

Acyl-Chain Elongation Drives Ketosynthase Substrate Selectivity in *trans*-Acyltransferase Polyketide Synthases**

Matthew Jenner, José Pedro Afonso, Hannah R. Bailey, Sarah Frank, Annette Kampa, Jörn Piel,* and Neil J. Oldham*

Abstract: Type I modular polyketide synthases (PKSs), which are responsible for the biosynthesis of many biologically active agents, possess a ketosynthase (KS) domain within each module to catalyze chain elongation. Acylation of the KS active site Cys residue is followed by transfer to malonyl-ACP to yield an extended β -ketoacyl chain (ACP = acyl carrier protein). To date, the precise contribution of KS selectivity in controlling product fidelity has been unclear. Six KS domains from *trans*-acyltransferase (*trans*-AT) PKSs were subjected to a mass spectrometry based elongation assay, and higher substrate selectivity was identified for the elongating step than in preceding acylation. A close correspondence between the observed KS selectivity and that predicted by phylogenetic analysis was seen. These findings provide insights into the mechanism of KS selectivity in this important group of PKSs, can serve as guidance for engineering, and show that targeted mutagenesis can be used to expand the repertoire of acceptable substrates.

Polyketide synthases (PKSs) are responsible for the production of a vast array of biologically active compounds.^[1] All PKSs build up polyketide products through a series of chain-elongation steps, and they are classified into types based upon their architecture. Bacterial type I modular PKSs are large multidomain enzyme complexes. Each module is dedicated to one round of chain elongation and the subsequent processing of its particular intermediate. The array of modules has been likened to a production line, with intermediates passed along in sequence. Within a PKS module, a single cycle of biosynthetic chain elongation minimally requires the activity of an acyltransferase (AT) to supply a malonyl or related extender unit, a ketosynthase (KS) domain to catalyze a Claisen-type chain elongation between the extender and growing acyl chain, and an acyl carrier protein (ACP) domain to tether the intermediates to the PKS through a thioester link

(Scheme 1 a).^[2] Chain elongation can be followed by modification of the β -keto product by processing domains such as ketoreductases (KR), dehydratases (DH), and enoylreductases (ER).^[3] These molecular factories therefore offer the prospect of novel bioactive natural products through rational engineering strategies,^[4] but questions remain as to how “acceptable” intermediates are recognized by PKS domains.

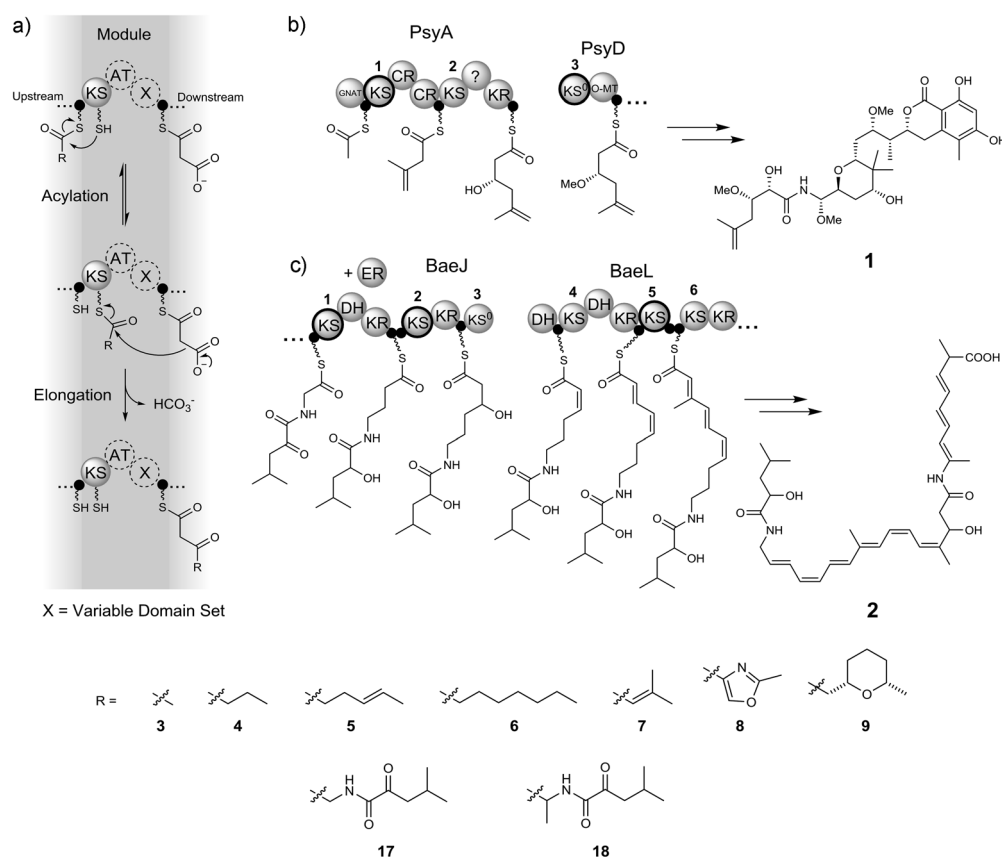
In “textbook” PKSs, such as that responsible for erythromycin biosynthesis, there is usually a 1:1 correspondence between PKS architecture and product structure. This principle of co-linearity has greatly assisted the assignment of each product to its synthase.^[5] PKSs that fall into this category are termed *cis*-AT PKSs, owing to the presence of an integral AT domain within each module. The *trans*-AT PKSs are an architectural variant of type I synthases that utilize separate AT enzymes.^[6] They often incorporate non-canonical modules and novel enzymatic domains, which results in poor biosynthetic assignment of clusters when using the co-linearity rules referred to above.^[7] *trans*-AT systems constitute approximately 40% of all bacterial multimodular PKSs^[8] and represent a major, but poorly characterized, enzyme class that is of high relevance for drug discovery.

One proposed mechanism for the maintenance of polyketide structural integrity is based on substrate specificity of the KS domains. Previous work on the *cis*-AT PKSs responsible for the biosynthesis of erythromycin and its relatives has revealed that unnatural substrates were able to acylate a KS domain, but no elongated product was observed to be released by a downstream thioesterase.^[9] It was suggested that the intermediate stalled on the KS domain. Clear evidence for a KS gatekeeper role has been found in the iterative *cis*-AT PKS that produces aureothin.^[10] By contrast, some chemobiosynthetic studies in which the PKS is fed a non-natural acyl starter unit have successfully produced polyketide analogues, and attempts to engineer artificial fusions of modules from eight *cis*-AT PKSs resulted in competent enzymatic assemblies, thus indicating more relaxed KS substrate selectivity in these cases.^[11] Recent work on pikromycin module 5 has provided new structural insights into the dynamics of the ACP domain within a module.^[12] It showed that the KR domain undergoes a large conformational change upon acylation, and that the position of the ACP domain within the module is dependent upon the degree of processing of its acyl chain. This mechanism may contribute to PKS selectivity by preventing access of the incorrect substrate to the downstream KS. The precise role of KS domains from *cis*-AT PKSs in controlling product fidelity remains unclear.

[*] M. Jenner, Dr. J. P. Afonso, H. R. Bailey, Dr. N. J. Oldham
School of Chemistry, University of Nottingham
University Park, Nottingham NG7 2RD (UK)
E-mail: neil.oldham@nottingham.ac.uk
S. Frank, Dr. A. Kampa, Prof. Dr. J. Piel
Institute of Microbiology
Eidgenössische Technische Hochschule (ETH) Zurich
Wolfgang-Pauli-Strasse 10, 8083, Zurich (Switzerland)

[**] We are grateful for funding from the Leverhulme Trust (RPG-2012-578) to J.A. and N.J.O., from the Biotechnology and Biological Science Research Council (BBSRC) for a studentship to M.J., and from the DFG (PI 430/8-1) and the EU (BlueGenics) to J.P.

Supporting information for this article is available on the WWW under <http://dx.doi.org/10.1002/ange.201410219>.



Scheme 1. KS catalysis and predicted substrates of the Psy and Bae KS domains. a) The catalytic cycle of a KS domain. Acylation by an upstream ACP loads the KS with an acyl intermediate, followed by elongation through a Claisen condensation between the acyl intermediate and a malonyl unit. In *cis*-AT PKSs, the AT domain is integral to the PKS, whereas in *trans*-AT systems, this activity is supplied by a separate AT domain. X represents optional domains. b) Partial proposed biosynthetic scheme for psymberin (**1**). c) Partial proposed biosynthetic scheme for bacillaene (**2**). KS: ketosynthase; KS⁰: non-elongating ketosynthase; KR: ketoreductase; DH: dehydratase; CR: crotonase (also known as enoyl-CoA dehydratase, ECH); O-MT: O-methyltransferase; C: NRPS condensation domain; A: NRPS adenylation; GNAT: acetyl-loading AT; and ●: ACP domains. KS domains are numbered and those used in this study are circled in bold.

In *trans*-AT PKSs, the situation is believed to be rather different. Here, KS domains have been shown to be closely correlated, at the sequence level, with their predicted substrates.^[13] Phylogenetic analysis gives rise to a series of KS clades, each linked to a specific types of intermediate (e.g., β -keto, β -hydroxy, enoyl, etc.). No such correlation was found for *cis*-AT PKSs. This approach provides improved functional prediction of *trans*-AT biosynthetic clusters compared to the co-linearity rules, thus suggesting that KS substrate selectivity is an important property of *trans*-AT PKSs. To test these predictions, we previously examined the initial acylation step of *trans*-AT KSs (Scheme 1 a). The specificity seen was not as well defined as the phylogenetic grouping might suggest.^[14] We suspected that further selectivity might be afforded at the elongation step of the KS-catalyzed reaction, in which the acyl chain is irreversibly transferred from the KS to ACP-bound malonate to form a new C–C bond. Currently, no conclusive data on the relative selectivity of these two steps exist for KSs from either *cis*- or *trans*-AT PKSs.

To provide new insights into the substrate selectivity exhibited during the elongation step of KS-catalyzed poly-

ketide biosynthesis in *trans*-AT PKSs, a range of KS domains from the psymberin (Psy) and bacillaene (Bae) PKSs^[15] were examined.

A new mass spectrometry based assay was developed to quantify ACP-bound elongated β -ketoacyl chains arising from the incubation of free malonyl-ACP with a pre-acylated KS domain (see the Supporting Information for details). A productive KS-catalyzed reaction results in the detection of β -ketoacyl-ACP. Quantification was made possible by the addition of an alkyl-ACP standard at the end of the incubation. Chain elongation catalyzed by PsyA KS1 was analyzed by using this assay. The natural substrate for this KS is the acetyl chain, which is predicted to be converted into an acetoacetyl unit (Scheme 1 b). Following incubation of acetylated PsyA KS1 with malonyl-ACP, tandem MS activation of the ACP-bound derivatives revealed the presence of elongated acetoacetyl-ACP, with an

associated decrease in malonyl-ACP, through detection of the ejected phosphopantetheinyl (PPant) ions (Figure 1, Figure S5 in the Supporting Information). PsyA KS1 is located in phylogenetic clade VI with other acetyl-accepting KS domains (Scheme 1 b, Figure S14). Previous work has shown that, functionally, PsyA KS1 is capable of accepting a range of substrates at the acylation stage.^[14a] This was tentatively attributed to the lack of evolutionary pressure upon the domain to confer selectivity towards an acetyl unit, owing to the presence of a highly specific upstream N-acetyltransferase (GNAT) loading domain.^[16] A set of seven simple acyl *N*-acetylcysteamine (SNAC) thioesters (**3–9**) were screened against Psy KS1 for elongation activity by first acylating the KS domain, and then incubating the product with malonyl-ACP according to the described assay method. PsyA KS1 showed a clear preference for elongation of the acetyl unit (**3**), and the longer carbon chains (**4–6**) were disfavored (Figure 2 a, Figure S7–13). There was no observable elongation for the β -methyl substrate (**7**), despite initial acylation of the KS. Furthermore, no elongation was observed with oxazolyl (**8**) or pyranlyl (**9**) substrates, which are moieties

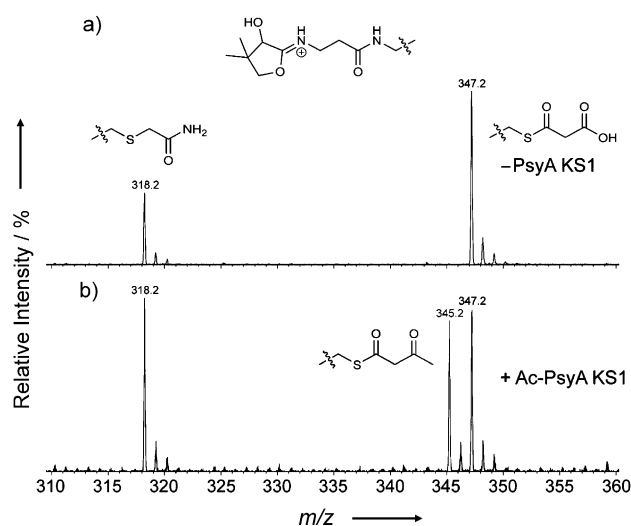


Figure 1. KS-catalysed production of β -ketoacyl chains. MS/MS spectra of the activated 7^+ PsyA ACP₃ species following acetyl elongation reactions in the absence (a) and presence (b) of PsyA KS1. Production of the acetoacetyl-ACP (PPant ion m/z 345.2) is only seen after incubation with the acetyl-KS domain. Internal standard (PPant ion m/z 318.2) was added after the elongation reaction at a final concentration of 10 μ M.

present in various PKS intermediates.^[17] Overall, these results suggest not only that PsyA KS1 imposes selectivity at the elongation step of its catalytic action, but that the selectivity is in excellent agreement with sequence-based phylogenetic predictions (Figure S14).^[13]

The non-elongating domain PsyD KS3⁰ (Scheme 1 b) was employed as a control for these experiments since it lacks an essential active-site His residue required for the decarboxylation of malonate^[7] and was therefore expected to yield no elongated product. Incubation of malonyl-ACP with PsyD KS3⁰ acylated with a range of acyl groups (3–9) generated no observable β -ketoacyl products (10–16), despite effective acylation of the KS domain.^[14a]

In contrast to PsyA KS1, BaeJ KS2 and BaeL KS5 are predicted to accept and elongate much longer acyl chains (Scheme 1 c). In phylogenetic terms, BaeJ KS2 is located in clade V (Figure S14) with other similar KS domains predicted to accept either fully saturated or β,γ -olefinic unbranched acyl chains. BaeL KS5 is located in clade IX and is also believed to accept unbranched intermediates (Scheme 1 c, Figure S14). Our previous acylation studies on BaeJ KS2 and BaeL KS5^[14a,17] indicated that unbranched acyl chains were clearly favored. Elongation assays conducted on BaeJ KS2 revealed a remarkably different substrate profile from that seen for PsyA KS1, with the longer acyl chains preferentially elongated to form their β -ketoacyl equivalents (11–13; Figure 2 b). By contrast, the short acetyl chain was elongated only poorly by BaeJ KS2 to yield little of the acetoacetyl-ACP (10).

The X-ray structure of BaeJ KS2, acylated with its natural substrate, shows that the entire 10-atom chain is accommodated within a relatively hydrophobic binding pocket.^[18] Presumably, favorable interactions between longer carbon chains and this pocket account for the observed substrate

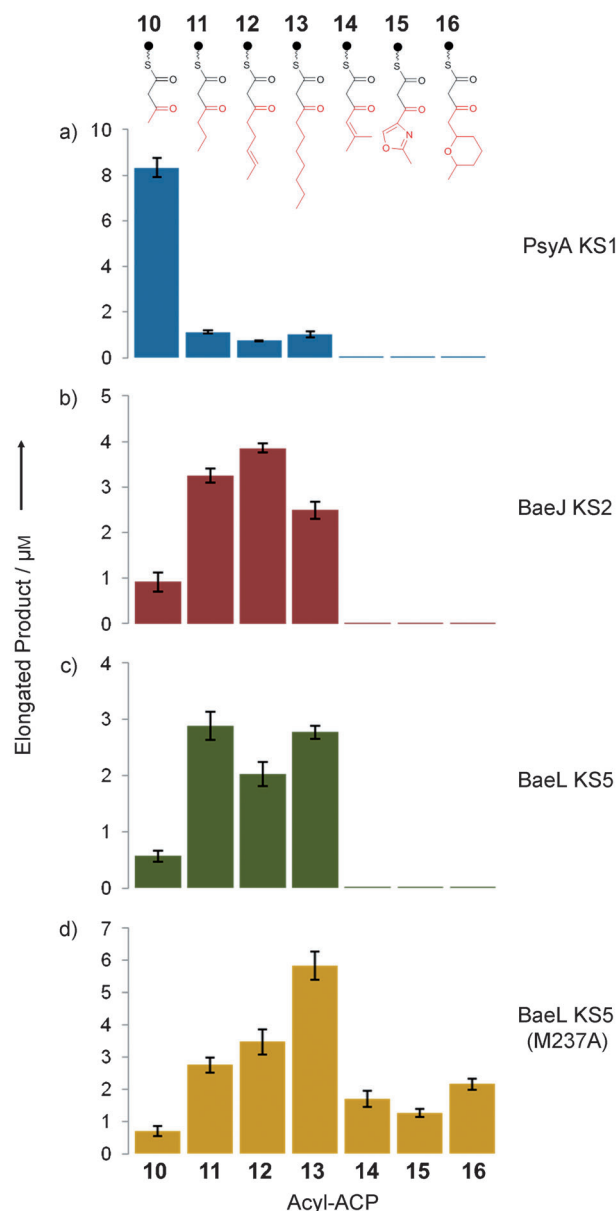


Figure 2. Elongation-based substrate selectivity profiles of KS domains. Elongation selectivity profiles for Psy and Bae KS domains were obtained by measuring the generation of β -ketoacyl products (10–16).

preference of BaeJ KS2. A similar elongation profile was produced by BaeL KS5, with a clear preference for longer unbranched acyl chains (Figure 2 c). In agreement with previous acylation data, no elongation was observed for a β -Me substrate (7), as evidenced by the absence of product 14. Furthermore, the oxazolyl (8) and pyranlyl (9) substrates yielded no elongated product. Overall, these data demonstrate that both BaeJ KS2 and BaeL KS5 show a preference for substrates bearing longer acyl chains, and that both KSs were unable to catalyze the elongation of β -branched chains, as predicted by phylogenetic analysis.

Previously, we have shown that unlike the wild type (WT) form of BaeL KS5, the active-site mutant BaeL KS5(M237A) was able to accept a β -methyl branched acyl chain at the

acylation stage.^[14a] Whether this KS variant had the ability to process the bulkier substrate fully to yield elongated product **14** remained an open question. The elongation profile of BaeL KS5(M237A) revealed a similar trend to that of WT BaeL KS5 with regard to straight-chain acyl units, and preferential elongation of longer acyl chains was observed. However, the mutant was also found to be competent to elongate the β -methyl branched chain, as evidenced by the detection of β -ketoacyl-ACP (**14**) in the assay (Figure 2d). This suggests that the single Met $\rightarrow$ Ala point mutation in the active site of KS5 not only permits acylation by the β -methyl SNAC but also allows the elongation step to be catalyzed. Pleasingly, the bulky oxazolyl (**8**) and pyranlyl (**9**) substrates were also elongated by this KS variant. This functional modification of BaeL KS5 highlights the attractive possibility of creating engineered *trans*-AT PKSs harboring KS domains with non-native selectivity profiles.

BaeJ KS1 (Scheme 1c) was also subjected to the elongation assay. Phylogenetically, BaeJ KS1 is located in clade XVI (Figure S14) and should accept and elongate 2-amidoacetyl intermediates. The elongation profile of BaeJ KS1 revealed a categorical preference for 2-amidoacetyl substrates, as evidenced by the elongation of **17** and **18**, with preference shown for the glycine substrate. There was no observable elongated product for any acyl chains, which did not contain the 2-amidoacetyl functionality (**3–6**; Table S1 in the Supporting Information).

The elongation assay performed with PsyA KS1 revealed a clear preference for the natural acetyl substrate over longer acyl chains, which contrasts with the rather broad substrate profile described for the acylation step.^[14a] To investigate whether the apparent lack of selectivity during acylation was due to the use of simple SNAC substrate analogues in an artificially bimolecular reaction, we expressed and tested the PsyA *apo*-ACP1–KS1 didomain to provide an accurate representation of intramolecular ACP–KS transfer. When the ACP was loaded with either acetyl- or butyryl-PPant chains, from the corresponding Coenzyme A, this construct showed similar transfer of the two acyl groups from ACP1 to KS1 (see Figures S16 and S17 and the Supporting Information for details of the controls). This result shows that the selectivity of KS acylation, even within a native didomain, is lower than that of the subsequent elongation step.

Our finding that KS substrate selectivity at the second elongation step exceeds that of acyl loading highlights the potential problem of KS enzymatic stalling. In order to restore enzymatic activity, either the acyl chain must be hydrolyzed from the active site Cys, or the upstream ACP must deacylate the KS in a reversal of the initial acylation step. Once on the upstream ACP, the acyl chain may be removed from the ACP, possibly through the action of an acylhydrolase (AH) or by cleavage at the β -position, as seen in the mupirocin system.^[19] In theory, both mechanisms are plausible, but we are unaware of any clear evidence in the literature for reversibility of the KS acylation step in a stalled situation. In order to test the ability of the upstream ACP domain to deacylate the KS active site, the ACP1–KS1 didomain was again utilized. The KS1 active-site Cys residue was acetylated prior to loading the PPant chain onto the apo-

ACP1 domain (Figure S19). Intramolecular transfer of the acetyl chain from the KS1 domain to the PPant chain of ACP1 was detected by MS/MS analysis as shown in Figure S21, a result that demonstrates the inherent reversibility of ACP $\leftrightarrow$ KS acyl transfer (Scheme 1a). Control measurements ruled out other sources of PPant acylation (see the Supporting Information for details).

During polyketide biosynthesis, the maintenance of product fidelity requires a mechanism for intermodular transfer of the correct intermediate and in *trans*-AT PKSs, the hypothesis that KS domains fulfil a gatekeeper role has been proposed.^[10,17,19] In principle, KS selectivity could be manifest at the initial acylation step, at the C–C forming elongation step, or both. Our previous work, based on examining substrate tolerance during the KS acylation step, showed that some selectivity does exist at this step. However, the selectivity is not as strictly defined as phylogenetic analysis would predict. Herein, we show that a high level of selectivity is observed during the KS-catalyzed elongation step, and this selectivity is in line with that predicted phylogenetically. Moreover, by using the PsyA ACP1–KS1 didomain, we confirmed that relatively low selectivity is exhibited at the acylation step, even for a tethered substrate. Thioester bonds are high-energy linkages, which form and break rapidly in the presence of a thiol or thiolate through the process of transthioesterification.^[20] Acyl transfer between an ACP and the immediate downstream KS may thus be difficult to control, leading to relatively limited enzymatic selectivity and a potentially reversible process. Indeed, it has been observed that a large excess of SNAC thiol is able to remove an acyl group from the KS active site through transthioesterification.^[21]

The differential selectivity observed in the KS acylation and elongation steps does raise a potential problem: namely nonproductive acylation of the active site by a substrate incapable of being elongated. Providing that KS acylation is reversible, however, this problem can be overcome, since the acyl chain can be transferred back to the upstream module. The rate constant for back transfer from KS to upstream ACP has been measured for the *cis*-AT DEBS module 2 and was found to be very low, thus leading to the conclusion that acylation is practically irreversible.^[21] It should be borne in mind, however, that these observations were made for a productive substrate under steady-state conditions, and not for a stalled substrate incapable of elongation. Our findings with PsyA ACP1–KS1 demonstrate that KS acylation in this *trans*-AT PKS didomain is a reversible process (in the absence of a downstream malonyl-ACP), and that this mechanism may allow the unloading of nonproductive substrates from the KS domain.

In summary, we have shown that five KS domains from the *trans*-AT PKSs responsible for the biosynthesis of psymberin and bacillaene exhibit substrate preferences that are in agreement with those predicted by phylogenetic analysis of their sequences. These findings provide functional testing of the proposal that KS domains from *trans*-AT PKSs show selectivity for their intermediates. Moreover, we also show that this selectivity can be modulated by rational enzyme modification.

Received: October 18, 2014
Revised: November 10, 2014
Published online: December 21, 2014

Keywords: biosynthesis · ketosynthases · mass spectrometry · polyketides · polyketide synthases

-
- [1] D. J. Newman, G. M. Cragg, *J. Nat. Prod.* **2007**, *70*, 461–477.
- [2] a) R. J. Heath, C. O. Rock, *Nat. Prod. Rep.* **2002**, *19*, 581–596; b) Y.-M. Zhang, J. Hurlbert, S. W. White, C. O. Rock, *J. Biol. Chem.* **2006**, *281*, 17390–17399.
- [3] a) J. Staunton, J. K. Weissman, *J. Nat. Prod. Rep.* **2001**, *18*, 380–416; b) S.-C. Tsai, B. D. Ames in *Complex Enzymes in Microbial Natural Product Biosynthesis, Part B: Polyketides, Aminocoumarins and Carbohydrates* (Ed.: D. A. Hopwood), Academic Press, **2009**, p. 459; c) M. A. Fischbach, C. T. Walsh, *Chem. Rev.* **2006**, *106*, 3468–3496; d) C. Hertweck, *Angew. Chem. Int. Ed.* **2009**, *48*, 4688–4716; *Angew. Chem.* **2009**, *121*, 4782–4811.
- [4] M. Till, P. R. Race, *Biotechnol. Lett.* **2014**, *36*, 877–888.
- [5] a) S. Kapur, et al., *Proc. Natl. Acad. Sci. USA* **2012**, *109*, 4110–4115; b) C. Khosla, Y. Tang, A. Y. Chen, N. A. Schnarr, D. E. Cane, *Annu. Rev. Biochem.* **2007**, *76*, 195–221.
- [6] a) J. Piel, *Nat. Prod. Rep.* **2010**, *27*, 996–1047; b) Y. Q. Cheng, G. L. Tang, B. Shen, *Proc. Natl. Acad. Sci. USA* **2003**, *100*, 3149–3154.
- [7] T. Gulder, M. Freeman, J. Piel in *Topics in Current Chemistry*, Springer, Heidelberg, **2012**, pp. 1–53.
- [8] R. V. O'Brien, R. W. Davis, C. Khosla, M. E. Hillenmeyer, *J. Antibiot.* **2014**, *67*, 89–97.
- [9] K. Watanabe, C. C. C. Wang, C. N. Boddy, D. E. Cane, C. J. Khosla, *J. Biol. Chem.* **2003**, *278*, 42020–42026.
- [10] B. Busch, et al., *Angew. Chem. Int. Ed.* **2013**, *52*, 5285–5289; *Angew. Chem.* **2013**, *125*, 5393–5397.
- [11] a) H. G. Menzella, et al., *Nat. Biotechnol.* **2005**, *23*, 1171–1176; b) S. Murli, et al., *Appl. Environ. Microbiol.* **2005**, *71*, 4503–4509; c) J. R. Jacobsen, C. R. Hutchinson, D. E. Cane, C. Khosla, *Science* **1997**, *277*, 367–369.
- [12] a) S. Dutta, et al., *Nature* **2014**, *510*, 512–517; b) J. R. Whicher, et al., *Nature* **2014**, *510*, 560–564.
- [13] T. Nguyen, et al., *Nat. Biotechnol.* **2008**, *26*, 225–233.
- [14] a) M. Jenner, et al., *Angew. Chem. Int. Ed.* **2013**, *52*, 1143–1147; *Angew. Chem.* **2013**, *125*, 1181–1185; b) C. Kohlhaas, et al., *Chem. Sci.* **2013**, *4*, 3212–3217.
- [15] a) J. Moldenhauer, X. H. Chen, R. Borriss, J. Piel, *Angew. Chem. Int. Ed.* **2007**, *46*, 8195–8197; *Angew. Chem.* **2007**, *119*, 8343–8345; b) M. Bielitz, J. Pietruszka, *Angew. Chem. Int. Ed.* **2013**, *52*, 10960–10985; *Angew. Chem.* **2013**, *125*, 11164–11190; c) K. M. Fisch, et al., *Nat. Chem. Biol.* **2009**, *5*, 494–501.
- [16] L. Gu, et al., *Science* **2007**, *318*, 970–974.
- [17] a) B. Kusebauch, N. Brendel, H. Kirchner, H.-M. Dahse, C. Hertweck, *ChemBioChem* **2011**, *12*, 2284–2288; b) P. Pöplau, S. Frank, B. I. Morinaka, J. Piel, *Angew. Chem. Int. Ed.* **2013**, *52*, 13215–13218; *Angew. Chem.* **2013**, *125*, 13457–13460.
- [18] D. C. Gay, et al., *Structure* **2014**, *22*, 444–451.
- [19] a) K. Jensen, et al., *Chem. Biol.* **2012**, *19*, 329–339; b) J. Wu, et al., *ChemBioChem* **2008**, *9*, 1500–1508.
- [20] P. J. Bracher, P. W. Snyder, B. R. Bohall, G. M. Whitesides, *Origins Life Evol. Biospheres* **2011**, *41*, 399–412.
- [21] J. Q. Wu, K. Kinoshita, C. Khosla, D. E. Cane, *Biochemistry* **2004**, *43*, 16301–16310.
-