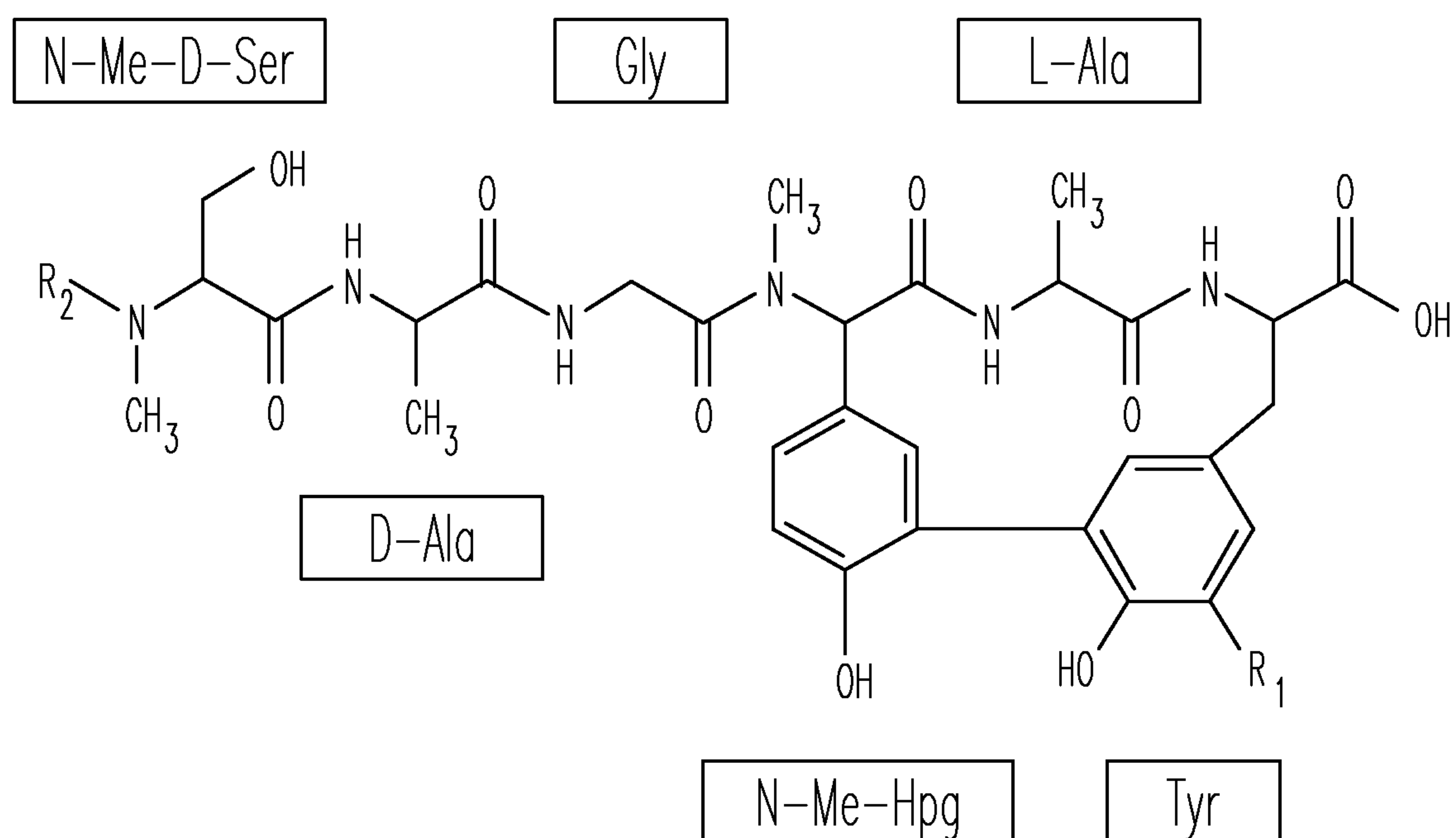
54. A bacterium genetically engineered to encode and/or express a signal peptidase without a proline at 5 to 7 amino acids N-terminal to the signal peptidase's catalytic serine, wherein the bacterium is *Escherichia coli*, *Klebsiella pneumonia*, *Salmonella enterica*, *Vibrio cholera*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, *Neisseria meningitides*, *Haemophilus influenza*, *Citrobacter koseri*, *Shigella flexneri*, *Bordetella pertussis*, *Mycobacterium tuberculosis*, *Staphylococcus aureus*, *Bacillus anthracis*, *Streptococcus mutans*, *Clostridium difficile*, *Enterococcus faecalis* and/or *Listeria monocytogenes*.

55. A mutant signal peptidase with a *Corynebacterium diphtheriae*, *Corynebacterium glutamicum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydophila pneumoniae*, *Francisella tularensis*, *Helicobacter pylori*, *Lactococcus lactis* subsp. *cremoris*, *Lactococcus lactis* subsp. *lactis*, *Propionibacterium acnes*, *Rhodococcus equi*, *Rhodococcus opacus*, *Staphylococcus carnosus*, *Staphylococcus cohnii*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus hominis* subsp. *hominis*, *Staphylococcus hominis* subsp. *novobiosepticus*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*, *Streptococcus dysgalactiae*, *Streptococcus mitis*, *Streptococcus oralis*, *Streptococcus pyogenes*, or *Streptococcus pneumoniae* signal peptidase amino acid sequence that is modified to have a proline substitution at a position 5 or at a position 7 amino acids N-terminal to the signal peptidase's catalytic serine.

56. A mutant signal peptidase with a *Escherichia coli*, *Klebsiella pneumonia*, *Salmonella enterica*, *Vibrio cholera*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, *Neisseria meningitides*, *Haemophilus influenza*, *Citrobacter koseri*, *Shigella flexneri*, *Bordetella pertussis*, *Mycobacterium tuberculosis*, *Staphylococcus aureus*, *Bacillus anthracis*, *Streptococcus mutans*, *Clostridium difficile*, *Enterococcus faecalis* or *Listeria monocytogenes* signal peptidase amino acid sequence that is modified by replacement of a proline with a selected amino acid, wherein the proline was at 5 to 7 amino acids N-terminal to the signal peptidase's catalytic serine.

57. The mutant signal peptidase of claim 56, wherein the selected amino acid is a serine.
58. A method of identifying an antibiotic effective for treating a bacterial infection involving an arylomycin-resistant bacterial species, comprising contacting the arylomycin-resistant bacteria with a test agent and observing whether the test agent inhibits growth of the arylomycin-resistant bacteria, wherein the arylomycin-resistant bacteria encodes or expresses a signal peptidase enzyme that has a proline residue 5 to 7 amino acids N-terminal to the signal peptidase catalytic serine.
59. A method of identifying a compound that has antibiotic activity against bacteria comprising contacting a culture of bacteria with the test compound and identifying whether the test compound inhibits growth of the bacteria, wherein the bacteria in the culture expresses a modified SPase that has a natural bacterial SPase amino acid sequence modified at position -5 to -7 relative to the catalytic serine by substitution or replacement of an amino acid at that position.
60. The method of claim 59, wherein an amino acid at position -5 and/or at position -7 relative to the catalytic serine is replaced with a proline.
61. The method of claim 59, wherein the amino acid at position -5 and/or at position -7 relative to the catalytic serine is a proline replaced by a selected amino acid.
62. The method of claim 61, wherein the selected amino acid is a serine.
63. The method of claims 58 to 62, wherein the test compound that inhibits the growth of the bacteria has antibiotic activity.

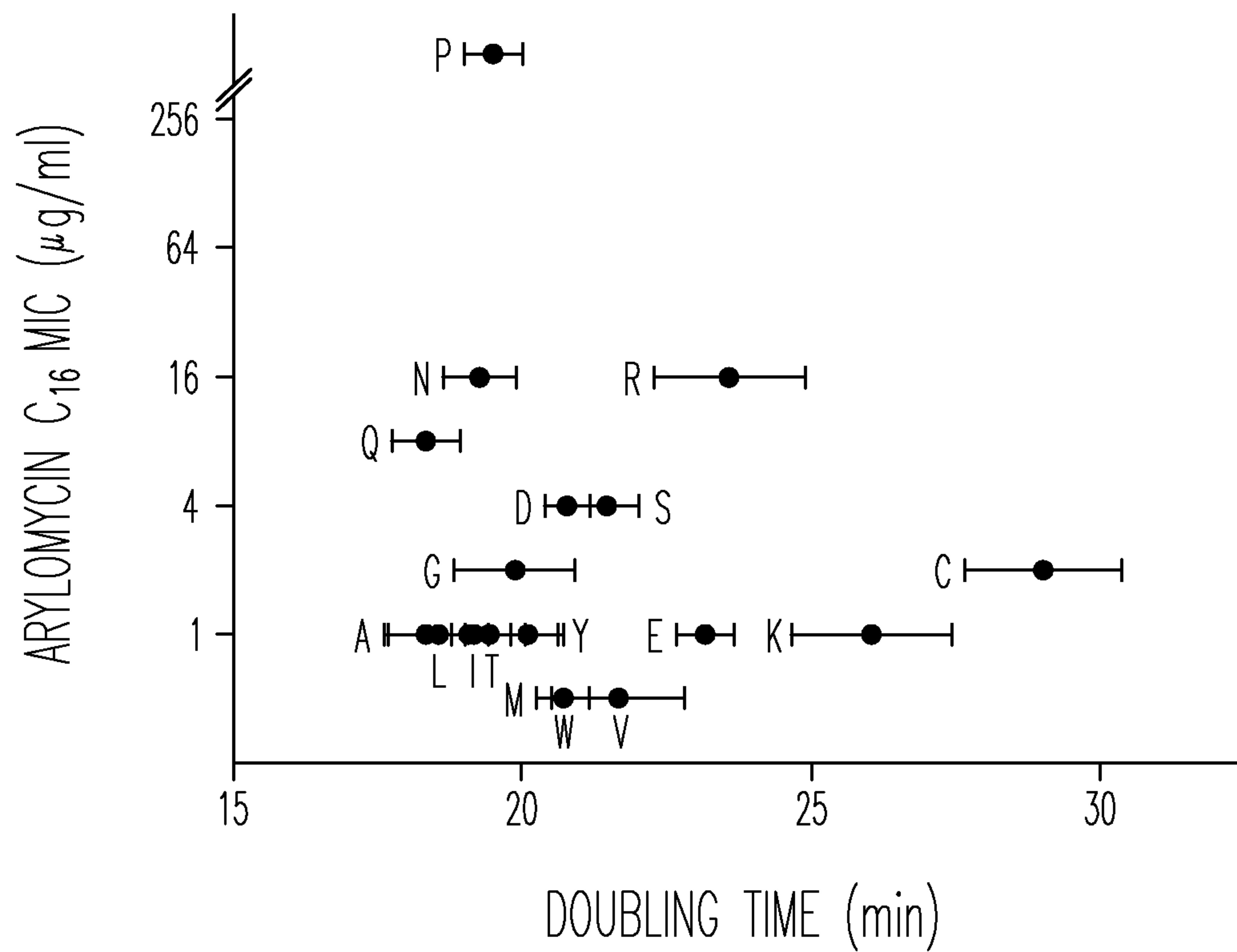
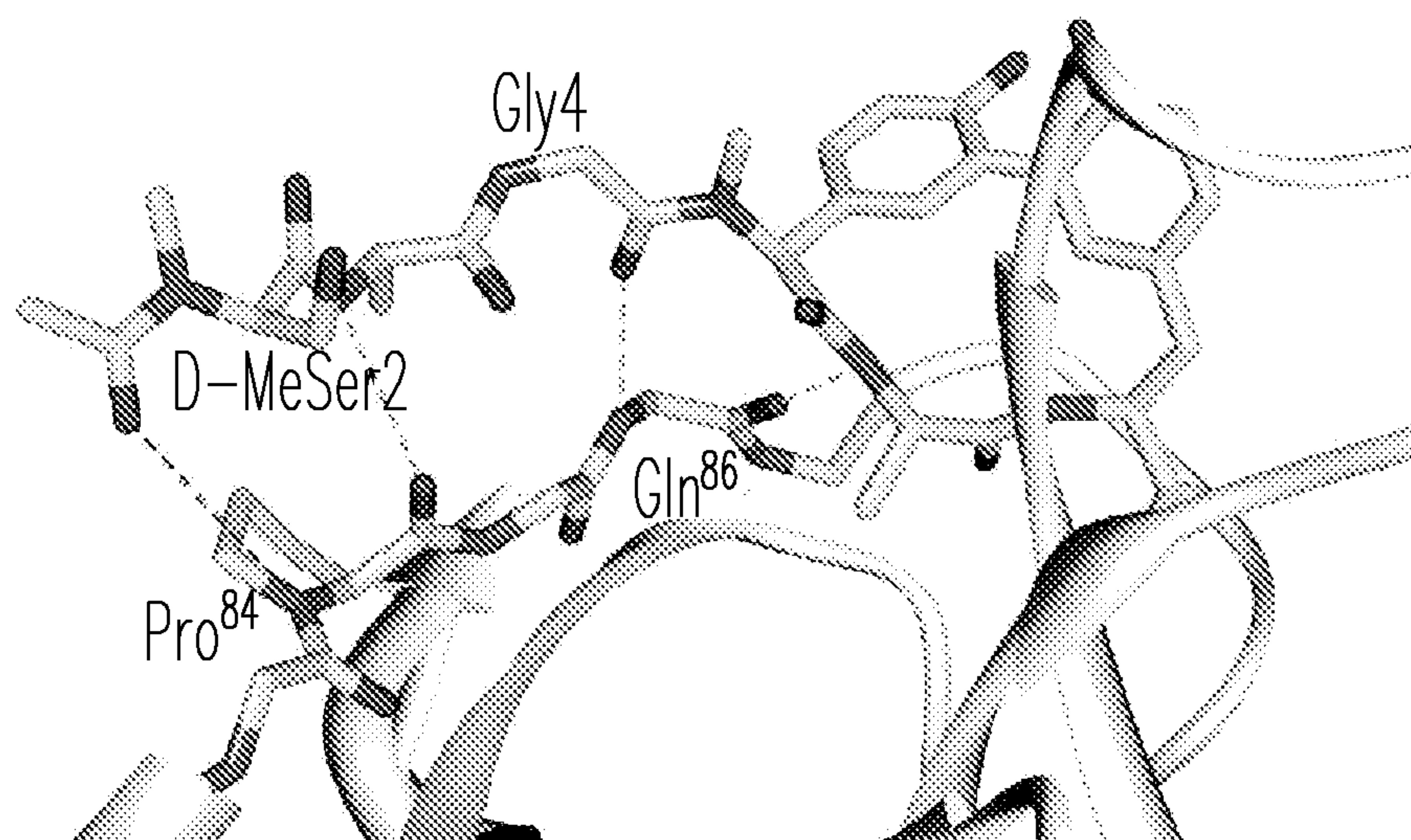
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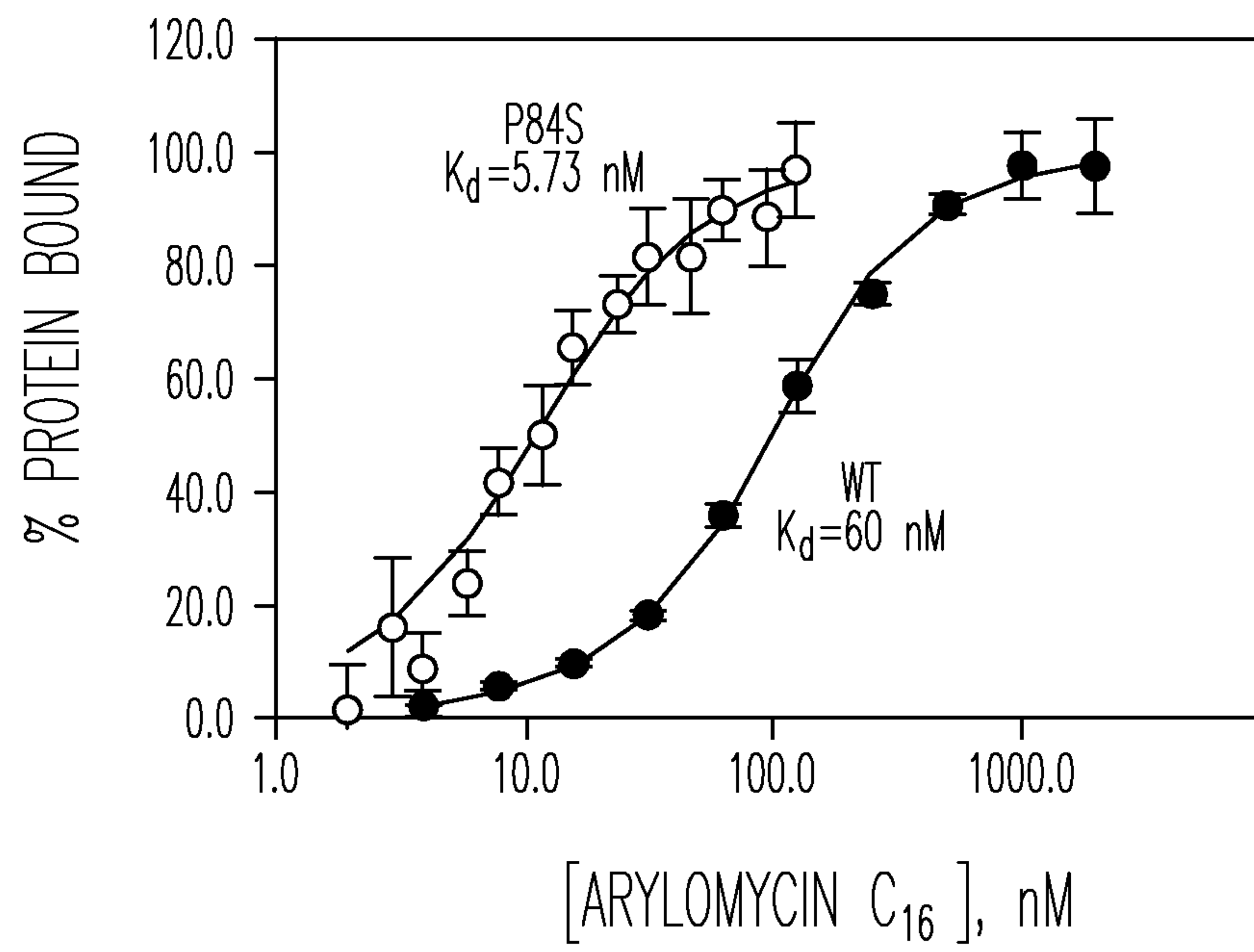
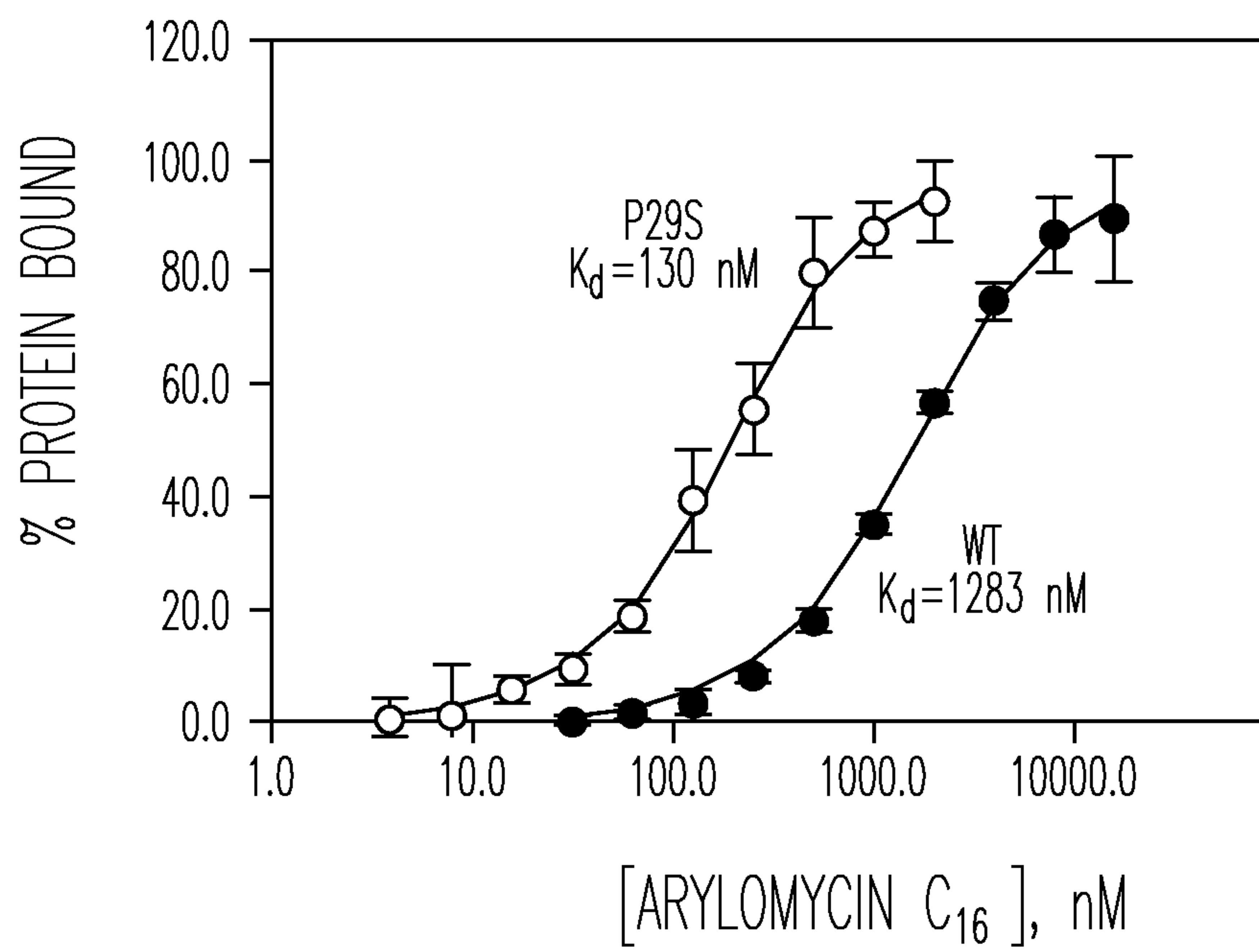
ARYLOMYCIN	R ₁	R ₁
A ₁	H	iso-C ₁₁
A ₂	H	iso-C ₁₂
A ₃	H	n-C ₁₂
A ₄	H	anteiso-C ₁₃
A ₅	H	iso-C ₁₄
B ₁	NO ₂	iso-C ₁₁
B ₂	NO ₂	iso-C ₁₂
B ₃	NO ₂	n-C ₁₂
B ₄	NO ₂	anteiso-C ₁₃
B ₅	NO ₂	iso-C ₁₃
B ₆	NO ₂	iso-C ₁₄
B ₇	NO ₂	anteiso-C ₁₅

Fig. 1

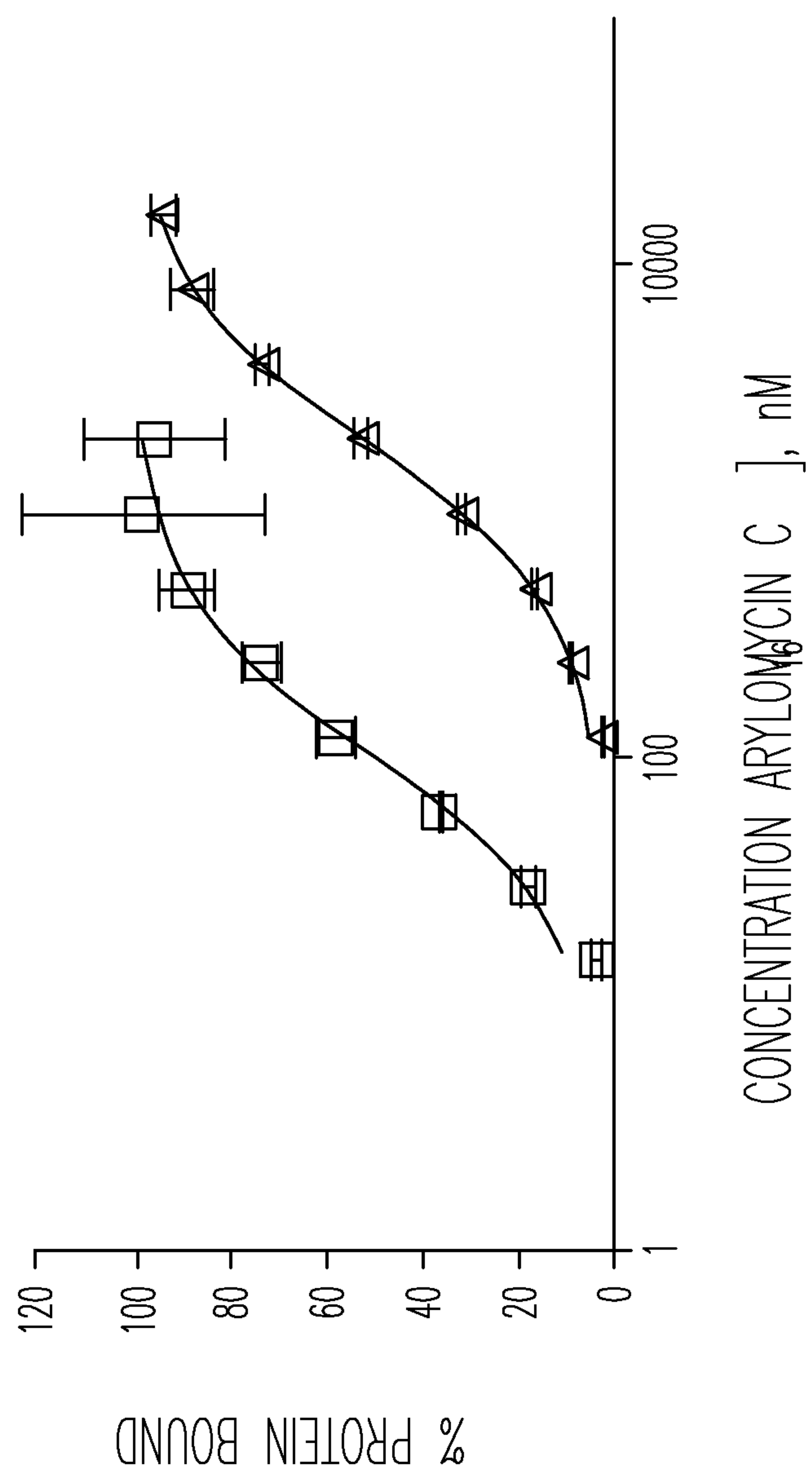
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*Fig. 2**Fig. 3A*

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*Fig. 3B**Fig. 3C*

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*Fig. 3D*

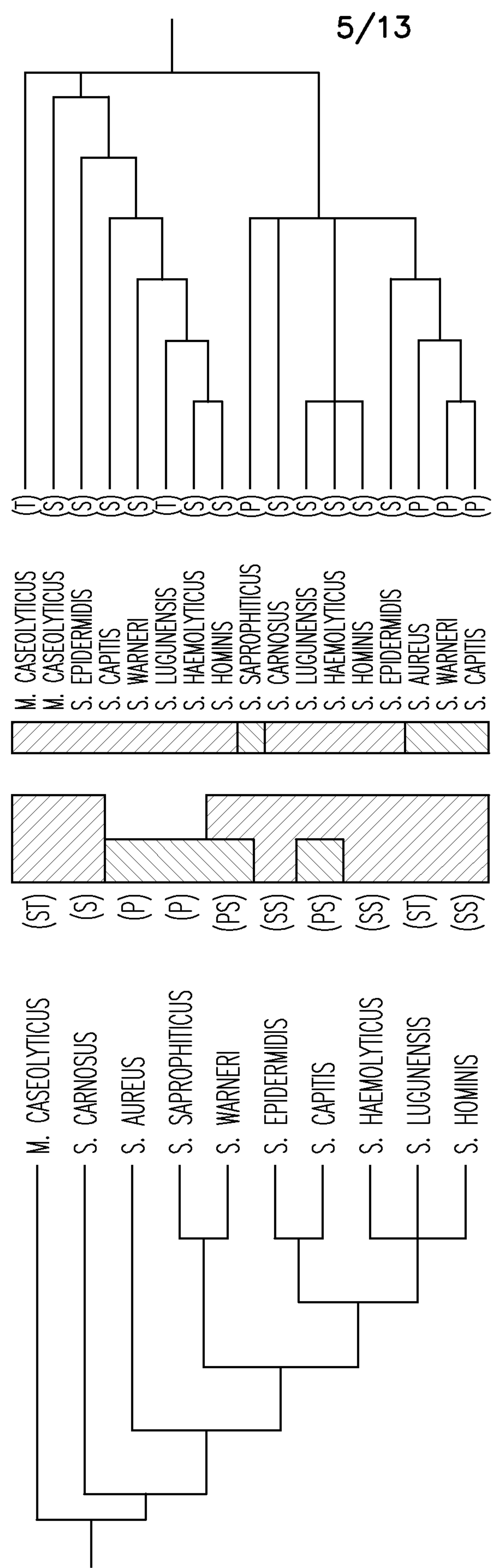


Fig. 4

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ORGANISM	AMINO ACID AT RESIDUE -7 FROM CATALYTIC SER
ABIOTROPHIA_DEFECTIVA	NKE
ACIDOTHERMUS_CELLULOLYTICUS	A
ACTINOMYCES_COLEOCANIS	A
ACTINOMYCES_ODONTOLYTICUS	V
ACTINOMYCES_SP_848_STR_F0332	A
ACTINOMYCES_UROGENITALIS	W
ACTINOSYNNEMA_MIRUMDSM	W
ANAEROCELLUM_THERMOPHILUM	L
ANAEROCOCCUS_HYDROGENALIS	A
ANAEROCOCCUS_LACTOLYTICUS	AL
ANAEROCOCCUS_PREVOTII	A
ANAEROCOCCUS_TETRADIUS	A
ANAEROCOCCUS_VAGINALIS	A
ANAEROMYXOBACTER_DEHALOGENANS	AA
ANAEROMYXOBACTER_SP_FW109-5	AA
ANAEROMYXOBACTER_SP_K	AA
ANAEROSTIPES_CACCAE	GRN
ANAEROTRUNCUS_COLIHOMINIS	LT
ARCOBACTER_BUTZLERI	A
ARTHROBACTER_AURESCENS	V
ARTHROBACTER_SP_FB24	VA
ATOPOBIUM_PARVULUM	V
ATOPOBIUM_RIMAE	V
ATOPOBIUM_VAGINAE	V
BACILLUS_HALODURANS	S
BEUTENBERGIA_CAVERNAE	A
BIFIDOBACTERIUM_ADOLESCENTIS	F
BIFIDOBACTERIUM_ANGULATUM	C
BIFIDOBACTERIUM_ANIMALIS	M
BIFIDOBACTERIUM_BIFIDUM	F
BIFIDOBACTERIUM_BREVE	F
BIFIDOBACTERIUM_CATENULATUM	F
BIFIDOBACTERIUM_DENTIUM	F
BIFIDOBACTERIUM_GALLICUM	M
BIFIDOBACTERIUM_LONGUM	VF
BIFIDOBACTERIUM_PSEUDOCATENULATUM	F
BLAUTIA_HANSENII	SN
BLAUTIA_HYDROGENOTROPHICA	VNS
BREVIBACTERIUM_LINENS	RS
BUTYRATE-PRODUCING_BACTERIUM_L2-50	TR
BUTYRATE-PRODUCING_BACTERIUM_M62-1	N
BUTYRATE-PRODUCING_BACTERIUM_SS2-1	RSN

Fig. 5A

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ORGANISM	AMINO ACID AT RESIDUE -7 FROM CATALYTIC SER
BUTYRIVIBRIO_CROSSOTUS	NNK
CALDANAEROBACTER_SUBTERRANEUS	L
CALDICELLULOSIRUPTOR_SACCHAROLYTICUS	L
CAMINIBACTER_MEDIATLANTICUS	A
CAMPYLOBACTER_COLI	A
CAMPYLOBACTER_CONCISUS	A
CAMPYLOBACTER_CURVUS	A
CAMPYLOBACTER_FETUS	A
CAMPYLOBACTER_GRACILIS	A
CAMPYLOBACTER_HOMINIS	A
CAMPYLOBACTER_JEJUNI	AIM
CAMPYLOBACTER_LARI	A
CAMPYLOBACTER_RECTUS	A
CAMPYLOBACTER_SHOWAE	A
CAMPYLOBACTER_UPSALIENSIS	A
CAMPYLOBACTERALES_BACTERIUM_GD1	A
CANDIDATUS_PROTOCHLAMYDIA	L
CARBOXYDIBRACHIUM_PACIFICUM	L
CARBOXYDOTHERMUS_HYDROGENOFORMANS	L
CATENULISPORA_ACIDIPHILA	VAAM
CELLULOMONAS_FLAVIGENA	A
CHLAMYDIA_MURIDARUM	L
CHLAMYDIA_TRACHOMATIS	L
CHLAMYDOPHILA_ABORTUS	L
CHLAMYDOPHILA_CAVIAE	L
CHLAMYDOPHILA_FELIS	L
CHLAMYDOPHILA_PNEUMONIAE	L
CLAVIBACTER_MICHIGANENSIS	S
CLOSTRIDIALESBACTERIUM1_7_47FAA	NQN
CLOSTRIDIALESGENOMO_SP_BVAB3	V
CLOSTRIDIUM_ACETOBUTYLICUM	RT
CLOSTRIDIUM_ASPARAGIFORME	NQN
CLOSTRIDIUM_BEIJERINCKII	GANN
CLOSTRIDIUM_BOLTEAE	NQN
CLOSTRIDIUM_BOTULINUM	STN
CLOSTRIDIUM_BUTYRICUM	NGNN
CLOSTRIDIUM_CELLULOVORANS	NNN
CLOSTRIDIUM_HATHEWAYI	QNN
CLOSTRIDIUM_HYLEMONAE	IRR
CLOSTRIDIUM_KLUYVERI	RIT
CLOSTRIDIUM_LEPTUM	V
CLOSTRIDIUM_METHYLPENTOSUM	VN

Fig. 5B

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ORGANISM	AMINO ACID AT RESIDUE -7 FROM CATALYTIC SER
CLOSTRIDIUM_NEXILE	RR
CLOSTRIDIUM_NOVYI	QQ
CLOSTRIDIUM_PERFRINGENS	KIKK
CLOSTRIDIUM_SCINDENS	FIRR
CLOSTRIDIUM_SPOROGENES	TK
CLOSTRIDIUM_TETANI	T
CLOSTRIDIUMSP_7_2_43FAA	KS
COPROCOCCUS_COMES	QR
COPROCOCCUS_EUTACTUS	NKR
CORYNEBACTERIUM_ACCOLENS	MQ
CORYNEBACTERIUM_AMYCOLATUM	V
CORYNEBACTERIUM_AURIMUCOSUM	LQL
CORYNEBACTERIUM_DIPHTHERIAE	V
CORYNEBACTERIUM_GENITALIUM	V
CORYNEBACTERIUM_GLUCURONOLYTICUM	I
CORYNEBACTERIUM_GLUTAMICUM	M
CORYNEBACTERIUM_JEIKEIUM	M
CORYNEBACTERIUM_KROPPESTEDTII	W
CORYNEBACTERIUM_LIPOPHILOFLAVUM	M
CORYNEBACTERIUM_MATRUCHOTII	L
CORYNEBACTERIUM_PSEUDOGENTIALIUM	MQ
CORYNEBACTERIUM_STRIATUM	MQ
CORYNEBACTERIUM_TUBERCULOSTEARICUM	QM
CORYNEBACTERIUM_UREALYTICUM	L
DELTA_PROTEOBACTERIUM_MLMS-1	A
DESULFOBACTERIUM_AUTOTROPHICUM	A
DESULFOHALOBIUM_RETBAENSE	A
DESULFOMICROBIUM_BACULATUM	A
DESULFONATRONOSPIRA_THIODISMUTANS	A
DESULFOTALEA_PSYCHROPHILA	A
DESULFOVIBRIO_AESPOEENSIS	NA
DESULFOVIBRIO_DESULFURICANS	A
DESULFOVIBRIO_MAGNETICUS	EA
DESULFOVIBRIO_PIGER	A
DESULFOVIBRIO_SALEXIGENS	A
DESULFOVIBRIO_VULGARIS	A
DESULFURIVIBRIO_ALKALIPHILUS	A
DETHIOBACTER_ALKALIPHILUS	V
DOREA_FORMICIGENERANS	RRN
DOREA_LONGICATENA	RRN
EGGERTHELLA_LENTA	AA

Fig. 5C

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ORGANISM	AMINO ACID AT RESIDUE -7 FROM CATALYTIC SER
EPULOPISCUM_SP_NT_B	HH
ETHANOLIGENENS_HARBINENSE	TT
EUBACTERIUM_ELIGENS	NR
EUBACTERIUM_HALLII	RRT
EUBACTERIUM_RECTALE	NIG
EUBACTERIUM_SAPHENUM	T
EUBACTERIUM_SIRAEUM	V
EUBACTERIUM_VENTRIOSUM	N
FAECALIBACTERIUM_PRAUSNITZII	I
FINEGOLDIA_MAGNA	TI
FRANCISELLA_NOVICIDA	N
FRANCISELLA_PHILOMIRAGIA	N
FRANCISELLA_TULARENSIS	N
FRANKIA_ALNI	A
FRANKIA_SP_CCI3	A
FRANKIA_SP_EAN1PEC	AA
FRANKIA_SP_EUI1	A
FRANKIA_SP_EUN1F	A
GARDNERELLA_VAGINALIS	V
GEOBACTER_BEMIDJIENSIS	A
GEOBACTER_LOVLEYI	AAL
GEOBACTER_METALLIREDUCTENS	A
GEOBACTER_SP_FRC-32	A
GEOBACTER_SP_M18	A
GEOBACTER_SP_M21	A
GEOBACTER_SULFURREDUCTENS	A
GEOBACTER_URANIIREDUCTENS	AA
GORDONIA_BRONCHIALIS	Q
HALIANGIUM_OCHRACEUM	A
HALOTHERMOTHRIX_ORENII	S
HELICOBACTER_ACINONYCHIS	A
HELICOBACTER_CANADENSIS	A
HELICOBACTER_CINAEDI	A
HELICOBACTER_HEPATICUS	A
HELICOBACTER_MUSTELAE	A
HELICOBACTER_PULLORUM	A
HELICOBACTER_PYLORI	A
HELICOBACTER_SP_ATCC_43879	G
HELICOBACTER_WINGHAMENSIS	A
HIRSCHIA_BALTICA	L
HYPHOMONAS_NEPTUNIUM	Q

Fig. 5D

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ORGANISM	AMINO ACID AT RESIDUE -7 FROM CATALYTIC SER
JONESIA_DENITRIFICANS	A
KINEOCOCCUS_RADITOLERANS	SAAT
KOCURIA_RHIZOPHILA	GV
KRIBBELLA_FLAVIDA	AM
KYTOCOCCUS_SEDENTARIUS	AT
LACTOBACILLUS_ACIDOPHILUS	N
LACTOBACILLUS_ANTRI	I
LACTOBACILLUS_BREVIS	RV
LACTOBACILLUS_CASEI	K
LACTOBACILLUS_COLEOHOMINIS	N
LACTOBACILLUS_CRISPATUS	NN
LACTOBACILLUS_DELBUECKII	N
LACTOBACILLUS_FERMENTUM	L
LACTOBACILLUS_GASSERI	NN
LACTOBACILLUS_HELVETICUS	NN
LACTOBACILLUS_INERS	N
LACTOBACILLUS_JENSENII	N
LACTOBACILLUS_JOHNSONII	NN
LACTOBACILLUS_PLANTARUM	MVM
LACTOBACILLUS_REUTERI	I
LACTOBACILLUS_RHAMNOSUS	K
LACTOBACILLUS_SALIVARIUS	V
LACTOBACILLUS_ULTUNENSIS	NN
LACTOBACILLUS_VAGINALIS	I
LACTOCOCCUS_LACTIS	L
LAWSONIA_INTRACELLULARIS	A
LEIFSONIA_XYLI	S
LEUCONOSTOC_CITREUM	L
LEUCONOSTOC_MESENEROIDES	LR
MACROCOCCUS_CASEOLYTICUS	TS
MARICAULIS_MARIS	A
MARINEACTINO_BACTERIUM	S
MARVINBRYANTIA_FORMATEXIGENS	TR
MICROCOCCUS_LUTEUS	MW
MICROMONOSPORA_AURANTIACA	TA
MICROMONOSPORA_CARONACEA	TA
MITSUOKELLA_MULTACIDA	L
NAKAMURELLA_MULTIPARTITA	V
NATRANAEROBIUS_THERMOPHILUS	VI
NAUTILIA_PROFUNDICOLA	A
NITRATIRUPTOR_SP_SB155-2	A

Fig. 5E

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ORGANISM	AMINO ACID AT RESIDUE -7 FROM CATALYTIC SER
NOCARDIOIDES_SP_JS614	A
NOCARDIOPSIS_DASSONVILLEI	A
OCEANICAULIS_ALEXANDRII	A
ORIBACTERIUM_SINUS	NL
ORIBACTERIUM_SP_F0262	QN
ORIENTIA_TSUTSUGAMUSHI	L
PARVIMONAS_MICRA	S
PEDIOCOCCUS_ACIDILACTICI	I
PEDIOCOCCUS_PENTOSACEUS	F
PELOBACTER_CARBINOLICUS	A
PELOBACTER_PROPIONICUS	AL
PEPTONIPHILUS_LACRIMALIS	L
PROPIONIBACTERIUM_ACNES	M
RHODOCOCCUS_ERYTHROPOLIS	IV
RHODOCOCCUS_JOSTII	V
RHODOCOCCUS_OPACUS	V
RICKETTSIA_BELLII	S
ROSEBURIA_INTESTINALIS	RRN
ROSEBURIA_INULINIVORANS	NR
ROTHIA_MUCILAGINOSA	G
RUBROBACTER_XYLANOPHILUS	A
RUMINOCOCCUS_GNAVUS	RR
RUMINOCOCCUS_LACTARIS	RN
RUMINOCOCCUS_OBEUM	TN
RUMINOCOCCUS_TORQUES	NRR
SACCHAROMONOSPORA_VIRIDIS	V
SACCHAROPOLYSPORA_ERYTHRAEA	V
SALINISPORA_ARENICOLA	TA
SALINISPORA_TROPICA	TA
SANGUIBACTER_KEDDIEII	A
SELENOMONAS_FLUEGGEI	LN
SELENOMONAS_SPUTIGENA	L
SHUTTLEWORTHIA_SATELLES	RT
SLACKIA_EXIGUA	AA
SLACKIA_HELIOTRINIREDUCENS	AL
SORANGIUM_CELLULOSUM	AQ
STACKEBRANDTIA_NASSAUENSIS	SSS
STAPHYLOCOCCUS_CARNOSUS	S
STAPHYLOCOCCUS_EPIDERMIDIS	SS
STAPHYLOCOCCUS_HAEMOLYTICUS	SS
STAPHYLOCOCCUS_HOMINIS	SS

Fig. 5F

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ORGANISM	AMINO ACID AT RESIDUE -7 FROM CATALYTIC SER
STAPHYLOCOCCUS_LUGDUNENSIS	TS
STREPTOCOCCUS_AGALACTIAE	FV
STREPTOCOCCUS_DYSGALACTIAE	A
STREPTOCOCCUS_MITIS	N
STREPTOCOCCUS_PNEUMONIAE	N
STREPTOCOCCUS_PYOGENES	A
STREPTOCOCCUS_SP_M143	N
STREPTOMYCES_SP_AA4	W
STREPTOSPORANGIUM_ROSEUM	ATA
SUBDOLIGRANULUM_VARIABLE	I
SULFURIMONAS_DENITRIFICANS	A
SULFUROSPIRILLUM_DELEYIANUM	AA
SULFUROVUM_SP_NBC37-1	SI
SYMBIOBACTERIUM_THERMOPHILUM	VW
SYNTROPHOBACTER_FUMAROXIDANS	AA
SYNTROPHOMONAS_WOLFEI	G
SYNTROPHUS_ACIDITROPHICUS	A
THERMOANAEROBACTER_ETHANOLICUS	L
THERMOANAEROBACTER_MATHRANII	L
THERMOANAEROBACTER_PSEUDETHANOLICUS	L
THERMOMONOSPORA_CURVATA	A
TROPHYMA_WHIPPLEI	V
TSUKAMURELLA_PAUROMETABOLA	Q
WEISSELLA_PARAMESENTEROIDES	M
WOLINELLA_SUCCINOGENES	A
XYLANIMONAS_CELLULOSILYTICA	LA
ALIS_PUTREDINIS	M
BACTEROIDES_CACCAE	SNW
BACTEROIDES_CAPILLOSUS	FV
BACTEROIDES_CELLULOSILYTICUS	STTSNS
BACTEROIDES_COPROCOLA	NS
BACTEROIDES_COPROPHILUS	SNS
BACTEROIDES_DOREI	SN
BACTEROIDES_EGGERTHII	N
BACTEROIDES_FINEGOLDII	N
BACTEROIDES_FRAGILIS	NS
BACTEROIDES_INTESTINALIS	TSTNT
BACTEROIDES_OVATUS	N
BACTEROIDES_PECTINOPHILUS	N
BACTEROIDES_PLEBEIUS	N
BACTEROIDES_SP_1_1_6	SN

Fig. 5G

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ORGANISM	AMINO ACID AT RESIDUE -7 FROM CATALYTIC SER
BACTEROIDES_SP_2_1_16	N
BACTEROIDES_SP_3_1_33FAA	N
BACTEROIDES_SP_4_3_47FAA	SS
BACTEROIDES_SP_9_1_42FAA	NSS
BACTEROIDES_SP_D1	N
BACTEROIDES_SP_D2	N
BACTEROIDES_SP_D20	SN
BACTEROIDES_STERCORIS	N
BACTEROIDES_THETAOTAOMICRON	SN
BACTEROIDES_UNIFORMIS	NS
BACTEROIDES_VULGATUS	SN
CAND_AZOBACTEROIDES	H
CHIT_PINENSIS	IA
DYAD_FERMENTANS	AA
MICR_MARINA	AAA
PARA_DISTASONIS	NT
PARA_JOHNSONII	NSS
PARA_SP_D13	TN
PEDO_HEPARINUS	A
PEDO_SP_BAL39	A
PORPHYROMONAS_ENDODONTALIS	N
PORPHYROMONAS_GINGIVALIS	N
PORPHYROMONAS_UENONIS	N
PREVOTELLA_BERGENSIS	N
PREVOTELLA_BIVIA	N
PREVOTELLA_BUCCAE	N
PREVOTELLA_BUCCALIS	N
PREVOTELLA_COPRI	N
PREVOTELLA_MELANINOGENICA	N
PREVOTELLAORIS	N
PREVOTELLA_RUMINICOLA	N
PREVOTELLA_SP_F0039	NF
PREVOTELLA_SP_F0108	N
PREVOTELLA_SP_F0295	N
PREVOTELLA_TANNERAE	N
PREVOTELLA_TIMONENSIS	N
PREVOTELLA_VERORALIS	N
RHOD_MARINUS	AL
SALINIBACTER_RUBER	L
SPHINGOBACTERIUM_SPIRITIVORUM	LA
SPIROSOMA_LINGUALE	AA

Fig. 5H