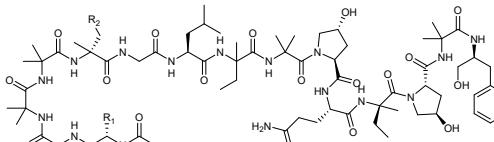
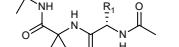
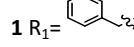
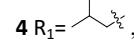
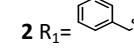
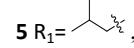
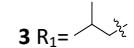
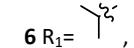
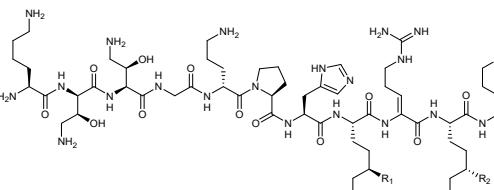
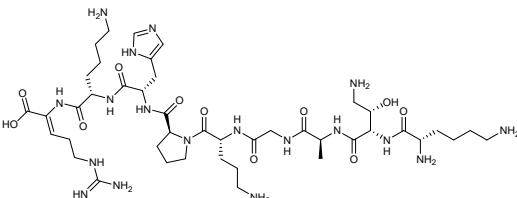
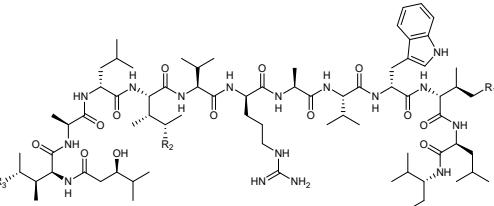
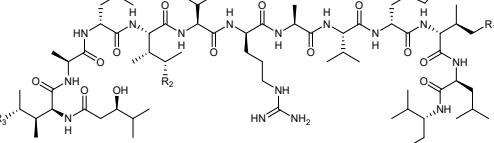
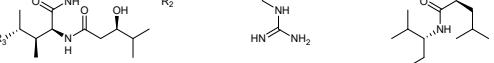
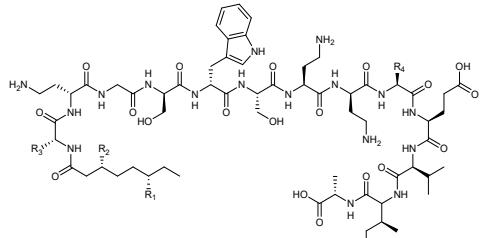


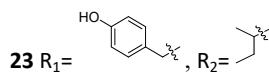
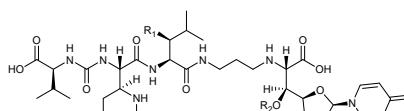
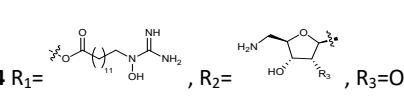
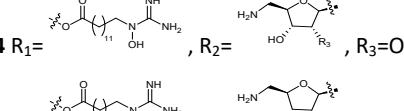
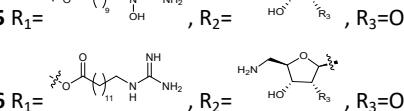
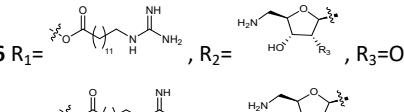
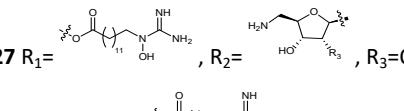
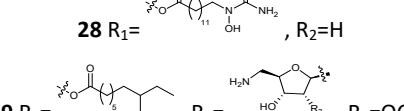
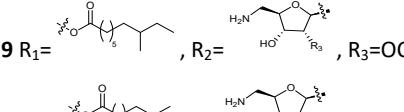
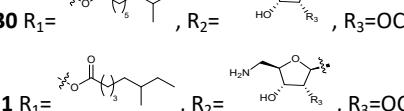
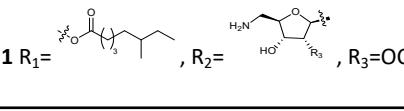
Medium-sized peptides from microbial sources with potential for antibacterial drug development

Table S1 Detailed information for all medium-sized antimicrobial peptides

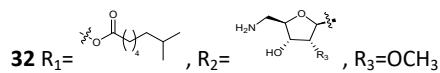
| 1. Linear peptides | | | | | | | | |
|--------------------|-----------------|---|--|-----------------------------------|--|---------------------|------|--|
| No. | Name | Structure | Strain No. | Source | Antimicrobial spectrum | Target | Ref. | |
| 1 | Emerimicin V |  | | | <i>E. faecalis</i> (64 µg/mL), VRE (64 µg/mL), MRSA (32 µg/mL) | | | |
| 2 | Emerimicin VI |  | | | MRSA (64 µg/mL) | | | |
| 3 | Emerimicin VII | | | <i>Acremonium tubakii</i> W. Gams | Soil sample (Salt Lake City, USA) | - | 1 | |
| 4 | Emerimicin VIII | 1 R ₁ =  , R ₂ =CH ₃ 4 R ₁ =  , R ₂ =H | | | Inactive | | | |
| 5 | Emerimicin IX | 2 R ₁ =  , R ₂ =H 5 R ₁ =  , R ₂ =H | | | | | | |
| 6 | Emerimicin X | 3 R ₁ =  , R ₂ =CH ₃ 6 R ₁ =  , R ₂ =H | | | | | | |
| 7 | NOSO-95A |  | Xenorhabdus nematophila K102 (CNCM I-4530) | - | <i>E. aerogenes</i> , <i>E. cloacae</i> , <i>E. coli</i> , <i>K. pneumoniae</i> , <i>P. mirabilis</i> , <i>S. marcescens</i> , <i>S. aureus</i> , <i>E. faecalis</i> (4-16 µg/mL) | bacterial ribosomes | 2-4 | |
| 8 | NOSO-95B | | | | | | | |

| | | | |
|-----------|----------------------------|---|---|
| 9 | NOSO-95C | 7 R ₁ =R ₂ =OH 8 R ₁ =OH, R ₂ =H 9 R ₁ =H, R ₂ =OH | |
| 10 | NOSO-95179 |  | semi-synthesis - |
| 11 | Aquimarin A |  | |
| 12 | Aquimarin B |  | <i>E. faecalis, S. aureus, A. baumannii, M. tuberculosis, P. agglomerans</i> - 5 |
| 13 | Aquimarin C |  | <i>Aquimaria</i> sp. Aq135 - |
| 14 | Aquimarin D | | (1-8 µm) |
| 15 | Aquimarin G | 11 R ₁ =H, R ₂ =R ₃ =Cl 14 R ₁ =CH ₃ , R ₂ =R ₃ =H | |
| 16 | Aquimarin H | 12 R ₁ =CH ₃ , R ₂ =R ₃ =Cl 15 R ₁ =R ₂ =H, R ₃ =Cl | |
| 17 | Tridecaptin A ₁ |  | <i>Paenibacillus terrae</i> NRRL B-30644 - Gram-negative bacteria (3.13-50 µg/mL) bacterial cell membranes 6-10 |

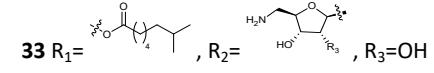
| | | | | |
|-----------|----------------------------------|---|---|----|
| 18 | Tridecaptin B ₁ | <i>Paenibacillus polymyxa</i> NRRL B-30509 | | |
| 19 | Octyl-Tridecaptin A ₁ | 17 R ₁ =CH ₃ , R ₂ =OH, R ₃ =CH(CH ₃) ₂ , R ₄ =Bn 18 R ₁ =CH ₃ , R ₂ =H, R ₃ =H, R ₄ =CH((S)-CH ₃)C ₂ H ₅ 19 R ₁ =H, R ₂ =H, R ₃ =CH(CH ₃) ₂ , R ₄ =Bn | total synthesis | |
| 20 | Syn-BNP 1 | <i>Paenibacillus mucilaginosus</i> K02 | <i>E. faecium</i> , MRSA, <i>A. baumannii</i> , <i>B. subtilis</i> , <i>L. rhamnosus</i> , Strep. <i>Sanguinis</i> , Strep. <i>Mitis</i> (4-64 µg/mL) | 10 |
| 21 | Syn-BNP 2 | <i>Xenorhabdus nematophila</i> | <i>C. albicans</i> , <i>S. pombe</i> , <i>S. cerevisiae</i> , <i>C. albidus</i> , <i>C. neoformans</i> , <i>S. chartarum</i> (4-32 µg/mL) | |
| 22 | Humimycin A | <i>Rhodococcus equi</i> Human microbiome | <i>S. aureus</i> , <i>S. epidermidis</i> , <i>S. mitis</i> , <i>S. mutans</i> , <i>S. delphini</i> , <i>S. intermedius</i> , <i>S. pseudointermedius</i> , <i>S. pneumoniae</i> , <i>S. sanguinis</i> , <i>R.</i> lipid II flippase (MurJ) | 11 |

| | | | | |
|-----------|---------------|---|---------------------------------|--|
| 23 | Humimycin B |  | <i>Rhodococcus erythropolis</i> | <i>mucilaginosa, R.</i> <i>dentocariosa</i> (4-32 µg/mL) |
| 24 | Muraymycin A1 |  | | |
| 25 | Muraymycin A2 |  | | |
| 26 | Muraymycin A3 |  | | |
| 27 | Muraymycin A4 |  | | |
| 28 | Muraymycin A5 |  | <i>Streptomyces</i> | <i>Staphylococcal</i> (2-16 µg/mL), <i>Enterococcal</i> (16- >64 µg/mL) and <i>Gram-negative bacteria</i> (8- >64 µg/mL) |
| 29 | Muraymycin B1 |  | <i>sp.</i> | <i>Polyprenyl-phosphate N-acetyl hexose-amine 1-phosphate transferase</i> |
| 30 | Muraymycin B2 |  | - | |
| 31 | Muraymycin B3 |  | | |
| 32 | Muraymycin B4 |  | | |
| 33 | Muraymycin B5 |  | | |

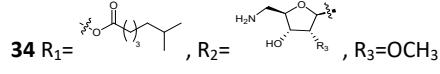
34 Muraymycin B6



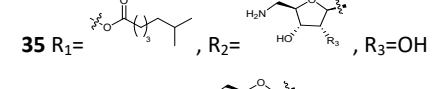
35 Muraymycin B7



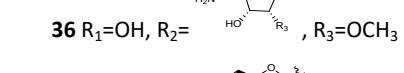
36 Muraymycin C1



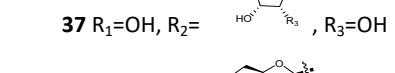
37 Muraymycin C2



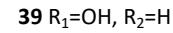
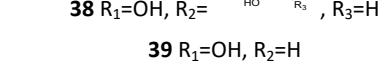
38 Muraymycin C3



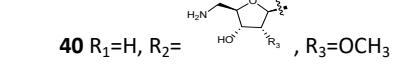
39 Muraymycin C4



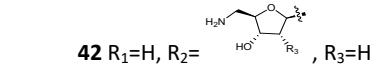
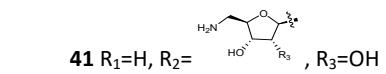
40 Muraymycin D1



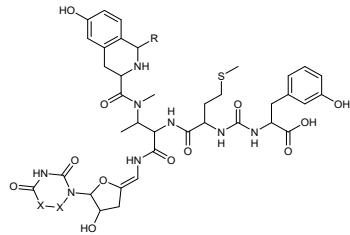
41 Muraymycin D2



42 Muraymycin D3



43 Napsamycin A



Streptomyces
sp. HIL Y-82

Soil sample (Andaman
Islands, India)

Pseudomonas aeruginosa
(6.25-50 mcg/ml)

ransloc-ase I
(MurX, known
as MraY
in

13

44 Napsamycin B

other bacteria)

45 Napsamycin C

43 R=H, X-X= CH=CH

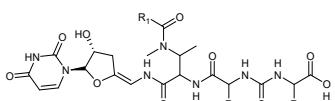
44 R=CH₃, X-X= CH=CH

45 R=H, X-X= CH₂-CH₂

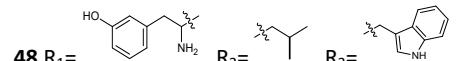
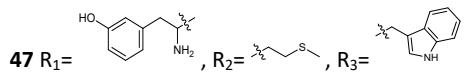
46 Napsamycin D

46 R= CH₃, X-X= CH₂-CH₂

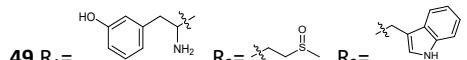
47 Sansanmycin A



48 Sansanmycin B



49 Sansanmycin C

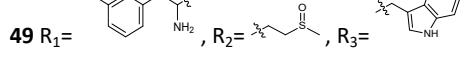


P. aeruginosa (16 µg/mL),

M. tuberculosis (2-16 µg/mL)

14-19

50 Sansanmycin D



Streptomyces
sp. SS

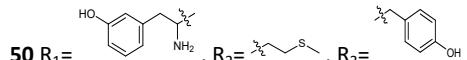
Soil sample

P. aeruginosa (16 µg/mL),

M. tuberculosis (2-16 µg/mL)

14-19

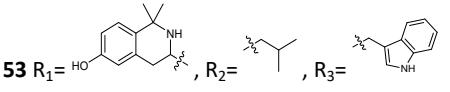
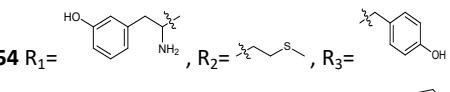
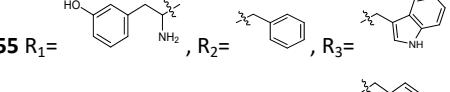
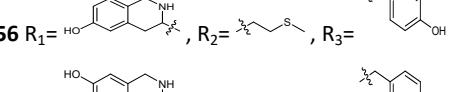
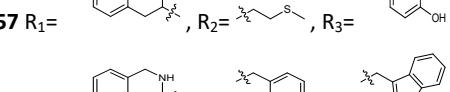
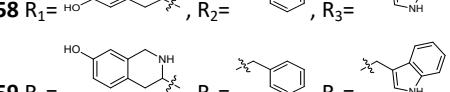
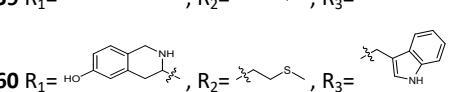
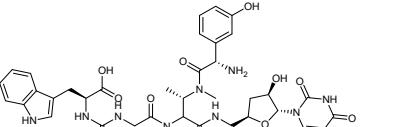
51 Sansanmycin E

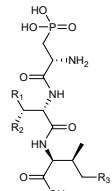


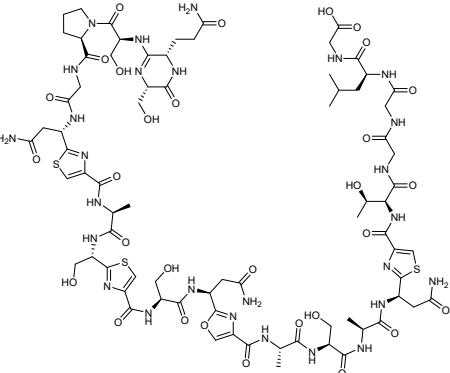
P. aeruginosa (16 µg/mL),

M. tuberculosis (2-16 µg/mL)

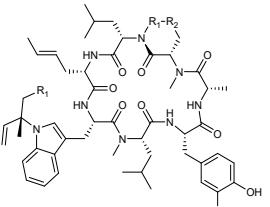
14-19

| | | | | | |
|-----------|---------------------|---|-----------------|---|--|
| 55 | Sansanmycin I |  | | | |
| 56 | Sansanmycin J |  | | | |
| 57 | Sansanmycin K |  | | | |
| 58 | Sansanmycin L |  | | | |
| 59 | Sansanmycin M |  | | | |
| 60 | Sansanmycin N |  | | | |
| 61 | Sansanmycin O |  | | | |
| 62 | Dihydrosansamycin A |  | total synthesis | - | P. aeruginosa (12.5-100 µm), M. tuberculosis (0.3-18.5 µm) |
| 63 | Dihydrosansamycin B |  | | | transloc-ase I (MurX, known as MraY in other bacteria) |
| | | | | | 20 |

| | | | | | | | |
|-----------|---------------------|---|--|--|---|--|--|
| 64 | Dihydrosansamycin C | | | | | | |
| 65 | Phosphonoalamide A | | | | | <i>E. coli, B. subtilis, B. cereus, B. megaterium</i> (6.25-200 µm) | |
| 66 | Phosphonoalamide B |  | 65 $R_1=R_2=R_3=H$ 66 $R_1=CH_3, R_2=OH, R_3=H$ 67 $R_1=R_2=H, R_3=CH_3$ 68 $R_1=R_2=CH_3, R_3=H$ | <i>Streptomyces</i> sp. NRRL B-2790 | - | | 21 |
| 67 | Phosphonoalamide C | | | | | N/A | |
| 68 | Phosphonoalamide D | | | | | | |
| 69 | Argolapho A | | 69 $R=$ 70 $R=H$ | <i>S. monomycini</i> NRRL B-24309 | - | <i>E. coli, S. aureus, S. enterica</i> (no MIC values) | UDP-N-acetylmuramyl-L-alanine synthetase |
| 70 | Argolapho B | | | | | | 22 |

| | | |
|----------------------------|---|---|
| 71 Klebsazolicin |  | <i>K. pneumoniae</i> ATCC 11296 - <i>E. coli</i> (32->1024 µg/mL), <i>K. pneumoniae</i> (128 µg/mL), <i>Yersinia pseudotuberculosis</i> (64 µg/mL) |
|----------------------------|---|---|

2. Cyclic oligopeptides

| | | | | | |
|--------------------------------------|--|---|---|-----------------------------------|--|
| 72 Ilamycin B ₁ |  | <i>M. tuberculosis</i> (2.4 µm) | | | |
| 73 Ilamycin B ₂ |  | | | | |
| 74 Ilamycin C ₁ |  | <i>Streptomyces atratus</i> SCSIO ZH16 marine-derived sample (South China Sea) | | | |
| 75 Ilamycin C ₂ | R ₁ 72 H | R ₂  | R ₃  | R ₄ NO ₂ | <i>M. tuberculosis</i> (0.0098-9.6 µm), <i>M. smegmatis</i> (0.12-30.7 µm) |
| 76 Ilamycin D | 73 H |  |  | NO ₂ | tyrosine hydrolytic protein C1 (ClpC1) 24-25 |
| 77 Ilamycin E ₁ | 74  |  | NO ₂ | | |

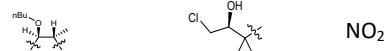
| | | | | | | |
|-----------|-------------------------|-----------|---|---|---|-----------------|
| 78 | Ilamycin E ₂ | | | | | |
| 79 | Ilamycin F | 75 |  |  | NO ₂ | |
| 80 | Ilamycin G | 76 | H |  |  | NO ₂ |
| 81 | Ilamycin H | 77 |  |  | NO ₂ | |
| 82 | Ilamycin I | 78 |  |  | NO ₂ | |
| 83 | Ilamycin J | 79 | H |  |  | NO ₂ |
| 84 | Ilamycin K | 80 | H |  |  | NO ₂ |
| 85 | Ilamycin L | 81 | H |  |  | NO ₂ |
| 86 | Ilamycin M | 82 | H |  |  | NO ₂ |
| 87 | Ilamycin N | 83 |  |  | NO ₂ | |
| 88 | Ilamycin O | 84 |  |  | NO ₂ | |
| 89 | Ilamycin P | 85 | H |  |  | NO ₂ |
| 90 | Ilamycin Q | 86 | H |  |  | NO ₂ |

Streptomyces
atratus SCSIO
ZH16 ΔilaR

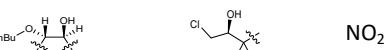
M. tuberculosis (0.0096-
10 μm)

| | | | | | |
|-----|----------------|----|---|------------------------------|--|
| | | | | | |
| 91 | Illumycin R | 87 | H | | |
| 92 | Rufomycin NBZ1 | 88 | H | | |
| 93 | Rufomycin NBZ2 | 89 | | | NO ₂ |
| 94 | Rufomycin NBZ3 | 90 | H | | |
| 95 | Rufomycin NBZ4 | 91 | | | NO ₂ |
| 96 | Rufomycin NBZ5 | 92 | H | | |
| 97 | Rufomycin NBZ6 | 93 | H | | |
| 98 | Rufomycin NBZ7 | 94 | H | | |
| 99 | Rufomycin NBZ8 | 95 | H | | |
| 100 | RufomycinSS 1 | 96 | H | | |
| 101 | RufomycinSS 2 | 97 | H | | |
| 102 | RufomycinSS 3 | 98 | | | NO ₂ |
| | | 99 | | | NO ₂ |
| | | | | <i>S. atratus</i> MMJ3502 | |
| | | | | - | <i>M. tuberculosis</i> (0.030- >10 µm), <i>M. abscessus</i> (0.54- >10 µm) |
| | | | | | 26 |
| | | | | semi-synthesis | |
| | | | | - | <i>M. tuberculosis</i> (12-4300 nM) |
| | | | | | 27 |

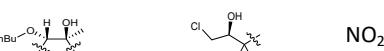
103 RufomycinSS 8



104 RufomycinSS 9



105 RufomycinSS 10



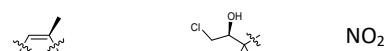
106 RufomycinSS 11



107 RufomycinSS 12



108 RufomycinSS 13

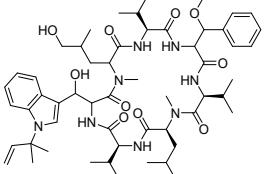
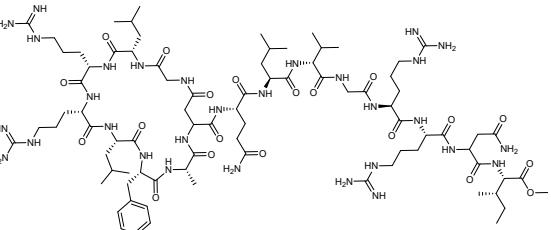
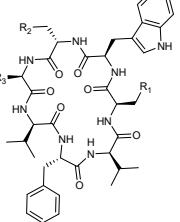
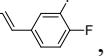
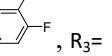
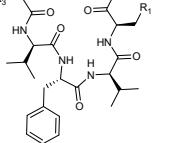
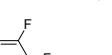
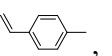
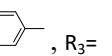


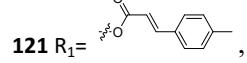
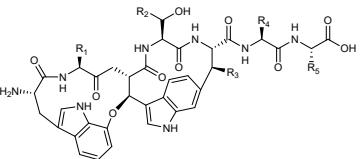
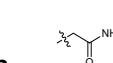
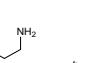
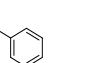
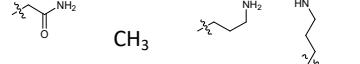
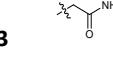
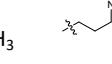
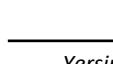
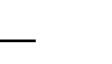
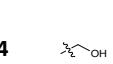
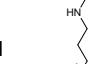
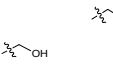
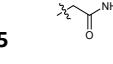
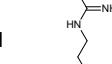
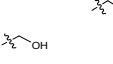
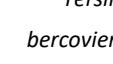
109 Rufomycin 6

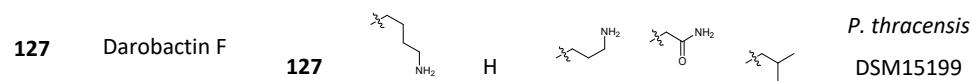
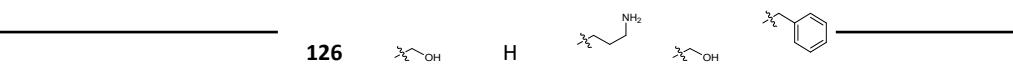


110 Rufomycin 7

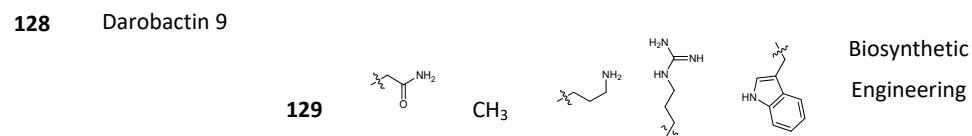
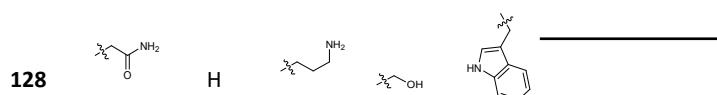


| | | | | | | | |
|------------|---------------------------------|---|---|---|---|--------------------|----|
| 111 | Metamarin |  | heterologous expression in <i>Streptomyces albus</i> J1074 (cosmids DFD0097_w371, DFD1080_w495) | soil sample | <i>M. tuberculosis</i> (0.16- 0.63 µg/mL) | ATPase of ClpC1 | 28 |
| 112 | Lassomycin |  | <i>Lentzea kentuckyensis</i> IS009804 | soil sample | <i>M. tuberculosis</i> (0.78-3.1 µg/mL), <i>M. avium subsp.</i> <i>paratuberculosis</i> (0.125- 0.25 µg/mL), <i>M.</i> <i>smegmatis</i> (0.78-2 µg/mL) | ATPase of ClpC1 | 29 |
| 113 | Asperver-siamide A |  | 118 R ₁ =  R ₂ =  R ₃ = CH ₃ | | <i>M. marinum</i> (23.4-87.5 µm), <i>M. tuberculosis</i> (100 µm) | | |
| 114 | Asperver-siamide B |  | 119 R ₁ = CH ₃ | | | | 30 |
| 115 | Asperver-siamide C |  | | | | | |
| 116 | Asperhepta-tide A | 113 R ₁ =OH, R ₂ =OH, R ₃ =CH ₃ | 118 R ₁ =  R ₂ =H, R ₃ =H | <i>Aspergillus versicolor</i> CHNSCLM-0063 | coral-derived fungus | - | |
| 117 | Asperhepta-tide B | 114 R ₁ =OH, R ₂ =H, R ₃ = CH ₃ | 119 R ₁ = CH ₃ | | <i>M. tuberculosis</i> (12.5-100 µm) | | 31 |
| 118 | Asperver-siamide A ₂ | 115 R ₁ =H, R ₂ =OH, R ₃ = CH ₃ | 120 R ₁ =  R ₂ =  R ₃ = | | | | |
| 119 | Asperversia-mide A ₆ | 116 R ₁ =OH, R ₂ =OH, R ₃ =H | 117 R ₁ =H, R ₂ =H, R ₃ = CH ₃ | | | | |

| | | | | | | | | | |
|------------|----------------------------------|---|--|---|--|---|---|--|-------|
| 120 | Asperversia-mide A ₁₅ |  | 121 R ₁ =  , R ₂ =  , R ₃ = CH ₃ | | | | | | |
| 121 | Asperversia-mide A ₁₆ | | | | | | | | |
| 122 | Darobactin A |  | <i>Photobacterium khanii</i> HGB1456 | bacterial insertase BamA | | | | | |
| 123 | Darobactin B | R ₁  122 | R ₂ H | R ₃  | R ₄  | R ₅  | <i>Photobacterium asymbiotica</i> ATCC43949 | | |
| 124 | Darobactin C |  |  |  |  |  |  | <i>Yersinia pestis</i> Angola Gram-negative bacteria (0.5-64 μm) | 32-35 |
| 125 | Darobactin D |  |  |  |  |  |  | <i>Yersinia enterocolitica</i> subsp. <i>enterocolitica</i> strain NCTC13629 | - |
| 126 | Darobactin E |  |  |  |  |  |  | <i>Yersinia bercovieri</i> stain SCPM-O-B-7607 | |

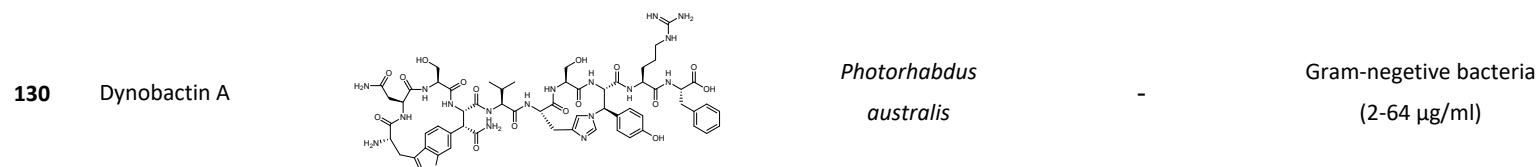


P. thracensis
DSM15199



Biosynthetic
Engineering

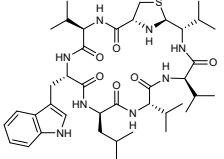
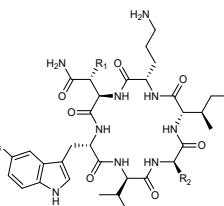
129 Darobactin 22

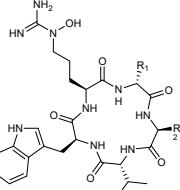


Photobacterium
australis

Gram-negative bacteria
(2-64 µg/ml)

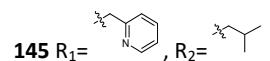
36

| | | | | | | | | |
|------------|--------------------|---|---|---|--|---|---|----|
| 131 | Lugdunin |  | <i>Staphylococcus lugdunensis</i> IVK28 | Human microbiome | MRSA, GISA, VRE, <i>L. monocytogenes</i> , <i>S. pneumoniae</i> , <i>B. subtilis</i> (1.5-12 µg/ml) | cell membranes | 37 | |
| 132 | Nicrophorusamide A |  | <i>Microbacterium</i> sp. UTG9 | a gut bacterium (the carrion beetle <i>Nicrophorus concolor</i>) | <i>S. aureus</i> , <i>E. faecalis</i> , <i>E. faecium</i> , <i>S. enterica</i> (8-128 µg/ml) | | 38-41 | |
| 133 | Nicrophorusamide B | R ₁  | R ₂  | R ₃ Cl | R ₄ CH ₃ | Inactive | 36 | |
| 132 | | | | | - | <i>S. aureus</i> , MRSA, QRSA, | | |
| 134 | Ulleungmycin A | 133 | H  |  | Cl CH ₃ | <i>Streptomyces</i> sp. KCB13F003 | <i>B. subtilis</i> , <i>S. pneumoniae</i> , <i>E. faecalis</i> (8-16 µg/ml) | 39 |
| 135 | Noursamycin A | 134 | OH  |  | Cl CH ₃ | <i>Streptomyces</i> <i>noursei</i> NTR-SR4 | <i>B. subtilis</i> , <i>S. typhimurium</i> , <i>M. luteus</i> , <i>M. phlei</i> (4-16 µg/ml) | 40 |
| 136 | Noursamycin C | 135 | OH  |  | Cl CH ₃ | | Inactive | |

| | | | | | | | | |
|------------|-------------------|------------|---|---|--|-----------------|---|-------|
| 137 | Noursamycin D | 136 | OH |  or  | Cl | CH ₃ | | |
| 138 | Noursamycin E | 137 | OH |  | Cl | H | | |
| 139 | Dechlorocuramycin | 138 | OH |  | Cl | H | | |
| | | 139 | OH |  | H | CH ₃ | <i>Streptomyces noursei</i> NBRC 15452 | 41 |
| 140 | Pentamino-mycin A | | |  | <i>Streptomyces</i> sp. RK88-1441 | - | N/A | |
| 141 | Pentamino-mycin B | | | | | - | <i>A. baumannii</i> (16-32 µg/ml) | |
| 142 | Pentamino-mycin C | 140 | R ₁ =  , R ₂ =  | | | | <i>M. luteus, B. subtilis, S. aureus, A. baumannii</i> (16 µg/ml) | 42-45 |
| 143 | Pentamino-mycin D | 141 | R ₁ =  , R ₂ =  | | <i>Streptomyces cacaoi</i> subsp. <i>cacaoi</i> NBRC 12748 | - | N/A | |
| 144 | Pentamino-mycin E | 142 | R ₁ =  , R ₂ =  | | | - | | |
| 145 | Pentamino- | 143 | R ₁ =  , R ₂ =  | | <i>Streptomyces</i> | - | Inactive | |

mycin F

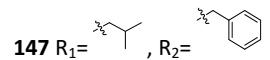
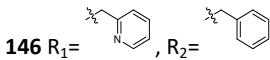
146 Pentamino-
mycin G



cacaoi subsp.

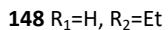
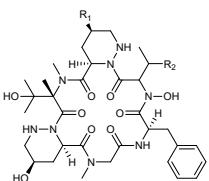
cacaoi CA-
170360

Pentamino-
147 mycin H



148 Pargamicin A

149 Pargamicin B



149 R₁=H, R₂=Me
Amycolatopsis
sp. ML1-hF4

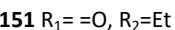
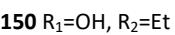
soil sample (Shinagawa,
Tokyo, Japan)

E. faecalis, VRE, *S.*
aureus, MREA, *M. luteus*,
E. faecium, *B. subtilis*, *B.*
cereus, *C. bovis*
(0.5-64 µg/ml)

-

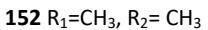
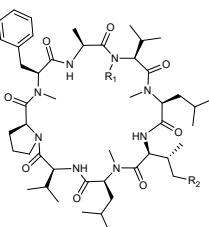
46-47

150 Pargamicin C



151 Pargamicin D

152 Broomeana-
mide A



Sphaerostilbella

wood-inhabiting fungi

C. neoformans (8 µg/ml),
C. albicans (64 µg/ml)

-

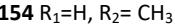
48

153 Broomeana-
mide B



broomeana

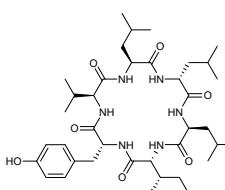
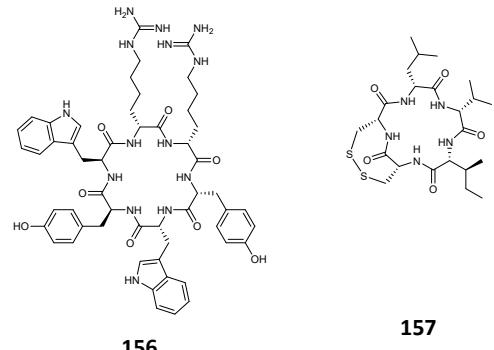
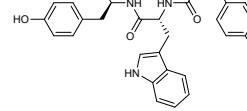
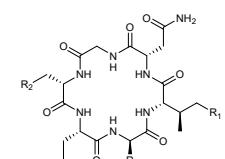
(the foothills of

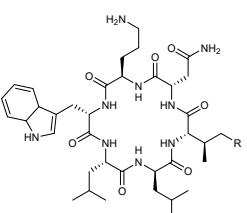
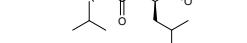


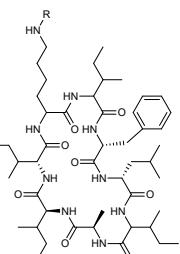
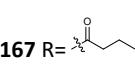
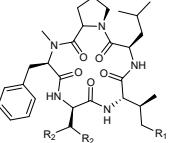
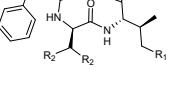
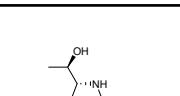
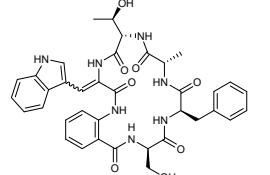
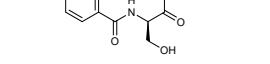
TFC201724

Himalayas)

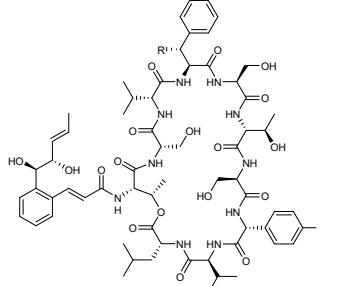
N/A

| | | | | | | | |
|-----|---------------------|---|---|---|--|---|-------|
| 154 | Broomeana-mide C | | | | | | |
| 155 | Thermoactinoamide A |  | <i>Thermoactinomyces vulgaris</i> strain ISCAR 2354 | A sample from coastal hot spring (Snæfellsness peninsula in West Iceland) | <i>S. aureus</i> (35 µm) | - | 49 |
| 156 | Photoditritide |  | <i>Photorhabdus temperata</i> Meg1 | - | <i>M. luteus, T. brucei rhodesiense, E. coli, P. falciparum</i> (3.0-27 µm) | - | 50 |
| 157 | Malformin E |  | <i>Aspergillus tamarii</i> FR02 | the roots of Ficus carica | <i>B. subtilis, S. aureus, P. aeruginosa, E. coli, P. chrysogenum, C. albicans, F. solani</i> (0.45-7.24 µm) | - | 51 |
| 158 | Desotamides A |  | <i>Streptomyces</i> sp. NRRL 21611 | soil sample (DeSoto Falls, GA) | <i>S. aureus, B. subtilis, S. pneumoniae, MRSE (clinical isolate shhs-E1)</i> | - | 52-54 |
| 159 | Desotamides B | R ₁ R ₂ R ₃ | | | | | |

| | | | | | | | | |
|------------|---------------|------------|----|---|---|--|---|--|
| 160 | Desotamides C | 158 | Me |  | CH ₂ CH(CH ₃) ₂ | <i>Streptomyces scopuliridis</i> SCSIO ZJ46 | a sediment sample collected in the South China Sea at a depth of 3536 m | Inactive |
| 161 | Desotamides D | 159 | H |  | CH ₂ CH(CH ₃) ₂ | | | |
| 162 | Desotamides E | 160 | Me |  | CH ₂ CH(CH ₃) ₂ | <i>Streptomyces</i> nov. sp. (MST-115088) | Soil sample from semiarid terrain (Wollogorang Station, Queensland) | <i>B. subtilis</i> (3.5-5.2 μm) |
| 163 | Desotamides F | 161 | Me |  | CH ₂ CH(CH ₃) ₂ | | | <i>B. subtilis</i> (1.0-1.2 μm), <i>S. aureus</i> (5.5-6.8 μm) |
| | | 162 | Me |  | CH(CH ₃) ₂ | | | |
| | | 163 | Me |  | CH(CH ₃)C ₂ H ₅ | | | |
| 164 | Wollamides A | | |  | 164 R=Me | <i>Streptomyces</i> nov. sp. (MST-115088) | Soil sample from semiarid terrain (Wollogorang Station, Queensland) | <i>B. subtilis</i> (1.8-2.0 μm), <i>M. bovis</i> (2.8 μm) |
| 165 | Wollamides B | | |  | 165 R=H | | | <i>B. subtilis</i> (1.9-2.2 μm), <i>S. aureus</i> (0.6-0.9 μm), <i>M. bovis</i> (3.1 μm) |

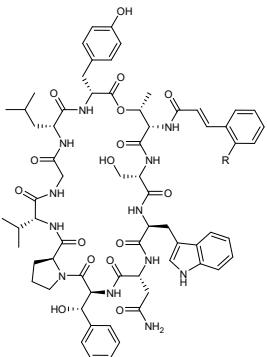
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|------------|-------------------|--|---|---------------------------------|---|--|---|-------|
| 166 | Surugamide A |  | 166 R=H | <i>Streptomyces</i> sp. JAMM992 | Deep-sea sediment sample collected from Kinko Bay (-106 m), Japan | <i>S. aureus</i> (10µm) | - | 55-56 |
| 167 | Acyl-surugamide A |  | 167 R=  | <i>Streptomyces</i> albus J1074 | - | <i>S. aureus</i> , <i>B. subtilis</i> , <i>S. cerevisiae</i> , <i>S. pombe</i> (3.5-32.5 µm) | - | |
| 168 | Ellisiamide A |  | 168 R ₁ =CH ₃ , R ₂ = CH ₃ | <i>Xylaria ellisii</i> sp. nov. | a leaf and stem endophyte of <i>Vaccinium angustifolium</i> (Nova Scotia, New Brunswick, and Ontario, Canada) | <i>E. coli</i> (100 µg/ml) | - | 57 |
| 169 | Ellisiamide B |  | 169 R ₁ =H, R ₂ =CH(CH ₃) ₂ | | | | - | |
| 170 | Ellisiamide C |  | 170 R ₁ = CH ₃ , R ₂ =CH(CH ₃)CH ₂ CH ₃ | | | inactive | - | |
| 171 | Sclerotide A |  | 171 Z | <i>Aspergillus sclerotiorum</i> | Marine sample (Putian Sea) | <i>C. albicans</i> (7 µm) | - | 58 |
| 172 | Sclerotide B |  | 172 E | PT06-1 | Salt Field, Fujian, China) | <i>C. albicans</i> (3.5 µm), <i>P. aeruginosa</i> (35.3 µm) | - | |

3 Cyclic depsipeptides

| | | | | | | | | |
|------------|---------------|---|-----------------|-------------------------------------|--|--|---|----|
| 173 | Atrovimycin A |  | 173 R=OH | <i>Streptomyces atrovirens</i> LQ13 | soil sample (Xinjiang Uygur Autonomous Region of China.) | <i>Fusarium oxysporum</i> f. sp. <i>Cucumerinum</i> (9.3 µm), <i>M. tuberculosis</i> (2.5 µg/ml) | - | 59 |
| | |  | 174 R=H | | | | - | |

174 Atrovimycin B

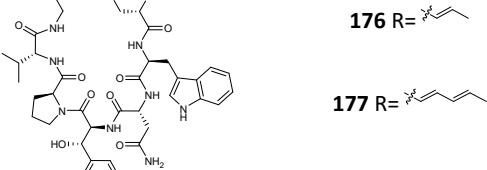
175 Atratumycin A



175 R=

Streptomyces atratus SCSIO ZH16 sediment sample

176 Atratumycin B

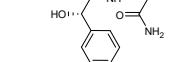


176 R=

M. tuberculosis (3.8-14.6 μm)

60-61

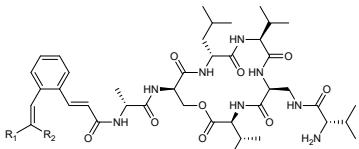
177 Atratumycin C



177 R=

Streptomyces atratus SCSIO ZH16 NS-80S engineered strain of *S. atratus* SCSIO ZH16

178 Coprisamide A



178 R₁=H, R₂=

A sample from gut of the dung beetle *Copris tripartitus* (Jeju Island, Republic of Korea)

62

179 Coprisamide B

179 R₁=

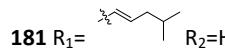
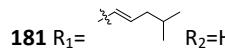
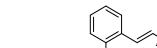
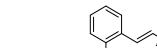
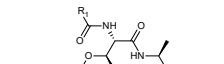
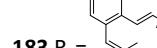
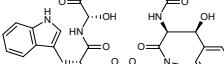
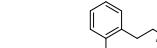
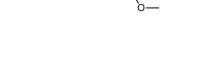
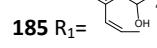
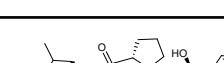
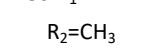
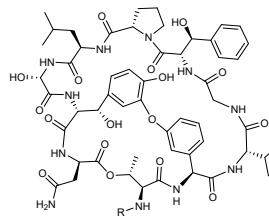
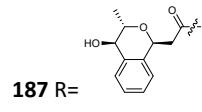
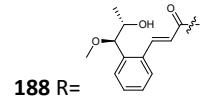
180 Coprisamide C

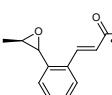
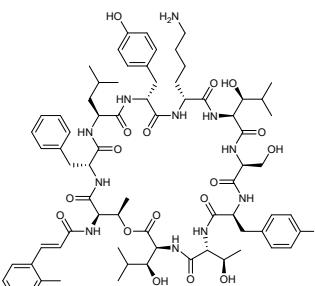
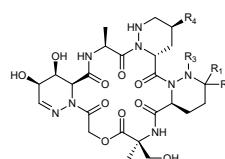
180 R₁=H, R₂=

Micromonospor a sp. UTJ3 Sample from the carrion beetle *Silpha perforata*

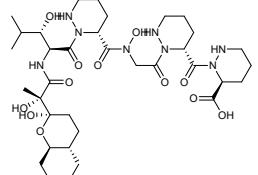
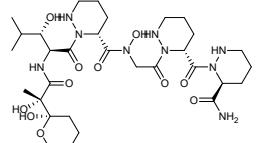
M. tuberculosis (82.8 $\mu\text{g/ml}$)

63

| | | | | |
|------------|---------------|---|---|--|
| 181 | Coprisamide D |  | 181 R ₁ =  R ₂ =H | inactive |
| 182 | Skyllamycin A |  | 182 R ₁ =  R ₂ =CH ₃ | <i>Streptomyces</i> sp. KY 11784 soil sample (Sakai-shi, Osaka, Japan) <i>S. aureus</i> (140 µm), <i>B. subtilis</i> (105 µm) |
| 183 | Skyllamycin B |  | 183 R ₁ =  R ₂ =H | <i>Streptomyces</i> sp. Acta 2897 Sandy soil sample (Warkworth, UK) |
| 184 | Skyllamycin C |  | 184 R ₁ =  R ₂ =H | <i>Streptomyces</i> sp. strain 1675 sediment sample from Westport Jetty, WA, USA |
| 185 | Skyllamycin D |  | 185 R ₁ =  R ₂ =CH ₃ | <i>Streptomyces</i> anulatus strain ATCC 11523 A sample from the New Zealand lichen <i>Pseudococcophyllum dissimilis</i> <i>B. subtilis</i> (8-32 µg/ml), <i>S. aureus</i> (16-64 µg/ml) |
| 186 | Skyllamycin E |  | 186 R ₁ =  R ₂ =CH ₃ | N/A |
| 187 | Nyuzenamide A |  | 187 R=  | <i>Streptomyces</i> sp. N11-34 deep sea derived sample (Toyama, Japan) <i>G. cingulata</i> (3.1 µg/ml), <i>T. rubrum</i> (6.3 µg/ml) |
| | | | 188 R=  | - 68-69 |

| | | | | | | | |
|------------|---------------|--|---|------------------------------------|---|---|---|
| 188 | Nyuzenamide B | 189 R= |  | <i>Streptomyces</i> sp. DM14 | river sediment sample (Dumulmeori, Republic of Korea) | inactive | |
| 189 | Nyuzenamide C | | | | | | |
| 190 | Cinnapeptin |  | <i>Streptomyces</i> <i>ghanaensis</i> | - | <i>B. subtilis</i> , <i>S. hominis</i> , <i>S. agalactiae</i> , <i>S. mutans</i> , <i>S. pombe</i> (5.7-11.4 µm) | - | 70 |
| 191 | Svetamycin A |  | | | <i>M. smegmatis</i> (32 µg/ml), MRSA (64 µg/ml) | | |
| 192 | Svetamycin B | R ₁ | R ₂ | R ₃ | R ₄ | <i>Streptomyces</i> sp. DSM 14386 | |
| 193 | Svetamycin C | 191 | H | H | H | Cl | Bought from DSMZ- German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany. |
| | | 192 | H | Me | H | Cl | N/A |
| | | | | | | | 71 |
| | | | | | | <i>M. smegmatis</i> (8 µg/ml), MRSA (16µg/ml), <i>M. tuberculosis</i> (54 µg/ml) | |

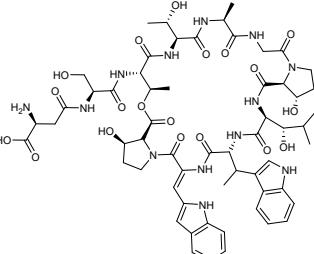
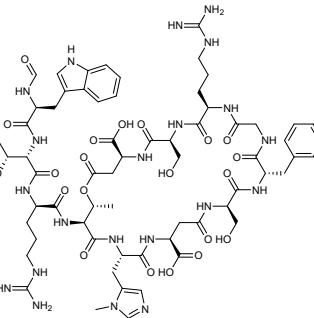
| | | | | | | | |
|------------|------------------|--|---|-----------------------------|--|--|---|
| 194 | Svetamycin D | | | | | | N/A |
| | | 193 | Me | Me | H | Cl | |
| 195 | Svetamycin F | 194 | H | π -band | | Cl | |
| | | 195 | H | H | H | Br | <i>M. smegmatis</i> (2-32 $\mu\text{g/ml}$), MRSA (16-64 $\mu\text{g/ml}$) |
| 196 | Svetamycin G | 196 | Me | Me | H | Br | |
| 197 | Meliponamycin A | | | | | | |
| 198 | Meliponamycin B | 197 R=H | 198 R=Me | | <i>Streptomyces</i> sp. ICBG1318 | Sample isolated from <i>M. scutellaris</i> nurse bees. | <i>P. larvae</i> (0.43 $\mu\text{g/ml}$), <i>S. aureus</i> (0.86-1.72 $\mu\text{g/ml}$), <i>L. infantum</i> (1.03-2.19 $\mu\text{g/ml}$) |
| | | | | | | | 72 |
| 199 | Dentigerumycin A | | | | | | |
| 200 | Dentigerumycin B | 199 R₁=CH₂CH₂CH₃, R₂=CH₃, R₃=H, R₄=OH, R₅=CH₃ | 200 R₁=CH₂CH₃, R₂=CH(S-OH)CH₃, R₃=OH, R₄=H, R₅=H | | <i>Pseudonocardia</i> spp. | Isolated from ant (<i>Apterostigma dentigerum</i>) nest (Gamboa, Panama) | <i>Escovopsis</i> sp. (2.8 μm) |
| | | | | | | | 73-76 |
| | | | | <i>Streptomyces</i> sp. M41 | isolated from a South African termite, <i>Macrotermes natalensis</i> | N/A | |

| | | | |
|------------|---------------------|---|---|
| | | 203 R ₁ =CH ₂ COOH, R ₂ =CH(S-OH)CH ₃ , R ₃ =OH, R ₄ =H, R ₅ =H | |
| 201 | Dentigerumycin C | | |
| 202 | Dentigerumycin D | 204 R ₁ =CH ₂ CH ₃ , R ₂ =CH ₃ , R ₃ =H, R ₄ =OH, R ₅ =CH ₃ |  |
| 203 | Dentigerumycin E | 201 |  |
| 204 | Dentigerumycin F | 202 |  |
| 205 | Marformycin A | 205 R ₁ =H, R ₂ =Me, R ₃ =H | |
| 206 | Marformycin B | 206 R ₁ =H, R ₂ =Me, R ₃ =Me | |
| 207 | Marformycin C | 207 R ₁ =OH, R ₂ =H, R ₃ =Me | <i>Streptomyces drozdzowiczae</i> marine-derived sample (South China Sea) |
| 208 | Marformycin D | 208 R ₁ =OH, R ₂ =Me, R ₃ =Me | <i>SCSIO 10141.</i> <i>M. luteus</i> (0.063-4 µg/ml) |
| 209 | Marformycin E | 209 R ₁ =OH, R ₂ =H, R ₃ =H | - |
| 210 | Marformycin F | 210 R ₁ =H, R ₂ =H, R ₃ =H | 77 N/A |

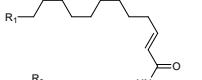
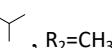
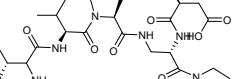
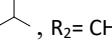
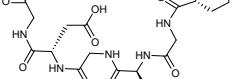
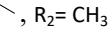
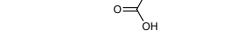
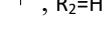
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|------------|------------------|--|---|---|--|--------------------|-------|
| 211 | Aurantimycin A | | <i>Streptomyces aurantiacus</i> | - | <i>B. subtilis, S. aureus, M. luteus, M. flavus, S. pyogenes, E. faecium</i> | (0.007-0.08 µg/ml) | 78 |
| 212 | Aurantimycin B | | <i>Streptomyces aurantiacus</i> | - | <i>B. subtilis, S. aureus, M. luteus, M. flavus, S. pyogenes, E. faecium</i> | (0.007-0.08 µg/ml) | 78 |
| 213 | Aurantimycin C | | <i>Streptomyces aurantiacus</i> | IMET43917 | <i>B. subtilis, S. aureus, M. luteus, M. flavus, S. pyogenes, E. faecium</i> | (0.007-0.08 µg/ml) | 78 |
| 214 | Krisynomycin A | | <i>Streptomyces fradiae</i> strain MA7310 | - | MRSA (16-32 µg/ml) | | |
| 215 | Krisynomycin B | | <i>Streptomyces canus</i> CA-091830 | sand sample (Kalahari Desert, South Africa) | inactive | Peptidase Type I | 79-80 |
| 216 | Krisynomycin C | | <i>Streptomyces canus</i> CA-091830 | sand sample (Kalahari Desert, South Africa) | inactive | Peptidase Type I | 79-80 |
| 217 | Ohmyungsamycin A | | <i>Streptomyces sp.</i> SNJ042 | Sample from a beach (Jeju, Republic of Korea) | <i>B. subtilis</i> (4.28-34 µg/ml), <i>K. rhizophila</i> (1.07-8.5 µg/ml), <i>P. hauseri</i> (2.14-17 µg/ml) | - | 81 |
| 218 | Ohmyungsamycin B | | | | | | |

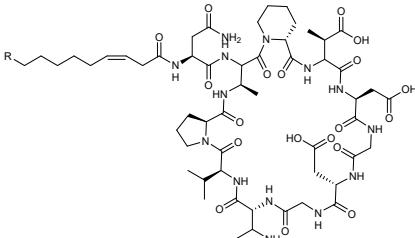
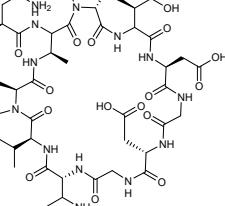
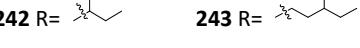
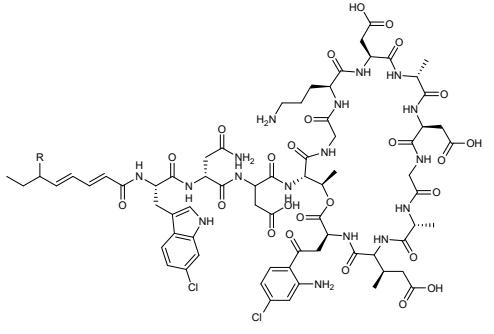
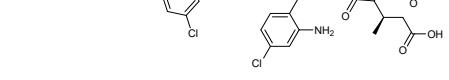
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|------------|----------------|---|--|---|--|--|-------|
| 219 | Ecumicin | 217 R ₁ =H, R ₂ =H, R ₃ =CH ₃ 218 R ₁ =CH ₃ , R ₂ =H, R ₃ =CH ₃ 219 R ₁ =CH ₃ , R ₂ =CH ₃ , R ₃ = | <i>Nonomuraea</i> sp. MJM5123 | - | <i>M. tuberculosis</i> (0.26 µg/ml) | ATPase of ClpC1 | 82 |
| 220 | Teixobactin | | <i>Eleftheria</i> <i>terrae</i> | - | Gram-positive bacteria (0.005-0.31 µg/ml) and Gram-negative bacteria (2.5-25 µg/ml) | peptidoglycan synthesis | 83 |
| 221 | Hypeptin | | <i>Lysobacter</i> sp. K5869 | - | Gram-positive bacteria (0.0625-16 µg/ml) | bacterial cell wall biosynthesis | 84 |
| 222 | Clavariopsin A | | <i>Clavariopsis</i> <i>aquatica</i> AJ117363 | stream sediment sample (Mt. Takao, Tokyo, Japan.) | <i>C. albicans</i> , <i>A. niger</i> , <i>A.</i> <i>fumigatus</i> , <i>B. cinerea</i> , <i>M.</i> <i>oryzae</i> , <i>C. orbiculare</i> , <i>A.</i> <i>alternata</i> | - | 85-86 |
| 223 | Clavariopsin B | 222 R ₁ =CH ₃ , R ₂ =CH(CH ₃) ₂ , R ₃ =CH(CH ₃)C ₂ H ₅ , R ₄ =CH ₃ , R ₅ =CH(CH ₃)C ₂ H ₅ , R ₆ =CH ₂ CH ₂ | | | (2-16 µg/ml) | | |

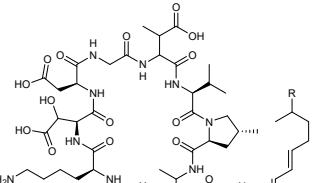
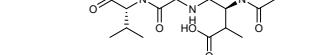
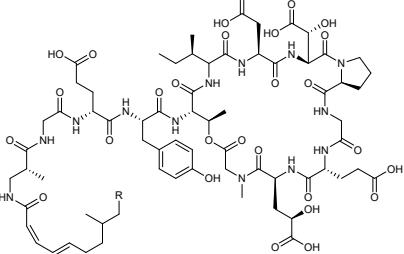
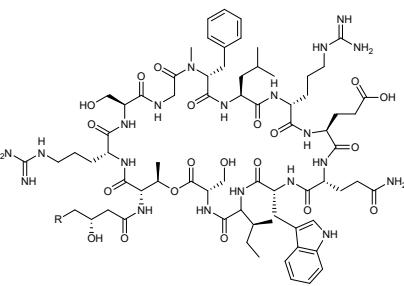
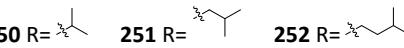
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|------------|----------------|---|---|---|-------------|----------|---|-------|
| 224 | Clavariopsin C | 223 R ₁ =H, R ₂ =CH(CH ₃) ₂ , R ₃ =CH(CH ₃)C ₂ H ₅ , R ₄ =CH ₃ , R ₅ =CH(CH ₃)C ₂ H ₅ , R ₆ =CH ₂ CH ₂ | | | | | | |
| 225 | Clavariopsin D | 224 R ₁ =CH ₃ , R ₂ =CH(CH ₃) ₂ , R ₃ =CH(CH ₃)C ₂ H ₅ , R ₄ =H, R ₅ =CH(CH ₃)C ₂ H ₅ , R ₆ =CH ₂ CH ₂ | | | | | | |
| 226 | Clavariopsin E | 225 R ₁ =CH ₃ , R ₂ =CH(CH ₃) ₂ , R ₃ =CH(CH ₃) ₂ , R ₄ =CH ₃ , R ₅ =CH(CH ₃)C ₂ H ₅ , R ₆ =CH ₂ CH ₂ | | | | | | |
| 227 | Clavariopsin F | 226 R ₁ =CH ₃ , R ₂ =CH(CH ₃) ₂ , R ₃ =CH(CH ₃)C ₂ H ₅ , R ₄ =CH ₃ , R ₅ =CH(CH ₃) ₂ , R ₆ =CH ₂ CH ₂ | <i>B. cinerea</i> (0.01-0.3 μg/disk), <i>A. alternata</i> (0.3-3 μg/disk) | | | | | |
| 228 | Clavariopsin G | 227 R ₁ =CH ₃ , R ₂ =CH(CH ₃) ₂ , R ₃ =CH ₂ CH(CH ₃) ₂ , R ₄ =CH ₃ , R ₅ =CH(CH ₃)C ₂ H ₅ , R ₆ =CH ₂ CH ₂ | | | | | | |
| 229 | Clavariopsin H | 228 R ₁ =CH ₃ , R ₂ =CH(CH ₃) ₂ , R ₃ =CH(CH ₃)C ₂ H ₅ , R ₄ =CH ₃ , R ₅ =CH ₂ CH(CH ₃) ₂ , R ₆ =CH ₂ CH ₂ | | | | | | |
| 230 | Clavariopsin I | 229 R ₁ =CH ₃ , R ₂ =CH(CH ₃) ₂ , R ₃ =CH(CH ₃)C ₂ H ₅ , R ₄ =CH ₃ , R ₅ =CH(CH ₃)C ₂ H ₅ , R ₆ =CH ₂ | | | | | | |
| 230 | Clavariopsin I | 230 R ₁ =CH ₃ , R ₂ =CH ₂ CH(CH ₃) ₂ , R ₃ =CH(CH ₃)C ₂ H ₅ , R ₄ =CH ₃ , R ₅ =CH(CH ₃)C ₂ H ₅ , R ₆ =CH ₂ CH ₂ | | | | | | |
| 231 | Ulleungamide A | | 231 R ₁ -R ₂ = | <i>S. aureus</i> (25 μg/disk), <i>S. typhimurium</i> (50 μg/disk) | | | | |
| 232 | Ulleungamide B | | 232 R ₁ -R ₂ = | <i>Streptomyces</i> sp. KCB13F003 | Soil sample | inactive | - | 87-88 |
| 233 | Ulleungamide C | | 233 R ₁ -R ₂ = | | | N/A | | |

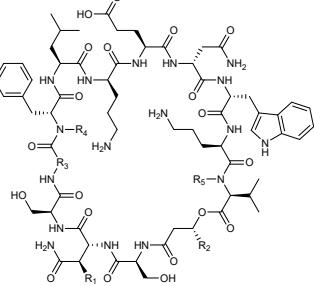
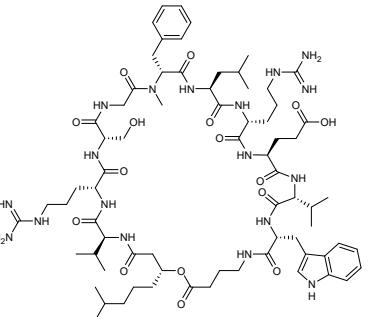
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| 234 | Ambobactin |  | <i>Streptomyces ambofaciens</i> F3 | an endophyte of <i>Platycladus orientalis</i> | <i>B. subtilis</i> , <i>B. cereus</i> , <i>S. aureus</i> , <i>E. coli</i> , <i>E. carotovora</i> , <i>P. syringae</i> , <i>pv. Actinidiae</i> , <i>A. solanacearum</i> , <i>X. oryzae</i> , <i>pv. Oryzae</i> . (3.13-25 µg/ml) | - | 89 |
| 235 | Evybactin |  | <i>P. noenieputensis</i> DSM 25462 | - | <i>M. tuberculosis</i> (0.0625-64 µg/ml), <i>E. coli</i> (0.0625-16 µg/ml) | DNA gyrase | 90 |

4 Cyclic liopeptides

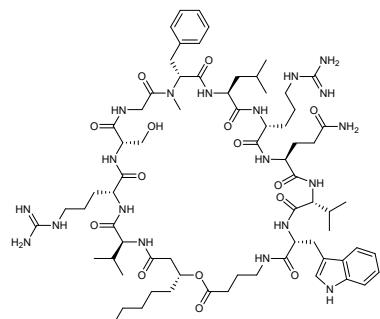
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| 236 | Glycinocin A |  | 236 R ₁ =  , R ₂ =CH ₃ | - | - | lipid carrier | |
| 237 | Glycinocin B |  | 237 R ₁ =  , R ₂ =CH ₃ | <i>Actinomycete</i> AW998 | - | <i>S. aureus</i> (5.5-17 µg/ml), <i>B. subtilis</i> (8.3-17 µg/ml) | undecylenyl phosphate (C55-P) |
| 238 | Glycinocin C |  | 238 R ₁ =  , R ₂ =CH ₃ | - | - | | 91 |
| 239 | Glycinocin D |  | 239 R ₁ =  , R ₂ =H | - | - | | |

| | | | | | |
|------------|---------------|---|--|--|--|
| 240 | Friulimicin A |  | N/A | | |
| 241 | Friulimicin B |  | <i>S. simulans</i> (0.078 µg/ml), <i>B. subtilis</i> (0.078 µg/ml) | lipid carrier undecylenyl phosphate (C55-P) | 92 |
| 242 | Friulimicin C |  | - | | |
| 243 | Friulimicin D |  | N/A | | |
| 244 | Taromycin A |  | <i>Saccharomonos</i> <i>pora</i> sp. CNQ- 490 | marine-derived sample | MRSA (12 µg/ml), <i>E.</i> <i>faecalis</i> (6-50 µg/ml) |
| 245 | Taromycin B |  | - | | 93-94 |
| | | 244 R=H | | | |
| | | 245 R=CH₃ | | | |

| | | | | | | | | |
|------------|-------------|---|---|---|-------------------------|---|--|----|
| 246 | Malacidin A |  | 246 R=Me | heterologous expression in <i>Streptomyces albus</i> J1074 (cosmids DFD0097-644, DFD0097-735 and DFD0097-388) | soil sample (USA) | multidrug-resistant Gram-positive pathogens (0.1-2 µg/ml) | cell wall synthesis precursor lipid II | 95 |
| 247 | Malacidin B |  | 247 R=Et | | | N/A | | |
| 248 | Cadaside A |  | | heterologous expression in <i>Streptomyces</i> <i>albus</i> J1074 (cosmid s DFD0097-431, DFD0097-157, DFD0097-262) | soil sample (Australia) | <i>S. aureus</i> (1 µg/ml), <i>E.</i> <i>faecalis</i> (4 µg/ml) | cell wall synthesis | 96 |
| 249 | Cadaside B |  | 248 R=CH₃ 249 R=H | | | | | |
| 250 | Lysocin E |  | | <i>Lysobacter</i> sp. RH2180-5 | soil sample (Japan) | <i>S. aureus</i> , <i>S. simulans</i> , <i>S.</i> <i>haemolyticus</i> , <i>S.</i> <i>pseudintermedius</i> , <i>B.</i> <i>subtilis</i> , <i>B. cereus</i> , <i>L.</i> <i>monocytogene</i> (1-4 µg/ml) | menaquinone on the cell membrane | 97 |
| 251 | Lysocin I | | | | | <i>M. smegmatis</i> (8 µg/ml), <i>S. aureus</i> (1-4 µg/ml), <i>S. epidermidis</i> (1 µg/ml) | - | 98 |
| 252 | Lysocin J |  | 250 R=  251 R=  252 R=  | <i>Lysobacter</i> <i>enzymogenes</i> | - | | | |

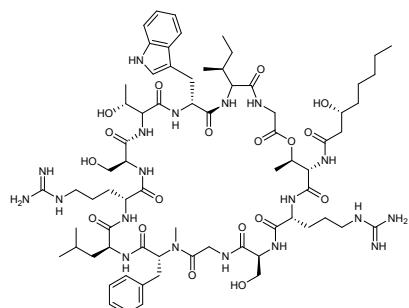
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|------------|-------------|--|--|---|--|--|-----------------|
| 253 | WAP-8294A1 |  | <i>Lysobacter</i> WAP-8294 | Soil sample (Shimoda City, Shizuoka Prefecture, Japan) | MRSA, <i>S. aureus</i> , <i>S. epidermidis</i> , <i>B. subtilis</i> , <i>E. faecium</i> (0.39-25 µg/ml) | menaquinone on the cell membrane | 99 |
| 254 | WAP-8294A2 | | | | | | |
| 255 | WAP-8294A4 | | | | | | |
| 256 | WAP-8294A8 | | | | | | |
| 257 | WAP-8294A9 | R ₁ | R ₂ | R ₃ | R ₄ | R ₅ | |
| | 253 | OH | (CH ₂) ₄ CH ₃ | CH ₂ | CH ₃ | CH ₃ | |
| 258 | WAP-8294A13 | 254 | OH | (CH ₂) ₃ CH(CH ₃) ₂ | CH ₂ | CH ₃ | CH ₃ |
| | 255 | OH | (CH ₂) ₄ CH(CH ₃) ₂ | CH ₂ | CH ₃ | CH ₃ | |
| | 256 | OH | ((CH ₂) ₃ CH(CH ₃) ₂ | CH ₂ | CH ₃ | H | |
| | 257 | OH | (CH ₂) ₃ CH(CH ₃) ₂ | (CH ₂) ₂ | H | CH ₃ | |
| | 258 | OH | (CH ₂) ₃ CH(CH ₃) ₂ | CH ₂ | CH ₃ | CH ₃ | |
| 259 | WBP-29479A1 |  | <i>L. antibioticus</i> ATCC 29479 | - | <i>S. aureus</i> (0.25-8 µg/ml) | - | 100 |

260 MBA1 wameb



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261 MBA2 lysomeb



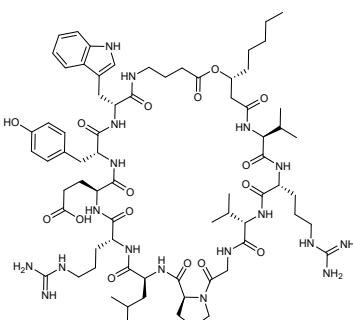
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Gram-positive bacteria
(0.5-64 µg/ml)

menaquinone

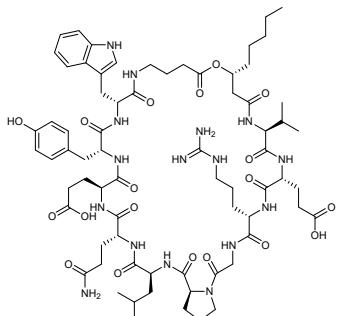
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262 MBA3
metameb



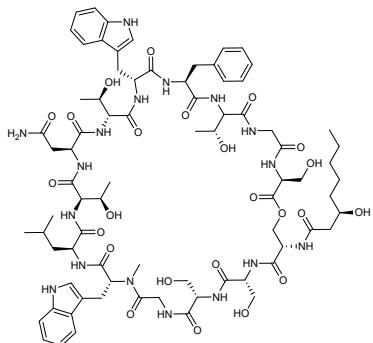
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263 MBA4 alcameb



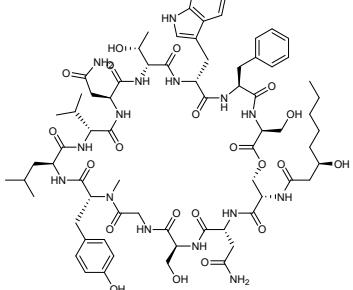
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264 MBA5 tabameb



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products

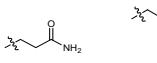
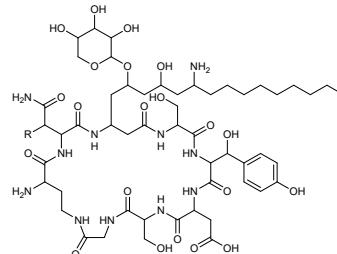
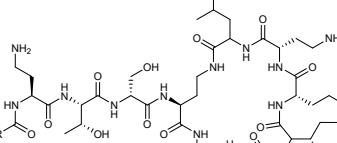
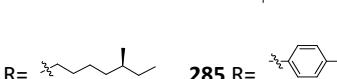
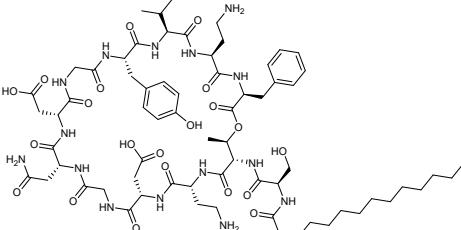
265 MBA6
mobimeb

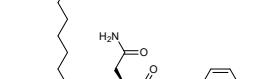
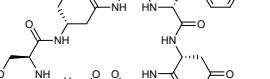
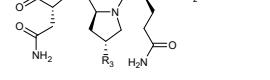
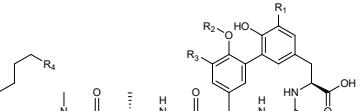


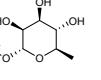
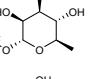
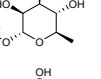
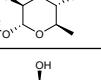
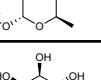
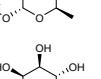
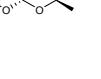
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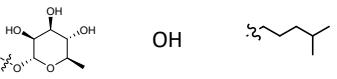
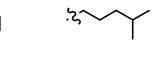
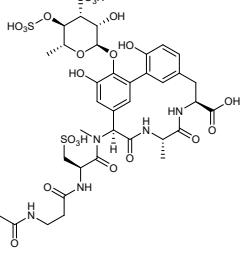
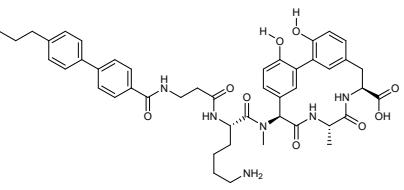
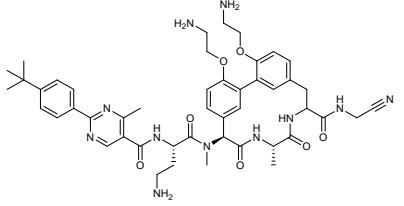
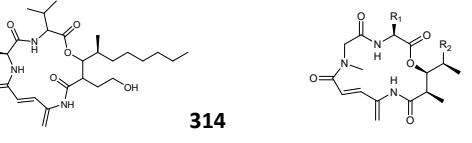
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|------------|---------------------|--|---|--|
| 266 | Burkholdine 1229 | | <i>P. infestans, A. solani, B. cinerea, M. figiensis, S. cerevisiae, A. niger, C. albicans</i> (0.4-12.5 µg/ml) | |
| 267 | Burkholdine 1097 | | | |
| 268 | Burkholdine 1119 | | <i>Burkholderia ambifaria</i> 2.2N. Soil sample (Pennsylvania State University, USA) | 102- 103 |
| 269 | Burkholdine 1213 | | <i>S. cerevisiae</i> (0.15-2 µg/ml), <i>A. niger</i> (0.15-2 µg/ml), <i>C. albicans</i> (0.5-64 µg/ml) | |
| 270 | Burkholdine 1215 | | | |
| 271 | Occidiofungin A | | <i>R. solani, A. fumigatus, A. niger, M. gypseum, T. mentagrophytes</i> , <i>A. alternata, M. phaseolina, G. candidum, P. spinosum, P. ultimum</i> (1-8 µg/ml) | |
| 272 | Occidiofungin B | | <i>Burkholderia contaminans</i> soil sample | in the intracellular actin cable |
| 273 | Occidiofungin C | | <i>MS14</i> | 104- 105 |
| 274 | Occidiofungin D | | | |

| | | | | | | | | | |
|------------|---------------|--|--|--|--|---|--|----------------------------|---|
| 275 | Gausemycin A | | <i>Streptomyces</i> sp. INA-Ac-5812 | <i>Staphylococcus</i> sp. (0.125-1 µg/ml) | - | 106 | | | |
| 276 | Gausemycin B | | | | | | | | |
| | | 275 R=H 276 R=COCH₂CH₂NH₂ | | | | | | | |
| 277 | Hassallidin A | | <i>Hassallia</i> sp. B0207 | Sample from epilithic cyanobacterium (Orrido Clough, Bellano, Italy) | <i>A. fumigatus</i> (4.8 µg/ml), <i>C. albicans</i> (4.8 µg/ml), <i>C.</i> <i>neoformans</i> (8 µg/ml) | - | | | |
| 278 | Hassallidin B | | | | | | | | |
| 279 | Hassallidin C | 277 R ₁ OH | 278 R ₂ | R ₃ H | R ₄ H | 279 N/A | 107- 110 | | |
| 280 | Hassallidin D | 279 | 278 R ₁ | R ₂ | R ₃ H | 280 <i>Anabaena</i> sp. SYKE748A | <i>C. albicans</i> (1.5 µm), <i>C.</i> <i>krusei</i> (1.5 µm) cell membranes | | |
| 281 | Hassallidin E | 279 | 280 | 278 R ₁ | R ₂ | 281 H or acetyl | 280 <i>Planktothrix</i> serta PCC 8927 | <i>C. albicans</i> (23 µm) | - |

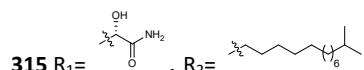
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| | | 281 | OH |  | H | | | | |
| 282 | Cepacidine A ₁ | | |  | <i>Pseudomonas cepacia</i> AF 2001. | Soil sample (Munichon, Kyunggi-Do, Korea.) | <i>C. albicans</i> , <i>C. glabrata</i> , <i>C. neoformans</i> , <i>S. cerevisiae</i> , <i>A. niger</i> , <i>M. canis</i> , <i>T. rubrum</i> (0.049-0.391 µg/ml) | - | 111 |
| 283 | Cepacidine A ₂ | | | | | | | | |
| | | 282 R=OH | 283 R=H | | | | | | |
| 284 | Macolacin | | |  | synthetic bioinformatic natural products | | Gram-negative bacteria (1-8 µg/ml), colistin- resistant pathogens (2-4 µg/ml) | lipid A | 112 |
| 285 | Biphenyl- macolacin | | |  | Semi-synthesis | | | | |
| 286 | Cilagycin | | |  | <i>Paenibacillus mucilaginosus</i> KNP414 and K02 | | Undecaprenyl phosphate and Undecaprenyl pyrophosphate (C55-PP) | | 113 |

| | | | | | | | | |
|------------|---------------|---|---|---------------------|---------------------|---|--|---|
| 287 | Iturin F1 |  | 287 R ₁ =CH ₃ , R ₂ =H, R ₃ =OH | | | | | |
| 288 | Iturin F2 |  | 288 R ₁ =H, R ₂ =CH ₃ , R ₃ =OH | <i>Bacillus</i> sp. | saline water sample | <i>A. flavus</i> , <i>N. crassa</i> , <i>C. albicans</i> , <i>P. griseofulvum</i> , | - | 114 |
| 289 | Iturin A8 |  | 289 R ₁ =CH ₃ , R ₂ =H, R ₃ =H | KCB14S006 | (Incheon, Korea) | <i>C. tropicalis</i> | - | 114 |
| 290 | Iturin A9 |  | 290 R ₁ =H, R ₂ =CH ₃ , R ₃ =H | | | (3.125-12.5 µg/ml) | | |
| 291 | Arylomycin A1 |  | | | | | | |
| 292 | Arylomycin A2 | R ₁ | R ₂ | R ₃ | R ₄ | | | |
| 293 | Arylomycin A3 | 291 | H | H | H |  | Gram-negative and gram-positive bacteria (0.25-16 µg/ml) | Signal Peptidase Type I (SPase I) |
| 294 | Arylomycin A4 | 292 | H | H | H |  | <i>Streptomyces</i> sp. TÜ 6075 | Soil sample (rain forest at Cape Coast, Ghana) |
| 295 | Arylomycin A5 | 293 | H | H | H |  | | |
| 294 | | 294 | H | H | H |  | | |
| 296 | Arylomycin B1 | 295 | H | H | H |  | | |
| 297 | Arylomycin B2 | 296 | NO ₂ | H | H |  | | |

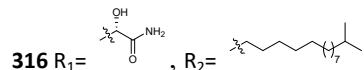
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|------------|---------------|------------|-----------------|---|----|---|-------------------------------------|
| 298 | Arylomycin B3 | 297 | NO ₂ | H | H |  | |
| 299 | Arylomycin B4 | 298 | NO ₂ | H | H |  | |
| 299 | Arylomycin B4 | 299 | NO ₂ | H | H |  | |
| 300 | Arylomycin B5 | 300 | NO ₂ | H | H |  | |
| 301 | Arylomycin B6 | 301 | NO ₂ | H | H |  | |
| 302 | Arylomycin B7 | 302 | NO ₂ | H | H |  | |
| 303 | Arylomycin C1 | 303 | H |  | OH |  | |
| 304 | Arylomycin C2 | 304 | H |  | OH |  | |
| 305 | Arylomycin C3 | 305 | H |  | H |  | |
| 306 | Arylomycin C4 | 306 | H |  | OH |  | <i>Streptomyces</i> sp. PTA-3546 |
| 307 | Arylomycin C5 | 307 | H |  | H |  | 116 |
| 308 | Arylomycin C6 | 308 | H |  | H |  | |
| 309 | Arylomycin C7 | 309 | H |  | H |  | |

| | | | | | | | |
|------------|---------------|------------|---|---|---|---|---|
| 310 | Arylomycin C8 | 310 | H |  |  | | |
| 311 | Arylomycin D | | |  | <i>Actinoplanes ferrugineus</i> MA738 | - | 79 |
| 312 | M131 | | |  | Total synthesis | - | |
| 313 | G0775 | | |  | | | 117 |
| 314 | Vinylamycin | 314 | |  | <i>Streptomyces</i> sp. MI982-63F1 | Soil sample (Institute of Microbial Chemistry, Shinagawa-ku, Tokyo, Japan) | <i>S. aureus, M. luteus, B.</i> <i>subtilis, C. bovis</i> (1.56-12.5 µg/ml) |

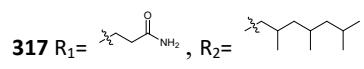
315 Rakicidin A



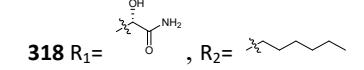
316 Rakicidin B



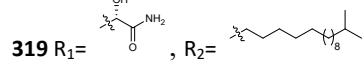
317 Rakicidin C



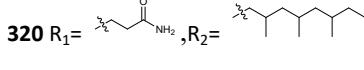
318 Rakicidin D



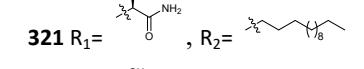
319 Rakicidin E



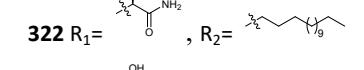
320 Rakicidin F



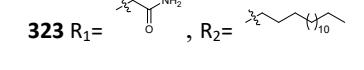
321 Rakicidin G



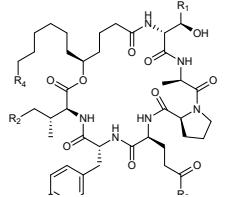
322 Rakicidin H



323 Rakicidin I



324 Simpicillium-tide J



325 Simpicillium-tide K

Micromonospor
a strain R385-2.

inactive

Streptomyces sp. (strain
GT 61042) - *B. subtilis* (50 µg/disk), *E.
coli*

Streptomyces sp. Marine sediment
MW064 sample

Micromonospora sp. TP-
A0860 - N/A

Streptomyces sp. marine sponge-
derived sample *B. subtilis*, *E. coli*
(25 µg/disk)

Micromonospor
a chalcea FIM - *C. difficile*, *P. anaerobius*,
P. gingivalis, *P. acnes*
(≤0.125-32 µg/ml)

A. versicolor (0.625
µg/disk), *C. australiensis*
(0.156 µg/disk)

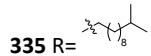
Micromonospora chalcea
FIM 02-523 -

inactive

119-
124

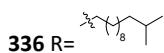
| | | | | | | | | |
|------------|----------------------|-------------------|-----------------------------------|-----------------------------------|---|--|--|---------|
| 326 | Simplicillium-tide L | | | | | | | |
| 327 | Simplicillium-tide N | 324 | R ₁ CH ₃ | R ₂ CH ₃ | R ₃ NH ₂ | R ₄ | A. solani (1.562-6.250 µg/disk), C. asianum (0.195-3.125 µg/disk) | |
| 328 | Simplicillium-tide O | 325 | CH ₃ | H | NH ₂ | | | |
| 329 | Verlamelin A | 326 | CH ₃ | H | NH ₂ | | C. miyabeanus (no MIC values), A. solani (no MIC values), F. oxysporum (2- | |
| | | 327 | CH ₃ | H | OH | | Lecanicillium sp. HF627 - 4 µg/disk), | 127 |
| 330 | Verlamelin B | 328 | CH ₃ | H | OCH ₃ | | C. cucumerinum (0.25-0.5 µg/disk), U. maydis (16->64 µg/disk) | |
| | | 329 | CH ₃ | H | NH ₂ | | | |
| | | 330 | H | H | NH ₂ | | | |
| 331 | Stechlisin B2 | | | | | | inactive | |
| 332 | Stechlisin F | | | Pseudomonas sp. FhG100052 | Sample from lake (Brandenburg, Germany) | M. catarrhalis (4 µg/ml) | - | 128-129 |
| 333 | Tensin | | | | | M. catarrhalis (32 µg/ml) | | |
| | | 331 R=H 332 R= | 333 R= | | | | | |
| 334 | Bacillopeptin A | | | 334 R= | Bacillus subtilis FR-2 | Sample from the rhizosphere of garlic (Fukagawa city, inactive | - | 130 |

335 Bacillopeptin B



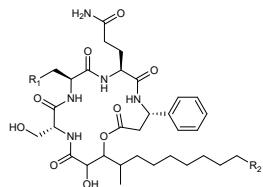
Hokkaido, Japan)

336 Bacillopeptin C



F. oxysporum, A. niger, A. oryzae, P. thomii, S. cerevisiae
(6.25-25 µg/ml)

337 Alveolaride A



P. oryzae (2 µg/ml), *U. maydis* (0.4 µg/ml), *Z. tritici* (1 µg/ml)

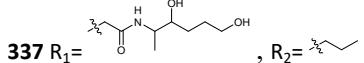
338 Alveolaride B

Microascus alveolaris strain PF1466

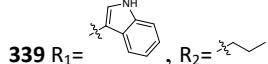
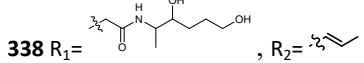
Soil sample (Okinawa Prefecture, Japan)

- 131

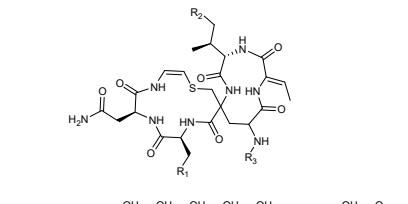
339 Alveolaride C

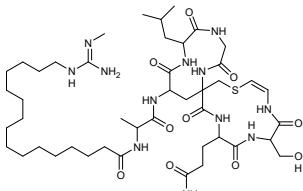
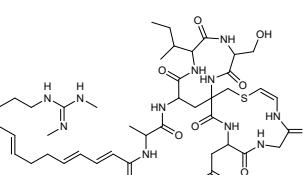


inactive



| | | | | | |
|------------|------------------|----------------|--|---|--|
| 340 | Bacilotetetrin A | | Marine sediment sample (Gageocho reef, Republic of Korea) | MRSA (8-32 µg/ml) | |
| 341 | Bacilotetetrin B | | | | |
| 342 | Bacilotetetrin C | | <i>Bacillus subtilis</i> 109GGC020 | | 132- 133 |
| 343 | Bacilotetetrin D | | marine sponge sample (Gageo reef, Republic of Korea) | <i>M. hyorhinis</i> (31 µg/ml) | |
| 344 | Bacilotetetrin E | | | | |
| 345 | Sclerotiotide A | | | | |
| 346 | Sclerotiotide B | | <i>Aspergillus sclerotiorum</i> PT06-1 | Marine sample (Putian Sea Salt Field, Fujian, China) | <i>C. albicans</i> (3.8-30 µm) |
| 347 | Sclerotiotide F | R ₁ | R ₂ | R ₃ | |
| 348 | Sclerotiotide M | 345 | H | H | |
| 349 | Sclerotiotide N | 346 | H | Me | <i>Aspergillus insulicola</i> |
| | | 347 | H | Me | a sample isolated from an unidentified sponge (Antarctic) |
| | | | | | <i>B. cereus, P. species, E. tarda, V. parahemolyticus, B.</i> |

| | | | | | |
|------------|-----------------|----------------|---|--|---|
| | 348 | H | Me |  | <i>subtilis</i> (1.56-25μm) |
| 350 | Sclerotiotide O | | | | |
| | 349 | H | Me |  | |
| | 350 | Me | Me |  | |
| 351 | Goadvionin A1 | | | | |
| 352 | Goadvionin A2 | | | $X_1 = \text{[Chemical structure of } X_1\text{]}$ | |
| 353 | Goadvionin A3 | | | $X_2 = \text{[Chemical structure of } X_2\text{]}$ | inactive |
| 354 | Goadvionin A4 | | | $X_3 = \text{[Chemical structure of } X_3\text{]}$ | <i>Streptomyces</i> sp. TP-A0584 |
| | | R ₁ | R ₂ | R ₃ | 136 |
| 355 | Goadvionin B1 | 351 |  | H | X ₁ |
| 356 | Goadvionin B2 | 352 |  | H | X ₂ |
| | | 353 |  | H | X ₃ |
| | | | | | <i>S. aureus</i> (6.4 μg/ml), <i>B.</i> <i>subtilis</i> (3.2 μg/ml), <i>M.</i> <i>luteus</i> (3.2μg/ml) |

| | | | | | | |
|------------|---------------|------------|---|---|----------------|---|
| 357 | Goadvionin B3 | 354 |  | H | X ₄ | |
| | | 355 |  | CH ₃ | X ₁ | inactive |
| 358 | Goadvionin B4 | 356 |  | CH ₃ | X ₂ | |
| 359 | Goadpeptin A | 357 |  | CH ₃ | X ₃ | |
| | | 358 |  | CH ₃ | X ₄ | N/A |
| 360 | Goadpeptin B | 359 |  | H | H | |
| | | 360 |  | CH ₃ | H | |
| 361 | Microvionin | |  | <i>Microbacterium arborescens</i> 5913 | - | MRSA (<0.46µg/ml), <i>S. pneumoniae</i> (<0.15 µg/ml) |
| 362 | Nocavionin | |  | <i>Nocardia terpenica</i> | - | N/A |

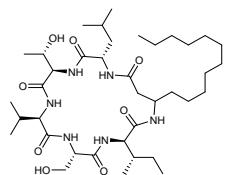
| | | | | | | |
|------------|---------------|--|--------------------------------------|--|--|---------|
| 363 | Fusaricidin A | | | | | |
| 364 | Fusaricidin B | | <i>Bacillus polymyxa</i> KT-8 | - | <i>S. aureus, M. luteus, B. subtilis, F. oxysporum, A. niger, A. oryzae, P. thomii</i> (<0.78-3.12 µg/ml) | 138-139 |
| 365 | Fusaricidin C | | | | σ (W)-regulated proteins | |
| 366 | Fusaricidin D | | | | | |
| 367 | Gacamide A | | <i>Pseudomonas fluorescens</i> PfO-1 | Genome Mining and Repair of the Defective GacA Regulator | <i>A. crystallopoietes</i> (32 µg/ml) | 140 |
| 368 | Bacaucin | | <i>Bacillus subtilis</i> CAU21 | - | MRSA (4µg/ml), VRE (16 µg/ml) | 141-142 |

| | | | | | |
|------------|---------------|--|--|--|--|
| 369 | Bacaucin-1 | | Semi-synthesis | <i>S. aureus</i> (4 µg/ml) | cell membranes |
| 370 | Bacaucin-1a | | - | GMP synthase | |
| 371 | Brevicidine | | <i>Brevibacillus laterosporus</i> DSM 25 | MRSA (2 µg/ml) | RNA polymerase |
| 372 | Laterocidine | | <i>Brevibacillus laterosporus</i> ATCC9141 | <i>E. coli</i> , <i>P. aeruginosa</i> , <i>A. baumannii</i> , <i>K. pneumoniae</i> , and <i>E. cloacae</i> | LPS 143- 144 |
| 373 | Brevicidine B | | <i>Brevibacillus laterosporus</i> DSM 25 | (1-16 µg/ml) | cell membrane, proton motive force of Gram- Negative Bacteria |
| 374 | SyCPA 2 | | synthetic- bioinformatic natural product | found in the genomes of eight species | Gram-positive bacteria, <i>A. baumannii</i> , <i>E. cloacae</i> (4-64 µg/ml) |
| | | | | - | 145 |

375 SyCPA 4

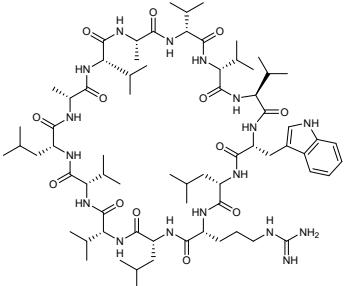
The meso-diaminopimelic acid moiety

376 SyCPA 116



376

377 SyCPA 153



377

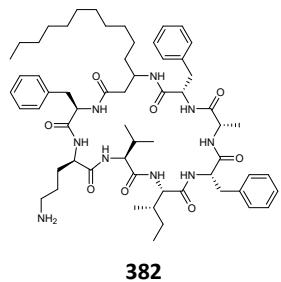
synthetic-bioinformatic natural product

found in the genomes of eight species

protein hydrolase ClpP

| | | |
|-------------------------|----------------|--|
| 378 SyCPA 12 | 378 | <p>cell membranes as cationic peptides</p> |
| 379 SyCPA 63 | 379 | <p>Gram-positive bacteria, Gram-negative bacteria (2-64 µg/ml) cell membrane</p> |
| 380 SyCPA 102 | | <p>synthetic- bioinformatic natural product</p> <p>found in the genomes of eight species</p> |
| 381 SyCPA 123 | | <p>cell membranes as cationic peptides</p> |

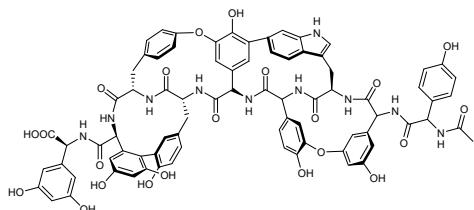
382 SyCPA 144



382

5. Other small-molecular antimicrobial peptides

383 Corbomycin



Streptomyces
sp. WAC01529

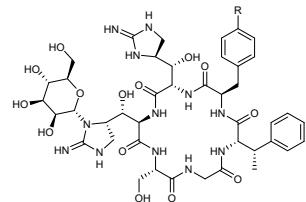
Alberta, Canada

Gram-positive bacteria
(0.5-4 $\mu\text{g/ml}$)

peptidoglycan
metabolism

146

384 Mannopepti-
mycin α



Streptomyces
hygroscopicus
LL-AC98

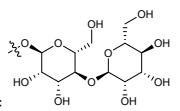
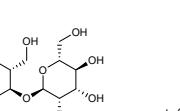
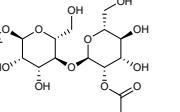
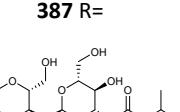
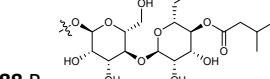
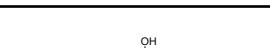
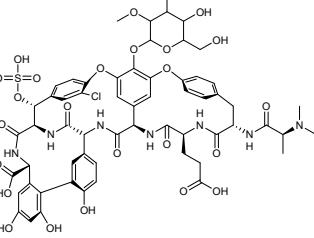
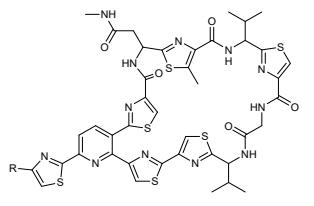
inactive

lipid II

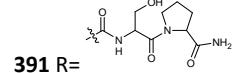
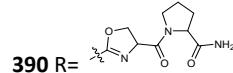
147

385 Mannopepti-
mycin β

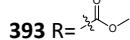
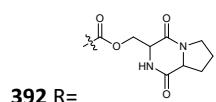
S. aureus, *S. hemolyticus*,
B. subtilis, *M. luteus*
(1-64 $\mu\text{g/ml}$)

| | | | | | | | | |
|------------|-----------------------------|---|--|---|--|---|-----|--|
| 386 | Mannopepti-mycin γ |  | 384 R= |  | 385 R=OH | | | |
| 387 | Mannopepti-mycin δ |  | 386 R= |  | 387 R= |  | | |
| 388 | Mannopepti-mycin ϵ |  | 388 R= |  | | | | |
| 389 | Pekiskomycin |  | <i>Actinomycetes</i> , coded WAC1420 and WAC4229 | - | VRE (no MIC value) | - | 148 | |
| 390 | Amythiamicin A |  | <i>Amycolatopsis</i> sp. MI481-42F4 | Soil sample (Nerimaku, Tokyo, Japan) | <i>S. aureus</i> , MRSA, <i>M. luteus</i> , <i>B. anthracis</i> , <i>B. subtilis</i> , <i>B. cereus</i> , <i>C. bovis</i> (0.32-5.12 μ m) | bacterial elongation factor Tu (EF-Tu) | 149 | |
| 391 | Amythiamicin B | | | | | | | |

392 Amythiamicin C

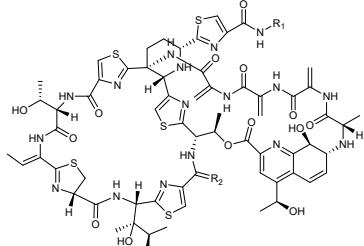


393 Amythiamicin D



394 Saalfelduracin A

S. aureus (0.25 µg/ml), *E.*
faecium (0.12 µg/ml), *B.*
anthracis (0.25 µg/ml)



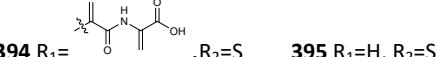
395 Saalfelduracin B

mycolatopsis
saalfeldensis
NRRL B-24474

150-
151

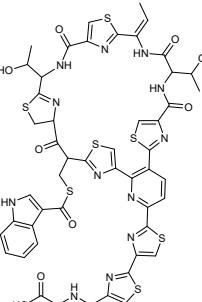
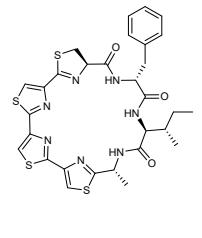
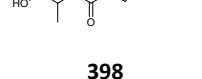
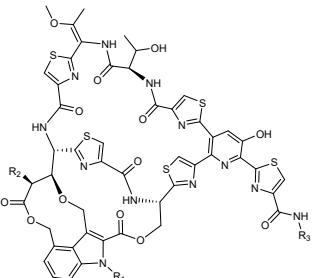
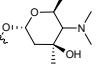
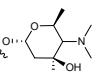
396 Saalfelduracin C

N/A



397 Saalfelduracin
D



| | | | | | | | | |
|------------|------------------|---|---|---|---|---|---|-----|
| 398 | Lactocillin |  |  | <i>Lactobacillus gasseri</i> JV-V03 | human urinary system | <i>S. aureus, E. faecalis, C. aurimucosum, G. vaginalis, S. sanguinis, S. sobrinus and S. mutans</i> (42-425 nM) | - | 152 |
| 399 | Marthiapeptide A |  |  | <i>Marinactinospora thermotolerans</i> SCSIO 00652 | Marine sediment (South China Sea) | <i>M. luteus, S. aureus, B. subtilis, B. thuringiensis</i> (2.0-8.0 µg/ml) | - | 153 |
| 400 | Nocathiacin I |  | | | | | | |
| 401 | Nocathiacin II |  | | <i>Nocardia</i> sp. WW-12651 | Soil sample (New Mexico, USA) | <i>S. pneumoniae, E. faecalis, E. faecium, S. aureus, S. epidermidis, S. haemolyticus, M. catarrhalis</i> | - | 154 |
| 402 | Nocathiacin III | R ₁ | R ₂ | R ₃ | | | | |
| 400 | OH |  |  |  | | | | |
| 403 | Nocathiacin IV | 400 | H |  |  |  | | |

| | | | | | | | | | |
|------------|-------------|------------|----|----|---|---|---|--|-----|
| 404 | Thiazomycin | 402 | OH | OH | | <i>Amycolatopsis fastidiosa</i> MA7332 | - | <i>Gram-positive bacteria</i> (no MIC values) | 155 |
| | | 403 | OH | | H | | | | |
| | | 404 | OH | | | | | | |

Reference

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