Table S1 Specification of new APD BGCs.

| | Organism | Apd1 accession | A-domain accession | Predicted APD |
|---|---|---|---|---|
| **A. Putative PBDs** | | | | |
| TOM | *Streptomyces bungoensis* | WP_061926485.1 | WP_061926494.1 | DH-EPL |
| | *Streptomyces phaeoluteigriseus* | OJT48496.1 | OQD56811.1 | DH-EPL |
| | *Streptomyces regensis* | KMS87272.1 | KMS87275.1 | DH-EPL |
| | *Streptomyces antibioticus* NRRL B-2032 | WP_051816305.1 | KOG74888.1 | DH-EPL |
| | *Streptomyces purpureus* | WP_040875304.1 | WP_019884141.1 | DH-EPL |
| | *Streptomyces* sp. NRRL B-1140 | WP_053671525.1 | WP_053671522.1 | DH-EPL |
| LIM | *Streptomyces sclerotialus* | WP_037773342.1 | WP_037773348.1 | DH-EPL |
| SIB | *Actinomadura echinospora* | SEG83572.1 | SEG83667.1 | DH-EPL |
| | *Streptomyces uncialis* | WP_073788394.1 | WP_073789160.1 | DH-PPL |
| | *Streptomyces* AmelKG-E11A | SCK10057.1 | SCK09874.1 | DH-PPL |
| | *Couchioplanes caeruleus* | WP_071803239.1 | WP 071803261.1 | DH-PPL |
| | *Micromonospora echinospora* | SCF40038.1 | SCF39935.1 | DH-PPL |
| | *Dermacoccus* sp. PE3 | WP_052947174.1 | WP_047312981.1 | DH-EPL/**8** |
| | *Nocardiopsis prasina* | WP_017545372.1 | WP_040694105.1 | DH-PPL |
| ANT | *Actinokineospora enzanensis* | WP_018681043.1 | WP_018681051.1 | DH-PPL |
| | *Nocardia tenerifensis* I | WP_040743483.1 | WP_040743488.1 | DH-PPL |
| | *Nocardia brasiliensis* | WP_014985053.1 | WP_014985045.1 | DH-PPL |
| | *Nocardia vulneris* | WP_043667451.1 | WP_043667671.1 | DH-PPL |
| POR | *Amycolatopsis jejuensis* | WP_033289431.1 | WP_033289433.1 | DH-PPL |
| **B. Putative non-PBD compounds** | | | | |
| 1,2 | *Streptomyces avermitilis* | WP_037650540.1 | 0/4 | APD **2/3** |
| | *Actinoplanes utahensis* | WP_043526719.1 | 0/6 | |
| 1,2,6 | *Streptomyces* sp. W007 | WP_007460155.1 | EHM24066.1 /6 |  |
| | *Streptomyces avicenniae* | WP_052847609.1 | 0/0 | |
| | *Amycolatopsis mediterranei* | YP_003767687.1 | 0/0 | |
| | *Nocardia tenerifensis* II | WP_051187886.1 | WP_051187885.1(1) /6 | |
| | *Streptomyces* sp. NRRL B-1347 | WP_051854982.1 | WP_030677493.1 /5 | |
| 1,2,3,4 | *Salinispora arenicola* | WP_051422804.1 | ?/? | APD **5** |
| 1,2,4,6 | *Micromonospora chokoriensis* | WP_030487095.1 | WP_036391166.1 /8 |  |
| | *Streptomyces mobaraensis* | WP_004940943.1 | WP_040888422.1 (2)/6 | |
| | *Streptomyces catenulae* | WP_030283633.1 | WP_037678228.1 (2)/4 | |
| 1,2,4,5,6 | *Streptomyces* sp. CNS654 | WP_050486887.1 | WP_050486890.1 (2)/4 | EPL, DH-EPL |
| | *Streptomyces scabrisporus* | WP_020555671.1 | WP_052174032.1 (2)/4 | |
| | *Streptomyces* sp. NRRL WC-3742 | WP_031068416.1 | WP_051836849.1 (2)/4 | |
| 1,2,3,4,6 | *Streptomyces antibioticus* DSM 40234 | WP_059197633.1 | KUN18767.1 (2)/3 | DH-PPL$_h$ |
| | *Amycolatopsis alba* | WP_039795848.1 | 0/3 | |
| | *Kibdelosporangium* sp. MJ126-NF4 | CTQ98696.1 | 0/1 | |
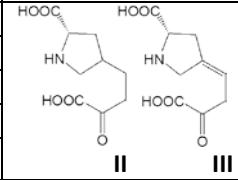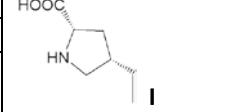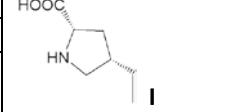
GenBank accession numbers of putative Apd1 and A-domain coding sequences used for the construction of phylogenetic trees in Fig. 9 and Fig. 10. The order of the A-domain used for the tree construction in respective NRPS protein chain (when applicable) is presented in brackets behind the A-domain accession number. Total number of A-domains identified in respective BGC is behind the slash. The question mark means that the length of available contig does not allow determining the presence/absence of the A-domain in the BGC with a sufficient certainty.