Phylogenomic analysis of type I polyketide synthase genes in pathogenic and saprobic ascomycetes

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Fungal type I polyketides (PKs) are synthesized by PK synthases (PKSs) and include well known secondary metabolites such as the anticholesterol drug lovastatin and the potent natural carcinogen aflatoxin. Other type I PKs are known to be virulence factors for some plant pathogens and pigments such as melanin. In this study, a phylogenomic approach was used to investigate the origin and diversity of fungal genes encoding putative PKSs that are predicted to synthesize type I PKs. The resulting genealogy, constructed by using the highly conserved PKS ketosynthase (KS) domain, indicated that: (*i*) Species within subphylum Pezizomycotina (phylum Ascomycota) but not early diverging ascomycetes, like *Saccharomyces cerevisiae* (Saccharomycotina) or *Schizosaccharomyces pombe* (Taphrinomycotina), had large numbers (7–25) of *PKS* genes. (*ii*) Bacteria and fungi had separate groups of *PKS* genes; the few exceptions are the likely result of horizontal gene transfer from bacteria to various sublineages of fungi. (*iii*) The bulk of genes encoding fungal PKSs fell into eight groups. Four groups were predicted to synthesize variously reduced PKs, and four groups were predicted to make unreduced PKs. (*iv*) Species within different classes of Pezizomycotina shared the same groups of *PKS* genes. (*v*) Different fungal genomes shared few putative orthologous *PKS* genes, even between closely related genomes in the same class or genus. (*vi*) The discontinuous distributions of orthologous *PKS*s among fungal species can be explained by gene duplication, divergence, and gene loss; horizontal gene transfer among fungi does not need to be invoked.

Type I fungal polyketide (PK) synthases (PKSs) are closely related to fatty acid synthetases (FASs) (1). Both are multifunctional enzymes with the same ancestral enzymatic domain structure, namely ketoacyl synthase (KS), acyl transferase (AT), ketoreductase (KR), dehydratase (DH), enoyl reductase (ER), and acyl carrier protein [also known as a phosphopantetheine attachment site (PP) domains]. The KS, AT, and PP domains are essential for both FASs and PKSs, whereas the KR, DH, and ER domains are present in all FASs, but some or all are absent in various PKSs. KR, DH, and ER domains catalyze, in a stepwise fashion, reduction of a keto to a hydroxyl group, dehydration of the hydroxyl to an enoyl group, and reduction of the enoyl to an alkyl group, respectively. PKSs that lack some or all of these domains produce partially reduced or fully oxidized PKs.

Fungal type I PKSs, like FASs, are monomodular enzymes; most are iterative and use their active sites repeatedly to synthesize a PK, adding a two-carbon molecule (i.e., a CoA ester) to the growing chain with each condensation. The noniterative fungal PKSs perform only one condensation cycle and make a diketide. Each one that has been characterized so far is encoded by a gene that resides in a gene cluster (genes adjacent along one stretch of a chromosome), along with a *PKS* gene encoding an iterative PKS (2, 3). The products of an iterative and a noniterative PKS are joined to make a branched PK. The diversity of PKs is generated, in part, through the use of the three optional PKS reducing domains.

Access to genomes of saprobic and pathogenic members of the Ascomycota allowed us to address the following questions regarding distribution and evolution of Type I *PKS* genes: (*i*) How many *PKS* genes are there in these genomes? (*ii*) Do type I *PKS* genes from fungi and bacteria fall into the same or different groups? (*iii*) How many subgroups of type I *PKS* genes are found in the Ascomycota? (*iv*) Do species in the different classes of Ascomycota share the same or have different subgroups of type I *PKS* genes? (*v*) What is the frequency of putative orthologs among distantly related fungi, including those that evolved independently as plant pathogens and among closely related species? (*vi*) Which evolutionary process can account for the phylogenetic distribution of *PKS* genes: gene duplication, divergence, gene loss, horizontal gene transfer (HGT), or all of these?

To address these questions, we performed phylogenetic analyses on the amino acid sequences of KS domains encoded by all previously characterized fungal *PKS* genes and by all putative *PKS* genes extracted from genomic sequences of five taxonomically diverse fungal species in the Ascomycota, subphylum Pezizomycotina (4) [the saprobe *Neurospora crassa* (5); the maize pathogens *Cochliobolus heterostrophus* (*Bipolaris maydis*) (6, 7) and *Gibberella moniliformis* (*Fusarium verticillioides*) (8); the cereal pathogen *Gibberella zeae* (*Fusarium graminearum*) (8); and the cosmopolitan dicot pathogen *Botryotinia fuckeliana* (*Botrytis cinerea*) (8)]. We also searched for *PKS* genes in the genomes of three earlier diverging ascomycetes [*Saccharomyces cerevisiae* (9), the plant pest *Eremothecium* (*Ashbya*) *gossypii* (10), (both in the Saccharomycotina), and the yeast saprobe *Schizosaccharomyces pombe* (11) (Taphrinomycotina)].

Materials and Methods

Detailed treatments of all section below are provided as *Supporting Materials and Methods*, which is published as supporting information on the PNAS web site.

DNA and Protein Genomic Databases. Four genomes were sequenced by Celera Genomics for the Torrey Mesa Research Institute (TMRI)/Syngenta: *B. fuckeliana* strain B05.10 (to ≈5× coverage), *C. heterostrophus* strain C4 (ATCC 48331) (to ≈5× coverage), *G. moniliformis* strain ATCC 38932 (FGSC 7600) (to ≈4× coverage), and *G. zeae* lineage 7 strain GZ3639 (12) (to ≈2× coverage). The shotgun sequence assemblies of these genomes were used for these studies, along with the genome

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Abbreviations: PK, polyketide; PKS, PK synthase; KS, ketoacyl synthase; AT, acyl transferase; DH, dehydratase; NPS, nonribosomal peptide synthetase; ME, methyl transferase; ER, enoyl reductase; KR, ketoreductase; PP, phosphopantetheine attachment site (acyl carrier protein of PKSs and thiolation of NPSs); AMP, adenylation; CON, condensation; HGT, horizontal gene transfer; TMRI, Torrey Mesa Research Institute; FAS, fatty acid synthase.

Data deposition: The sequences reported in this paper have been deposited in the GenBank database [accession nos. AY495643–AY495666 (*C. heterostrophus PKS2–25*), AY495606–AY495625 (*B. fuckeliana PKS1–20*), AY495591–AY495605 (*G. moniliformis PKS1–15*), AY495626–AY495641 (*G. zeae PKS1–16*), and AY495642 (*PKS1* from *Didymella maydis*)].

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sequences of *N. crassa* (5), *S. cerevisiae* (9), *E. gossypii* (10) (sequenced by Syngenta), and *S. pombe* (11). The protein databases for *C. heterostrophus*, *B. fuckeliana*, and *G. moniliformis* were compiled by using four gene models that were found to generate the largest numbers of predicted proteins: GENEMARK.HMM (13) (*Arabidopsis* and *Caenorhabditis* models), FGENESH (14) (dicot model), and GENSCAN (15) (*Arabidopsis* model). *N. crassa*, *S. cerevisiae*, and *S. pombe* protein databases are available at the National Center for Biotechnology Information.

PKS Gene Identification. To retrieve *PKS* genes or predicted proteins from each genome, we used the consensus sequence of the KS domain, the most highly conserved domain in type I PKSs and FASs (1), as a query in TBLASTN searches of the TMRI genome assemblies; in PSI-BLAST searches of the TMRI protein databases of *C. heterostrophus*, *B. fuckeliana*, and *G. moniliformis*; and in PSI-BLAST searches of the eukaryote protein database (www.ncbi.nlm.nih.gov/BLAST) for *N. crassa*, *S. cerevisiae*, and *S. pombe.* The PSI-BLAST searches were also used to retrieve all previously published fungal PKS protein sequences from National Center for Biotechnology Information.

PKS Gene Annotation. The protein sequences of the KS domains obtained from TBLASTN and PSI-BLAST searches were used as queries to retrieve the complete PKS protein sequences from the protein databases. The *C. heterostrophus*, *B. fuckeliana*, and *G. moniliformis* PKS-predicted sequences from each of the four protein databases were retrieved and aligned by CLUSTALW by using the amino acid substitution matrix BLOSUM62, implemented in MEGALIGN (DNASTAR, Madison, WI), and the protein predictions and corresponding DNA sequences were evaluated for their predicted introns. The predicted PKS proteins from *N. crassa* were also aligned to verify intron predictions. The predicted proteins were submitted to Hidden Markov Model searches, implemented in TIMELOGIC (TimeLogic, Carlsbad, CA), to determine their multidomain PKS protein structures.

KS-Domain Genealogy Construction and Evaluation. The predicted KS domains of all newly sequenced fungal genomes plus those from all previously published PKS protein sequences from ascomycete fungi, the homologous FASs from animals (1), and representative type I PKSs from bacteria (Table 1, which is published as supporting information on the PNAS web site) were aligned with CLUSTALW (Table 2, which is published as supporting information on the PNAS web site) and phylogenetically analyzed with neighbor joining and maximum parsimony in PAUP4.0b8 (Sinauer, Sunderland, MA), by using the settings given in *Supporting Materials and Methods*. The resulting KS-domain genealogy was evaluated to rank major clades and subclades of PKS enzymes. The criteria used to categorize proteins in major clades and subclades were moderate bootstrap support, similar domain structure, and similar chemical characteristics of the resulting PK products for those PKSs that have been previously characterized. KS-domain genealogy was also used to predict putative phylogenetic orthologs that are expected to encode enzymes of identical or nearly identical biochemical function (16, 17). The criteria used to predict proteins as orthologs were bootstrap values >80%, identical predicted domain structure (or nearly so), and chemical characteristics similar to those of the resulting PK product for those proteins whose product has been characterized previously. Putative orthologs were further supported by a KS-domain genealogy that was consistent with the currently understood organismal phylogeny (4), applicable when three or more orthologs are present. Alternative phylogenetic hypotheses were tested for significance with a Kishino–Hasegawa test (18). The hypothesis underlying the constraint tree is rejected if the difference in logarithm likelihood compared to the unconstrained tree divided by the SD (Ln L/SD) is >1.96 ($P \leq 0.05$) (19).

Results and Discussion

Species Within the Pezizomycotina Have Many _PKS_ Genes. The four newly sequenced genomes have large numbers of putative *PKS* genes: 15 in *G. moniliformis*, 16 in *G. zeae*, 20 in *B. fuckeliana*, and 25 in *C. heterostrophus* (Table 3, which is published as supporting information on the PNAS web site). The *PKS* genes in *G. zeae* were represented as fragments, due to the small contig size and many gaps in the 2× coverage; however, a search of the publicly available *G. zeae* genome {albeit a different strain [PH-1 (NRRL 31084, but the same lineage, lineage7)]} did not reveal additional *PKS* genes beyond those we identified in our 2× coverage. These numbers are greater than those of the saprobe *N. crassa*, which is thought to produce only one PK, namely PK-derived melanin, yet contains seven putative *PKS* genes, only one of which is a melanin-type *PKS* gene (5). By contrast, the three earlier-diverging ascomycetes (*S. pombe, S. cerevisiae*, and *E. gossypii*) lacked identifiable *PKS* genes, including those involved in pigment formation.

KS-Domain Genealogy and Prediction of PK Structure. KS-domain genealogy (Fig. 1) was used to infer the genealogy of type I PKSs. The predicted fungal and bacterial PKSs grouped in three main clades (20–22). Together, these three major clades grouped into a larger clade of type I PKSs, which was sister to the clade of FASs found in animals. All of the type I PKSs and FASs grouped into a larger clade, which was sister to the type II PKSs found in bacteria and to the bacterial and mitochondrial acyl-ACP synthetases (1). KS-domain genealogy suggested that the ancestral domain structure of type I PKSs was KS-AT-DH-ME-ER-KR-PP, because these domains were present, and in this order, in the PKS protein sequences in members of two of the three main clades of PKSs, one of which (the bacterial PKS clade) was in a basal position.

Two of these three main clades of microbial type I PKSs were identified as exclusively fungal and correlated with the two largest structural classes of fungal PKs: reduced and unreduced (1). Each main fungal PKS clade was further divided into four groups, each with a typical domain structure, depending on the loss of ancestral domains, or the gain of novel domains (mapped onto Fig. 1 and listed in Table 3). The third major clade included all bacterial PKSs, and within this clade were nested two small, additional fungal clades, the first of which comprised the 6-methylsalicylic acid synthases, and the second of which was a nonribosomal peptide synthetase (*NPS*)/*PKS* hybrid gene found in *C. heterostrophus*.

Fungal PKSs Producing Reduced PKs. The first main fungal clade included the PKSs that synthesize variously reduced, and usually linear, PKs (Fig. 1). The characterized PKs serve as precursors to toxins that are active in animals [e.g., lovastatin (2), citrinin (3), and fumonisin (23)] and to toxins that are active in plants [e.g., T-toxin (6), and PM-toxin (24)]. These reduced PKs frequently are synthesized from CoA thioesterified carboxylic acids other than acetyl and malonyl CoA, and the extent of keto-group processing varies from one condensation cycle to the next (1). In addition, one or more sites may be methylated by a ME domain (3, 25). However, many of the predicted PKSs in the PKS clade that produces reduced PKs have highly divergent and presumably nonfunctional ME domains.

The clade of PKSs that synthesize reduced PKs was subdivided into four subclades (I—IV), each of which had a typical domain structure (Fig. 1). Reducing PKS subclade I included *Aspergillus terreus* LovF and its ortholog *Penicillium citrinum* MlcB, which synthesize the diketide portion of lovastatin (2) and citrinin (3), respectively, and *C. heterostrophus* PKS1 and its ortholog *Didy-*

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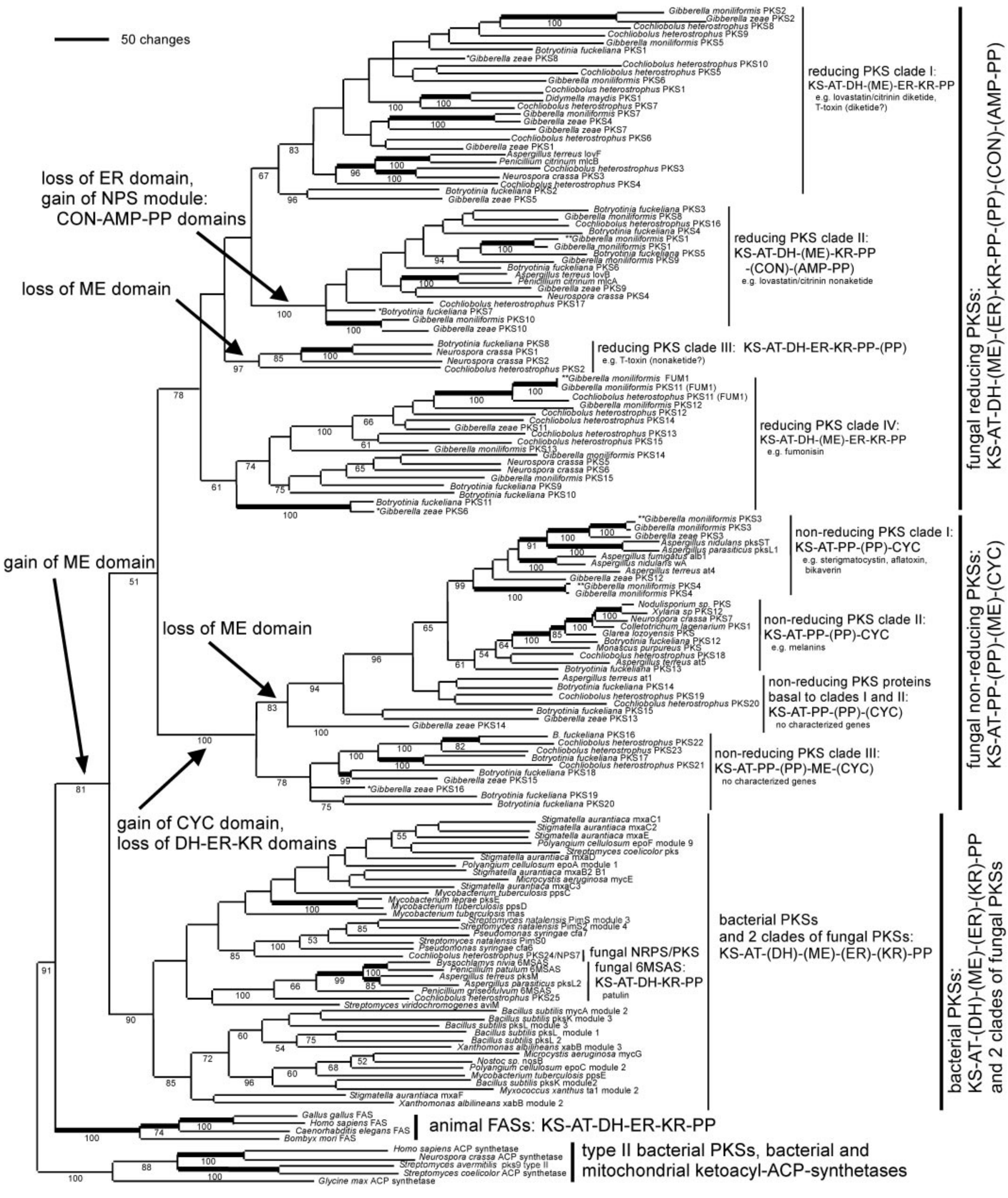

Fig. 1. Genealogy of type I PKSs, inferred by maximum parsimony analysis of the KS domain. Major clades and subclades are indicated by vertical bars, each of which shares a common organization of domains (those in parentheses are variable in their presence/absence within that clade). Branch length indicates number of inferred amino acid changes. Numbers below branches indicate percentage bootstrap support for each clade. All branches present in a strict consensus of the maximum parsimony trees received bootstrap support. Bold branches indicate putative orthologs, which were inferred as described in *Materials and Methods*. Monophyletic gains and losses of domains are noted by arrows. Three *G. moniliformis* PKSs were previously represented by GenBank submissions; these are noted with double asterisks. The accession numbers for all sequences obtained from GenBank are given in Table 1. Three *G. zeae* and one *B. fuckeliana* PKSs represented by partial C-terminal fragments of the KS domain were mapped onto the tree that was based on an alignment that included only N-terminal

mella (*Mycosphaerella*) *maydis* PKS1, which are necessary for the synthesis of structurally similar linear PKs, T-toxin (6), and PM-toxin (26), respectively.

Reducing PKS subclade II was characterized by enzymes that have lost the ER domain (Fig. 1); PKs synthesized by PKSs in this clade are predicted to either lack reduced alkyl groups or to contain alkyl groups whose reduction is completed by the product of an external ER domain-containing gene [e.g., *A. terreus lovC* (25), *P. citrinum mlcG* (3)]. The PKSs of this clade were also found to have either a condensation (CON) domain typical of NPSs (25) or an entire NPS module consisting of a CON domain, an adenylation (AMP) domain, and a PP domain (Table 3 and Fig. 1). Genealogies of the AMP and CON domains, along with those from characterized fungal and bacterial NPS proteins, grouped the AMP domains with those that adenylate amino acids that are subsequently *N*-methylated and grouped the CON domains with those that condense *N*-methylated amino acids (analysis not shown). These data suggest that the PKSs in this subclade gained an *N*-methylated amino acid-type NPS module (described in refs. 27–30). However, none of these PKSs had an *N*-methylation domain that is found between the AMP and CON domains of *N*-methylated amino acid type NPS modules. Many of these PKSs also lacked AMP and PP domains; these PKSs were scattered throughout this subclade, suggesting that the AMP and PP domains have been lost repeatedly, including those from the only two characterized proteins, *A. terreus* LovB and its ortholog *P. citrinum* MlcA, which synthesize the cyclic nonaketide portion of lovastatin and citrinin, respectively (3, 25). Each cyclic PK is derived from the action of the CON domain on a methylated keto group. This mode of action suggests that the loss of the AMP and PP domains was involved in a change of function of the CON domain from acting on methylated amino acids to acting on methylated keto groups. Uncharacterized PKSs with the same domain structure are predicted to make cyclic PKs. PKSs that have lost the entire C-terminal NPS module, consisting of the CON, AMP, and PP domains, are also scattered throughout this clade. The inferred polyphyletic losses of the CON, AMP, and PP domains were tested by constraint topologies forcing subsets of sequences into clades, which were subjected to parsimony analyses, and the likelihoods of the resulting genealogies were compared to the likelihood of the maximum parsimony tree found without these topological constraints. The Kishino–Hasegawa tests (18) rejected the alternative hypothesis of a monophyletic origin of the four PKSs that lack the entire NPS-like module via a sequential loss of first the AMP-PP domains and then the CON domain [$P < 0.0001$) (19)] or single loss of all three domains ($P = 0.0302$).

PKSs in reducing subclade III all lacked a ME domain, and two of the four PKSs had an additional PP domain. The only characterized protein is *C. heterostrophus* PKS2, which, along with PKS1, is required for synthesis of T-toxin (S. E. Baker, personal communication).

Reducing PKS subclade IV, like subclades I and II, included PKS enzymes that may or may not have a conserved ME domain. The only characterized PKS in this subclade is *G. moniliformis* FUM1, which makes the linear PK precursor of the toxin fumonisin (31, 32).

The PKSs that lack conserved and putatively functional ME domains are scattered throughout reducing PKS clades I, III, and IV and comprise reducing PKS clade II. The alternative hypothesis of a monophyletic loss of ME domains in the reducing PKS clade was rejected by the Kishino–Hasegawa test ($P < 0.0001$).

Fungal PKSs Producing Unreduced PKs. The second main fungal clade included fungal PKSs that synthesize unreduced, and usually cyclic, i.e., aromatic, PKs that are precursors to toxins [e.g., sterigmatocystin (33) and aflatoxin (34)] and pigments [e.g., melanin (35), bikaverin (36), and green spore pigment (37)]. All PKSs within this clade lacked ER, DH, and KR domains, which is interpreted as a single loss of these reducing domains, compared to the inferred ancestral domain structure of type I PKSs (Fig. 1, arrows). The nonreducing fungal PKSs are predicted to synthesize PKs in which the keto groups are either not reduced or may be reduced by enzymes other than a PKS. Unreduced PKs are typically synthesized from acetyl- and malonyl-CoA. PKS proteins with an additional PP domain were scattered throughout the nonreducing PKS clade, as was the case for reducing PKS subclade III. The functional significance of these duplicated PP domains is not known.

A Claisen-type cyclase (38) domain was present at the C terminus of all PKS proteins in sister subclades I (toxins and nonmelanin pigments) and II (melanin). The PKSs that make melanin precursors are encoded by the most widely distributed fungal *PKS* genes and have been characterized in *Colletotrichum lagenarium* (*PKS1*) (35), *Glarea* sp., *Nodulisporium* sp. (39), and *C. heterostrophus* (*PKS18*) (B. Robbertse and S. Baker, personal communication). *N. crassa PKS7* maps to the same region as the *per* locus; *per* mutants have nonmelanized perithecia and ascospores (40). The melanin-type *PKS* gene is not ubiquitous, because the two *Gibberella* genomes lacked a gene within unreduced PKS clade I, which correlates with a lack of melanized structures in their life cycles.

All PKSs basal to nonreducing PKS subclades I and II are uncharacterized. These basal PKSs occur both with and without the Claisen-type cyclase (CYC domain); the PKSs without CYC are predicted to make unreduced noncyclic PKs. We propose calling this clade the nonreducing PKSs, because this character is invariable, whereas not all PKSs in this clade are likely to make aromatic (cyclic) PKs. Several of these basal PKSs formed a subclade (nonreducing PKS subclade III) characterized by a ME domain located after the PP domain [KS-AT-PP-(PP)-ME-(CYC)], the apparent result of a domain rearrangement. The other PKSs basal to nonreducing subclades I and II do not have ME domains; we hypothesize that the genes encoding these PKSs diverged after the loss of the ME domain that was retained in nonreducing PKS subclade III (Fig. 1, arrow).

Other Fungal and Bacterial PKSs. The third main fungal PKS clade comprised the 6-methylsalicylic acid-type (i.e., simple aromatic) of PKSs that make 6-methylsalicylic acid, a precursor to toxins [e.g., patulin (41)]. These toxins have been characterized from *Aspergillus* spp. (27, 42), *Byssochlamys nivea*, and *Penicillium* spp. (27). The *C. heterostrophus* genome had a PKS in this clade, but the other Pezizomycotina genomes did not. This fungal clade was nested within the large clade that comprised all bacterial type I PKSs. A second fungal clade was also nested within this bacterial clade and was represented by a single member, *C. heterostrophus* PKS24. *PKS24* is a hybrid *NPS/PKS* gene, predicted to encode an enzyme that synthesizes a partly reduced PK decorated with a single amino acid.

Origin of *PKS* Genes in the Ascomycota. Fungal genome sequences available were limited to the three subphyla of Ascomycota, i.e., Taphrinomycotina, Saccharomycotina, and Pezizomycotina, as

fragments; these are marked with a single asterisk. Alignment was based on 4,862 amino acids from the KS domain; 462 characters were informative, 20 were uninformative, and 4 were constant. Parsimony was performed with 100 random additions. Shown is one of 18 most-parsimonious trees of 17,859 steps, consistency index (CI) = 0.2763, rescaled CI = 0.1491. The maximum parsimony trees generated by coding gaps as either 21st amino acid or as missing were not significantly different from each other or from the tree generated by neighbor joining.

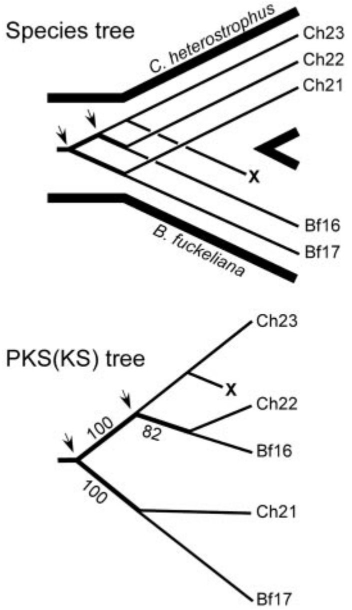

Fig. 2. Species tree (*Upper*) depicts the inferred gene duplication and gene losses necessary to account for the distribution of these PKS proteins present in fungal nonreducing PKS subclade III (*Lower*). Arrows indicate the two gene duplication events, and X indicates the extinction of the ortholog of *C. heterostrophus PKS23* in the lineage leading to *B. fuckeliana*.

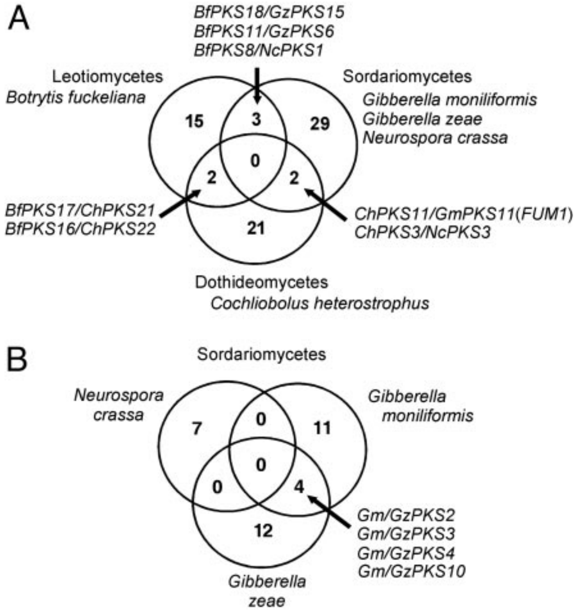

Fig. 3. Venn diagrams showing predicted *PKS* gene orthologs shared between and among taxa, inferred as described in *Materials and Methods*. (*A*) Among the classes Leotiomycetes (represented by *B. fuckeliana*), Dothideomycetes (*C. heterostrophus*), and Sordariomycetes (*N. crassa*, *G. moniliformis*, and *G. zeae*). (*B*) Among the Sordariomycetes: *N. crassa*, *G. moniliformis*, and *G. zeae*.

well as to one of the three subphyla of Basidiomycota, Hymenomycetes (*Phanerochaete chrysosporium*, www.jgi.doe.gov/programs/whiterot.htm). *PKS* genes were found only in the genomes of Pezizomycotina. It is possible that these genes have been lost in the non-Pezizomycotina taxa or that *PKS* genes came to the Pezizomycotina via HGT, perhaps from the bacterial *PKS* genes that form the sister clade to the main fungal clade. However, until fungal genomes from other Basidiomycota and from Zygomycota and Chytridiomycota are sequenced, this question will remain unresolved.

Diversification of *PKS* Genes Among Species in the Pezizomycotina. The diversity of *PKS* genes and PKs found in Pezizomycotina led to speculation, including our own (6, 43), that HGT is involved in generating and maintaining this diversity (ref. 44 and references therein). However, other discontinuous genome events such as gene duplication and differential gene loss are alternative explanations to HGT for the distributions of *PKS* genes (45).

We have data for genomes of species within three classes (Sordariomycetes, Dothideomycetes, and Leotiomycetes) of the Pezizomycotina (Table 3). For the fungal-reducing PKSs, all three classes are represented in each of the four subclades. For the fungal-nonreducing PKSs, all three classes are represented, but not in each of the four subclades. We also have data from a fourth class, Eurotiomycetes, in the form of many PKS proteins in GenBank from *Penicillium* and *Aspergillus* species (Table 1); these PKSs were found in two of the four fungal-reducing PKS subclades and three of the four fungal-nonreducing PKS subclades. This phylogenomic distribution (Fig. 1) is consistent with the hypothesis that all eight types of *PKS* gene were present in the common ancestor of the four classes of the Pezizomycotina, before the radiation of Pezizomycotina 300–700 million years ago (46).

Evidence for gene duplication and gene loss was observed; for example, in nonreducing PKS subclade III, a clade with many strongly supported internal branches (Fig. 2). Using only the genomes of *C. heterostrophus* and *B. fuckeliana*, two gene duplications in an ancestor of these two fungi would account for the present distribution of three pairs of paralogs, *ChPKS21/BfPKS17*, *ChPKS22/BfPKS16*, and *ChPKS23*, provided that the counterpart of *C. heterostrophus PKS23* was lost in the lineage leading to *B. fuckeliana*. HGT does not need to be invoked.

It would seem possible to distinguish between gene duplication and loss and HGT by comparing the time of divergence of *PKS* genes to that of genes taken to represent the organismal divergence. Similar divergence times for the two types of gene would favor gene duplication. More recent divergence for the *PKS* genes would favor HGT. Although rates of nucleotide substitution have been estimated for fungal tubulin genes (47), substitution rates for *PKS* genes are not known and will require data sets with large numbers of orthologous *PKS* genes.

The *N. crassa* genome is remarkable for its lack of duplicated genes (5), due presumably to repeat-induced point mutation that alters nucleotides in both copies of duplicated genes and renders them nonfunctional. If HGT were the main method of generating *PKS* gene diversity, *N. crassa* might be expected to have as many *PKS* genes as the other fungi. However, *N. crassa* has by far the fewest *PKS* genes, suggesting that gene duplication may be more important than HGT for generating *PKS* gene diversity.

Origins of Fungal *PKS* Genes in the Bacterial *PKS* Gene Clade. We found two *PKS* genes in *C. heterostrophus*, each sister to different *PKS* genes from bacteria. Several branches uniting the fungal and bacterial *PKS* genes in the bacterial PKS clade were so well supported that it seems certain that these fungal sequences belong in the bacterial clade. Kishino–Hasegawa tests rejected the alternative hypothesis that these sequences are fungal in origin [*C. heterostrophus PKS24* ($P = 0.0001$) and *C. heterostrophus PKS25* and the other members of the MSAS clade ($P < 0.0001$)]. These fungi may have acquired these *PKS* genes by one or more HGT events from bacteria.

Orthologs. Gene duplication and loss have left few putative orthologous matches among fungal *PKS* genes, and in no case were orthologous genes found for members of all of the three classes (Sordariomycetes, Dothideomycetes, and Leotiomycetes) for which we have genomic sequence (Fig. 3*A*). Few orthologs were observed among members of the Sordariomycetes, even within a genus (Fig. 3*B*); the *N. crassa PKS* genes have no orthologs in *G. zeae* or *G. moniliformis*, and only four *PKS* genes of 25 are orthologous between *G. zeae* and *G. moniliformis.*

Orthologous *PKS* genes found among closely or distantly related species reflect examples of nearly identical PKs being produced by different fungi. For example, citrinin and lovastatin are nearly identical compounds, made by closely related *P. citrinum* (3, 24) and *A. terreus* (25), respectively. Both citrinin and lovastatin require two PKSs for their synthesis; *A. terreus LovF* and *P. citrinum MlcB* genes are orthologs, and *LovB* and *MlcA* genes are orthologs. We note that both pairs of proteins receive strong bootstrap support (Fig. 1) and have identical domain structures, which is why we used these criteria to predict orthologs among the uncharacterized proteins. Another example of orthologs that fit these criteria, *C. heterostrophus* PKS1 (6) and *D. maydis* PKS1 (26), synthesize nearly identical compounds (T- and PM-toxins, respectively), and the biological activities of these toxins on the fungal host, maize, are identical (24). In a third example, *Dothistroma pini* makes dothistromin with products of genes that are orthologous to those of the aflatoxin biosynthetic pathway found in *Aspergillus* spp. (48).

PKS Diversity in Ascomycota. Given that a fungal species has as many as 25 *PKS* genes, our small sampling of fungal genomes predicts that an astonishingly large number of PKs are produced by species of Pezizomycotina. The unknown PKs may be toxins and pigments, or they may be involved in developmental processes that require small molecule signaling, such as growth and hyphal fusion, aerial hyphae formation, conidiation, and sexual reproduction. For example, in *Dictyostelium discoideum*, a type II PKS produces the 12-carbon PK precursor for a diffusible signaling molecule (DIF-1, a chlorinated alkyl phenone), which induces the differentiation of prestalk-O cells (49).

This inventory and categorization of all type I *PKS* genes in the genomes of five species within the Pezizomycotina is a starting point in our understanding of the diversity of PKs generated by these multidomain enzymes. A better understanding of the function of these compounds requires the characterization of PKs, including their modification and decoration by enzymes that are part of the biochemical pathway [some or all of which may be found in gene clusters (50, 51)], and the analysis of their roles in the biology of these fungi (52).

We thank Steven Briggs, President and Chief Executive Officer of TMRI, for his helmsmanship. Intermediate genome assembly of raw shotgun sequences was performed with in-house software (Don Hutchinson, TMRI). The gene predictions were created by Darrell Ricke (TMRI). Preliminary analyses of *PKSs* in *C. heterostrophus* were conducted by Barbara Robbertse and Scott E. Baker (TMRI). S.K. was supported by a collaborative agreement between University of California, Berkeley, and TMRI/Syngenta. The *C. heterostrophus*, *B. fuckeliana*, *G. moniliformis*, and *G. zeae* genome sequences were provided by Celera Genomics (Rockville, MD) for TMRI/Syngenta. The genome of *E. gossypii* was sequenced by SBI Technology/Syngenta (Research Triangle Park, NC). The genome of *P. chrysosporium* was made available by the U.S. Department of Energy (http://genome.jgi-psf.org/whiterot1/whiterot1.home.html).

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Supporting Materials and Methods

DNA and Protein Genomic Databases. Four genomes were sequenced by Celera Genomics for Torrey Mesa Research Institute (TMRI)/Syngenta: *Botryotinia fuckeliana* strain B05.10 (to ≈ 5× coverage), *Cochliobolus heterostrophus* strain C4 [American Type Culture Collection (ATCC) 48331] (to ≈ 5× coverage), *Gibberella moniliformis* strain (ATCC 38932) (FGSC 7600) (to ≈ 4× coverage), and *Gibberella zeae* lineage 7 strain GZ3639 (1) (to ≈ 2× coverage). The shotgun sequence assemblies of these genomes were used for these studies, along with the genome sequence of *Neurospora crassa* (2), *Saccharomyces cerevisiae* (3), *Eremothecium gossypii* (4) (sequenced by Syngenta), and *Schizosaccharomyces pombe* (5). The more complete coverage (≈ 10×) of *G. zeae* [lineage 7 strain PH-1 (NRRL 31084), available from the Whitehead Institute (www-genome.wi.mit.edu/annotation/fungi/*Fusarium*/index.html)], was used to check whether our 2× genome coverage of *G. zeae* lacked any putative *polyketide* (*PK*) *synthase* (*PKS*) genes.

The protein databases for *Cochliobolus heterostrophus*, *B. fuckeliana*, and *G. moniliformis* were compiled by using four gene models that were found to generate the largest numbers of predicted proteins: GENEMARK.HMM (6) (*Arabidopsis* and *Caenorhabditis* models), FGENESH (7) (dicot model), and GENSCAN (8) (*Arabidopsis* model). *N. crassa*, *S. cerevisiae*, and *S. pombe* protein databases are available at NCBI (www.ncbi.nlm.nih.gov).

***PKS* Gene Identification.** Initially, we searched our 2× coverage of fungal genomes available at TMRI for *PKS* genes. Because 2× coverage yielded average contig lengths shorter than the expected length of most *PKS* genes (5,000-7,500 bp), most *PKS* genes were represented as fragments. When greater coverage was available, the process was repeated, but no additional genes were found. We used the ketoacyl synthase (KS) domain, the most highly conserved domain in type I PKSs and in fatty acid synthases (FASs) (9), as a query. The KS domain is composed of a KSn Protein Families database Pfam00109.6) and a KSc (Pfam2801.6) domain (www.sanger.ac.uk/Software/Pfam). The consensus sequences of the two Pfams were concatenated and used in TBLASTN to retrieve *PKS* genes from each genome. In addition, to find *PKS* genes that may have been missed in a TBLASTN search, the concatenated Pfams were used in PSI-BLAST as a query against the predicted protein databases from *C. heterostrophus*, *B. fuckeliana*, and *G. moniliformis* and against the protein databases from *N. crassa*, *S. cerevisiae*, and *S. pombe* [available in the eukaryote protein database (www.ncbi.nlm.nih.gov/BLAST)]. The PSI-BLAST searches were also used to retrieve all previously published fungal *PKS* genes from NCBI. After the initial phylogenetic analyses were performed (described below), representative KS domains from each clade were used as queries in TBLASTN searches against all databases described above to identify any previously missed *PKS* genes.

***PKS* Gene Annotation.** The protein sequences of the KS domains obtained from TBLASTN and PSI-BLAST searches were used as queries to retrieve the complete PKS protein sequences from the protein databases. The *C. heterostrophus*, *B. fuckeliana*, and *G. moniliformis* PKS-predicted sequences from each of the four protein databases were retrieved and aligned by CLUSTALW by using the amino acid substitution matrix BLOSUM62, implemented in MEGALIGN (DNASTAR, Madison, WI). This was done to evaluate, manually, the predicted introns removed from each sequence by each algorithm. *PKS* genes frequently have large numbers of introns, particularly so in the *KS* domain (which can have up to nine introns each). None of the algorithms reliably removed all of the introns, nor were all of the 5' and 3' ends correctly predicted. The majority of introns in the *PKS* genes were therefore predicted manually by using progressive alignments with previously annotated PKS proteins as a guide. The predicted PKS proteins from *N. crassa* were also aligned to verify intron predictions. The predicted proteins were submitted to Hidden Markov Model searches, implemented in TIMELOGIC (TimeLogic, Carlsbad, CA), to determine their multidomain structures.

KS Domain Genealogy Construction and Evaluation. The predicted KS domains of all newly sequenced filamentous fungal genomes plus those from all previously published PKS protein sequences from ascomycete fungi, the homologous FASs from animals (9), and representative type I PKSs from bacteria, including those that occur as nonribosomal peptide synthetase (NPS)/PKS hybrids (Table 1) were aligned with CLUSTALW (NEXUS file provided as Table 2) and phylogenetically analyzed with neighbor joining and maximum parsimony (MP) in PAUP4.0b8 (10). MP was performed with the following settings: gaps treated alternately as "21st amino acid" and as missing, 100 repetitions performed with random sequence addition, branch swapping by tree bisection-reconnection (TBR), and heuristic search performed with multiple trees saved and steepest descent invoked. Only the MP genealogies were retained.

The resulting KS-domain genealogy (randomly selected from the MP trees) was evaluated to rank major clades and subclades of PKS enzymes. The criteria used to categorize proteins in major clades and subclades were moderate bootstrap support (performed with MP, with 100 repetitions with 10 random additions per repetition, MaxTrees set to 1,000), similar domain structure, and similar chemical characteristics of the resulting PK products for those PKSs that have been previously characterized (e.g., PKSs producing lovastatin and citrinin). KS-domain genealogy was also used to distinguish orthologous genes that are expected to encode functionally homologous enzymes (11, 12). The criteria used to categorize proteins as orthologous were bootstrap values >80%, identical predicted domain structure (or nearly so), and similar chemical characteristics of the resulting PK product (e.g., ascomycete-type melanin). Putative orthologs were further evaluated by comparing their topology in the KS domain genealogy to that of the currently understood organismal phylogeny (13). The latter is applicable when three or more orthologs are present.

Alternative phylogenetic hypotheses were tested for significance with a Kishino--Hasegawa (K-H) test (14). The hypothesis was stated as a tree with a topology constraining the taxon in question as a monophyletic group. The constrained tree was imported as a PAUP file and analyzed to find the best tree given the constraint, by using parsimony and the settings described above to find the MP tree without the constraint. The likelihood of the resulting tree was compared to that of the most likely tree, given no constraint. The hypothesis underlying the constraint tree is rejected if the difference in logarithm likelihood divided by the standard deviation (Ln L/SD) is > 1.96 ($P \leq 0.05$) (15).

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Table 1. GenBank accession nos. for previously published sequences included in Fig. 1

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Species	Protein (module)	Accession nos.
Aspergillus fumigatus	alb1	AAC39471
Aspergillus nidulans	pksST	AAA81586
A. nidulans	wA	CAA46695
Aspergillus parasiticus	pksL2	AAC23536
A. parasiticus	pksL1	AAC41675
Aspergillus terreus	at1	BAB88688
A. terreus	at4	BAB88689
A. terreus	at5	BAB88752
A. terreus	lovB	AAD39830
A. terreus	pksM	AAC49814
A. terreus	lovF	AAD34559
Bacillus subtilis	pksK module 2	NP_389599
B. subtilis	pksK module 3	NP_389599
B. subtilis	pksL module 1	CAB13602
B. subtilis	pksL module 2	CAB13602
B. subtilis	pksL module 3	CAB13602
B. subtilis	mycA pks1 module 2	AAF08795
Bombyx mori	FAS p270	AAB53258
Byssochlamys nivea	6MSAS	AAK48943

Caenorhabditis elegans	FAS	NP_492417	
Colletotrichum lagenarium	pks1	BAA18956	
Gallus gallus	FAS	P12276	
Glarea lozoyensis	PKS1	AAN59953	
Glycine max	beta-ketoacyl synthetase	AAF61730	
Gibberella moniliformis	FUM1	AAD43562	
G. moniliformis	PKS1	CAC44633	
G. moniliformis	PKS3	CAC88775	
G. moniliformis	PKS4	CAB92399	
Homo sapiens	FAS	AAC50259	
H. sapiens	3-oxoacyl-ACP-synthetase	NP_060367	
Microcystis aeruginosa	mycE	AAF00958	
M. aeruginosa	mycG	AAF00957	
Monascus purpureus	PKS1	CAC94008	
Mycobacterium leprae	pksE	AAA17364	
Mycobacterium tuberculosis	mas	CAB06108	
M. tuberculosis	ppsD	CAB06093	
M. tuberculosis	ppsE	CAB06094	
Myxococcus xanthus	ta1 module 2	CAB38084	
Neurospora crassa	PKS1	XP_325868	
N. crassa	PKS2	XP_324368	
N. crassa	PKS3	XP_324222	
N. crassa	PKS4	XP_329445	
N. crassa	PKS5	XP_330288	
N. crassa	PKS6	XP_330106	

N. crassa	PKS7	XP_322886	
N. crassa	3-oxoacyl-ACP-synthetase	AAB81078	
Nodulisporium sp.	melanin PKS	AAD38786	
Nostoc sp. GSV224	nosB	AAF15891	
Penicillium citrinum	mlcA	BAC2056	
P. citrinum	mlcB	BAC20564	
Penicillium griseofulvum	pks2	AAB4968	
Penicillium patulum	6MSAS synthetase	CAA39295	
Pseudomonas syringae	cfa6	AAD03047	
P. syringae	cfa7	AF098795	
Sorangium cellulosum	epoA module 1	AAF26919	
S. cellulosum	epoC module 2	AAF2692	
S. cellulosum	epoF module 9	AAF62885	
Stigmatella aurantiaca	mxaB2, B1	AAK57186+AAK57185	
S. aurantiaca	mxaC1	AAK57187	
S. aurantiaca	mxaC2	AAK57187	
S. aurantiaca	mxaC3	AAK57187	
S. aurantiaca	mxaD	AAK57188	
S. aurantiaca	mxaE	AAK57189	
S. aurantiaca	mxaF	AAK57190	
Streptomyces natalensis	PimS0	CAC20930	
S. natalensis	PimS2 module 3	CAC20921	
S. natalensis	PimS2 module 4	CAC20921	
Streptomyces viridochromogenes	aviM	AAK83194	
Streptomyces coelicolor	act typeII	NP_823552	

Streptomyces avermitilis	pks9 typeII	NP_823551	
Xanthomonas albilineans	xabB module 2	AAK15074	
X. albilineans	xabB module 3	AAK15074	
Xylaria sp.	PKS12	AAM9354	

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Table 2. KS domain alignment used for phylogenetic analyses in NEXUS format

```
#NEXUS

begin data;
  dimensions ntax=144 nchar=486;
  format datatype=Protein interleave gap=- missing='.';
  matrix
[                                    1                                                      60]
Bf_PKS7                             AIAIVGNSCRL--PGGSHCPSKLWDL-LKSPIDLVAEIRQNRFNA----AGFYHPRAEHS
Aspergillus_terreus_at1             AI--VGMSCRF--PGGADDPERFWEL-LEEGRDVHKKVPADRFDVDLHCDPTDKRK----
Aspergillus_terreus_at4             AI--VGYSGRF--PSA-ASNEAFWEL-LRAGRDVHREIPRDRFDWETYYDPTGKRR----
Aspergillus_terreus_at5             AI--VGMAGRF--PNS-DDLESFWST-LRQGLDLHRRVPPDRFDIDAHYDPTGKKL----
Gm_PKS5                             AVIGSVAISRLMRRAKIHEINHSRTI-LTTAR-VIHEVRPNRMKN----KSIMSMLLSLI
Ch_PKS9                             AV--VGFGFKF--PQDVTNAETLWKL-LIERRSTMTEIPKNRWNI----DGFYKENGHRP
Ch_PKS8                             AI--IGMNMKF--PGDAVSAQSFWKL-IVSARNVSKEVPADRFKI----DSFYHPDPNRL
Gz_PKS2                             AIV--GYSFKL--PQGVEDDDAFWDV-LENRRNLMTDWPESRVKT----DSFAHPDRRSS
Gm_PKS2                             AIV--GYSFKL--PQGAEDDDVFWDV-LENRRNLMTEWPESRVKT----DSFANNKH---
Ch_PKS10                            AVI--GLDAKL--PCDGDSVQQFFDF-LIAGRSARKPVPSDRYNA----DAFWHPD-HHR
Ch_PKS5                             AI--VGLATRF--PQEAYNTEQLWQF-LLAKRCAHTPIPEGRMGP-----GHYHPDPEHG
Ch_PKS7                             AI--VGMSFRG--PGSANNIENLFKM-ICEKRESRTAIPKSRWNN----KAFYHPNFQRH
Ch_PKS1                             AV--VGMSFRG--PGDATNVEKLLNM-ISEGRESRAEVQAKKWDP----EGFYHPDSSRH
Didymella_maydis_PKS1               AI--VGLSFRG--PGDATSAENLLRM-VAESRESRSPIPSQKWNA----SGHYHPDPSRQ
Gz_PKS4                             AI--VGLACRF--PGDATSPSKFWDL-LKSGKDAYSE-TTDRYNA----QAFYHPNSKRQ
Gz_PKS7                             AV--VGIGLRF--PGDASSPEELWKV-LERGESQWSEFPKDRLNI----DGYYHPGGDRQ
Gm_PKS7                             AI--VGIGLRF--PGDASSPEELWKV-LERGESQWSEFPKDRLNI----DGYYHPSGDRQ
Ch_PKS6                             AI--IGIAFRG--PGDARDPEAFYRM-LIEGRSARTEIPKDRYNV----DAFYHPDPERL
Gz_PKS1                             AV--IGIGCRF--PGNSSNPEALWKL-LSDARSMYSKVPPDRYNV----DGFRHPSNKLN
Ch_PKS4                             AI--IGMSCRF--SGMADTPGAFWQM-LSKGMTSWSRDARDRFKL----ESFWHPRNDLS
Gm_PKS6                             AV--IGVSGRF--PGDATSPRHLWDL-LKEGRNALSDVPESRFNI----DGFYHPDGGRA
Nc_PKS1                             AI--VGMACRM--PGNVSTPAEFWEL-CTRARSGWSETPKQRFNS----ARFHHPNQGKG
Bf_PKS8                             AI--VGISCRL--PGNVSTPDEFWEL-CSRARSGWSEIPKERFDT----ASFYHPNPGKA
Nc_PKS2                             AI--VGMSCRL--PGGVETPGDFYRM-MCRGRSGWSKVPKDRFNQ----EAYNHPDPDHK
Ch_PKS2                             AI--IGMSCRF--PGKVASLEDFWDM-LSNSKHGYRQFPRERFNW----EAFYHPNQSRK
Aspergillus_terreus_lovF            AM--VGMGCRF--GGGATDPQKLWKL-LEEGGSAWSKIPPSRFNV----GGVYHPNGQRV
Penicillium_citrinum_mlcB           AI--VGMGCRF--AGDATSPQKLWEM-VERGGSAWSKVPSSRFNV----RGVYHPNGERV
Ch_PKS3                             AI--IGMSCRF--AGGATDPEKLWQL-CAEGRTGWSEIPEDRFKI----DGHYHPRPDNL
Nc_PKS3                             AI--IGMSCRF--AGDVDSPSKLWDL-LAQGKSAWSEIPKDRFNI----DGFHHPNFEKL
Bf_PKS2                             AI--VGISCRF--PAGANSPEELWSL-ISQGKSAWSDVPEDRFNW----KSFLHPSSDVV
Gz_PKS5                             AI--IGVGCRL--PGGANNLDNLWKL-LSESRNGQTEIPKDRWNA----DAWFDAYPDAK
Gm_PKS1_CAC44633                    AI--IGSACRF--PGDSSSPSKLWDL-LKSPRDLLTKVPPNRYNA----DAFYHADSKHH
Gm_PKS1                             AI--IGSACRF--PGDSSSPSKLWDL-LKAPRDLLTEVPSNRYNA----DAFYHADSKHH
Bf_PKS5                             AI--IGMACRF--PGGSNSPSKLWDL-IKSPRNLSKRVPDERFNS----EAFFHTNGSYH
Gm_PKS9                             AV--VGTACRF--PGGCNTPSKLWDL-VFSSRDVLQKVPPARFNV----DSFYHSDPTHH
Aspergillus_terreus_lovB            VV--VGSGCRF--PGDANTPSKLWEL-LQHPRDVQSRIPKERFDV----DTFYHPDGKHH
Penicillium_citrinum_mlcA           VV--VGSGCRF--PGGVNTPSKLWEL-LKEPRDVQTKIPKERFDV----DTFYSPDGTHP
Gz_PKS9                             ....................SKLWDL-LKRPKDVSKEIPEDRFNL----DRFYHKDSSHH
Ch_PKS16                            AI--VGSACRF--AGGANSPSKLWDL-LRNPKDIRSNITDKRFNA----NGFYHPDGSHH
Bf_PKS6                             AV--IGTGCRF--PGGASSPSKLWNL-LHHPYDLTQKVPSSRFNI----KAFYHPNGEHH
Bf_PKS3                             AI--IGSSCRF--TGASNT-SKLWEL-LKEPRDVLSKIPEERFLA----EGFYHQDGQHH
Ch_PKS17                            AV--VGVGCRF--PGGCNTPSKLWDL-ICEQRDIQSKIPAERYNS----DAFYNEDGSKP
Gz_PKS10                            AI--IGTFCRF--HGGANTPSKLWDL-LIEKRDVQSSIPPVRFNV----DAFIAVM-DKN
Gm_PKS10                            AI--IGTSCRF--PGGANTPSKLWDL-LCEKRDVQSRIPNDRFNV----DAFYSTNGDKN
Nc_PKS4                             AI--VGSSCRF--TGEATSPAKLWEL-LKDPKDLTREVPKDRFNV----EGFYHPDGEYH
Bf_PKS4                             AI--IGRGCRL--AGGCQSPSELWNF-LQTPYDVSQEFPPDR------------NSASRH
Gz_PKS11                            AICGMSV----RLPGGLHSPQDLWEF-LVSKGDARGPVPESRYNA----SSYWSEKM-KP
Ch_PKS14                            ICGMGL-----RLPGGNTTPQEFWEF-LINKGDGRVRVPMSRYNV----SAYHETTK-RP
Ch_PKS12                            AICGMAI----RLPGALKTPAQFWTF-LTEKKDARAPIPFARFDA----EAFYSASG-KS
Gm_PKS12                            AICGTAL----RLPGGISNCQDYWDL-LYHGLDARRPIPSSRFNI----NGFNDSLG-GK
Ch_PKS13_pseudogene                 TIVGMAM----RLLGRVHNVEDLWEM-LIAKKSGLVDILKKRYNA----EGFQSDTP-MV
Ch_PKS11_FUM1                       AIVGLGM----RLPGAIHTAEQLWKT-IVQKRSTRCEIPASRFSV----DGFHSPSA-KP
Gm_FUM1_AAD43562                    AIVGMGM----RLPGGIHTPDELWGM-LVEKRSTRCEIPPTRFSV----DGFHSPSS-KP
Gm_FUM1                             AIVGMGM----RLPGGIHTPDELWGM-LVEKRSTRCEIPPTRFSV----DGFHSPSS-KP
Ch_PKS15                            AIVGMGM----RLPGNCHNSEAFWDL-LINQRDGMIDIPSSRWNS----EGFYDPHG-RP
Nc_PKS5                             AI--VGMACRW--PGGVHDPSQFWEF-LRNKVNGWKEFDDPRFSS----AGFHHPNSDRP
Gm_PKS15                            AI--VGMSCRL--PGGVNNPKEFWEF-LVNGESGYSDFPEERLNI----DSWYHPESVRP
Nc_PKS6                             AI--IGMGCRL--PGGSHSSSKLWEL-LKAGRTAQSRFPPSRFNI----DGFYHPNSDRP
Gm_PKS14                            CI--VGMACRL--PGGIRSPDDLWDF-MIQKESAYGPVPADRYNI----DGFYHHQNNLS
Bf_PKS9                             ........CRL--PGGLTTPDELWDF-LLAKKDARCRVPHSRYDI----DSYY-SDTKKP
Gm_PKS13                            AI--VSMACRL--PGGIDKPLDLWDH-VRAGRSSATAIPKDRFNA----ENFLSMDPNQK
Bf_PKS10                            AI--IGFACRL--PGGNTTPKKLWEF-LERGDIASNKVPKSRFNI----EGHWD-GSQKP
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Bf_PKS11                            AI--CGMACRL--PGGLTTPDELWDF-LLAKKDARCRVPHSRYDI----DSYY-SDTKKP
Penicillium_patulum_6MSAS           AV--VGMACRV--AGGNHNPELLWQS-LLSQKSAMGEIPPMR---WEPYYRR-DARNEKF
Byssochlamys_nivea_6MSAS            AV--VGMACRV--AGGNNNPEQLWHS-LLEKRDASGEIPPLR---WEPYYRR-DPRNAKE
Aspergillus_terreus_pksM            AV--VGMACRL--AGGNNSPEELWQS-ILNRKDASGEIPSMR---WEPYYRR-DIRNPKI
Aspergillus_parasiticus_pksL2       AV--VGMGCRL--PGNNNTPEELWRS-ILQKVDASSEIPRTR---WEPY-QQ-NAHNARS
Penicillium_griseofulvum_pks2       AI--IGMACRV--PGDVKSPSALWQF-LLQKGDASGDMPSWR---WDPYRQR-HPRNAAA
Ch_PKS25                            AI--VGLSCRT--AGRIDSLDSLWDF-LLQKKHASSEIPPRR---WEPWRQR-SMLEGNI
Nc_PKS7                             AI--VGMAGRF--PDA-ANHEKLWEL-LEKGLDVHRLVPPDRFDIKTHYDPTGKAI----
Colletotrichum_lagenarium_PKS1      AI--VGMAGRF--PDA-ASHEKLWEL-LAKGLDVHRVVPADRFPVATHYDITGKAV----
Nodulisporium_sp_PKS1               AI--VGMAGRF--PDS-ASHEALWEL-LEKGIDAHRVIPADRFPVDTHYDPTGKAI----
Xylaria_sp_PKS12                    AI--VGMAGRF--PDS-ESVEALWEL-LEAGIDAHRVIPADRFPVDTHYDPTGKAI----
Bf_PKS12                            AI--VGMAGRF--PDA-ASHEKLWEL-LENGLDVHREVPKDRFDVATHFDPTSKIR----
Glarea_lozoyensis_PKS1              AI--VGMAGRF--PDA-ASHELLWEL-LEKGLAVHREVPPDRFPVKTHVDPSGKTV----
Monascus_purpureus_PKS1             AI--VGMSGRF--PGG-QDLEEFWDV-LQRGLDMHKEIPPDRFDAKAHTDPSGKGK----
Bf_PKS13                            AI--VGMSGRF--PNS-ADHEAFWAL-LEQGLDVHREIPSNRFDAKLHCDPSGKGK----
Ch_PKS18                            AI--VGMSGRF--PGA-ANPEALWDL-LERGLDVHREVPADRFDAKAHCDPSGKGK----
Bf_PKS14                            AV--VGMACRF--PGGADDTERFWDL-LAQGRDVHRPVPADRFDIESHVDPTGERS----
Ch_PKS20                            AV--VGMSCRL--PGGANDLELFWKL-MVDKRDVHTMIPPDRFELSTHFDPTGQIQ----
Aspergillus_nidulans_wA             AI--IGMSGRF--PEA-DSPQDFWNL-LYKGLDVHRKVPEDRWDADAHVDLTGTAT----
Aspergillus_fumigatus_alb1          AI--IGMSGRF--PEA-DGIEAFWDL-LYKGLDVHKKVPPERWDVDAHVDLTGTKR----
Gz_PK12                             AI--VAMSGRF--PDA-ADLGEFWDL-LYEGRDVHRQIPEDRFNAELHYDATGRRK----
Gm_PKS3_CAC88775                    AI--VAMSGRF--PGA-KDNEAYWDL-LYKGLDVHKPVPSLRWDQQTHVDPTGAGK----
Gm_PKS3                             AI--VAMSGRF--PGA-KDNEAYWDL-LYKGLDVHKPVPSLRWDQQTHVDPTGAAK----
Gz_PKS12                            AI--VAMSGRF--PGA-KDNEAYWDL-LYKGLDVHKPVPSLRWDQKTHVDPTGKAK----
Gm_PKS4_CAC92399                    AI--IGFSGRF--PEA-DNLDEFWDL-LIRGLDVHKPVPEERFARD-HYDPTGQRK----
Gm_PKS4                             AI--IGFSGRF--PEA-DNLDEFWDL-LIRGLDVHKPVPEERFARD-HYDPTGQRK----
Aspergillus_parasiticus_pksL1       AI--VSMSGRF--PES-PTTESFWDL-LYKGLDVCKEVPRRRWDINTHVDPSGKAR----
Aspergillus_nidulans_pksST          AI--VSMSGRF--PEA-PSTDSFWDL-LYKGLDVCKEVPLRRWDVKTHVDPSGKAR----
Gz_PKS13                            AI--VGMAGRG--PGS-DNVEEFWNVIM-SKLDLCEEIPEDRFNLSEFYRSKHDSG----
Bf_PKS15                            AI--VGMAGRG--PGS-DNVEEFWNVIMLCKQILTKQIPPSRFSISDFHDPTGETK----
Bf_PSK19                            AV--IGMSGRF--PDA-ESVDELWEL-LLQGKSTVKRADVERLQL----SQTGNHT----
Ch_PKS22                            AI--VGAACRL--PGA-NNMEELWDL-LAGGVSKAEEIRPDRIPLHASFRASQD------
Bf_PKS16                            AV--IGASCRL--PGA-NNLEELWDL-ISKGTSVAKEVPNDRFDIHHSFRASQD--WKFA
Ch_PKS19                            AI--VGMSCRL--PGGSTDTEKFWEV-LEAGLDVSRQIPADRFDINTHYDPEGKDL----
Ch_PKS23                            AI--TGAACRL--PKA-NDLEELWNL-LSAGISTCEEIRLDRVSMHESFRAMQNEKWK--
Ch_PKS21                            AV--IGVAINV--AGA-SSATEFWDL-LASGKSQHQLVTDDKFTFETTFRENDPKR----
Bf_PKS17                            AV--VGMACQL--PGA-EDLEEYWKI-LSSGKSQHTEIPQERFSMETAWREADSER----
Bf_PKS18                            AI--CGMACRL--PGGLTTPDELWDF-LLAKKDARCRVPHSRYDIDSYYSDTKKPG----
Bf_PKS20                            AV--VGMACRT--AAG-DTAEDLWEA-IQTGRTTEREIDSKR------FPDAVMKD----
Homo_sapiens_FAS                    VIAGMFG----KLPE-SENLQEFWDN-LIGGVDMVTDDDRR----WKAG---LYGLPRRS
Gallus_gallus_FAS                   VIAGIAG----KLPE-SENLQEFWEN-LLNGVDMVTEDDRR----WKPG---IYGLPKRN
Caenorhabditis_elegans_FAS          VISGVSG----RFPR-CDNVKMFGDM-LLAGEDLVTEDSLR----WTPG---FCDLPKRH
Bombyx_mori_FAS_p270                YVTGVSG----YFPD-SDSVKHLQEN-LFNKVDLISSDDRR----WKLA---HPEIPQRT
Ch_PKS24_3p_of_nps7                 AI--VSMACRL--PGQVSSPEEYWDL-LEHGADVITDVPKDR---WDADAFY-DPNPGTP
Nc_3_oxoacyl_ACP_synthetase         VVTGLGAI-----TPLAVGIRPTWRRLL-DSHSGIVSVA--DLEPQDKWKELTSTVGGLV
Homo_sapiens_3_oxoacyl_ACP_synth    VITGIGLV-----TPLGVGTHLVWDRLI-GGESGIVSLV--G----EEYKSIPCSVAAYV
Glycine_max_beta_ketoacyl_synth     VITGMGLA-----SVFGNDVEGYYEKLL-AGESGITAID--RFDA----SKFPTRFGGQI
Streptomyces_coelicolor_act         VITGVGVR-----APGGNGTRQFWELLT-SGRTATRRIS--FFDP----SPYRSQVAA--
Streptomyces_avermitilis_pks9       ------MR-----APGGGNAKEFWELIS-SGTSAIRTIS--LFDA----SGFRSRIAG--
Bacillus_subtilis_pksK_mod2         AI--IGISCEF---PGAKNHDEFWEN-LRDGKESIAFFNKEELQRFGISKEIAENADYVP
Bacillus_subtilis_pksK_mod3         AI--VGISGRF--PGAMDIDE-FWKN-LEEGKDSITEVPKDR---WDWREHYGNPDTDVN
Bacillus_subtilis_pksL_mod1         AI--IGLAGRY--PKAANIHE-FWNN-LKEGKDCVSEIPESR---WDWQRL--EGITSPS
Bacillus_subtilis_pksL_mod2         AI--IGISGRY--PQADNIDE-LWEK-LRDGRDCITEIPADR---WD-HSLYYDEDKDKP
Bacillus_subtilis_pksL_mod3         AI--VGMSGRY--PGARNVRE-YWDN-LVHARNAIRDIPTSR---WD-VDKYYDPVLNKK
Bacillus_subtilis_mycA_pks1_mod2    AI--IGMSLNV--PGASNKSD-FWHL-LENGEHGIREYPAPR---VKDAIDYLRSIKSER
Microcystis_aruginosa_mycE          AV--VGMACRF--PGGINSPEKYWSF-CQAGLDAIVEVPKSR---WDISKLY-SQKPTL-
Microcystis_aruginosa_mycG          AI--IGMTGQF---PGAKNLTTFWEN-LKNGIETISFFSEEELQESGVSSELFNQPNYVR
Mycobacterium_leprae_pksE           AV--VGIGCRF--PGNVTGPDSFWQL-LVDGGDAISEVPPDR---WDADAFY-DPDPSAS
Mycobacterium_tuberculosis_mas      AV--IGMGCRL--PGGINSPDKLWES-LLRGDDLVTEIPPDR---WDADDYY-DPEPGVP
Mycobacterium_tuberculosis_ppsC     AV--IGMGCRF--PGGVNNPEQFWDL-LCAGRSGIVRVPAQR---WDADAYY-CDDHTVP
Mycobacterium_tuberculosis_ppsD     AV--VGIGCRF--PGNVTGPESFWQL-LADGVDTIEQVPPDR---WDADAFY-DPDPSAS
Mycobacterium_tuberculosis_ppsE     AV--VGMAGRF---PGAKDVSAFWSN-LRRGKESIVTLSEQELRDAGVSDKTLADPAYVR
Myxococcus_xanthus_ta1_mod2         AV--IGISCQL---PGAADPWRFWKN-LREGRDSVVAYRHEELRELGVPEEVLRDSRYVA
Nostoc_sp_nosB                      AI--ISLAGRF---PKAKDIDSFWQN-LYDGVESISRLTDEELITSGVSLDLLNNPNYVK
Pseudomonas_syringae_cfa6           AI--IGMSCRY--PGGANSPEALWTL-LMQERDAISEYPTDRG--WDTTKLY-DSEPGRF
Pseudomonas_syringae_cfa7           AI--VAMGCRL--PGGLASPEALWRL-VEAGEALSSALPSDRG--WQLDSLF-PADSPLR
Sorangium_cellulosum_epoA_mod1      AI--VGAGCRL--PGGVIDLSGFWTL-LEGSRDTVGQVPAER---WDAAAWF-DPDLDAP
Sorangium_cellulosum_epoC_mod2      AV--IGMSGRF---PGARDLDEFWRN-LRDGTEAVQRFSEQELAASGVDPALVLDPNYVR
Sorangium_cellulosum_epoF_mod9      AI--IGIGCRF--PGGADTPEAFWEL-LDSGRDAVQPLD-RR---WALVGVH-PSEEVP-
Stigmatella_aurantiaca_mxaB2_B1     AV--IGLGCRF--PGGAVDGSSYWKI-LRDGVDALREVPESR---WDVPGHF-DSTRGVP
Stigmatella_aurantiaca_mxaC1        AI--VGMACRF--PQ-ADNVEAFWRL-LQGGVDAVREIPLER---WPKDEVA-DIGDGAM
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Stigmatella_aurantiaca_mxaC2       AI--VGMGCRF--PGGANEPEAYWRL-LSDGVDAVREVPADR---WQSSTDA-AEHKGT-
Stigmatella_aurantiaca_mxaC3       AI--VGIGCRV--PQAS-GPEAFWKL-LEGGVDAIREVPASR---WKVEDYY-DPQPGVP
Stigmatella_aurantiaca_mxaD        AI--VGTSCRV--PGGARTPEAFWRL-LHGGVDAITEVPRDR---WDAEALF-DPDPNKQ
Stigmatella_aurantiaca_mxaE        AI--IGMGCRF--PGGGNDPESYWNL-LCNGVDAVTEVPSSR---WTREEME-RMDPEAL
Stigmatella_aurantiaca_mxaF        AI--VGMACRY--PQ-ASDPEAFWRL-LAGGNHAITEIPPER---WDINRLY-DRDPAAA
Streptomyces_natalensis_PimS0      AI--VGMACRL--PGGADSPDALWEL-LADGTDAMSPFPTDRG--WDLDRLF-DEDADRP
Streptomyces_natalensis_PimS2_mod3 AI--VGMSCRF--PGGVRSPRQLWDL-VSEGVDAISDFPVNRG--WNT-GLF-HPDPDNP
Streptomyces_natalensis_PimS2_mod4 AI--IGMSCRY--PGGVGSPEDLWRL-VTEGGDATGEFPADRG--WDAEGLY-DPDPDRA
Steptomyces_viridochromogenes_aviM AV--VGIGCRF--PGGVNSPGEFWDL-LTAGRNTVGEMPPDR---WEEYRDF-GPRFDAA
Xanthomonas_albilineans_xabB_mod2  AI--VAMHCEV--PGAGENTEALWSF-LRSDVNAIRPIESTRPDLWAAMRAY----PGLA
Xanthomonas_albilineans_xabB_mod3  AI--IGLAGRF--PGADTLEE-FWNN-LRNGQSSMGEVPGER---WD-HQHYFDSERQAP

[                                   61                                                      120]
Bf_PKS7                            GTSNVTKAYLLEG--DPWTFDNEFFKISAREAESMDPQQR....................
Aspergillus_terreus_at1            NTSLTPFGCFIDQ---PGLFDAGFFDMSPREAANTDPMHRLALVTAYEALEQSGF-----
Aspergillus_terreus_at4            NTSRVKYGCWIDE---PGLFDTKFFNMSPRKPENTDPAQRLAITTTYEAMEMAGM-----
Aspergillus_terreus_at5            NSTHTPYGCFIEK---PGLFDPRFFNMSQREAYQTDPMGRLALVTAYEALEMSGF-----
Gm_PKS5                            KTFALR-AHFLKG--EIAAFDAPFFSITPAEAGGMDPQQRGLL----ENTYRA-LENAGC
Ch_PKS9                            GTVKNRGGHFLSD--DPARFDAPFFSIQPAEAECMDPQQRLLL----ETSYHA-LENAGI
Ch_PKS8                            DSIRIRNAHFMTE--DPRAFDAPFFNMSHAEASVLDPQQRGLL----EGAYRT-FENAGI
Gz_PKS2                            HSRRKKLRRWIRC--..............................EGVLTA-CLVACL
Gm_PKS2                            QKWNGKGGHFISD--DAAAFDAPFFSLTAKEASAMDPMQRWTL----EATYHA-FENAGL
Ch_PKS10                           DAIASKQGHFMNS--SVKAFDAPFFGITPAEAAALDPQQRLLL----ESSYAA-LENAGY
Ch_PKS5                            GTHAV--AHFLAE--DPAYFDSSFFGITKGEAMSLDPQQRVVL----ENVYLA-LENSGF
Ch_PKS7                            GSHNVEYGHFFHD--DISKFDAPFFNMTKEEAAALDPAQRLLL----ESTYEA-LENGGI
Ch_PKS1                            GTHNVEYGHWFQQ--DVYNFDAPFFNVSPAEAAALDPQQRMLL----ECSYEA-FENSGT
Didymella_maydis_PKS1              GSHIVEYGHWFQQ--DVYEFDAPFFNLSAVESAALDPQQRMLL----ECTYEA-FENSGM
Gz_PKS4                            NVLPVTGGHFLKQ--DPHVFDAAFFNITAAEAISLDPKQRIAL----EVAYEA-FENAGK
Gz_PKS7                            GSISFRGAHFIKS--DFAAFDASFFAVAAEDAKAIDPQQRILL----EASYEA-LENAGI
Gm_PKS7                            GSISFRGAHFIKG--NFASFDASFFSISAEDAQAIDPQQRILL----EASYEA-LENAGI
Ch_PKS6                            GSIQQRYAHFLQQ--DFKAFDAPFFSITPKEAKAMDPTHRILL----EAAYEG-FENAGL
Gz_PKS1                            TTIA-EGAHFLSE--NIAAFDAAFFNIAPIDAKSMDPQQR..................GI
Ch_PKS4                            GSFNASGLHLLRQ--NPAAFDNDFFSISGLEAKAMDPQQRLML----ELAYET-FENAGL
Gm_PKS6                            GTLNTKQGYFLKS--DVDKFDAGFFSITPEEARGMDPTQRILL----ELAYEG-LENAGL
Nc_PKS1                            GTLNPVGGNFLNV--DLAAFDAPFFGLTEKEAISMDPQQRLLL----ECTFEA-LESAGI
Bf_PKS8                            GCFNAAGGNFLKE--DVGLFDAPFFSLTAQEATSMDPQQRILL----ECTFEA-LESAGI
Nc_PKS2                            GTFNSQGGYFIKQ--DLSGFDAAFFDVTRREAEAMDPAQRLLM----ECTYEA-LESGGI
Ch_PKS2                            DCIDVNCGYFLDG--DIAEFDAQFFKMNGTDA---DPQGRMIL----ECVYEALENAGGS
Aspergillus_terreus_lovF           GSMHVRGGHFLDE--DPALFDASFFNMSTEVASCMDPQYRLIL----EVVYEA-LEAAGI
Penicillium_citrinum_mlcB          GSTHVKGGHFIDE--DPALFDAAFFNMTTEVASCMDPQYRLML----EVVYES-LESAGI
Ch_PKS3                            NTTNVKGACFLDE--DVGNFDATFFNLPAETAAV-----SIII----CSSLPC-ILTKGN
Nc_PKS3                            NGTNVIGGHFMKE--DVGLFDAHFFNLSAETAAALDPQFRLQL----ESTYEA-LESAGI
Bf_PKS2                            GTINSRGGHFIDQ--DIRTFDAGFFGIPPAEANAMDPQHRLQL----ETAYEA-LENAGI
Gz_PKS5                            QSMVTKYGYFLQD--DISQFDAKFFGISSAEANSMDPQQRLFL----MTTYEA-LEDAGI
Gm_PKS1_CAC44633                   GTTNVRHSYFLNE--DPARFDNNFFNIQPGEAEAIDPQQRLLM----EVVYQG-LCASGQ
Gm_PKS1                            GTTNVRHSYFLSE--DPASFDNNFFNIQPGEAEAIDPQQRLLM----EVVYQG-LCASGQ
Bf_PKS5                            GATDSREAYFLEE--DVALFDNAFFNIQPGEAEAVDPQQRLLM----ETVYDS-LCAGGQ
Gm_PKS9                            GTTNVTQSYFLDE--DVTKFDNGFFGIQPMEAEAMDPQQRLLL----ETVYDS-VVDAGL
Aspergillus_terreus_lovB           GRTNAPYAYVLQD--DLGAFDAAFFNIQAGEAESMDPQHRLLL----ETVYEA-VTNAGM
Penicillium_citrinum_mlcA          GRTNAPFAYLLQE--DLRGFDASFFNIQAGEAETIDPQQRLLL----ETVYEA-VSNAGL
Gz_PKS9                            GTANVRRSYLLDE--DVRLFDTQFFGISPGEAQAMDPQHRVLL----EVVYEA-IESAGK
Ch_PKS16                           GHMNVLQSYLLEE--DTRLFDAEFFGINPVEAKAMDPQQRLLL----EVVYES-IESAGL
Bf_PKS6                            GTHNATKSYFLNE--DPTTFDAPFFNINPREAEALDPQQRLLL----ETVYEA-LEAAGL
Bf_PKS3                            GTSNVLHSYLLDE--NPLAFDSAFFHIHNREAECIDPQQRLLL----ENVYET-IESACY
Ch_PKS17                           GCTNVNHGYFLDE--DIRAFDAAFFRMNPAEVEAVDPQQRMLL----ETVFEA-LESAGT
Gz_PKS10                           GCTDVKKAYLWAE--DTRLFDASFFKINPREAEAMDPQQRLLL----EAVYEA-TESAGL
Gm_PKS10                           GCTDVKRAYLLSE--DIRVFDASFFKINPREAEAMDPQQRLLL----EAVYEA-TEAAGL
Nc_PKS4                            GTTNSAKAYFLEQ--DHRLFDASFFNITPKEAEAIDPQQRMLL----EVVYEA-LESAGY
Bf_PKS4                            STS--TRGYFLSQ--DVREFDASFFSLSPLEAQAMDPQHRLLL----ETVYEA-LEEAGI
Gz_PKS11                           GTVKTQYGYFLDESIDIASVDTSFFTMRKDEVGKADPQQRQML----EVAREC-LEDAGE
Ch_PKS14                           TTVATEYGYFLDEDVKLGAMDTSRFSMSRADVEFSDPQQRHLL----EVVMEA-LEDAGE
Ch_PKS12                           GYFNSKNGYYLDDSAEVGALDTSLFRMSQQESERMDPQAKILL----ELAREC-FESAGE
Gm_PKS12                           DSIKTRHGYFIED--DLSRLDTSFFSLTKNELERVDPQQRLLL----EVTHEC-LEDAGE
Ch_PKS13_pseudogene                GTMQTKHGYFLND-IDLTQFDALFFSFSYKEAERIDLAQRQLL----EIIYEC-LENVGE
Ch_PKS11_FUM1                      GSVAMRHGHFLDEFDDLHRLDTSLFSMGITEVNDIDPQQRMLL----EVVYEC-MESSGQ
Gm_FUM1_AAD43562                   GSIAMRHGHFLDDKDDLHRLDTSFFSMGMTEVSDIDPQQRMLL----EVAYEC-MQSSGQ
Gm_FUM1                            GSIAMRHGHFLDDKDDLHRLDTSFFSMGMTEVSDIDPQQRMLL----EVAYEC-MQSSGQ
Ch_PKS15                           GTTKVNKGNFLG-SIDPADFDGSFFSMSAAQIAKVDPQHRVLL----ETTYEA-LENAGE
Nc_PKS5                            GSMSMKGAFLAEQ--DARLFDHTFFGMTGLEVETMDPSQRKLL----EVAYEA-IESAGE
Gm_PKS15                           GSVVTKGGYFLKH--DMNEFDNEFFGITAAEARLMDPAQKQLM----EVVFES-AEAAGV
Nc_PKS6                            GSLNMEGGYFIED--DIRGFENSFFGINNLEATYMDPQQRKLL----EVVFET-FENAGF
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Gm_PKS14                            GATNVPGGYFINE--DVRQFDNAFFDINNLEATYMDPQQRKIL----EVVYEC-LVSSGT
Bf_PKS9                             GTVSTEYGYFLDESVDIWKFDPAFFGIVQEEAKAMDPQQRKLL----ECVYES-FESGGI
Gm_PKS13                            GEQAFRGAHFVKR--DIKQFDHKFFGISKDTATAMDPQQKQLL----EVVYEC-LESANI
Bf_PKS10                            RTMRPCGGMFLED-IDPADFDASFFEISRSEAISMDPNQRQML----EVVFEG-LENAGI
Bf_PKS11                            GTVSTDGGHFLKD--DIKAFDASFFGINPIEATVSDPQQRLLL----EIAYEA-FENAGL
Penicillium_patulum_6MSAS           LKNTTSRGYFLDR---LEDFDCQFFGISPKEAEQMDPQQRVSLEVASEALEDAGIPAKSL
Byssochlamys_nivea_6MSAS            LSKTTSRGYFLDN---LEDFDGQFFGISPKEAEQMDPQQRISLEVAWEALEDAGIPAKSL
Aspergillus_terreus_pksM            LDQTTKRGYFLDH---VENFDAAFFGVSPKEAEQMDPQQRLSLEVTWEALEDAGIPPQSL
Aspergillus_parasiticus_pksL2       IGKVPRRGYFVKN---IENFDASFFNISPKEAEQMDPQQRLALEVTWEALENAGIPLSSL
Penicillium_griseofulvum_pks2       LAKTTAKGYFVND---IDHFDAAFFAISPREAEQMDPQQRIALEVAWEALENAGISPSRL
Ch_PKS25                            FDSVTRKGYFLDD---LEGFDAAFFGISPREAEHMDPHQRPSLELTYEGLQNAGIRPDRL
Nc_PKS7                             NTSHTPYGCWIEQ---PGLFDPRFFNMSPREAFQTDPMQRMALTTAYEALEMSGY-----
Colletotrichum_lagenarium_pks1      NTSHSQYGCWIEN---PGYFDPRFFNMSPREAFQTDPMQRMALTTAYEALEMCGY-----
Nodulisporium_sp_PKS1               NTSHTPYGNWIEN---PGHFDPRFFNMSPREAFQTDPMQRLALTTAYEALEMSGY-----
Xylaria_sp_PKS12                    NTSHTPYGNWIKN---PGHFDPRFFNMSPREAFQTDPMQRMALMTAYEALEMSGY-----
Bf_PKS12                            NTSHTPYGCWIEN---PGLFDPRFFNMSPREAYQTCPMQRLGLATAYEALEMAGY-----
Glarea_lozoyensis_PKS1              NTSHTPFGCWIEN---PGLFDPRFFNMSPREAFQTDPMQRMALSTAFEALEMSGY-----
Monascus_purpureus_PKS1             NKSHTPFGCFVEN---AGLFDPRFFNMSPREAAQTDPMQRLALITAYEALEMAGY-----
Bf_PKS13                            NKTHSPFGCFIDE---PGKFDPRFFNMSPREAMQTDPMQRLAISTAYEAMEMSGF-----
Ch_PKS18                            NKSHTPYGCFIDE---PGLFDPRFFNMSPREAAQTDPMGRLALTTAYEALEMSGY-----
Bf_PKS14                            NTSKTPYGCFVDN---PGLFDALFFGMSPREAEQTDPMHRLALVTAYEALESSGY-----
Ch_PKS20                            NTTQTSYMNHIDS---PGLFDAGFFNISPKEAEQMDPMHRLALVTVYEALEMSGY-----
Aspergillus_nidulans_wA             NTSKVPYGCWIRE---PGLFDPRFFNMSPREALQADPAQRLALLTAYEALEGAGF-----
Aspergillus_fumigatus_alb1          NTSKVPYGCWINE---PGLFDARFFNMSPREALQADPAQRLALLSAYEALEMAGF-----
Gz_PK12                             NTSKVMNGCFIKE---PGLFDARFFNMSPKEGEQSDPGQRMVLETAYEALEMAGI-----
Gm_PKS3_CAC88775                    NTSATPFGCWLDD---PSEFDARFFNISPREAPQIDPAQRLALMTAYEAIEQAGI-----
Gm_PKS3                             NTSATPFGCWLDD---PSEFDARFFNISPREAPQIDPAQRLALMTAYEAIEQAGI-----
Gz_PKS12                            NTSATPFGCWLDE---PGQFDARFFNISPREAPQVDPAQRLALMTAYEAIEQAGI-----
Gm_PKS4_CAC92399                    NTSQVQYGCWLKS---AGYFDTQFFHMSPKEAMQTDPAQRLALLTAYEALEMAGV-----
Gm_PKS4                             NTSQVQYGCWLKS---AGYFDTQFFHMSPKEAMQTDPAQRLALLTAYEALEMAGV-----
Aspergillus_parasiticus_pksL1       NKGATKWGCWLDF---SGDFDPRFFGISPKEAPQMDPAQRMALMSTYEAMERAGL-----
Aspergillus_nidulans_pksST          NKGATRWGCWLDF---AGEFDPRFFSISPKEAPQMDPAQRMALMSTYEAMERGGI-----
Gz_PKS13                            CTTTTKFGCFMDK---PGHFDNRFFHISPREALLMDPGHRQFLMTTYEALEMAGY-----
Bf_PKS15                            NSLITTHGAFLRH---PGLFDNKLFNVSPKEALQMDPLQRLLLLCTYEALEKAGY-----
Bf_PSK19                            -DTSW-WGNWLRD---PTAFDHRFFKKSSREAIAWDPQQRVLLQVVYEALESSGYFG---
Ch_PKS22                            -----------QK---VDGFDHTFFRTNPKEATYMDPQQRILLELAYQAMDSSGYLRSHK
Bf_PKS16                            GKRKF-FGNFLEN---VEDFDHAFFRTNPREAVNMDPQQRILLELAYEAMESSGYLRSHK
Ch_PKS19                            NKTMTQYGCFIEE---PGMFDPSFFNMSPREAMVVDPQMRLSLVTAYEALERAGY-----
Ch_PKS23                            --PKW-FGNFIDG---ADEFDWNFFRSNVKAAANMDPQQRILLELTYEALDSAGYLRRHR
Ch_PKS21                            -K--W-YGNFIDG---VEDFDHKFFKKTPRESTGMDPQQRLLLQCAYQAVEMSGYFND-N
Bf_PKS17                            -K--W-FGNFVEN---YNTFDHKFFKKSPREMASTDPQHRLMLQIAYQTVEQSGYFGS-L
Bf_PKS18                            -TVSTEYGYFVDD---IDAFDHKFFQKSPREAASMDPQQRFLLECSYNALLSSGYFG---
Bf_PKS20                            -KM---WGNFLSD---IDSFDHRFFKKSKREAMALDPHQRTILETTYHALESATCFGGGQ
Homo_sapiens_FAS                    GKLK-----------DLSRFDASFFGVHPKQAHTMDPQLRLLLEATYEAIVDGGINPD--
Gallus_gallus_FAS                   GKLK-----------DIKKFDASFFGVHPKQAHTMDPQLRLLLEVSYEAILDGGINPT--
Caenorhabditis_elegans_FAS          GKLK-----------VLNKFDAGFFQVTPKQANFMDPQVRLLLEASWEAMVDAGINPT--
Bombyx_mori_FAS_p270                GKIN-----------NVNKFDASFFGVHYKQAHTMDPMCRILLEKAYEAIVDAGLNPK--
Ch_9497_PKS24_3p_of_nps7             GKSHCRRGGFLAS---IDEFDASFFGISPKEARAMDPAQRIMLETCWEGFERAGYTDRQL
Nc_3_oxoacyl_ACP_synthetase         PTPARNKQNVDEQHT----WKAADW-LEPSDQXRMSLFAQYSVAATEMALQDAGWKPTRQ
Homo_sapiens_3_oxoacyl_ACP_synth    P-RGSDEGQFNEQ----------NF-VSKSDIKSMSSPTIMAIGAAELAMKDSGWHPQSE
Glycine_max_beta_ketoacyl_synth     -------------RG----FSAEGY-IDGKNDRRLDDCLRYCIVAGKKALENADLAPDNH
Streptomyces_coelicolor_act         ------EADFDP--------VAEGF--GPRELDRMDRASQFAVACAREAFAASGLDPDT-
Streptomyces_avermitilis_pks9       ------ECDFDP--------VAEGF--SAQEIRRMDRSAQLAVAATREAVADAGLDLAE-
Bacillus_subtilis_pksK_mod2         AKASID---------GKDRFDPSFFQISPKDAEFMDPQLRMLLTHSWKAIEDAGYAARQI
Bacillus_subtilis_pksK_mod3         -KTDIKWGGFIDG---VAEFDPLFFGISPREADYVDPQQRLLMTYVWKALEDAGCSPQSL
Bacillus_subtilis_pksL_mod1         GKDISKWGGFIDD---PDCFDPQFFRITPREAETMDPQERLFLETCWETIEDAGYTPKTL
Bacillus_subtilis_pksL_mod2         GKTYSKWGGFMKD---VDKFDPQFFHISPREAKLMDPQERLFLQCVYETMEDAGYTREHL
Bacillus_subtilis_pksL_mod3         GKVYCKSMGMLDD---IEHFDPLFFNIPPSEAELMDPQHRIFLQEGYKAFEDAGYNARTL
Bac_subtilis_mycA_pks1_mod2         NEKQFVRGGYLDE---IDRFDYSFFGLAPKTAKFMDPNQRLFLQSAWHAIEDAGYAGDTI
Microcystis_aruginosa_mycE          GKMNTAYGGFLQE--NITEFDARFFSISAKEAASMDPQQRLLLEVAWEALENANLPLKNL
Microcystis_aruginosa_mycG          ARPILE---------QVEYFDSEFFGYTDREAELLDPQQRLLLECSWECLENAGYNPNTY
Mycobacterium_leprae_pksE           GRMTTKWGGFVP---DVDAFDAEFFGITPREAVAMDPQHRMLLEVAWESLEHAGIAPDSL
Mycobacterium_tuberculosis_mas      GRSVSRWGGFLDD---VAGFDAEFFGISEREATSIDPQQRLLLETSWEAIEHAGLDPASL
Mycobacterium_tuberculosis_ppsC     GTICSTEGGFLTSW-QPDEFDAEFFSISPREAAAMDPQQRLLIEVAWEALEDAGVPQHTI
Mycobacterium_tuberculosis_ppsD     GRMTTKWGGFVS---DVDAFDADFFGITPREAVAMDPQHRMLLEVAWEALEHAGIPPDSL
Mycobacterium_tuberculosis_ppsE     RAPLLD---------GIDEFDAGFFGFPPLAAQVLDPQHRLFLQCAWHALEDAGADPARF
Myxococcus_xanthus_ta1_mod2         VRSSIE---------DKECFDPHFFGLTARDASFMDPQFRLLLMHAWKAVEDAATTPERL
Nostoc_sp_nosB                      ASAVLS---------DIELFDANFFAYSAKEAELIDPQQRLFLELAWEAIEKAGYDPHTY
Pseudomonas_syringae_cfa6           GKISTRTSGFLHD---ASAFDPAFFGISPREALTLEPQQRLLLEVCWEALERAGIDPASL
Pseudomonas_syringae_cfa7           ERVAGWRGGFLDE---VAGFDAAFFRISDREALAMDPQQRLLLEVSWEVLERAGIVPATL
Sorangium_cellulosum_epoA_mod1      GKTPVTRASFLSD---VACFDASFFGISPREALRMDPAHRLLLEVCWEALENAAIAPSAL
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Sorangium_cellulosum_epoC_mod2      AGSVLE---------DVDRFDAAFFGISPREAELMDPQHRIFMECAWEALENAGYDPTAY
Sorangium_cellulosum_epoF_mod9      -----RWAGLLTE--AVDGFDAAFFGTSPREARSLDPQQRLLLEVTWEGLEDAGIAPQSL
Stigmatella_aurantiaca_mxaB2_B1     GKMYGTRGGFLDD---VEHFDAEFFGISPREAASLDPQQRLVLEVAWEALENAGLAPDQL
Stigmatella_aurantiaca_mxaC1        -----RWGGFL-D--SVDSFDPGFFGISPREAVRMDPQQRLLLEVAWEALEDAGLDVDKL
Stigmatella_aurantiaca_mxaC2        -----RWGGFL-D--RVDGFDPEFFGIAPREAVAMDPQQRLLLEVAWEALENAGLPKSRL
Stigmatella_aurantiaca_mxaC3        GKTYTRWGGFLDG---ADQFDAQFFGIAPREAANMDPQQRLLLEVAWESLEHAGIAPARL
Stigmatella_aurantiaca_mxaD         GRTYARWGGFIDG---VDRFDAAFFGVSPREASRMDPQQRMLLEVAWEALERAGQPPDQL
Stigmatella_aurantiaca_mxaE         EKLGARWGAFI-N--KVDQFDADFFGISPREAHRMDPQQRILLEVAWEALERAGQDMTQL
Stigmatella_aurantiaca_mxaF         GKVTSRWGAYLD---QVDGFDPLFFGISPKEALHMDPQQRLMLELTWEALEDAGIAAEGL
Streptomyces_natalensis_PimS0       GTSYAREGGFLHD---AGDFDAGFFGLSDQEATATDPQQRLLLEAAWETFERAGIDPQSL
Streptomyces_natalensis_PimS2_mod3  GTTYSTQGGFLHD---AGEFDASFFGISPREALSMDPQQRLLLETTWEAFEHAGIDPTTV
Streptomyces_natalensis_PimS2_mod4  GHTYSTRGGFLHD---AADFDASFFGISPREALAMDPQQRLLLETSWEAMERAGIDPATL
S_viridochromogenes_aviM            LRTAIRSGSFLDD--DIAGFDAEFFGISPREAELMDPQQRLMLEVAWQALEHAGIPPHTL
Xanthomonas_albilineans_xabB_mod2   GEQLPRYAGFLDD---VDAFDAAFFGISRREAECMDPQQRKVLEMVWKLIEQAGHDPLSW
Xanthomonas_albilineans_xabB_mod3   GKTYSRWGAFLRD---IDGFDAAFFEWPDSVALESDPQARIFLEQAYAGIEDAGYTPGSL

[                                    121                                                     180]
Bf_PKS7                             ............................................................
Aspergillus_terreus_at1             ---VLNRTPATHCKRVGTFYGQASDDYREASSGQ-N--------VDTYYITGGCRAFATG
Aspergillus_terreus_at4             ---VRNRTPSTQQDRVGVFFGTTSDDWRGVNSGQ-D--------VGTYFIPGGNRAFVPG
Aspergillus_terreus_at5             ---VPNRTPSSMLDRIGTFYGQTSDDWRTLNAAE-K--------IDMYYIPGTIRAFATS
Gm_PKS5                             P--MNKVLGTNTGVFIGCFT----REYEAIMFKET----EIQQRYFA-TGTGTT--MLAN
Ch_PKS9                             T--MQDAVGTRTSVHVGCLL----QEYSQISQRDA----QMPGDYRI-VGSS-GLAMLSN
Ch_PKS8                             P--MESLSRTPTSVYCASFS----RDGETITGRDF----ASQSRYHA-TANG-S-SMLSN
Gz_PKS2                             P--VDSLKGSRTAVFSASML----EDYCRVTAVDP----DNLERTAV-TGSIVS-CIIPN
Gm_PKS2                             P--VESLKGSRTAVFSASML----EDYSRMTIVDP----DNLERTAV-TGSTVS-CIIPN
Ch_PKS10                            T--LQEILGSNTGVYTGSFV----YDYRDVMIKDT----DVAL-T-Y-SGTGTVPSTLAG
Ch_PKS5                             T--LEQVAGSNTSVYVSGFN----HDHLAILNSDP----ETTLRHRV-T--GLTNSMHSN
Ch_PKS7                             P--LEKIVGTKTSVFVGSFA----TDYTDLLTRDP----ESVPMYQC-TNSGQSRAMISN
Ch_PKS1                             P--MSKIVGTDTSVFVSSFA----TDYTDMLWRDP----ESVPMYQC-TNSGFSRSNLAN
Didymella_maydis_PKS1               P--LNKLVGTDTSVFTAVFC----TDYTDMLWRDP----EMVPMYQC-TNSGATRANMAN
Gz_PKS4                             P--LKQVAGTTTACFVGSSM----SDYRDAVVRDF----AHNPKYHV-LGTCEE--MIAN
Gz_PKS7                             R--KEDVDGTDAAVYVGSFV----KDYEQVCLRDP----DWQPQYAA-TGNGIA--IMAN
Gm_PKS7                             R--KEDIDGSDAAVYVGSFV----KDYEQVCLRDP----DWQPQYAA-TGNGIA--IMAN
Ch_PKS6                             T--LDQVSGTQTSCYIGTFT----ADFPNLQARDN----EGPSIYHA-TGMS-S-SLASN
Gz_PKS1                             R--MEDTTGSDTSCYVGTFT----RDWSDMLMRDP----ETAPKYSG-AGIGSG--MQAN
Ch_PKS4                             T--IKALEKSKTGVYCASTY----QDYDQILGRDP----ELSAKYRF-TGTGAS--MLAN
Gm_PKS6                             K--IDEVANQHMSCYIGACQ----HDYWDLQAYDM----DSAPKYTA-TGTG-P-ALLSN
Nc_PKS1                             PK--HTIAGKDVGVFVGGSF----PEYESHLFRDP----DTIPMHQ---ATGCAYAMQSN
Bf_PKS8                             PK--HEIVGKDVGVFVGGSF----SEYESASFVDT----DSVPMYQ---ATG-KFFLVSN
Nc_PKS2                             PR--EHIAGTRTGVFIGGNY----GEHRFSHIRDL----DTIPSFD---ATGNQPAFLSG
Ch_PKS2                             Q---ESIVGSKVGVFSTSNT----SDYTLSLKDDI----YSMPALV---GVLATACMLSN
Aspergillus_terreus_lovF            P--LEQVSGSKTGVFAGTMY----HDYQGSFQRQP----EALPRYFI-TGNAGT--MLAN
Penicillium_citrinum_mlcB           T--IDGMAGSNTSVFGGVMY----HDYQDSLNRDP----ETVPRYFI-TGNSGT--MLSN
Ch_PKS3                             SAWIPSSGSCSRAPTRPSRM----QDYHDAGLRDV----TTLPRFFL-VGVGSA--MASN
Nc_PKS3                             T--LQDVAGSNTSVYAGSFF----RDYHESLIRDP----DTLPRFLL-MGTGAA--MASN
Bf_PKS2                             S--LEKVRGSSTSVYVAIFN----RDYDRMMFKDT----NDIAKYHL-LGSGEA--IASN
Gz_PKS5                             P--VETLRGSNTGVYASIFE----RSYDRMGHKDL----STIGRTHL-NGTGES--ILSN
Gm_PKS1_CAC44633                    T--IEGLRGSPTAVYVGVMC----DDWSGIITRDL----EVFPQYG---ATGMARSIMSN
Gm_PKS1                             T--IEGLRGSSTSVYVGVMC----DDWNGILTRDL----EVFPQYG---ATGMARSIMSN
Bf_PKS5                             T--IEGLRGSNTGIYVGMMC----DDWAQAINRDW----ESTMTYA---ATGQSRAIVSN
Gm_PKS9                             R--PEGLRCEQTSVFVGQMC----DDWAQMLAKDW----DDIPTYM---GTGVSRAVMSN
Aspergillus_terreus_lovB            R--IQDLQGTSTAVYVGVMT----HDYETVSTRDL----ESIPTYS---ATGVAVSVASN
Penicillium_citrinum_mlcA           R--IQGLQGSSTAVYVGMMT----HDYETIVTREL----DSIPTYS---ATGVAVSVASN
Gz_PKS9                             T--IHGLHNSDTAVYVGLMC----TDYYVIQAADL----NSVPTYN---ATGVANSNASS
Ch_PKS16                            S--IDRLRGSDTAVFAGLMC----GDYEARMLRDL----DQVPTHF---ATGTSRAVMSN
Bf_PKS6                             S--IEEMQGTSTAVYVGLMC----ADYFDVLMRDI----EDIPQYL---ATGTARSIMSN
Bf_PKS3                             P--METIRGSDTGVFVGLMC----ADYYDVQMRDP----ETLPQYF---STGTARSIVSN
Ch_PKS17                            T--IDQLQGTDTAVYVGCMT----SDYVEMLLRDP----LDFPKYM---APGTARSILSN
Gz_PKS10                            P--MEDLKGSDTAVYVGCMT----GYYHEMLMREP----QDMPKYM---ATGTARSILSN
Gm_PKS10                            P--MEDLKGSDTAVYVGCMT----GDYHEMLMRDP----QDMPKYM---ATGTARSILSN
Nc_PKS4                             T--LQDYSGKKVAVFAGVMT----ADYDTLSQRDD----LSVSQYY---ATGNARSIISN
Bf_PKS4                             P--AETLRGSDTAVYTGVMF----HDYLSLSSQDH----MAIPKYH---ITGTAPNKASN
Gz_PKS11                            FDW----KGRPIGCFMGSFG----EDWVEMFAKEA----QQYGIYRV---MGYGDFMLSN
Ch_PKS14                            ANF----RGKKIGCYFGNMC----EDWGEMMNRDP----LWHGANKI---DGYQDWMLAN
Ch_PKS12                            TDW----RGKDIGTYVGSFG----NDWLEMAAKDR----LDKNMYKV---SGYSDFLLSN
Gm_PKS12                            ITY----RGKQVGCYVGTFG----DDWLIMNAKEP----LQGGLYAT---TGGADLMMAN
Ch_PKS13_pseudogene                 TEW----RSKEIGYYVGSFG----EDWLNENIMDA----HMLGIYRA---LRFIDFFLAN
Ch_PKS11_FUM1                       VNW----QGSNIGCYVGVWG----EDWLDLHAKDL----FDSGTYRV---SGSHDFAISN
Gm_FUM1_AAD43562                    TNW----RGSNIGCYVGVWG----EDWLDLHSKDL----YDSGTYRV---SGGHDFAISN
Gm_FUM1                             TNW----RGSNIGCYVGVWG----EDWLDLHSKDL----YDSGTYRV---SGGHDFAISN
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Ch_PKS15                             SNF----RGKKVGVYVGMFA----DDYVEMQSKDS----EPHEFLSL---TGHLDLFGSN
Nc_PKS5                              T--WESVSGTRTGVFVGNFC-L---DHWMIQSRDW----DNPRPYAF-TGAGTS--ILAN
Gm_PKS15                             S--AQELRGSKTGVYIGNFG-L---DQALMALKDS----EFMSPYTS-TGISGT--ILSN
Nc_PKS6                              T--LDQVSDANIGCYVGNFV-T---DFITMQLKDS----EYTHRYSA-TGLGTT--ILAN
Gm_PKS14                             S--MEAIAGSNTGVYVANFT-V---DYQPLQLRDP----DYLHRYVT-TGSGAT--IMSN
Bf_PKS9                              T--LSQLSGSNTGCYIGNFT-S---DYYLQGHRDH----NNPKPYSL-LGSGYT--IISN
Gm_PKS13                             S--METISKSKIGCYCAMFV-S---DYHDMLMQDP----EYLPTFIA-IGTTRT--MLAN
Bf_PKS10                             P--LESLDGAPVGCFVGSYA-SGKSDYHDMQMRDP----EQRVSGHA-VGTGRA--ILSN
Bf_PKS11                             T--LEQLSGSNTGVYVGQWA-S---DYQEMLLRDI----DFPPIYQA-SGVGAA--ISSN
Penicillium_patulum_6MSAS            S-------GSDTAVFWGV----NSDDYSKLV--LE----D-LPNVEAWMGIGTAYCGVPN
Byssochlamys_nivea_6MSAS             S-------GSDTAVFWGV----NSDDYSKLL--LE----D-LPNIEAWMGIGTAYCGVPN
Aspergillus_terreus_pksM             S-------GSETAVFMGV----NSDDYSKLL--LE----D-IPNVEAWMGIGTAYCGVPN
Aspergillus_parasiticus_pksL2        S-------GSDAAVFMGV----NSDDYGKLL--LE----D-LPHVEPWMGIGTAYCGVAN
Penicillium_griseofulvum_pks2        A-------GSDTSVYMGV----NSDDYGKLV--LE----D-LTGVGAHMGVGTAYCGIPS
Ch_PKS25                             A-------GSDTAVY--I----DPNDYSRML--ME----D-LQAIEAWSGIGTAHHGISN
Nc_PKS7                              ---VPNRTPSTRLDRIGTFYGQTSDDWREINAAQ-E--------VDTYFITGGVRAFGPG
Colletotrichum_lagenarium_pks1       ---VPNRTPSTRLDRIGTFYGQTSDDWREINAAQ-E--------VDTYYITGGVRAFGPG
Nodulisporium_sp_PKS1                ---VPNRTPSTRLDRIGTFYGQTSDDWREINAAQ-E--------VDTYYITGGVRAFGPG
Xylaria_sp_PKS12                     ---VPNRTPSTRLDRIGTFYGQTSDDWREINAAQ-E--------VDTYFITGGVRAFGPG
Bf_PKS12                             ---VPNRTHSTKLDRIGTFYGQTSDDWREINAAQ-D--------VDTYFITGGVRAFG--
Glarea_lozoyensis_PKS1               ---TPNRTPSTRLDRVGTFYGQTSDDWREINAAQ-E--------VDTYFITGGVRAFGPG
Monascus_purpureus_PKS1              ---SPNRTPSTRLDRIGTFYGQTSDDWREVNEAQ-D--------IDTYFITGGVRAFGPG
Bf_PKS13                             ---VRDRTPSTQAHRIGTFYGQTSDDWREINAAQ-D--------IDTYFITGGVRAFGPG
Ch_PKS18                             ---VPNRTPSTKLERIGTFYGQTSDDWREINAAE-N--------IDTYFITGGVRAFAPG
Bf_PKS14                             ---VHGR--GIHQRRVGTFYGCSSDDYREVNTGQ-D--------IGTYFIPGGCRAFGPG
Ch_PKS20                             ---SPNRTRSTSSPRVGTYHGQASDDWRELNASQ-N--------IGTYAVPSGERGFANG
Aspergillus_nidulans_wA              ---VPDSTPSTQRDRVGIFYGMTSDDYREVNSGQ-D--------IDTYFIPGGNRAFTPG
Aspergillus_fumigatus_alb1           ---VPNSSPSTQRDRVGIFMGMTSDDYREINSGQ-D--------IDTYFIPGGNRAFTPG
Gz_PK12                              ---VPDRPPSTQRDRVGVFYVHPSDDWREVNSGQ-N--------VDTYFIPGGNRAFTPG
Gm_PKS3_CAC88775                     ---VPDATPSTRPDRVGIFYGVTSNDWMETNSAQ-N--------IDTYYIPGGNRAFIPG
Gm_PKS3                              ---VPDATPSTRPDRVGIFYGVTSNDWMETNSAQ-N--------IDTYFIPGGNRAFIPG
Gz_PKS12                             ---VPDATPSTRPDRVGVFYGVTSNDWIETNSAQ-N--------IDTYFIPGGNRAFIPG
Gm_PKS4_CAC92399                     ---VPDRTPSTQRNRVGVYYGTTSNDWGEVNSSQ-D--------VDTYYIPGANRAFIPG
Gm_PKS4                              ---VPDRTPSTQRNRVGVYYGTTSNDWGEVNSSQ-D--------VDTYYIPGANRAFIPG
Aspergillus_parasiticus_pksL1        ---VPDTTPSTQRDRIGVFHGVTSNDWMETNTAQ-N--------IDTYFITGGNRGFIPG
Aspergillus_nidulans_pksST           ---VPDTTPSTQRNRIGVFHGVTSNDWMETNTAQ-N--------IDTYFITGGNRGFIPG
Gz_PKS13                             ---SDGATRAVDPARIATFFGQCNDDWHDVSHHTLG--------CDAYTLQGVQRAFGAG
Bf_PKS15                             ---ARDSSTSTHPSKIGTYFGQTVDDWKDINAQ-MG--------IDTHYLPSLDRAFHPG
Bf_PSK19                             P------SSTSETDDYGCYVGAVMNSYYE-NLACHP--------PNTYATIGTGRAFLSG
Ch_PKS22                             RE---------NGDNIGCFIGASFNEYLD-NTSAHA--------PTAYTSTGTIRAFLCG
Bf_PKS16                             RE---------NNDPIGCFIGASFVEYLD-NTNSNA--------PTAYTSTGTIRAFLCG
Ch_PKS19                             ---VANRTQSTRLQRIGTYYGQAADDYREVNQGQ-E--------VGTYYIPGGCRAFGPG
Ch_PKS23                             RE---------NGDKVGCFIGASYVEYAD-NTNAYP--------PTAYSAVGTIRAFLCG
Ch_PKS21                             KQQANADANGPDPKNIGCYIGMCGNDYVA-NTSHHA--------PNAFTATGTLRSFVAG
Bf_PKS17                             NAD----------KHIGCFLGVGNVDYEA-NVACYP--------ATAYSATGNLKSFVAG
Bf_PKS18                             RQLISGDKGGNEQNDVGCFFGVCGSDYND-NIASHP--------PNAFSSLGSLRAFLSG
Bf_PKS20                             KQEAETHERTQNKDTTGCFIGMIAPDYSL-NLASHP--------ASPYTGIGMHRSYVAG
Homo_sapiens_FAS                     -----SLRGTHTGVWVGV----SGSETSEALSRDPE-------TLVGYSMVGCQRAMMAN
Gallus_gallus_FAS                    -----ALRGTDTGVWVGA----SGSEALEALSQDPE-------ELLGYSMTGCQRAMLAN
Caenorhabditis_elegans_FAS           -----DLRGSKTGVFVGC----SASETSGMLTQDPD-------TVTGYTLTGCVRSMFSN
Bombyx_mori_FAS_p270                 -----ELRDTKTGVFIGA----CFSESEKTWFYEKM-------QVNGFGITGCSRAMLAN
Ch_9497_PKS24_3p_of_nps7              R-------GSRTGVYMGV----CS---IPAHSTAL----C-LQELGGYDATGSAGATMSG
Nc_3_oxoacyl_ACP_synthetase          E--DLEATGVCMGSGIGNLDDF-YNTSVTYDKEGYKRV--S-PLFVPKIXINLGAGHIAM
Homo_sapiens_3_oxoacyl_ACP_synth     A--DQVATGVAIGMGMIPLEVV-SETALNFQTKGYNKV--S-PFFVPKILVNMAAGQVSI
Glycine_max_beta_ketoacyl_synth      SKIDKERAGVLVGSGMGGLTVF-SDGVQALIEKGHRKI--T-PFFIPYAITNMGSALLGI
Streptomyces_coelicolor_act          --LDPARVGVSLGSAVAAATSL-EREYLLLSDSGRDWEVDA-AWLSRHMFDYLVPSVMPA
Streptomyces_avermitilis_pks9        --TDPHRCGVSVGSAIGGTMSL-DREYNVLSDGGRKWLLDH-EYAVPHMYNYLVPTSIAA
Bacillus_subtilis_pksK_mod2          -PQTSVFMSASNNSY--------R---ALLPSDTTE-SLETPDGYVSWVLAQSGT--IPT
Bacillus_subtilis_pksK_mod3          S-------GTGTGIFIGT----GNTGYK-DLFHRA----NLPIEGHAA-TGHMIPSVGPN
Bacillus_subtilis_pksL_mod1          AKPKGRNKRQHVGVFAGV----MHKDYT---LVGA----EEASAENVF-PLSLNYAQIAN
Bacillus_subtilis_pksL_mod2          GRKRDAELGGSVGVYVGV----MYEEYQ---LYGA----QEQVRGRSL-ALTGNPSSIAN
Bacillus_subtilis_pksL_mod3          NEKK-------CGVYLGI----MSNEYG-VMLNR---------QSRAN-ATGNSFAIAAA
Bac_subtilis_mycA_pks1_mod2          S-------GSQLGVYVGY----SKVGYDYERLLSA----NYPEELHHY-IVGNLPSVLAS
Microcystis_aruginosa_mycE           A-------DNKVGVFVGI----TSIDHALKVYGTN----Y-D-QIDSFFGSGNALSAAAG
Microcystis_aruginosa_mycG           QGSIGIFAGASMNTYLINNC-YPNRGKLDSNDELQPFTLDSMGGFQTMVANDKDY--LTT
Mycobacterium_leprae_pksE            S-------GTRTAVMMGL----SSWDY--TIVNIE----R-RADIDAYLSTGTPHCAAVG
Mycobacterium_tuberculosis_mas       A-------GSSTAVFTGL----THEDY--LVLTTT----A-GGLASPYVVTGLNNSVASG
Mycobacterium_tuberculosis_ppsC      R-------GTQTSVFVGV----TAYDYMLTLAGRL----R-PVDLDAYIPTGNSANFAAG
Mycobacterium_tuberculosis_ppsD      S-------GTRTGVMMGL----SSWDY--TIVNIE----R-RADIDAYLSTGTPHCAAVG
Mycobacterium_tuberculosis_ppsE      DGSIGVYGTSSPSGYLLHNL-LSHRDPNAVLAEGLNF-----DQFSLFLQNDKDF--LAT
Myxococcus_xanthus_ta1_mod2          -GPCGVFMTASNSFY--------HQGSPQFPADGQP-VLRTAEEYVLWVLAQAGS--IPT
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Nostoc_sp_nosB                      NGLIGVYAGVGMNRYLVNNL-YPHHQLLET-----------VDPLQLTISNDKDF--LPT
Pseudomonas_syringae_cfa6           H-------GSLTGVYAGI----MGTEYGTQIQ--H----A-SEDVTGYGYMGTATCVAAG
Pseudomonas_syringae_cfa7           K-------NSATGVFLGA----NQNGYLADLQ--R----R-NPAADGYRLQGGLSSIISG
Sorangium_cellulosum_epoA_mod1      V-------GTETGVFIGI----GPSEYEAALPRAT----A-SAEIDAHGGLGTMPSVGAG
Sorangium_cellulosum_epoC_mod2      E-------GSIGVYAGAN----MSSYLTSNLHEHP----A-MMRWPGWFQTLIGNDKDYL
Sorangium_cellulosum_epoF_mod9      D-------GSRTGVFLGA----CSSDYSHTVAQQR----R-EEQ-DAYDITGNTLSVAAG
Stigmatella_aurantiaca_mxaB2_B1     A-------GSKTGVFMGV----MSSDYMARLLKEN----D-ATRFDGYMATGNGYSFVPG
Stigmatella_aurantiaca_mxaC1        S-------GSRSGVFIGA----CNDDY-HCMQVER----P-ETG-DAFSATGVAASVLSG
Stigmatella_aurantiaca_mxaC2        A-------GTRTGVFVGV----CGYDY-AMLQAER----D-VEG-DVYSVIGCSNSVIAG
Stigmatella_aurantiaca_mxaC3        A-------NTRTGVFIGI----GSNEYAMLNGVGS----A-SAAGDAYIATGNDSSFAAG
Stigmatella_aurantiaca_mxaD         A-------GSRTGVFLGI----IGSDYAQLQARLL----G-DSP-DIYHLTGTSLNAAAG
Stigmatella_aurantiaca_mxaE         A-------GSRTGVFVGI----YSDDY-ALLQVGN----P-SAR-DSSSVTGALNCVVPG
Stigmatella_aurantiaca_mxaF         Q-------GSPTAVCFGV----VWTDYEAMLQRMG----L-R-RISSYTSSGSHHSIVAN
Streptomyces_natalensis_PimS0       R-------GSRTGVFTGA----MDRGYGTSAS--A----A-PSAWESMLITGTAGSAVSG
Streptomyces_natalensis_PimS2_mod3  H-------GTTTGTFIGS----TYQEY--GLG--V----E--DGSAGHLVTGTSPSVLSG
Streptomyces_natalensis_PimS2_mod4  R-------GSSTGTFIGA----SYQDY-RAFG--A----G-PDGAEGHLITGTISSVLSG
S_viridochromogenes_aviM            A-------GTDTGVFAGV----CTYDYGA--GRLE----D-LPNIDAWTGIGAAVCAVSN
Xanthomonas_albilineans_xabB_mod2   G-------GQPVGLFVGA----HTSDYGELLASQP----QLMAQCGAYIDSGSHLTMIPN
Xanthomonas_albilineans_xabB_mod3   SKS------QRVGVFVGV----MNGYY----------------------SGGARFWQIAN

[                                    181                                                  240]
Bf_PKS7                             ............................................................
Aspergillus_terreus_at1             RINYFFKFSGPSFNCDTACSSGLASIQMACTSLLHGDA-DTVVAGGLNVLCDSDG-FTGL
Aspergillus_terreus_at4             RISYFFRFSGPSLSIDTACSSSFAAIQAACSYLWRGEC-DTAIAGGTNILTNPDN-FAGL
Aspergillus_terreus_at5             RINYHFKFKGPSYNVDTACSSSFAAIQLACTSLLAKEC-DTALAGGLNVMTTPDL-FAGL
Gm_PKS5                             RLSYFYDLHGPSISLDTACSSSLNACHLACNSLRLGEC-DMALAAGYNLFYNPD-TIIPL
Ch_PKS9                             RLSWFYDFSGPSMTVDTACSGGLVALHLACQELLAGSV-NMSLVCGTNLCLLPDSTAL-L
Ch_PKS8                             RISHFFDLAGPSLTVDTACSSGLYALHLGVQSILTGES-TMSLVCGANTFITPESQALAL
Gz_PKS2                             RVSWYFDLRGPSINVNNACSSSLTAVDMACKALNSGDAYSQAVVTGTNVLLDPSI-FQVL
Gm_PKS2                             RVSWYFDLRGPSIHVNTACSSSLSAVDMACKALKSGDA-SSAVVTGANLLLDPSI-FQVL
Ch_PKS10                            RVAWFFDFRGPAFTVDTACSSSMVALHQAVIGLKSRECNLVALACGTNVILSPEFG-QQL
Ch_PKS5                             RVSWFFDLKGPSVTIDTACSSSMAALHLGSQSLRTGES-DMSIITGVTILNYPGD-VNGM
Ch_PKS7                             RLSYFFDLHGPSVTVDTACSGSLVALHLACQSLRAGEA-KSAIAAGVNVVLNHEF-MTTM
Ch_PKS1                             RISYSFDLKGPSVLVDTACSGGLTALHLACQSLLVGDV-RQALAAGSSLILGPEM-MVTM
Didymella_maydis_PKS1               RVSYSFDLKGPSITVDTACSGGLTALHLACQSLVTGES-TQAVVSGSSLILGPET-MVTM
Gz_PKS4                             RISHFFDIHGPSATVHTACSSSLVAIHLACQSLLSGDA-EMALAGGVGMILTPDG-TMQL
Gz_PKS7                             RISYFFNLHGPSMTIDTGCSGSLVSVHLAAQSLRTKET-SLAIAAGAGMILTPNT-MMPM
Gm_PKS7                             RISHFFNLHGPSMTIDTGCSGSLVSVHLASQSLRAKET-SLAIAAGAGMILTPNT-MMPM
Ch_PKS6                             RLSWFYNLRGPSLTIDTACSSSLTAFHLACQSLRTGES-EMSVVGGANLMFGPDMSIL-L
Gz_PKS1                             RVSWFFDWHGPSLTLDTACSSSLVALHLACQSINDGVS-KVAVAAGTTLMLNPDM-PMWM
Ch_PKS4                             RISYFFDLRGPSMTIDTACSSTLVAIHEACSALRMGEI-DQALIGGVNLILDPD-KLMVQ
Gm_PKS6                             RISWFFNLKGPSVTIDTACSSTLTALHLAGQSIRNGES-DSALVGGLGLHLLPNFGVF-M
Nc_PKS1                             RISHFFDLRGPSFTADTACSSSMVAIHLACQSLRTGES-SAALVGGCHLNMLPEF-WISF
Bf_PKS8                             RISHFFDLRGPSFTMDTACSSSLVALHQACQSIRNGEC-KSAITGGCHLNMLPEN-WISM
Nc_PKS2                             RLAYYFNLHGPTFTVDTACSSSLHALHLAVQSIRNGEC-DAAVVGASHLITQPDV-WVSM
Ch_PKS2                             IVSNTFDLKGPSVSIDTACSSAFYALQLASQSLRSGET-EMCIVSGCALNISP-WRWTML
Aspergillus_terreus_lovF            RVSHFYDLRGPSVSIDTACSTTLTALHLAIQSLRAGES-DMAIVAGANLLLNPDV-FTTM
Penicillium_citrinum_mlcB           RISHFYDLRGPSVTVDTACSTTLTALHLACQSLRTGES-DTAIVIGANLLLNPDV-FVTM
Ch_PKS3                             RLSHYFDLRGASMSIDTGCSTTLTALHQACNDLRNGES-DMSVVSGANLMLNPDM-FITM
Nc_PKS3                             RLSHFFDLRGPSMSVDTGCSTTLTALHQACQSLRSGES-TMSIVGGANIMFNPDM-FLAM
Bf_PKS2                             RISYTFDLKGPSMTVDTGCSGSLVALHQACQGLRSGDT-DMALVGGTSLILSPDT-MVPM
Gz_PKS5                             RVSYCFDLRGPCMTIDTGCSGSLVGLHQACQSLRLGES-ELALVGGSQLVIQPDV-LYTV
Gm_PKS1_CAC44633                    RISYFFDWHGPSMTIDTACSSSLVAVHQAIQTLRSGES-EVAIAAGANLILTPGM-YIAE
Gm_PKS1                             RISYFFDWHGPSMTIDTACSSSLVAVHQAIQTLRSGES-QV...................
Bf_PKS5                             RLSYFFDWHGPSMTVDTACSSSLVAVHQGVTSLRNGEC-PVVIAAGVNLILGPGM-WIAE
Gm_PKS9                             RVSYFFDWHGPSMSIDTACSSSLVAVHEAVRTLRSGES-NVAVAAGANLILLPGM-YICE
Aspergillus_terreus_lovB            RISYFFDWHGPSMTIDTACSSSLVAVHLAVQQLRTGQS-SMAIAAGANLILGPMT-FVLE
Penicillium_citrinum_mlcA           RVSYFFDWHGPSMTIDTACSSSLAAVHLAVQQLRTGES-TMAVAAGANLILGPMT-FVME
Gz_PKS9                             RVSYFFNWHGPSMTIDTACSSSLVAVHEAVQALRNGTS-RMAVACGTNLILSPLP-FISE
Ch_PKS16                            RVSYFFDWHGPSVTIDTACSSSLVAVHHAVQALRSGDS-HAAVACGSNLIFGPEM-YVIE
Bf_PKS6                             RISYFFDWKGPSMTIDTACSSSLVAVHNAISTLRSGQS-RTAIAAGANLIFGPEM-YIGE
Bf_PKS3                             RVSYFFDWKGPSLTIDTACSSSLVAVHQAVSALRNGEC-RSAVAAGVNLIFGPEM-FNGE
Ch_PKS17                            RISYFYDWHGPSMTIDTACSASLVAVHEAVQALRSGIS-RVACAAGSNAILGPEN-FVIE
Gz_PKS10                            RISYLFDWKGPSMTIDTACSSSLVAVYDAVTALRNGVS-RIACAGGVNLILGPEM-MISE
Gm_PKS10                            RISYLFDWKGPSMTIDTACSSSLVAVYDAVTALRNGVS-KIACAGGANLILGPEM-MISE
Nc_PKS4                             RVSYFFNFHGPSMTIDTACSSSLVALHQAVLSLRSGEA-EMACVSGVNLILTPEQ-FVVE
Bf_PKS4                             RISYFFDWHGPSVTVDTACSSSLVALDHAVQQLRSGSS-TLAVAAGANLLLDGRP-FIGF
Gz_PKS11                            RVSYELDLMG..................................................
Ch_PKS14                            RISYEFGLTGPSMTIRTACSSALTGLAEAFAAIQRGIC-EGAIVAGSNLILAPGMT-QQM
Ch_PKS12                            RLSYEYDLRGPSMTIRTACSASLMGLHEACLAIRNGDC-SAALVGGSNLFWSPDTM-ADM
Gm_PKS12                            RISYEYDFQGPSMVIKTGCSSSAVALHEACRAIQRGDA-SSAIVGGANMIMTPALT-ATM
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Ch_PKS13_pseudogene                 RVLYEYNWTGLSMIVKIGCSASLVALHLAVKALGARSC-SAAIVIGCNLMTSPLIT-VVY
Ch_PKS11_FUM1                       RISYEYNLKGPSYTIKAGCSSSLIALHEAVRAIRAGDC-DGAIVAGTNLIFSPTMS-MAM
Gm_FUM1_AAD43562                    RISYEYDLKGPSFTIKAGCSSSLIALHEAVRAIRAGDC-DGAIVAGTNLVFSPTMS-VAM
Gm_FUM1                             RISYEYDLKGPSFTIKAGCSSSLIALHEAVRAIRAGDC-DGAIVAGTNLVFSPTMS-VAM
Ch_PKS15                            RVSHEFDWTGPSMTIKTGCSASLVCLDQAVKALRAGDC-DAAIVGGANLIMSPALS-CAL
Nc_PKS5                             RISYIFNLQGPSLTVDTACSSSMYALHLAVNAIRAGDC-DSAIVASANWIADPGVQIALD
Gm_PKS15                            RINYALDLNGPSFTVDTACSSSIYALHLACLGLQNGDC-DAAFVGAANAIRSIEAQLFST
Nc_PKS6                             RISHVFNMKGPSFVIDTACSSSLYCLHAAVAALIAGEC-DSAIVAGANLIQSPEQQLATM
Gm_PKS14                            RISHVFNLHGPSLSVDTACSSSIYAFHQAIKAIKAGDC-DSAIVASANLILSPEPHIAAA
Bf_PKS9                             RVSYLFDLCGPSLTIDTACSSSLYSLHIACRALQTKEI-DAAVVGGTNLMLAVETQMSTD
Gm_PKS13                            RISHALDLGGPSVTIDTACSGALVALHLACQALQAGEC-DGAVIGASNLFLSPDYALSLT
Bf_PKS10                            RLSYEFDLQGPSMTIDTACSGSLVGLDVACRYLQSREI-DSAIIATSNLYLNPEHVMDLG
Bf_PKS11                            RISYCFNLHGPSLTLDTGCSASLVALHQAVHSLRAGET-DKCFVAGVNLQLDPQRYGYQN
Penicillium_patulum_6MSAS           RISYHLNLMGPSTAVDAACASSLVAIHHGVQAIRLGES-KVAIVGGVNALCGPGL-TRVL
Byssochlamys_nivea_6MSAS            RISYHLNLMGPSTAVDAACASSLVAVHHGVQAIKSNEP-KIAIVGGVNAICGPGL-TRVL
Aspergillus_terreus_pksM            RISYHLNLMGPSTAVDAACASSLVAIHHGRQAILQGES-EVAIVGGVNALCGPGL-TRVL
Aspergillus_parasiticus_pksL2       RISYHLNLMGPSTAVDAACASSLVAIHLGRQAILSGES-KVAIVGGVNAIFGPGL-TSVL
Penicillium_griseofulvum_pks2       RISYLLDLMGPSVALDAACASSLVAVHHARQAIRAGET-DLAIAGGVNALLGPGL-TRVL
Ch_PKS25                            RISYHPDLRGPSRAVDAACASSLVALHLARGAIVSGES-TLAICSGVNVICTPEI-TCML
Nc_PKS7                             RINYHFGFSGPSLNIDTACSSSAAALQVACTALWARDC-DTAIVGGLSCMTNPDI-FSGL
Colletotrichum_lagenarium_pks1      RINYHFGFSGPSLNVDTACSSSAAALNVACNSLWQKDC-DTAIVGGLSCMTNPDI-FAGL
Nodulisporium_sp_PKS1               RINYHFGFSGPSLNIDTACSSSAAALQVACTSLRAKEC-DTAIVGGLSCMTNSDI-FSGL
Xylaria_sp_PKS12                    RISYYFGFSGPSLNIDTACSSSAAAMHVACTSLWAKEC-DTAIVGGLSCMTNSDI-FSGL
Bf_PKS12                            RINYHFGFSGPSFNIDTACSSSAAALQLACTSLWAGDC-DTAVVGGLSCMTNPDI-FSGL
Glarea_lozoyensis_PKS1              RINYHFGFSGPSFNVDTACSSSAAALQLAYTSLCAKDC-DTAIVGGLSCMTNSDI-FAGL
Monascus_purpureus_PKS1             RINYHFKFSGPSFNVDTACSSSMAALHVACNSLWTGDC-DMAITGGLNIMTNPDI-FAGL
Bf_PKS13                            RINYHFGFSGPSYSVDTACSSSMAAINLAVTSLRAGDC-DTVFAGGMNVMTNPDI-FSGL
Ch_PKS18                            RINYYFKFSGPSYSVDTACSSSLAAIQLACTSLWAGDC-DTACAGGLNVLTNPDI-FSGL
Bf_PKS14                            RINYFMKFWGPSYSIDTACSSSLAAIQTACTSLWSGDI-DMAITGGMNIITNSDS-YAGL
Ch_PKS20                            RINYFFKFNGPSFNMDTACSSGLAAVNAACSALWAGDV-DIAIAGGLNVITDPDN-LSAR
Aspergillus_nidulans_wA             RINYYFKFSGPSVSVDTACSSSLAAIHLACNSIWRNDC-DTAITGGVNILTNPDN-HAGL
Aspergillus_fumigatus_alb1          RINYYFKFSGPSVSVDTACSSSLAAIHLACNAIWRNDC-DTAISGGVNLLTNPDN-HAGL
Gz_PK12                             RLNYFFKFSGPSASVDTACSSSLAALHLACNSLWRNDC-DTAIAGGTNVMTNPDN-FAGL
Gm_PKS3_CAC88775                    RINYFFKFSGPSYAVDTACSSSLAGIHLACNALWQGDV-DTAIAGGTNVLTNPDY-HAGL
Gm_PKS3                             RINYFFKFSGPSYAVDTACSSSLAGIHLACNALWQGDV-DTAIAGGTNVLTNPDY-HAGL
Gz_PKS12                            RINYFFKFSGPSYAVDTACSSSLAGIHLACNALWQNDV-DTAIAGGTNVLANPDF-HAGL
Gm_PKS4_CAC92399                    RVNYFFKFTGPSIAVDTACSSSLAAINLAITSLKNRDC-NTAIAGGTNVMTNPDN-FAGL
Gm_PKS4                             RVNYFFKFTGPSIAVDTACSSSLAAINLAITSLKNRDC-DTAIAGGTNVMTNPDN-FAGL
Aspergillus_parasiticus_pksL1       RINFCFEFAGPSYTNDTACSSSLAAIHLACNSLWRGDC-DTAVAGGTNMIYTPDG-HTGL
Aspergillus_nidulans_pksST          RINFCFEFSGPSYSNDTACSSSLAAIHLACNSLWRGDC-DTAVAGGTNMIFTPDG-HTGL
Gz_PKS13                            RIAFQFKWEGPTYSLDSACASTASSIHLACTSLLAKET-DMAVAGAANVVGYPHS-WTSL
Bf_PKS15                            RVAHYFKWGGGFYSVDTACSSSLTCAHLACEALNNREL-DMTIVAGGSLLGAPEI-FSGL
Bf_PSK19                            SISHHFGWIGPSLTIDTACSSSLVAINTACRAIWSGEC-TRAVAGGTNVISSPGD-YQNL
Ch_PKS22                            KISYYFGWSGPAEVIDTACSASLVAINRACRAILSGEC-AQALAGGINIMSGINN-FMDL
Bf_PKS16                            KISYYFGWSGPSEVIDTACSSSLVAIHRAVRAIQSGEC-PMALTGGINIMTGINN-YLDL
Ch_PKS19                            RINYFFKFAGPSYSIDTACSSGLAAIEVACQALWSGEV-DTAVAGGVNILTNPDG-FTGL
Ch_PKS23                            KLSHCYGWTGPAEVIDTACSSSLVAINRACRSIQSGEC-PMAIAGGVNIISSVHN-YLNL
Ch_PKS21                            KLSHYFGWLGPSLTLDTACSASAVAIHTACRAILSGEV-TAALAGGTNTISEPGV-YQNL
Bf_PKS17                            KISHYFGWTGPSLTIDTACSSSSVSIHYACRSILSGEC-NSALAGGINIITSPNW-YHNL
Bf_PKS18                            KVSHFFGFTGPSVIYDTACSSSAVAIDAACKSLQAGDC-SAALAGGVSLYTSPYF-YENL
Bf_PKS20                            RLSHHFGWTGPSQTIDTACSSSMVAIHQACRSIQTGEC-TRAVAGGVNLITNLVL-YDAL
Homo_sapiens_FAS                    RLSFFFDFRGPSIALDTACSSSLMALQNAYQAIHSGQC-PAAIVGGINVLLKPNTS-VQF
Gallus_gallus_FAS                   RISYFYDFTGPSLTIDTACSSSLMALENAYKAIRHGQC-SAALVGGVNILLKPNTS-VQF
Caenorhabditis_elegans_FAS          RISYTFDLQGPSFSVDTACSSSLLALQLAVDSIRQGQC-DAAIVAGAHLTLTPTAA-LQF
Bombyx_mori_FAS_p270                RISYWLGVTGPSYTVDSACSSSLYALEHAFRAIRDGHC-DAAIVGGSNLCLHPFVS-LQF
Ch_9497_PKS24_3p_of_nps7            RLSYALGLEGPALTVDTACSSSLVTTHLACNALRQGEC-DMAVSGGITLLLTPGM-HVEF
Nc_3_oxoacyl_ACP_synthetase         RYGFR----GPNXSATTACTTGAHSIGDASRFIAFGDA-DVMVAGGSESCIHP-LTFAGF
Homo_sapiens_3_oxoacyl_ACP_synth    RYKLK----GPNHAVSTACTTGAHAVGDSFRFIAHGDA-DVMVAGGTDSCISP-LSLAGF
Glycine_max_beta_ketoacyl_synth     DLGFM----GPNYSISTACATSNYCFYAAANHIRRGEA-DLMIAGGTEAAIIP-IGLGGF
Streptomyces_coelicolor_act         EVAWAVGAEGPVTMVSTGCTSGLDSVGNAVRAIEEGSA-DVMFAGAADTPITP-IVVACF
Streptomyces_avermitilis_pks9       DVAWTVGAEGPVSLVSTGCTAGIESVSHAARLIREGSA-DVMLAGGSDASLSP-ICVACF
Bacillus_subtilis_pksK_mod2         MISHKLGLRGPSYFVHANCSSSLIGLHSAYKSLLSGES-DYALVGGATLHTESNIGYVHQ
Bacillus_subtilis_pksK_mod3         RMSYFLNIHGPSEPVETACSSSLVAIHRAVTAMQNGDC-EMAIAGGVNTILTEEA-HISY
Bacillus_subtilis_pksL_mod1         RVSYFCNFHGPSMAVDTVCSSSLTAVHLALESIRHGEC-DVALAGGVNLSLHPNK-YMTY
Bacillus_subtilis_pksL_mod2         RVSYYFDFHGPSIALDTMCSSSLTAIHLACQSLQRGEC-EAAFAGGVNVSIHPNK-YLML
Bacillus_subtilis_pksL_mod3         RIPYFLNLKGPAIPIDTACSSSLVGTHLARQALINKEI-DMALVGGVSLYLTPES-YMSM
Bac_subtilis_mycA_pks1_mod2         RIAYFLNLKGPAVTVDTACSSSLVAVHMACKALLTGDC-EMALAGGIRTSLLPMR-I---
Microcystis_aruginosa_mycE          RLSYFLNLHGPCLSIDTACASSLVAVHQGIRSLRNREC-ELALVGGVNLILEPAI-TISL
Microcystis_aruginosa_mycG          RISYKLNLHGPSVNVQTACSTGLVVVHLACQSLISGES-DMALAGAASINSPQKIGYLYQ
Mycobacterium_leprae_pksE           RISYLLGLRGPAMAVDTACSSSLVAIHLACQSLRLRES-DVALAGGVQLILSPFT-AIAL
Mycobacterium_tuberculosis_mas      RIAHTLGLHGPAMTFDTACSSGLMAVHLACRSLHDGEA-DLALAGGCAVLLEPHA-SVAA
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Mycobacterium_tuberculosis_ppsC     RLAYILGARGPAVVIDTACSSSLVAVHLACQSLRGRES-DMALVGGTNLLLSPGP-SIAC
Mycobacterium_tuberculosis_ppsD     RIAYLLGLRGPAVAVDTACSSSLVAIHLACQSLRLRET-DVALAGGVQLTLSPFT-AIAL
Mycobacterium_tuberculosis_ppsE     RISHAFNLRGPSIAVQTACSSSLVAVHLACLSLLSGEC-DMALAGGSSLCIPHRVGYFTS
Myxococcus_xanthus_ta1_mod2         MVSYKLGLKGPSLFVHTNCSSSLSALYVAQQAIAAGDC-QTALVGAATVFPSANLGYLHQ
Nostoc_sp_nosB                      RVAYKLNLTGTAVNVQTACSTSLVAVHLACQSLLNYEC-DMALAGGVTLSIPQKIGYLHQ
Pseudomonas_syringae_cfa6           RVSYCLGLQGPALAIDTACSSSLVAIHTACEALRSNDC-QLALAGGVTVMPTPGV-LIDF
Pseudomonas_syringae_cfa7           RIAFVLGLRGPEMTVDTACSASLTDIHLAVQSLRRHEC-SLALAGGVTDMDTPEV-FAEF
Sorangium_cellulosum_epoA_mod1      RISYVLGLRGPCVAVDTAYSSSLVAVHLACQSLRSGEC-STALAGGVSLMLSPST-LVWL
Sorangium_cellulosum_epoC_mod2      HVSYRLNLRGPSISVQTACSTSLVAVHLACMSLLDREC-DMALAGGITVRIPHRAGYVYA
Sorangium_cellulosum_epoF_mod9      RLSYTLGLQGPCLTVDTACSSSLVAIHLACRSLRARES-DLALAGGVNMLLSSKT-MIML
Stigmatella_aurantiaca_mxaB2_B1     RVSYVLGLQGPCMPVDTACSSSLVALHLASESLRAGES-NLALAGGVNLILSPET-MICL
Stigmatella_aurantiaca_mxaC1        RLSYLFNLQGPSLVVDTACSSSLVSLHLACQSLRNREC-NMALAGGVNLILSPQS-VLLV
Stigmatella_aurantiaca_mxaC2        RLSYLMDLRGPAMTVDTACSSSLVALHLASQSLRNREC-DAALVGGVNLLLSQRP-SSWL
Stigmatella_aurantiaca_mxaC3        RLAYLLRFQGPTMSLNTACSSSLVAVHLACQSLRAGES-NLALAGGVNMTLAPHS-TIYL
Stigmatella_aurantiaca_mxaD         RLSYTLGLQGPCMSIDTACSSSLVALHVACQSLRNREC-DLALSAGVNLMLMPDA-TIAL
Stigmatella_aurantiaca_mxaE         RLSYLLDFQGPCLAVDTACSSSLVALHLATQSLRNQEC-SMALACGVNLILSPLS-SSRV
Stigmatella_aurantiaca_mxaF         RVSYVLGLRGPSMAIDTACSSSLSAVHLACESLRRGES-TMALVGGVNLTIAPDS-TVGL
Streptomyces_natalensis_PimS0       RIAYTYGLEGPALTVDTASSSSLVALHLACRSLRSGET-DLALAGGVTVMATPAP-FAHF
Streptomyces_natalensis_PimS2_mod3  RLAYLFGLEGPAVTVDTACSSSLVALHLACQSLRNGES-SLALAGGATVMTNPNP-FVAF
Streptomyces_natalensis_PimS2_mod4  RLSYTYGFEGPAVSLDTACSSSLVALHLACQSLRNGES-SLALAGGVSIMSTPGA-FVGF
S_viridochromogenes_aviM            RVSHALDLRGPSLSIDTACSASLVALHTAAQSLRLGEC-TVALAGGVNLLVSPGQ-TIAL
Xanthomonas_albilineans_xabB_mod2   RASRWFNFTGPSEVINSACSSSLVALHRAVQSLRQGES-SVALVLGVNLILAPKV-LLAS
Xanthomonas_albilineans_xabB_mod3   RVSYQFDFRGPSLAVDTACSASLTAIHLALESLRSGSC-EVALAGGVNLLVDPQQ-YLNL

[                                    241                                                 300]
Bf_PKS7                             ............................................................
Aspergillus_terreus_at1             SRGHFLSKT-GGCKTFD---------CNADGYCRGDGVGSVVMKRLDDAQRD--NDNILG
Aspergillus_terreus_at4             DRGHFLSTT-GNCNTFD---------DEASGYCRSDAVGSVILKRLEDAEADN--DPIFA
Aspergillus_terreus_at5             SRAHFLSKT-GSCKTFD---------DGADGFCRGDGVGTVVLKRLEDAEADN--DPILA
Gm_PKS5                             TALGFLSPD-GRCYSFDERA------NR---YSRGEGFGMVVLKRLSDAIRDG--DCIRA
Ch_PKS9                             SSLNMMSKD-SVCYSFDERA-------S--GYARGEGFGVLVLKRLSEAIADG--NNIRG
Ch_PKS8                             SNGGFLSVD-GKSYSFDAKA-------N--GYARGEGFGFVLLKPLDAAIRDG--DVVRA
Gz_PKS2                             ANQGFLSPD-GVCYSFDERA------N---GYARGEGVIAVVLKPVQAAIENG--DMIRA
Gm_PKS2                             ANQRFLSPD-GVCYSFDERA------N---GYARGEGVIAVVLKPVQAAIENG--DMVRA
Ch_PKS10                            NGLGVLSPQ-GASKSFD---------KEANGYGRGEGISVVVLKRMSDAIRDG--DTIRA
Ch_PKS5                             SHQGFLSPD-GRCFSFDHRA-------N--GFARGEGAGTVIVKRLSDALRNG--DTIRA
Ch_PKS7                             SMMKFLSPD-GRCYAFDERG-------N--GYGRGEGVGTVFLKPLADALKDG--DPIRA
Ch_PKS1                             SMMKFLSPD-GRCYAFDERA-------N--GYARGEGVAVLLLKRLEDALADN--DTIRA
Didymella_maydis_PKS1               SMMRFLSPD-GRCYAFDDRA-------N--GYARGEGVTVLLLKRLDDALANG--DTIRA
Gz_PKS4                             NNLGFLNPE-GHSRSFDKDA-------G--GYGRGEGCGILVLKKLDKAIQDG--DNIRA
Gz_PKS7                             TALNFLSPD-GKCFTFDSRA-------N--GYGRGEGIGVVVMKRLSDALRDN--DTIRA
Gm_PKS7                             TALNFLSPD-GKCFTFDSRA-------N--GYGRGEGIGVVVMKRLSDAIRDN--DTIRA
Ch_PKS6                             GAAKILSPE-GKSKMWDANA-------D--GFARGEGFGVTILKPLDTALRDG--DTIRA
Gz_PKS1                             SNMSFLSAD-GLSKSFDASA-------D--GYGRGEGIAAVILKSLDQAVRDR--DPIRA
Ch_PKS4                             SSMQFLSPD-GRCYSFDARA-------S--GYSRGEGVAGIMLKPLSKALKDR--DTIRA
Gm_PKS6                             SSMSFLSAD-NKCHSFDASA-------N--GYARAEGGGFVVLKRLDKALADG--DTIRA
Nc_PKS1                             STCRLLSDA-GRSFSFDNRG-------T--GFGRGEGCGMIVLKPLDQAIKDK--DPIRA
Bf_PKS8                             NKYRLFSDE-GRSFSFDSRG-------T--GYGRGEGCGLIVLKPLEQALKDN--DNIRA
Nc_PKS2                             SMLRLFSDE-GRTYAFDHRA------RS--GYARGEGCAVIILKPVEKAFKDN--DHIFS
Ch_PKS2                             SNLTMLNPD-GLSKSFDPQA-------DA-GYVRGEGAASIIVKPLDAAIRDN--DRVHC
Aspergillus_terreus_lovF            SNLGFLSSD-GISYSFDSRA-------D--GYGRGEGVAAIVLKTLPDAVRDG--DPIRL
Penicillium_citrinum_mlcB           SNLGFLSPD-GISYSFDPRA-------N--GYGRGEGIAALVIKALPNALRDQ--DPIRA
Ch_PKS3                             SSIALISKD-GRSFAFDSRA-------N--GYGRGEGAATIVLKRLDDAIRDG--DPIQC
Nc_PKS3                             SSMTLISKD-GRSWAFDSRA-------N--GYGRGEGSATVVLKPLDAALRDG--DPIRA
Bf_PKS2                             DKRSVLDPS-GKSFVFDDRG-------V--GYGRGEGVATIVLKRLKDALNAG--DHVRA
Gz_PKS5                             SGMGMLNPD-GKSYAFDSRG-------A--GYGRGEGVATIVLKRLDNAIKDG--DRIHA
Gm_PKS1_CAC44633                    SKLSMLSPS-GRSKMWDQDV-------N--GYARGEGIAAVVLKPLSAAIRDN--DHIDC
Gm_PKS1                             ....................................GIAAVVLKPLSAAIRDN--DHIDC
Bf_PKS5                             SKLHMLSPT-GTSKMWDESA-------D--GYARGEGIASVVMKRLSDALRDG--DPIEC
Gm_PKS9                             SKLRMISPT-GRSRMWDANA-------D--GYARGEGFASVILKTLSQALADG--DPIEC
Aspergillus_terreus_lovB            SKLSMLSPS-GRSRMWDAGA-------D--GYARGEAVCSVVLKTLSQALRDG--DTIEC
Penicillium_citrinum_mlcA           SKLNMLSPN-GRSRMWDAAA-------D--GYARGEGVCSIVLKTLSQALRDG--DSIEC
Gz_PKS9                             SNLSMLSPT-GKSRMWDADA-------D--GYARGEGVAAVVLKPLSAAIEDN--DVIEC
Ch_PKS16                            SKLKMLSPD-SLSRMWDKDA-------N--GYARGEGVTAVVLKTLSQALADN--NRIEV
Bf_PKS6                             SNLHMLSPT-GRSQMWDSRA-------D--GYARGEGTAAIVLKTLKNALEDG--DDIEY
Bf_PKS3                             ANLKMLSPT-GTCKMWDASA-------D--GYARGEGCG--MLKLLEDAIRDG--DRIES
Ch_PKS17                            SKLQLLSPT-GRSRMWDAAA-------D--GYARGEGAAALIMKKLSHALADG--DEVYC
Gz_PKS10                            SKLHMLSPT-GRSRMWDASA-------N--GYARGEGVAAIMMKTLSQALADG--DHIEG
Gm_PKS10                            SKLHMLSPT-GRSRMWDASA-------N--GYARGEGVAAIMMKTLSQALADG--DHIQG
Nc_PKS4                             SSLHMLSPT-GRCHMWDDRA-------D--GYARGEGVAAIFIKPLSKALADG--DRIEA
Bf_PKS4                             NNMGMLSPT-GSCKMWDTEA-------D--GYARGEGILAMLLKPLRLALADG--DNIQC
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Gz_PKS11                            ............................................................
Ch_PKS14                            TEKGILSPN-GSCKTFSA---------DADGYARGEAFTAVFVKPLDAAIRDG--NPIRA
Ch_PKS12                            SEQGVTSPN-ASCRSFDA---------DADGYARAEAVNLIYIKPLSAAIKHG--NPIRA
Gm_PKS12                            SSGEVLAPD-ASCKTFDA---------AADGYARAEAITAVYIKPLSDAIRDG--NPIRA
Ch_PKS13_pseudogene                 TKHRLLSKT-GKCKTFDV---------ASDGYRRGEAVNAVYIKRLSDAIRDG--NTIRA
Ch_PKS11_FUM1                       TEQGVLSPD-ASCKSFDA---------NANGYARGEAINAIFLKGLSSALRDG--DPIRA
Gm_FUM1_AAD43562                    TEQGVLSPD-ASCKTFDA---------NANGYARGEAINAIFLKPLNNALREG--DPIRA
Gm_FUM1                             TEQGVLSPD-ASCKTFDA---------NANGYARGEAINAIFLKPLNNALREG--DPIRA
Ch_PKS15                            VAQGVNSAD-GICRSFDA---------KATGYGRGEAVSSLLVKRLDDALRDG--NPIRA
Nc_PKS5                             KLG-ALSAS-ARCHTFDARA------E---GYARGEGFGAIYLKRPSLAIADM--SPIRA
Gm_PKS15                            KLG-ALSKT-SHCHTFDASA------D---GYARADGIGSVYIMRLSDALKSG--RPIRA
Nc_PKS6                             KAG-VLSKT-STCHTFDSSA------D---GYGRADGIGAILVKRLSDAIRDG--DPIRS
Gm_PKS14                            KSG-VLSST-GMCLTFDESA------S---GYGRAEGVNSIYVKRLSSAVKDG--NPIRA
Bf_PKS9                             KVG-VLSAT-STCHTFDESA------D---GYGRAEGVGAIFLKRLSDAIRDN--DPIRG
Gm_PKS13                            RLG-AIAAD-GQCKTFDASA------N---GYGRGEGTNAVYVKRLSDALRDG--DSIRA
Bf_PKS10                            AVGNAHSPT-GLCHTFDIDA------D---GYVKAEAVSSIIVKRLSDAIRDR--DPIRA
Bf_PKS11                            KLS-MFSKQ-GKSFTFDHRA------KTASGYGRGEGCSGVVLMPLSQAQKQG--FPIRA
Penicillium_patulum_6MSAS           DKAGAISSD-GSCKSFD---------DDAHGYARGEGAGALVLKSLHRALLDH--DNVLA
Byssochlamys_nivea_6MSAS            DQAGAISPE-GFCRSFD---------DNAKGYGRGEGAGAIVLKGLRQAVLEG--DHILA
Aspergillus_terreus_pksM            DKAGATSTE-GRCLSFD---------EDAKGYGRGEGAAVVILKRLSTAIRDG--DHIRA
Aspergillus_parasiticus_pksL2       DKAGALSSD-GRCHSFD---------DTASGYGRGEGAAVVILKNMAEAVKNG--DHILA
Penicillium_griseofulvum_pks2       DEAGAISAD-GKCRSFD---------DSANGYGRGEGAGVVILKRLEKALTDG--DRVLA
Ch_PKS25                            QKAGALKAD-SVCRSFN---------AAASGYARGEEWGIIILKRLSAAQEDN--DHILA
Nc_PKS7                             SRGQFLSKK-GPCATFD---------NEADGYCRGDGCASVVVKRLEDAQAD--NDRVLA
Colletotrichum_lagenarium_pks1      SRGQFLSKT-GPCATFD---------NGADGYCRADGCASVIVKRLDDALAD--KDNVLA
Nodulisporium_sp_PKS1               SRGQFLSKE-HNCNTFD---------NDADGYCRADGCASVIVKRLDDALAD--KDNILA
Xylaria_sp_PKS12                    SRGQFLSKN-NNCNTFD---------NDADGYCRVDGCASVIVKRLDDALAD--KDNILA
Bf_PKS12                            SRGQFLSKN-GPCATFD---------HDADGYCRADGIGTVIIKRLDYALAENSKDNVLA
Glarea_lozoyensis_PKS1              SRGQFLSKT-GPCATFD---------NDADGYCRADGVGTIIVKRLEDAISD--KDNVLA
Monascus_purpureus_PKS1             SKGQFLSKV-GPCQTFD---------NNADGYCRGDGIGTLILKRLTDAQAD--KDNILG
Bf_PKS13                            SKGQFLSKT-GSCKTYD---------DSADGYCRGDGVVTLILKRLDDAVAD--QDPILG
Ch_PKS18                            SKGQFLSKT-GSCKTYD---------NDADGYCRGDGCGSVVLKRYEDAIAD--KDNILG
Bf_PKS14                            SKGHFLSPT-GGCKTWD---------EGADGYCRADGVGSVVLKRLEDAEAD--NDNILA
Ch_PKS20                            KGSLFVS--CGTMQSLG---------RAADGYCRADGVGSVVIKRLDDALAD--NDKILA
Aspergillus_nidulans_wA             DRGHFLSRT-GNCNTFD---------DGADGYCRADGVGTVVLKRLEDALADN--DPILG
Aspergillus_fumigatus_alb1          DRGHFLSRT-GNCNTFD---------DGADGYCRADGVGTIVLKRLEDAEADN--DPILG
Gz_PK12                             DRGHFLSRT-GNCNTFD---------DGADGYCRADGVGTIILKRLEDAEADN--DPILG
Gm_PKS3_CAC88775                    DRGHFLSRT-GNCKTFD---------DGADGYCRGEGVATIIIKRLDDAIAEN--DPILG
Gm_PKS3                             DRGHFLSRT-GNCKTFD---------DGADGYCRGEGVATIIIKRLDDAIAEN--DPILG
Gz_PKS12                            DRGHFLSRT-GNCKTFD---------DGADGYCRGEGIATIIMKRLDDALAEN--DPILG
Gm_PKS4_CAC92399                    DRGHFLSRT-GNCKAFN---------DGADGYCRADGIGTLILKRLPDAIADS--DPIFG
Gm_PKS4                             DRGHFLSRT-GNCKAFD---------DGADGYCRADGIGTLILKRLPDAIADS--DPIFG
Aspergillus_parasiticus_pksL1       DKGFFLSRT-GNCKPYD---------DKADGYCRAEGVGTVFIKRLEDALADN--DPILG
Aspergillus_nidulans_pksST          DKGFFLSRT-GNCKAFD---------DAADGYCRAEGVGTVFIKRLEDALAEN--DPILA
Gz_PKS13                            SKSGVLSDT-GNCKTFR---------DDADGYCRADFVGTVVLKRLEDAIAHN--DNILA
Bf_PKS15                            GKGGFLSAT-GGCKTFH---------DDADGYCRGEALGVVVLKRLEDAVREN--DNILA
Bf_PSK19                            QSGGFLSST-GQCRPFD---------ASADGYCRGEGVGAVVLKRLSEAVTDK--DNILG
Ch_PKS22                            GKAGFLSPT-GQCKPFD---------KNADGYCRADGGGLVVLKLLRHARADG--DNILG
Bf_PKS16                            AKAGFLSPT-GQCKPFC---------ESADGYCRAEGGGLIVLKLLKQAVADG--DQILS
Ch_PKS19                            SKGHFLTKGHNACKTWD---------ASADGYCRADGVGSIVIKRLEDAQAD--KDNILG
Ch_PKS23                            GKAGFLSPT-GQCKPFD---------ESADGYCRGEGAGLVVLKPLKQALADG--DQVLA
Ch_PKS21                            AGASFLSPT-GPCKPFD---------ANADGYCRGEAVSAVFLKSLSQAQKDG--DAIIG
Bf_PKS17                            SGASFLSPT-GQCKPFD---------AKGDGYCRGEGVGAVLLKKLSSAVADG--DQVLG
Bf_PKS18                            GAASFLSPT-GATKPFD---------AEADGYCRGEGVGIVVLKRLENAITDG--DPILG
Bf_PKS20                            RVGGFLSKT-AGCKAFD---------VGADGYCRGEAVGVVVLKSLNKALKDG--DHIQG
Homo_sapiens_FAS                    LRLGMLSPE-GTCKAFDTAG---------NGYCRSEGVVAVLLTKKSLA------RKVYT
Gallus_gallus_FAS                   MKLGMLSPD-GACKAFDVSG---------NGYCRSEAVVVVLLTKKSMA------KRVYA
Caenorhabditis_elegans_FAS          LRLGMLTDK-GSCRSFDESG---------DGYCRTEGVAAIFIQRKKKA------QRLYA
Bombyx_mori_FAS_p270                SRLGVLSPD-GKCKSFDNSA---------NGYARSEAIVVCFLQKAKDS------RRVYA
Ch_9497_PKS24_3p_of_nps7            SQLKGMSAD-GRCRAF---------AEDTQGTGWAEGCTMVLLKRLNDAIRDG--DKIHA
Nc_3_oxoacyl_ACP_synthetase         GRSRSLXTAYNH----DPTSACRPFDKDRAGFVVSEGAAVLILEELEHAKRRGA--RILA
Homo_sapiens_3_oxoacyl_ACP_synth    SRARALST--NS----DPKLACRPFHPKRDGFVMGEGAAVLVLEEYEHAVQRRA--RIYA
Glycine_max_beta_ketoacyl_synth     VACRALSQR-ND----DPKTASRPWDKERDGFVMGEGAGVLVMESLEHAMKRGA--PIIA
Streptomyces_coelicolor_act         DAIRATTAR-ND----DPEHASRPFDGTRDGFVLAEGAAMFVLEDYDSALARGA--RIHA
Streptomyces_avermitilis_pks9       DAIKATTPR-ND----EPATASRPFDRTRNGFVLAEGSAMLVLEELNHARERGA--RVYA
Bacillus_subtilis_pksK_mod2         PGL-NFSSD-GHIKAFDASA---------DGMIGGEGVAVVLLKKAADAVKDG--DHIYA
Bacillus_subtilis_pksK_mod3         SKAGMLSTD-GRCKTFS---------ADANGYVRGEGVGMVMLKKLEDAERDG--NHIYG
Bacillus_subtilis_pksL_mod1         GVWDMFSTD-GHCRTFG---------KDGDGYVPAEGIGAVLLKPLRQAEEDG--DRIYA
Bacillus_subtilis_pksL_mod2         GQNKFMSSK-GRCESFG---------QGGDGYVPGEGVGAVLLKPLSKAVEDG--DHIYG
Bacillus_subtilis_pksL_mod3         CEAGMLSPD-GQCKAFD---------NGANGFVPGEGAGALVLKRLKDAEADR--DHIYG
Bac_subtilis_mycA_pks1_mod2         -GLDMESSD-GLTKTFS---------KDSDGTGSGEGVAAVLLKPLQAAIRDG--DHIYG
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Microcystis_aruginosa_mycE          SQSGMMSPD-GRCKTFDASA---------NGYVRGEGCGVLILKTLSEAQKNG--DHILA
Microcystis_aruginosa_mycG          EGL-IMSPD-GHCRAFDAEA---------KGTIFGSGVGVIMLKRLSDALADH--DHIYA
Mycobacterium_leprae_pksE           SKWSALSPT-GRCNSFDANA---------DGFVRGEGCGVVVLKRLVDALRDQ--DRVLA
Mycobacterium_tuberculosis_mas      SAQGMLSST-GRCHSFDAD---------ADGFVRSEGCAMVLLKRLPDALRDG--NRIFA
Mycobacterium_tuberculosis_ppsC     SRWGMLSPE-GRCKTFDASA---------DGYVRGEGAAVVVLKRLDDAVRDG--NRILA
Mycobacterium_tuberculosis_ppsD     SKWSALSPT-GRCNSFDANA---------DGFVRGEGCGVVVLKRLADAVRDQ--DRVLA
Mycobacterium_tuberculosis_ppsE     PGS-MVSAV-GHCRPFDVRA---------DGTVFGSGVGLVVLKPLAAAIDAG--DRIHA
Myxococcus_xanthus_ta1_mod2         RGL-NFSSA-GRVKAFDAAA---------DGMIAGEGVAVLVVKDAAAAVRDG--DPIYC
Nostoc_sp_nosB                      EGM-ILSPD-GHCRAFDAKA---------QGTIASSGAGIVVLKRLKDAIADR--DHIHA
Pseudomonas_syringae_cfa6           SQQRVLAPD-GRCKAF---------SASADGVGLGEGVGMLVLERLSQAQAKG--RLILG
Pseudomonas_syringae_cfa7           TRQNGLAAD-GYCKAF---------AEQADGTCFAEGAGVLLLERLADAQRAG--HPVLA
Sorangium_cellulosum_epoA_mod1      SKTRALATD-GRCKAFSAEA---------DGFGRGEGCAVVVLKRLSGARADG--DRILA
Sorangium_cellulosum_epoC_mod2      EGG-IFSPD-GHCRAFDAKA---------NGTIMGNGCGVVLLKPLDRALSDG--DPVRA
Sorangium_cellulosum_epoF_mod9      GRIQALSPD-GHCRTFDASA---------NGFVRGEGCGMVVLKRLSDAQRHG--DRIWA
Stigmatella_aurantiaca_mxaB2_B1     CSMQALASD-GRCKTFDASA---------DGYVRGEGCGVLVLKRLSDAQRDG--DSILA
Stigmatella_aurantiaca_mxaC1        SKLQALSPD-GRSKAFDASA---------NGFTRGEGCGIVVLKRLSDALADG--DHILA
Stigmatella_aurantiaca_mxaC2        SKLMALSPD-GRCRTFDSRA---------NGFVRGEGCGVVVIKRLSDALASG--DNVLG
Stigmatella_aurantiaca_mxaC3        AQLRALSQD-GRCKTFDASA---------DGYVRSEGCGIVVLKRLSDAKRDG--DDVLA
Stigmatella_aurantiaca_mxaD         SSSRGLSPD-GRCKTFDAAA---------NGFVRAEGCVVLVLKRLSDALASG--DEILS
Stigmatella_aurantiaca_mxaE         SRAQALAPD-GRCKTFDARA---------NGFVRGEGCGVVVLKRLSDAIAAG--DPILA
Stigmatella_aurantiaca_mxaF         SKLGALSPD-GRCYTFDARA---------NGYVRGEGAGVAVLKPLSRAIADG--DPIYC
Streptomyces_natalensis_PimS0       SRLRALSPD-SRSMAY---------ADAANGSAWSEGAGLLLLERLSDARRNG--HRVLA
Streptomyces_natalensis_PimS2_mod3  SRQRALAGD-GRCKAF---------SEGADGMTLAEGVGVLVLERLSDAQRNG--HEILA
Streptomyces_natalensis_PimS2_mod4  SRQRAMAAD-GRCKAY---------SDQADGMSLAEGVGLVLVERLSDARRNG--HQVLA
S_viridochromogenes_aviM            GTAGALAPD-GRSKPFAASAGRYAVAASADGYGRGEGCGVLVIKLLTDAVRDG--DRVLA
Xanthomonas_albilineans_xabB_mod2   ASAGMLSPD-GRCKTLDAAA---------DGFVRSEGIAGVILKPLAQALADG--DRVYG
Xanthomonas_albilineans_xabB_mod3   AGAAMLSAG-ASCRPFG---------EAADGFVAGEACGVVLLKPLKQARADG--DVIHA

[                                    301                                                      360]
Bf_PKS7                             ............................................................
Aspergillus_terreus_at1             VILASATNHSANA-ISITHPHAQTQADLFRHILTQSGVS----PLEVDYVEMHGTGTQAG
Aspergillus_terreus_at4             VIVGTNTNHCGQT-DSITRPHEGDQVSVFKRIVRHSGID----PLDISYVEMHGTGTQAG
Aspergillus_terreus_at5             VVLGTATNHSSEA-VSITRPHGPAQEALYRKILKHTGVD----PVDVSYVEMHGTGTQAG
Gm_PKS5                             IVRGSSSNQDGNS-PGITQPTRQAQVDLINAAYRSAGLSKTQT----RFFEAHGTGTPVG
Ch_PKS9                             VIRSTGCGQDGNT-PSITSPSQSAQERLIRETYARAGLSLDETR----YFEAHGTGTKAG
Ch_PKS8                             VVRATGANQDGRT-PSITQPSQQAQLDLLRDTYRVAGLNVADTG----YVEAHGTGTPVG
Gz_PKS2                             VIRSIGSNQDGHT-PILTQPSSQSQEELIRHVYKQAGLSMSDT----RYVEAHGTGTPVG
Gm_PKS2                             VIRSIGSNQDGHT-PILTQPSSQSQEELIRHVYGQAGLSMSDT----RYVEAHGTGTPVG
Ch_PKS10                            VIRNSGIGHDGKG-APLPAPVRESQVNLVRRCYAQAKIDPSET----RLFEAHGTGTVQT
Ch_PKS5                             VVRGTGINQDGRT-PGLTLPSSDAQERLIRTTYASAGLNFDDTT----LVEAHGTGTKQG
Ch_PKS7                             VIRGSASNQDGKT-SGITLPNPVAQEALIKDVYHVADLNPIDTS----IVEAHGTGTAAG
Ch_PKS1                             VIRGTGCNQDGKT-PGITMPNSVSQEALIRSVYKKAALDPLDTT----YVECHGTGTQAG
Didymella_maydis_PKS1               VIRGTGRNPDGKT-TGIAMPSGLAQEALIRSVYAKTGLDLLDTA----YIECHGTGTQAG
Gz_PKS4                             VIRASGVNSDGWT-QGVTMPSSEAQAALIKHVYETRGLDYGATQ----YVEAHGTGTKAG
Gz_PKS7                             VIRATKVNQDALK--GITLPSKEAQVANIHSVYESAGLDFSQTG----YVECHGTGTKAG
Gm_PKS7                             VIRATKVNQDGHT-TGITLPSKEAQVANIKSVYESAGLDFSQTG----YVECHGTGTKAG
Ch_PKS6                             VVLATATNEDGHT-PGISLPNSEAQQDLIRRAYQMAGVDPAETG----YVEAHGTGTMAG
Gz_PKS1                             VI..........................................................
Ch_PKS4                             ILRGTSVVSDGKT-LGITMPSMDSQVEAITRAYEQAGLVLADTT----YIEAHGTGTIAG
Gm_PKS6                             VLRSTGSNQDGRT-LGITQPSASRQEELIRATYASAGLTFDKTN----FFEAHGTGTKVG
Nc_PKS1                             VIAATGLNQDGKT-PGITVPHGPAQEDLIRKVYGRAGLDPNLCG----FVEAHGTGTRVG
Bf_PKS8                             VIRGSGINQDGKT-PGITMPNGSAQESLMKWVYESAGIDPKDTG----YVEAHGTGTKVG
Nc_PKS2                             VISHSGVSHNGRT-VGIVAPSPDEQEQLLRDVFTAAKIDPREVG----FFEAHGTGTKKG
Ch_PKS2                             VLSDIGVNHNGRTN-GYTLPDARMQASLMRELQVRLDIKPDEFG----FVEAHAPGTRVG
Aspergillus_terreus_lovF            IVRETAINQDGRT-PAISTPSGEAQECLIQDCYQKAQLDPKQTS----YVEAHGTGTRAG
Penicillium_citrinum_mlcB           VIRETALNQDGKT-PAITAPSDVAQKSLIQECYDKAGLDMSLTS----YVEAHGTGTPTG
Ch_PKS3                             VIKETGLNQDGKT-ETITTPSQAAQIDLMRRLYKKAGLDPKDTG----YFEAHGTGTPTG
Nc_PKS3                             VIRDSGINQDGKT-ETITTPSGEAQEALIRACYERAGLDPGQTT----YFEAHGTGTPTG
Bf_PKS2                             VIRNTGINQDGKT-SGIALPSQVAQQALANHVFKQVGLDPCKIN----YVEAHGTGTIAG
Gz_PKS5                             IIANSGMNQDGKT-PGLNTPSGEAQAALSRRVYQEAGLNPADTS----FVEAHGTGTQAG
Gm_PKS1_CAC44633                    IIRATGVNQDGRT-PGLTMPSATAQADLIRSTYARAGLDINKPEDRPQFFHAHGTGTPAG
Gm_PKS1                             IIRATGVNQDGRT-PGLTMPSAAAQADLIRSTYARAGLDINKPEDRPQFFHAHGTGTPAG
Bf_PKS5                             VIRGTGVNQDGKT-PGLTMPNGKAQADLIRDTYQRAGLDIHDPRDRPQFFHAHGTGTQAG
Gm_PKS9                             IIRETGVNQDGKT-PGLTVPSNIAQTALIRDVYQRAGLDITKPSDRPQLFHAHGTGTKAG
Aspergillus_terreus_lovB            VIRETGVNQDGRT-TGITMPNHSAQEALIKATYAQAGLDITKAEDRCQFFEAHGTGTPAG
Penicillium_citrinum_mlcA           VIRETGINQDGRT-TGITMPNHSAQEALIRATYAKAGLDITNPQERCQFFEAHGTGTPAG
Gz_PKS9                             IIREVGVNQDGKT-RGITMPSAQAQASLIRQTYAKAGLDPATPEGRCQFFEAHGTGTPAG
Ch_PKS16                            VIRETGMNSDGAT-PGITMPSASAQRDLIRSVYRKAGLDPESAEDRPQYIEAHGTGTPAG
Bf_PKS6                             IIRETGVNSDGKS-KGITMPLAASQADLIRQTYARAGLDCTKPSERCQYFEAHGTGTPAG
Bf_PKS3                             VIRETGVNSDGRT-MGITMPSASSQEKLIKETYRRAGLD------RCQFFEAHGTGTLAG
Ch_PKS17                            IIRETGVNSDGRT-NGITMPSAEAQAALIRKTYARAGLDPLK--DGCQFFEAHGTGTQAG
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Gz_PKS10                              IIREIGVNSDGRT-NGITLPSPDAQKVLIRHTYRNAGLDVFK--DRCQFFEAHGTGTPAG
Gm_PKS10                              VIREIGVNSDGRT-NGITLPSPEAQKFLIRQTYKKAGLDVFK--DRCQFFEAHGTGTPAG
Nc_PKS4                               IIRETGVNSDGRS-KGITMPNWEAQSALIQDTYRRSGLNARDPIDRCQFFEAHGTGTAAG
Bf_PKS4                               VIRETGVNHNGRT-SGITLPSASAQTSLIRDVYHRAGLDPTNPSDRPQYIEAHGTGTQAG
Gz_PKS11                              ............................................................
Ch_PKS14                              VIRAAVANSDGKT-QGITQPNGYAHEAMIRLAYKQAGITV-SKYPQTAYFECHGTGTSVG
Ch_PKS12                              IIRGSSLNADGKT-PGPSMPSSSSQAALIRRAYQNAGIPE-SEIIRTAFVECHATGTATG
Gm_PKS12                              IVKGTAVNCDGKC-VSLVTPNGAAHEALMRKAYCDNGLDP-KD---TAFVECHGTGTPTG
Ch_PKS13_pseudogene                   VIWASATNYDGRK-IRMLNLNTLVQEALICKTYAKASIT---NYRETGFFKCYGIGMLVG
Ch_PKS11_FUM1                         VVRATSSNSDGKT-PGMSMPSSESHMTLIQHAYHEAGLNP-KD---TVFVEAHGTGTPVG
Gm_FUM1_AAD43562                      LVRATSSNSDGKT-PGMSMPSSESHEALIRRAYGEVFLDP-KD---TCFVEAHGTGTSVG
Gm_FUM1                               LVRATSSNSDGKT-PGMSMPSSESHEALIRRAYGEVFLDP-KD---TCFVEAHGTGTSVG
Ch_PKS15                              IIRSTACNDDGKT-PGITQPNTVAHEALIRAAYRTAGISE-EDLNKTGFFECHGTGTAVG
Nc_PKS5                               MIRGTAINSNGRT-GGITRPSANGQETVIREAYRNAGNLPFRDTS---YFECHGTGTYVG
Gm_PKS15                              VIRGTAIGANGRG-DGMTKPDSEGQARTIRMAYKNAGITDLAQTG---YFECHGTGTPVG
Nc_PKS6                               VIRGTAINSNGKT-NGITLPSADGQEAVIRKAYAQAG-LGFNETD---YIECHGTGTAVG
Gm_PKS14                              VIRGSALNANGRT-PGISLPDSDFQELAMRKAYSDAN-LDVSGTD---YVECHGTGTAVG
Bf_PKS9                               VIRGTATNANGKT-SGITQPSAKGHETVMRTAYEFAG-LDPRDTS---YFETHGTGTQVG
Gm_PKS13                              VIRGTSSNSSGAT-PAITEPSGRAQADTILQAYAQAGINDFSETG---YFECHGTGTPVG
Bf_PKS10                              VIRGSATNSDGRT-PGIASPSAEA-SAAIRAAYANAGITNLNDTA---YLECHGTGT--G
Bf_PKS11                              VVQNSVANQDGKT-NGITVPSAEAQSAAIEKAYSQVGLVPYAD-----YVEAHGTGTAVG
Penicillium_patulum_6MSAS             VIKGSAVCQDGKTN-GIMAPNSVAQQLAANNAL-S---AANIDPHTVRYVEAHATSTPLG
Byssochlamys_nivea_6MSAS              VIKGSAVAQDGKTN-GIMAPNAKAQELVARTAL-K---VAKIDPRTIRYVEAHATSTPLG
Aspergillus_terreus_pksM              IIKGSAVAQDGKTN-GIMAPNAKAQELVAWNAL-R---TAGVDPLTVGYVEAHATSTPLG
Aspergillus_parasiticus_pksL2         TLKGTAVAQDGRTN-GIMAPNQKAQELVARKAL-D---VARVDASTIDYVEAHATSTPVG
Penicillium_griseofulvum_pks2         VLKGSAVASDGKTL-GIMAPNAQAQILVAQKAL-K---EARVTPDSISYIEAHATSTSLG
Ch_PKS25                              MLKSSASALDGKTR-GIMAPNGAAQVDVARQALCR---AGNIDPCTVDYIEAHATSTPLG
Nc_PKS7                               VVLGTATNHSADA-ISITHPHGPTQSTLSQAILDDAGVD----PHDVDYVEMHGTGTQAG
Colletotrichum_lagenarium_pks1        VILGTATNHSADA-ISITHPHGPTQSILSRAILDDAGVD----PLDVDYVEMHGTGTQAG
Nodulisporium_sp_PKS1                 VILGTQTNHSADA-ISITHPHGPTQSILSSSILDEAGVD----PLDVDYVEMHGTGTQAG
Xylaria_sp_PKS12                      VILGAQTNHSADA-ISITHPHGPTQSVLSTSILDEAGVD----PHDVDYVEMHGTGTQAG
Bf_PKS12                              VILGSATNHSADA-VSITHPHGGTQEILYKRILNNAGVD----PNDIDYVEMHGTGTQAG
Glarea_lozoyensis_PKS1                VILGSATNHSADA-VSITHPHGGTQEILYRSILRKAGVD----PLDIDYVEMHGTGTQAG
Monascus_purpureus_PKS1               VILSTATNHSAEA-ISITHPHGKTQEALYKKVLDQSGVD----PEEICYVEMHGTGTQAG
Bf_PKS13                              VIAGIATNHSAEA-VSITHPHAGAQKFLFQKVMDEARVD----IRDVKYVEMHGTGTQAG
Ch_PKS18                              CILGAATNHSAEA-VSITHPHAGAQEYLYNKVLSNAGVD----AHEISYVEMHGTGTQAG
Bf_PKS14                              VVLAAGTDHSAEA-VSITHPHDLAQIHLFNQIVKRSGID----PLSVGYVEFHGTGTGAG
Ch_PKS20                              TILAANTNHSADA-ISITHPHAPKQAQNYQRVMSQAGFS----PLDVSYVELHGTGTQAG
Aspergillus_nidulans_wA               VINGAYTNHSAEA-VSITRPHVGAQAFIFKKLLNEANVD----PKNISYIEMHGTGTQAG
Aspergillus_fumigatus_alb1            VINAAYTNHSAEA-VSITRPHVGAQAFIFNKLLNDTNTN----PHEIGYVEMHGTGTQAG
Gz_PK12                               VILGAYTNHSAEA-VSITRPHAGAQEYIFSKLLRESGTD----PYNVSYIEMHGTGTQAG
Gm_PKS3_CAC88775                      VVLGAHTNHSAES-ESITRPHVGAQRVIFNKILNEAAVD----PYSVSYVEMHGTGTQAG
Gm_PKS3                               VVLGAYTNHSAES-ESITRPHVGAQRVIFNKILNEAAVD----PYSVSYVEMHGTGTQAG
Gz_PKS12                              VVLGAYTNHSAES-ESITRPHAGAQQAIFNKILNQADVD----PYTVGMC..........
Gm_PKS4_CAC92399                      VILGAHTNHSAES-VSITRPLADAQEYLFKKLLNETGIH----PHDVSYVEMHGTGTQAG
Gm_PKS4                               VILGAHTNHSAES-VSITRPLADAQEYLFKKLLNETGIH----PHDVSYVEMHGTGTQAG
Aspergillus_parasiticus_pksL1         VILDAKTNHSAMS-ESMTRPHVGAQIDNMTAALNTTGLH----PNDFSYIEMHGTGTQVG
Aspergillus_nidulans_pksST            TILDIKTNHSAMS-DSMTRPFKPAQIDNMSALLSTAGIS----PLDLSYIEMHGTGTQVG
Gz_PKS13                              VVAASGRNHSGNS-SSITTSDAKAQEKLYRKMMHNARVS----PNDISYVEMHGTGTKVG
Bf_PKS15                              VIKGTERNSNAGA-ASITYPGQEAQEKLFGRLLRKASVD----PHDVGFVEMHGTGTQAG
Bf_PSK19                              VIVGSAANQNHNF-SHITVPHADSQANLYNKVMKMGNVR----PETVTYVEAHGTGTRVG
Ch_PKS22                              VIPGIATNQGGLS-ASITVPHSPAQMTLYRRILKQAAMK----PEQVSYVECHGTGTQAG
Bf_PKS16                              VIPGAATNQGGLS-SSLTIPSSPAQVQLYQNILNKAKMK----ADQVSYVEAHGTGTQAG
Ch_PKS19                              VILAAGTNHSAEA-VSITHPHAGHQSYLSRQIIRQAGID----PLDVSYVELHGTGTQAG
Ch_PKS23                              VISGSSTNQGGLS-ENLTLTHPPAQVDLYKSVLKGAKMS----PRHVSYIEAHGTGTSQG
Ch_PKS21                              VISGTAVAQNSND-TPIVVPNAPSLSTLFRSVLETSNLN----AQDVSVVEAHGTGTPVG
Bf_PKS17                              VISSTGVYQNGND-TAITVPISDSLSDLFLHVLHKAKLE----PKDISVVEAHGTGTPVG
Bf_PKS18                              VIAGSAVNQSMNS-TSITVPNLESQSVLFEKVAALAGSS----PSEFTYVEAHGTGTPVG
Bf_PKS20                              VLLATGNNQNMNH-TSITNPVLESQTALYRDVLARAGVN----PEDISYVEAHGTGTRAG
Homo_sapiens_FAS                      TILNKGTNTDGFKEQGVTFPQ-DIQEQPIRSLYQSAGVA----PESFEYIEAHGPGTKVG
Gallus_gallus_FAS                     TIVNAGSNTDGFKEQGVTFPSGEMQQQLVGSLYRECGIK----PGDVEYVEAHGTGTKVG
Caenorhabditis_elegans_FAS            TVVHAKSNTDGHKEHGITFPSGERQAQLLQEVYSEAGID----PNSVYYVEAHGTGTKVG
Bombyx_mori_FAS_p270                  QLLHAKTNCDGYKEQGITYPAGHIQKLLLREFYEECSIP----PSELEFVEAHGTGTRVG
Ch_9497_PKS24_3p_of_nps7              LLRGTAVNHGGRSAPGLTVPSGTAQQRLVHAAL-A---SANLTPGDIDYVEAHGTGTKLG
Nc_3_oxoacyl_ACP_synthetase           ELTGYGCSGDAHHMTAPR-DDGSGAFLSMNXALKNAGCQ----PGDVDYINAHATGTAVX
Homo_sapiens_3_oxoacyl_ACP_synth      EVLGYGLSGDAGHITAPD-PEGEGALRCMAAALKDAGVQ----PEEISYINAHATSTPLG
Glycine_max_beta_ketoacyl_synth       EYLGGAVNCDAYHMTDPR-SDGLGVSTCIQSSLEDAGVS----PEEVNYINAHATSTLAG
Streptomyces_coelicolor_act           EISGYATRCNAYHMTGLK-ADGREMAETIRVALDESRTD----ATDIDYINAHGSGTRQN
Streptomyces_avermitilis_pks9         EIGGWDVRANAYHMTGLR-TEGPELAKAIEVALRMAGRV----PEQVDYVNAHGSGTKQN
Bacillus_subtilis_pksK_mod2           LLRGIGVNNDGADKVGFYAPSVKGQADVVQQVMNQTKVQ----PESICYVEAHGTGTKLG
Bacillus_subtilis_pksK_mod3           VIRGTAENHGGRAN-TLTSPNPKAQADLLVRAY-R---QADIDPSTVTYIEAHGTGTELG
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Bacillus_subtilis_pksL_mod1         VIKGSAVNHVGTVS-GISVPSPVSQADLIETCL-E---KTGIDPRTISYVEAHGTGTSLG
Bacillus_subtilis_pksL_mod2         IIKGTAINHGGKTN-GYSVPNPNAQADVIKKAF-V---EAKVDPRTVSYIEAHGTGTSLG
Bacillus_subtilis_pksL_mod3         IIIGSGINQDGKTN-GITAPSAKSQMDLERDIY-E---TYGIHPESISYVEMHGTGTKQG
Bac_subtilis_mycA_pks1_mod2         VIKGSAINQDGTTV-GITAPSPAAQTEVIEMAW-K---DAGIAPETLSFIEAHGTGTKLG
Microcystis_aruginosa_mycE          LLRGSAVNHNGAAA-GLTVPSGPAQQELLRQAL-A---DARIVPEDVSYIEAHGTGTSLG
Microcystis_aruginosa_mycG          VIKGSAINNDGGQKLGFTAPGGEGQIAAATEALAFAGVD----ANTISFVEAHGTGTPLG
Mycobacterium_leprae_pksE           VVRGSATNQDGRSN-GMTAPNALAQRDVITTAL-R---LADITPDSVNYVETHGTGTVLG
Mycobacterium_tuberculosis_mas      VVRGTATNQDGRTE-TLTMPSEDAQVAVYRAAL-A---AAGVQPETVGVVEAHGTGTPIG
Mycobacterium_tuberculosis_ppsC     VVRGSAVNQDGASS-GVTVPNGPAQQALLAKAL-T---SSKLTAADIDYVEAHGTGTPLG
Mycobacterium_tuberculosis_ppsD     VVRGSATNSDGRSN-GMTAPNALAQRDVITSAL-K---LADVTPDSVNYVETHGTGTVLG
Mycobacterium_tuberculosis_ppsE     VIRGSAINNDGSAKMGYAAPNPAAQADVIAEAHAVSGID----SSTVSYVECHGTGTPLG
Myxococcus_xanthus_ta1_mod2         LVRKVGINNDGQDKVGLYAPSATGQAEVIRRLFDRTGID----PASIGYVEAHGTGTLLG
Nostoc_sp_nosB                      IIKGSAINNDGAMKVGFTAPSVSGQAAVIAEAQAIAGVD----AETISYIEAHGTATPLG
Pseudomonas_syringae_cfa6           VIRGSAVNQDGASN-GLTAPNGTAQQQVIRHAL-A---NAGLQPEDVDAVDAHGTGTRLG
Pseudomonas_syringae_cfa7           VIRGTAINQDGASN-GLTAPSGPAQEQVIQLAL-Q---NARLRSLDIDVVEAHGTGTALG
Sorangium_cellulosum_epoA_mod1      VIRGSAINHDGASS-GLTVPNGSSQEIVLKRAL-A---DAGCAASSVGYVEAHGTGTTLG
Sorangium_cellulosum_epoC_mod2      VILGSATNNDGARKIGFTAPSEVGQAQAIMEALALAGVE----ARSIQYIETHGTGTLLG
Sorangium_cellulosum_epoF_mod9      LIRGSAMNQDGRST-GLMAPNVLAQEALLRQAL-Q---SARVDAGAIDYVETHGTGTSLG
Stigmatella_aurantiaca_mxaB2_B1     LIRGSAVNHDGASG-GLTVPNGPSQQAVVQRAL-D---NARIAPALVGYIEAHGTGTPLG
Stigmatella_aurantiaca_mxaC1        TIRGSAINQDGKST-GLTTPNVLSQQALIRQAL-E---SSGLKAEQVSYVEAHGTGTPLG
Stigmatella_aurantiaca_mxaC2        VIRASAVNQDGGST-GLTAPNVLSQQALIRDAL-K---SANLSPKEIGYIEAHGTGTPLG
Stigmatella_aurantiaca_mxaC3        VIRGSAVNHDGPSS-ALTVPNGDAQQQVLRAAL-A---NAGVAPADVDYIEAHGTGTSLG
Stigmatella_aurantiaca_mxaD         LIAGSAVNQDGASS-GLMVPNGPAQERVIEQAL-A---SGGLKPSQISFVEAHGTGTSLG
Stigmatella_aurantiaca_mxaE         LVRGSAVNQDGKSA-GLTAPNVLAQQALIRQAL-Q---SANLEPSEIDCVEAHGTGTSLG
Stigmatella_aurantiaca_mxaF         VIRGSAINNNGGSN-GLTAPNTQAQAEVIRQAC-A---RAGVAPTDVQYVEAHGTGTQLG
Streptomyces_natalensis_PimS0       LVRGSAVNQDGASN-GLTAPSGPAQQRVIRQAL-A---DAGLTPQDVDAVEGHGTGTPLG
Streptomyces_natalensis_PimS2_mod3  VVRGSAINQDGASN-GLSAPNGPSQQRVIRQAL-A---NSGLTPADIDAVEAHGTGTALG
Streptomyces_natalensis_PimS2_mod4  VIRGSAVNQDGASN-GLTAPNGPSQQRVIRQAL-A---NAEVDPDGIDVIDGHGTGTALG
S_viridochromogenes_aviM            VLRGSAFNQDGRTN-GIMAPCGQAQEHVMRRAL-T---AAGVAADTVDFVEAHGTGTRLG
Xanthomonas_albilineans_xabB_mod2   LVRGVAVNHGGRSNS-LRAPNVNAQRQLLIRTY-Q---EAGVEPASVGYVELHGTGTSLG
Xanthomonas_albilineans_xabB_mod3   VIRGSMINAGGHTS-AFSSPNPAAQAEVVRQAL-Q---RAGVAPDSISYIEAHGTGTVLG

[                                    361                                                        420]
Bf_PKS7                             ............................................................
Aspergillus_terreus_at1             DAVEMESVTSVFSPG------RTMR-----PHPLHIGSVKGNVGH-GEAAAGVTALIKTL
Aspergillus_terreus_at4             DATEMNSVLSVFVPEYK--RMQMTP-----ARPLYLGSAKANIGH-AESASGVSSLIKVM
Aspergillus_terreus_at5             DGTEMKSITNVFAPRD---KGRRQP-----DQLIHLGALKANIGH-GEASAGVASLIKTV
Gm_PKS5                             DPIEASAISGAFLEYCSEQE------------PMVVGAVKTNIGHLEGSAG.........
Ch_PKS9                             DPCEAAAINSVFSA-RTPED------------PIFVGALKSNMGHPEGASG-IAGVIKTL
Ch_PKS8                             DPIEASAIGQAFRDGRSLDR------------PLYIGSVKASIGHLEGASG-LAGVIKAV
Gz_PKS2                             DPIEVKAIGRCFQEHRSHSE------------PLYVGSVKANIGHLE-GASALASLVKCI
Gm_PKS2                             DPIEVEAIGRCFQAHRSPSE------------PLYVGSVKANIGHLE-GASALASLVKCV
Ch_PKS10                            REIQLRLVPLVTSSAAIGQKKS----------PIYIGALKSNIGH-TEGNSGVASFIKAV
Ch_PKS5                             DAIEARGIAQAF--KSRRKDK-----------PLYLGSVKASVGHLEGAAG-VAGIIKSV
Ch_PKS7                             DPLELRALTNSFCGANRPEDR-----------PLIIGSIKSNLGHLEGASG-IAAVVKAV
Ch_PKS1                             DTTEASALSKVFSPGRR---L-----------PLLIGSVKTNIGHLEGASG-LAGVVKSI
Didymella_maydis_PKS1               DTTEARAISNVFGPGRQ---V-----------PLAIGSVKTNIGHLEAASG-LAGVLKCI
Gz_PKS4                             DPVETGAIHRTIGQGASKNRK------------LWVGSVKPNIGHLEAAAG-VASVIKGV
Gz_PKS7                             DWRELKAISESLGSVRGIDN------------PIVVGSLKPNIGHLEGAAG-VAGLIKGV
Gm_PKS7                             DWRELKAISESLCTVRDIDN------------PMVVGSIKPNIGHLEGAAG-VAGLIKGV
Ch_PKS6                             DPLEAKAILKTVGSVEGRKS-S-----------LYVGSVKTNIGHLEGAAG-VAGVIKAA
Gz_PKS1                             ............................................................
Ch_PKS4                             DKAEALAFTTTIGKDRREK--------------IIVGSVKSNLGHIENASG-LASVIKTV
Gm_PKS6                             DPIECSVIGNVF--GKTRER------------PVYVGSVKSNIGHLEGASG-LAGLVKTI
Nc_PKS1                             DPIEATAIHNVLGQERSPRN------------PLWIGSVKSNIGHLEGASG-IAGVIKAA
Bf_PKS8                             DPIEATALYNVFGEGRNARN------------PLFIGSVKSNIGHLEAASGGIISVIKTA
Nc_PKS2                             DPIEATAIYKAVGRYLSADD------------PLYIGSSKPNVGHLECASG-LVSVIKGV
Ch_PKS2                             DPIEISALQEVFSTSARTLED-----------PLLIGSVKANVGHL-ESSSGFPSLIKAA
Aspergillus_terreus_lovF            DPLELAVISAAFPGQQ-----------------IQVGSVKANIGHTEAVSG-LASLIKVA
Penicillium_citrinum_mlcB           DPLEISAISAAFKGH-----------------PLHLGSVKANIGHTEAASG-LASIIKVA
Ch_PKS3                             DPLEVGAIAAVFKDSRPTTT------------PLPIGSIKPNVGHTECASG-LASIVKVV
Nc_PKS3                             DPIEVKAIARVFKDSRKGNGEDAL---------LRIGSVKTNIGHTETASG-VAAIIKVA
Bf_PKS2                             DLAETKSIANVFCTE--RKKT------------LYIGSIKSNIGHLESASG-AAGLLKAI
Gz_PKS5                             DREEIGSISKVFCEDSGRTDD------------LYIGSVKTNIGHLEATSG-IAGLLKSI
Gm_PKS1_CAC44633                    DPREAEASTVRSI--PDV-----------KDDKLYVGSIKTVLG-HTEGTAGLASLIGTA
Gm_PKS1                             DPREAEAIYRAFY--SDV-----------KDDKLYVGSIKTVLG-HTEGTAGLASLIGTA
Bf_PKS5                             DPQESQAIDSAFFSGPDK-----------KLETMAVGSIKTIIGYHTEGTAGLASLIGSV
Gm_PKS9                             DPKEAEAIFRAFFGDDQP-----------HDEKLNVISIKTQIG-HTEGTAGLASLLGTM
Aspergillus_terreus_lovB            DPQEAEAIATAFFGHEQVARSDG-----NERAPLFVGSAKTVVG-HTEGTAGLAGLMKAS
Penicillium_citrinum_mlcA           DPQEAEAIATAFFGHKDGTIDSD-----GEKDELFVGSIKTVLG-HTEGTAGIAGLMKAS
Gz_PKS9                             DPQEAEALKTAFFPNETDSVTNGTNGLLSEADNLLVGSIKTVIG-HTEGTAGLAGLIKAC
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Ch_PKS16                            DPIEAEALSTAFFGEGAKMTT-----------PIYTGSIKTVLG-HTEGSAGLAALLKVT
Bf_PKS6                             DPVEAEAISSAFFPQRSDILNS---------EPLHVGSIKTVIG-HLEGAAGLAGIIKAG
Bf_PKS3                             DRQEAEAISRAFDLYQTSHLMQD-------NLPLSVGSIKTIVG-HLEGCAGIAGLLKAS
Ch_PKS17                            DPQEARAIHDVFFPELRDS--A---------DVLYVGSVKTVIG-HLEGAAGVAGLIKAA
Gz_PKS10                            DPLEGRAIHKAFFDGSDIV--N---------EPMYVGSVKTAIG-HLEGCAGFAGMIKVI
Gm_PKS10                            DPLEARAIHEAFFTDGDIV--S---------EPMYVGSVKTAIG-HLEGCAGLAGLIKAL
Nc_PKS4                             DPNEARAIEDAFFGRNVSTSSQDT----AEVSKLLVGSVKTVIG-HTEGAAGLAGLFKVV
Bf_PKS4                             DPLEAEALAAAFSLTSSQP--D--------EAHMLVGSIKTVIG-HTEGAAGLAGVLKAS
Gz_PKS11                            ............................................................
Ch_PKS14                            DPIETGAVARVFGEN--------------G---IHITSVKPNVGH-TEGASGLVSLIKAV
Ch_PKS12                            DPIEATAVGNVFGNG--------------G---VYIGSVKPNVGH-SEGASGITSIIKAV
Gm_PKS12                            DPIEATAVGKVFGG----------------EKWVFITSVKPNLGH-SEGSAGLSSVIKCV
Ch_PKS13_pseudogene                 DPLKVGAVANVFGES--------------GV-LIRVVGIKLNVGH-SEGAAGILSTIKAI
Ch_PKS11_FUM1                       DPLEAIAISRVFGGR--------------KERPFYLGSVKPNLGH-SEGASGISSVLKVV
Gm_FUM1_AAD43562                    DPLEATAIARVFGGS--------------SDNKLYIGSVKPNLGH-SEGASGVSSVMKAV
Gm_FUM1                             DPLEATAIARVFGGS--------------SDNKLYIGSVKPNLGH-SEGASGVSSVMKAV
Ch_PKS15                            DPIEVGAVARVFGKD--------------G---MIIGSVKSNIGH-SEGASGNTSVIKAI
Nc_PKS5                             DPIEVAALGRVFAPERSSD------------DPLLIGSVKSNVGH-GEGASALASIMKVV
Gm_PKS15                            DPIETHSVGSVFAEHREQD------------DPLLIGSVKTNLGH-SEATAGITALIKTV
Nc_PKS6                             DPIEVEAVSRVF--KKPQG------------APLLIGSVKSNLGH-SEAASGLSSIIKVA
Gm_PKS14                            DPIEVEAIGRVF--DRGSG------------GKLLLGSVKTNVGH-SEAASGLTSVLKVV
Bf_PKS9                             DPIEIKGVGNFFFNGTDRQ-------------KLLVGSVKTNVGH-SEAASALASIIKVC
Gm_PKS13                            DCIELGAVGSVFSESHKTQ------------DALWVGSTKPNVGH-SEAASGLSSLIKVV
Bf_PKS10                            DPTEVKGAASAFSGTRSAD------------KPLIIGSVKSNLGH-AEPSAGISGILKAV
Bf_PKS11                            DPIEARAIAKVLGAGRESD------------SPLPIGSLKANIGH-TESAAGLTGLIKAV
Penicillium_patulum_6MSAS           DPTEISAIASVY-------GAD--R---PADDPCYIGSIKPNIGHL-EAGAGVMGFIKAV
Byssochlamys_nivea_6MSAS            DPTEISAIAGVY-------GLG--R---QPEDPCYIGSIKPNIGHL-EAGAGAMGFIKAV
Aspergillus_terreus_pksM            DPTEVSAVSAVY-------GKG--R---PEGNPCFIGSVKPNVGHL-EAGAGAVGFIKAV
Aspergillus_parasiticus_pksL2       DPTEVSAISAVY-------GKG--R---SPDKPCYIGSVKPNVGHL-EAGAGAVGFIKAV
Penicillium_griseofulvum_pks2       DPTETSALAGVY-------GAGSGR---HPCNPCYIGSIKPNIGHL-EAGAGVMGLIKAV
Ch_PKS25                            DPVEIKAMAGVY-------G--PVR---SPENPCYLGSIKPNVGHL-ETAAGAINIVKTV
Nc_PKS7                             DGTEMVSVTNVFAPAQ---R-KRPQ-----DRPLYLGAIKANVGH-GEAASGITALCKVL
Colletotrichum_lagenarium_pks1      DGTEMVSVTNVFAPAD---R-KRPA-----DRPLYLGAVKSNIGH-GEAASGVTALTKVL
Nodulisporium_sp_PKS1               DGTEMVSVTDVFAPAN---R-HRPA-----DRPLYLGAVKANVGH-GEAASGVTALIKVL
Xylaria_sp_PKS12                    DGTEMVSVTSVFAPAE---R-HRPA-----DRPLYLGSVKSNVGH-GEAASGVTALIKVL
Bf_PKS12                            DGTEMKSVTNVFAPAD---R-KRRP-----DQPLYLGAVKANVGH-GEAASGVTALIKCL
Glarea_lozoyensis_PKS1              DGTEMKSVTNVFAPAD---R-KRTA-----EQPLYLGAVKANVGH-GEAASGITALIKVL
Monascus_purpureus_PKS1             DGTEMSSVSNVFAPEA---N-NRGA-----NQKLYLGSVKANIGH-GEAASGVTAMIKVL
Bf_PKS13                            DGVEMDSVSSIFAPSN---NLRRRL-----DQPLFVGSVKSNVGH-GEAVSGATALVKIM
Ch_PKS18                            DGIEMTSVTNAFAPRH---R-QRTP-----EQTLHLGAIKANIGH-GEAASGINSLVKVL
Bf_PKS14                            DPTEMSSVTKVFANG------QP-R-----TTDLHIGSVKSNVGH-GEAAAGIMAFIKTM
Ch_PKS20                            DREEAKSVSHIFAPVAP----RRKK-----KYRLRLGAVKSNIGH-GGVAAGIASFIKVL
Aspergillus_nidulans_wA             DAVEMQSVLDVFAPDHR-----RGP-----GQSLHLGSAKSNIGH-GESASGVTSLVKVL
Aspergillus_fumigatus_alb1          DAVEMQSVLDVFAPDYR-----RGP-----ANSLYLGSAKSNIGH-GESASGVTSLVKVL
Gz_PK12                             DATEMTSVLKTFAPTSGFG--GRLP-----HQNLHLGSVKANVGH-GESASGIIALIKTL
Gm_PKS3_CAC88775                    DATEMSSVLETFAPPVAEGKVARPE-----SQKLYIGSAKANIGH-GEAASGVCSVIKVL
Gm_PKS3                             DATEMSSVLETFAPPLAEGKVARPD-----SQKLYIGSAKANIGH-GEAASGVCSVIKVL
Gz_PKS12                            .....SKILVT............................KSHIGH-GEAASGACSVIKVL
Gm_PKS4_CAC92399                    DAVEMRSVLNSFAFDH-----SRPR-----DKSLYLGSVKANVGH-AESASGVLAIIKVL
Gm_PKS4                             DAVEMRSVLNSFAFDH-----SRPR-----DKSLYLGSVKANVGH-AESASGVLAIIKVL
Aspergillus_parasiticus_pksL1       DAVEMESVLSVFAPSETA----RKA-----DQPLFVGSAKANVGH-GEGVSGVTSLIKVL
Aspergillus_nidulans_pksST          DAVEMESVLSLFAPDETF----RPR-----DKPLYVGSAKANIGH-GEGVSGVTSLIKVL
Gz_PKS13                            DPAEMGALASLFSH-------RRTP------KPVVVGGVKANVGH-SESAAGVASLLKCI
Bf_PKS15                            DNVEINSVRKVFAQ-------NRGR-----DNPLNIGAVKATVGH-SEAAAGIASLIKSL
Bf_PSK19                            DPVEVSSIRDAYG-----GP---QR-----DSTLYFASIKGNIGH-TEAAAGVSGLIKVL
Ch_PKS22                            DPLEIASVREVFC-----GG---DR-----QGNLHVGSLKGNIGH-CETAAGVASLLKVL
Bf_PKS16                            DPLEVASIREVFG-----GS---ER-----TNSLYLGSIKGNIGH-CETGAGVAGLVKLI
Ch_PKS19                            DFEEMKGVLDVYAPNTF---PNRRS-----DQKLHIGSAKSNVGH-GESVAGTTALIKVL
Ch_PKS23                            DPLEVSSIREVFG-----AS---DR-----PNKVYLGSIKGNTGH-AESAAGVAGLIKII
Ch_PKS21                            DPAEYAAIRRIFGQEKDNGI---KR-----PVPLQLGSVKGLVGH-TEGSSGAVSLVKVL
Bf_PKS17                            DPAEYKGIQRVFG-----GP---DS-----SHKVSLTSVKGLIGH-TECASGVASLLKVI
Bf_PKS18                            DPIEINAIRKVFG-----GA---HR-----SIPLHVASVKGNIGH-LEGASGVASLIKVL
Bf_PKS20                            DPIEIKSIRQVLG-----GK---DR-----HSILQIGSVKSNIGH-AEGASGIVSLIKVL
Homo_sapiens_FAS                    DPQERNGITRALCATRQ--------------EPLLIGSTKSNMGH-PEPASGLDALAKVL
Gallus_gallus_FAS                   DPQEVNGIVNVFCQCER--------------EPLLIGSTKSNMGH-PEPASGLAALAKVI
Caenorhabditis_elegans_FAS          DPQEANAICEVFCSKRT--------------DSLLIGSVKSNMGH-AEPASGVCSLTKIL
Bombyx_mori_FAS_p270                DPEELLAIDEIFCTGRS--------------GPLLLGSIKSNLGH-SEPASGLCSIAKMC
Ch_9497_PKS24_3p_of_nps7            DPIEGTALAEVF-------SGSRST---ES-EPLWIGSVKSNIGHT-QAAAGLAGLLKAI
Nc_3_oxoacyl_ACP_synthetase         DAAXAIAIRSLMMGEE----------..DDXSRITVNXTKGAIGHLLGAAGAIESVF-SI
Homo_sapiens_3_oxoacyl_ACP_synth    DAAENKAIKHL---------------FKDHAYALAVSSTKGATGHLLGAAGAVEAAF-TT
Glycine_max_beta_ketoacyl_synth     DLAEINAIKKV---------------FKD-TSGIKINATKSMIGHCLGAAGGLEAIA-TV
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Streptomyces_coelicolor_act         DRHETAAYKRAL---------------GEHARRTPVSSIKSMVGHSLGAIGSLEIAA-CV
Streptomyces_avermitilis_pks9       DAHETDAFKRTL---------------GDHAYRTPVSSIKSMIGHSLGAIGSIEIAA-CA
Bacillus_subtilis_pksK_mod2         DPIELAALTNVYRQYTNKTQF------------CGIGSVKTNIGHL-DTAAGLAGCIKVV
Bacillus_subtilis_pksK_mod3         DPIEINGLKAAFKELSNMRGESQPD---VPDHRCGIGSVKSNIGHL-ELAAGISGLIKVL
Bacillus_subtilis_pksL_mod1         DPIEIQGLVKAFRQYTQDR------------QFCSIGSVKSNIGHA-ESAAGISGLSKVA
Bacillus_subtilis_pksL_mod2         DPIEITGLSKVFTQETDDK------------QFCAIGSAKSNIGHC-ESAAGIAGVTKVL
Bacillus_subtilis_pksL_mod3         DPIELEALSTVFQEKTDKK------------QFCAIGSVKSNIGHT-SAAAGVAGVQKVL
Bac_subtilis_mycA_pks1_mod2         DPVEFNGLCKAFEKVTEKK------------QFCAIGSVKANIGHL-FEAAGIVGLIKSA
Microcystis_aruginosa_mycE          DPIELNAIASVY-------GKRSD--------PLYVASVKTNIGHL-EAAAGMAGIIKTI
Microcystis_aruginosa_mycG          DPIEVDALAKVYQ--GANEGE------------CALGSVKTNIGHM-QIASGIAGLIKAT
Mycobacterium_leprae_pksE           DPIEFESLAATY-------G----R---GE-SSCALGSVKTNIGHL-EAAAGVAGFIKTV
Mycobacterium_tuberculosis_mas      DPIEYRSLARVY-------GAG---------TPCALGSAKSNMGHS-TASAGTVGLIKAI
Mycobacterium_tuberculosis_ppsC     DPIELDSLSKVF-------SDRAGS---DQ-L--VIGSVKTNLGHL-EAAAGVAGLMKAV
Mycobacterium_tuberculosis_ppsD     DPIEFESLAATY-------GLGKGQ---GE-SPCALGSVKTNIGHL-EAAAGVAGFIKAV
Mycobacterium_tuberculosis_ppsE     DPIEIQGLRAAFEVSQTSRSA-----------PCVLGSVKSNIGHL-EVAAGIAGLIKTI
Myxococcus_xanthus_ta1_mod2         DPVEVSALSEAFRTFTDRRGY------------CRLGSVKSNLGHL-DTVAGLAGLIKTA
Nostoc_sp_nosB                      DPIEIAALTQAFSQTTDKKGF------------CAIGSLKTNLGHL-DTAAGVAGLIKTV
Pseudomonas_syringae_cfa6           DPIEANALLATY-------GQ-RPA---ER--PLLLGSIKSNTGHT-QAAAGVASLMKMV
Pseudomonas_syringae_cfa7           DPIEAGALINTY-------GRGRPP---ER--PLWLGSLKSNIGHT-QLAAGVASVIKMV
Sorangium_cellulosum_epoA_mod1      DPIEIQALNAVY-------GLGRD----VA-TPLLIGSVKTNLGHP-EYASGITGLLKVV
Sorangium_cellulosum_epoC_mod2      DAIETAALRRVFDRDASTRRS------------CAIGSVKTGIGHL-ESAAGIAGLIKTV
Sorangium_cellulosum_epoF_mod9      DPIEVDALRAVM-------GPARA----DG-SRCVLGAVKTNLGHL-EGAAGVAGLIKAA
Stigmatella_aurantiaca_mxaB2_B1     DPIELRALGAVL-------GKGRP----AD-RPFFIGSVKTNIGHL-EPAAGIAGVIKTI
Stigmatella_aurantiaca_mxaC1        DPIEAEALRETY-------GVPRP----DG-SVCGIGSVKTNVGHL-ESAAGIAGIMKVV
Stigmatella_aurantiaca_mxaC2        DPIEVEALRETY-------GVRRD----DG-FPCFLGSAKTNIGHL-EAAAGMAGLIKVL
Stigmatella_aurantiaca_mxaC3        DPIEVQALANVL-------GQGRT----SE-QRLLIGSVKTTIGHL-EAAAGIAGLIKVV
Stigmatella_aurantiaca_mxaD         DPIELQALARVL-------GTGRS----AE-TPLFVGSVKTNVGHL-EATAGLTGVLKTA
Stigmatella_aurantiaca_mxaE         DPIEMEALHEVY-------GSGRS----AK-QALVVGAAKTNIGHL-ESAAGIAGIIKMV
Stigmatella_aurantiaca_mxaF         DPMEARALGEAL-------GAGRPS---DK--PLHIGSCKTNIGHL-EAAAGITGLIKVA
Streptomyces_natalensis_PimS0       DPIEAQALLATY-------GQQRPV---ER--PLWLGSVKSNFGHT-QAAAGVVGVIKTV
Streptomyces_natalensis_PimS2_mod3  DPIEAQALLATY-------GPGRDP---DS--PLLLGSVKSNIGHT-QSAAGVAGVIKMV
Streptomyces_natalensis_PimS2_mod4  DPIEAQALLATY-------GQGRDP---EH--PLLLGSVKSNIGHT-QMASGVASVIKMV
S_viridochromogenes_aviM            DPMEIGAIAAVY-------GRDRS----GQ-EPCAVGSVKSNIGHL-EGAAGVAGVIKAI
Xanthomonas_albilineans_xabB_mod2   DPIEIQALKEAF-------IALGAQ---AAPSNCGIGSVKSALGHL-EAAAGLTGLIKVL
Xanthomonas_albilineans_xabB_mod3   DAVELGALNKVFDKRAAP---------------CPIGSLKANIGHA-ESAAGIAGLAKLV

[                                    421                                                     480]
Bf_PKS7                             ............................................................
Aspergillus_terreus_at1             LAFQKQAIPKHVGIK--TMLNP--KFP-GLDSLNIHIALEQ-VPWPRN--DARTRYALVN
Aspergillus_terreus_at4             LMMKHGEIPPHCGIK--NRINH--NYPLYLEQRGVRIALNV-TAWKRDALPSGKRSVFLN
Aspergillus_terreus_at5             IMMQKNAIPHHVGIK--TTMNK--TFPHDLNERGVRIAFKE-TPWVRPDGGK-RR-AYLN
Gm_PKS5                             ............................................................
Ch_PKS9                             LVLEKGIIPPNVYPERINPAVTAAGPNLRF--PLEPVTWP-T-SG-V-------RRASVN
Ch_PKS8                             LSLEKAVIPPIAMFEKVNPAIDAADLQLAF--PKEAIPWP-A-SE-V-------RRASVS
Gz_PKS2                             CNLEKGVILPNALLQKMNPAMNADTY--SIEVPIHNVQWPV-------Q---GLRRVSLN
Gm_PKS2                             LILEKGVIPPNALLQKTNTALKADSY--NITVPTKSIEWPT-------E---GLRRVSLN
Ch_PKS10                            LTLESGIIPANAHFKEVNHAI---PKKWHFKFPTVATPYPKTPSG--------VRRVSIN
Ch_PKS5                             LALENGVIPPQANFEKANPKIPFQKWNLS--IADKAVPWP-T-QG-L-------RRVSIN
Ch_PKS7                             LMLEQEVILPNQNFEKPNPRIPFVDWKL--RVATNVQPWD-S-SG-P-------LRVSIN
Ch_PKS1                             LMLEQGVILPNRNFEETKHENPAGKMELAYKVPTTLECWN-N-VK-T-------RRVSIN
Didymella_maydis_PKS1               LMLENEIILPNRNFKHANLNIPLEEWKL--RVPTTVEPWN-S-MT-T-------RRASVN
Gz_PKS4                             LAMENSLIPPNIHFASPNPEIPLDEWNM--AVPTKLTPWPAA--R-T-------KRMSVS
Gz_PKS7                             LTLEHAKIPPNINLDKPNPDIDFKNWKV--KVPTKLLDWPLP--G-L-------RRVSVN
Gm_PKS7                             LALEHAKIPPNINFEKPNPDIDFKEWKV----PTELLDWPVS--G-L-------RRVSVN
Ch_PKS6                             LAVERGLIPQNLWFEKLNPEINLPE-NVEI--PLKLTPWP-S-DG-P-------RRASIN
Gz_PKS1                             ............................................................
Ch_PKS4                             LMIENGVIPPVPTFEKSSEQLPVDQ--MGITIPREAILWPAGTH----------KRASIN
Gm_PKS6                             YSLESGVISPTYGLENVNPKIKLDEWKINL--PTEKIKWP-A--G-L-------RRASIN
Nc_PKS1                             LMLERGFILPNHDFKQPNPRIPWKEWNLE--VPVTQRPWA---RG-K-------KYISVN
Bf_PKS8                             MMLERGFILPNHDFKTPNENIPFSKWHLQ--VPISQRPWP---RA-K-------KFASVN
Nc_PKS2                             LSLYYGFILPNADFDKENPGIPFKEWNMT--VAKQQKPWP---AH-K-------KYACVN
Ch_PKS2                             MMLKKGLVVPNANFENESMNSHLKEKNMR--VPISTQPW----KG-K-------TYIAIN
Aspergillus_terreus_lovF            LAVEKGVIPPNARFLQPSKKL-LKDTHI--QIPLCSQSWIPT-DG-V-------RRASIN
Penicillium_citrinum_mlcB           LALEKGLIPPNARFLQKNSKLMLDQKNI--KIPMSAQDWPVK-DG-T-------RRASVN
Ch_PKS3                             KAIEKGLIPPAANLETINPKLKLGEWNL--KIPRATEPW--N-AS-L-------RRASVN
Nc_PKS3                             LALERGQIPPSINFETPNAKLSLDEWKL--KVPTELEEWVGK-DG-I-------RRASIN
Bf_PKS2                             LVLEKGLIPPNVNLSNHKKGLDLEQSNI--VVPSKIEKLSVDEDG-K-------SRIAIN
Gz_PKS5                             LILKHGQIPATLNFIKPKPSLKLYEKKI--KIPSELTKLPTPQNG-P-------PRVSLN
Gm_PKS1_CAC44633                    LAIQNKTIPPNMHFDVLNPKIK--PFYDNLEVPTKAIAWPETHKGQP-------RRASIN
Gm_PKS1                             LAIQNKTIPPNMHFDVLNPKIK--PFYDNLEVPTKAIAWPEPYQGQP-------RRASIN
Bf_PKS5                             MAIKHGVFPPNLHFQNLSPKVA--PFYNHLHIPTTATPWPELPSGVP-------RRISCN
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Gm_PKS9                              MAMKNATVPPNMHFETLNPDIE--PFYSNLEVPTSAKAWPNVH-GSV-------RRASIN
Aspergillus_terreus_lovB             FAVRHGVIPPNLLFDKISPRVA--PFYKNLRIPTEATQWPALPPGQP-------RRASVN
Penicillium_citrinum_mlcA            FAVRNGVIPPNLLFEKISPRVA--PFYTHLKIATEATEWPIVAPGQP-------RRVSVN
Gz_PKS9                              MALKHAV-PPNLLFNRLNPALE--PFTK................................
Ch_PKS16                             QAMQNSTVPPNLWFQQINPKLK--PFYGNLQIPTHALIWPKPFGRRP-------KRASIN
Bf_PKS6                              LALKEKTIPPNLHFQSLNSAIE--PFYGNLNVPTAPLPWP--AVEGP-------LRASVN
Bf_PKS3                              LALQHSFIPPNMHFQELNPEIE--PFYQNLKVVTSLQPWPLIPDNTP-------RRASIN
Ch_PKS17                             EAVRRAVVPPNMLLQKLNPAIE--PFCVNLKVPTQSLPWPHLPLGGP-------RRASVN
Gz_PKS10                             EAVKTGIIPPNQLFETLNPAVK--PYTSNLKLPVESQPWPKLTEGFP-------RRASVN
Gm_PKS10                             EAVKRGVIPPNQLFENLNPALK--PYVSNLRLPTESKPWPKLAPGSA-------RRASVN
Nc_PKS4                              HAMINGTVPPNLHFNRLQPAVA--KYYSHLHVPTKALAWPSVAAGQP-------RRATVN
Bf_PKS4                              LAIQHGIIPPNLGFQQLNKKVA--PYCTNMDVVTSVQPWPAMASNTP-------RRVSIN
Gz_PKS11                             ............................................................
Ch_PKS14                             MSLENRTIPPNIKFTTPNPKIPFKE--AKLTVPVEPTPFPE-------D---RCERVSVN
Ch_PKS12                             LALENRVIPPNIKFETPNPKIPFLE--KDLKVPTDCLGWPK-------D---KLERVSVN
Gm_PKS12                             LALEHQMIPPNIKLVNPNPNSK-PT--MPSSVPLSPTQFPS-------D---RQNRVSIN
Ch_PKS13_pseudogene                  LTLEHKTIPPNIYFNIPNPRSTFKS--ARLAVPTEPLPWPT-------D---HTKRISVN
Ch_PKS11_FUM1                        LALENRKIPPNINFSIPNPKIPFNE--ANMVVPCEVLPWPE-------N---QPLRASVN
Gm_FUM1_AAD43562                     LALENRTIPPNINFSTPNPKIPFSE--MNMAVPVDAIPWPR-------D---RPLRVSVN
Gm_FUM1                              LALENRTIPPNINFSTPNPKIPFSE--MNMAVPVDAIPWPR-------D---RPLRVSVN
Ch_PKS15                             LSMEHQIIPPNVNFETPNPKIPWKE--ANLRVPTECMKWPS-------D---RLERASVN
Nc_PKS5                              LALEHGAIPPIYDLQTRNPNIDFEGA--KVQPVTEVTPWPKD------R---L-QRASIN
Gm_PKS15                             LAIENELIPPTIGIENFNPNIKFQDW--KLHVVQEATAWPSNIP---------IRRASVN
Nc_PKS6                              MALEKGEIPPTYGVKNINPKIKTDEW--NVQIVTETTPWPKNLPHNAGR---LFRRAGVN
Gm_PKS14                             KSFEKGQVPPTRGIVNLNPKLVLAER--NLMIAQDAHDWPRDL-----------RRASIN
Bf_PKS9                              LAMEKRTIPATIGIKKLNPXVDFKGG--RIEVVQKMTPWPKGFS---------VCRASIN
Gm_PKS13                             LALEKGEIPPNTNYKTPNPKIDFDGW--RVRVPTAPQPWPS-------K---SIRRASVN
Bf_PKS10                             MAIENGIIPGNPTFLKPSP---FAGL--KVKATRTAIPWPES----------SIRRASVN
Bf_PKS11                             LMLEHNMIPPQVNFEKANPEIDLDAL--NLRIPITLESRP-------------LKRISVN
Penicillium_patulum_6MSAS            LAIQKGVLPPQANLTKLNSRIDWKT--AGVKVVQEATPWPES-D------PIR--RAGVC
Byssochlamys_nivea_6MSAS             LALKKGILPPQANLQKLNSKVDWDH--AGVKVVQEATKWPES-D------EVR--RAGVC
Aspergillus_terreus_pksM             MAVEKAIFPPQTNLKRLNSRIDWDQ--AGVKVVQEALEWPGNED------DVR--RAGVC
Aspergillus_parasiticus_pksL2        MSVQKGILPPQANLKTLNTRVNWNE---GVRVVQDIEDWPSSGY------P-R--RAGVC
Penicillium_griseofulvum_pks2        LVLRHGQVPPQANLQTLNSKIAWKK--SLLCPARELVTLPH-GT------PSRPLRAAVA
Ch_PKS25                             LSVQRGIIPPQRLLENFNTNIDWDS--SGLKVLREGKIWPENGV----------WRAAVC
Nc_PKS7                              LMLHKNAIPPHVGIKKGSIINK--TFPKDLSDRNVNIAFHL-TPFKR-RDGKPRR-VFIN
Colletotrichum_lagenarium_pks1       MMMRKNAIPPHVGIKKE--INK--TFPKDLSERNVNIAFHL-TPFKR-RDGKPRR-IFVN
Nodulisporium_sp_PKS1                MMLKKNAIPPHIGIKKE--INK--TFPKDLGERGVNIAFHK-TPFTR-KDGKPRK-VFVN
Xylaria_sp_PKS12                     MMLQRNAIPPHIGIKKE--INK--TFPKDLGQRGVNIAFHK-TPFLR-KDGKPRR-LFVN
Bf_PKS12                             MMLQKNAIPPHVGIKK--TINQ--GFPKDLAERNVHIAFKN-TPLPRKKSGAPRR-IFVN
Glarea_lozoyensis_PKS1               MMLQKNAIPPHVGIKN--TINV--GFPKDLAERNVNIAFHK-TPL-RARAGMPRR-VFLN
Monascus_purpureus_PKS1              LMLRKNAIPPHIGIKR--DINK--GFP-DLAARNIKIAFDL-TPLPR-EAGKLRK-VFVN
Bf_PKS13                             MMLKKSMIPPHCGIK--TKINQ--TFPKDLKDRNLNMAFKP-TPFPRPTNGK-RY-VFMN
Ch_PKS18                             MMMKKNAIPANVGIKG--VMNK--TFPKDLAQRNVHIETTQ-VAWPR-KGAEKRK-IFLN
Bf_PKS14                             LVFQKSTIPPHVGIK--TGLNP--ALPKDLDQRGIVIPYTA-TSWEKS--SSQKRLAMVN
Ch_PKS20                             LMYQKSAIPPQIGVKK---LNP--TLPPDLEERTIGLNWEY-VEWPRPKTGS--RLAIVN
Aspergillus_nidulans_wA              LMMKENMIPPHCGIK--TKINH--NFPTDLAQRNVHIAL-QPTAWNRPSFGKRQI--FLN
Aspergillus_fumigatus_alb1           LMLKQNMIPPHCGIK--TKINH--NFPTDLAQRNVHIAF-KPTPWNRPVSGKRKM--FIN
Gz_PK12                              LMMEKNMIPPHCGIK--TKINH--HFPTDLTQRNVHIAK-VPTSWTRSGQANPRI-AFVN
Gm_PKS3_CAC88775                     QMLKKDTIVPHCGIK--NKINH--RFPTDLEQRNVRIAM-GPTQWKKGTEINPRR-VFVN
Gm_PKS3                              QMLKKDTIVPHCGIK--NKINH--RFPTDLDQRNVRIAL-EPTGWKKGTETNPRR-VFVN
Gz_PKS12                             QMMQKNTIVPHCGIK--TKINH--RFPTDLEERNIRIAF-EPTPWERINLDTPRR-VMVN
Gm_PKS4_CAC92399                     LMMQKNTIPPHCGIK--TKINQ--GFPKDLDHRGVRIALKDSVDWSRPEGGK-RR-VLVN
Gm_PKS4                              LMMQKNTIPPHCGIK--TKINQ--GFPKDLDHRGVRIALKDGVDWTRPEGGK-RR-VLVN
Aspergillus_parasiticus_pksL1        MMMQHDTIPPHCGIKPGSKINR--NFP-DLGARNVHIAF-EPKPWPRTHTPRR---VLIN
Aspergillus_nidulans_pksST           LMMKNDTIPPHCGIKPGSRINR--NYP-DLPARNVHIAF-EPKPWPRTDTPRR---VLIN
Gz_PKS13                             MMFQKNILPPQAGMPH--ALNP--NFP-PLSEINIEIP-SEPSTFESPVSQP--RRILLN
Bf_PKS15                             LILREGSIPTQPDWPF--KLNH--KFP-DLEASNIMIA-DGKGRLVPRPNGDGKRRIVVN
Bf_PSK19                             LMMKHRKIPRQASYK---ELNP--QIPS-LDQDRMAIPTSV-MPW-----NPPVRLACVN
Ch_PKS22                             AMLQKQRIPPLASFK---SLNP--KIPA-LAPDKMAVAKQVE-AW-----DAPLRAACVN
Bf_PKS16                             AMINKGVIPPLASHN---NLNP--KIPA-LEPDRMAITTKAI-PW-----IAKFRAACVN
Ch_PKS19                             LMLQKNAIPPHIGIK--TEVNP--RLPKDLDQRNVAIPFSM-TEWKSD--GKKKRIAAVN
Ch_PKS23                             AMLQKKSIPPHASFN---TLNP--KIPS-LGPDKITIARNLE-PW-----NIPFRAALVN
Ch_PKS21                             CMLHEATIPPQASHT---VMNP--AIGA-TKSDGIQITLQP-KPW-----NADFKAALIN
Bf_PKS17                             LMVQEGFIPPQASFT---SVNP--NLGL-TPDDKIEISAQL-KPW---------------
Bf_PKS18                             LMMKHKSIPKQANHL---SLNP--KIRA-LEPDKIKIPLQT-TPW-----EADLRIASIN
Bf_PKS20                             LMMKHGKIPIQAQFR---TLNT--NIPA-LETDKMAISTSLQKQW-----SDDLRLALVN
Homo_sapiens_FAS                     LSLEHGLWAPNLHFHSPNPEIP-ALLDGRLQVVDQPLPVRGGN-------------VGIN
Gallus_gallus_FAS                    LSLEHGLWAPNLHFNDPNPDIP-ALHDGSLKVVCKPTPVKGGL-------------VSIN
Caenorhabditis_elegans_FAS           LSIERQLIPPNLHYNTPNQYIP-GLTDGRLKVVTEPTALPGGL-------------IGIN
Bombyx_mori_FAS_p270                 IAYTTGYIPPNLNYSIPREGVS-ALVDGRMNVITDKQAWNRGM-------------SGIN
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Ch_9497_PKS24_3p_of_nps7             LAMQHNKIPRTLHAEKPTSAVDWQG--ANMALVQEPQPWLPQAD------R--PRRAGVS
Nc_3_oxoacyl_ACP_synthetase         LAIAEGXIPPTLNLTSPNVGVGFNFVPVQ----------------AQQ-KEVK--VAMSN
Homo_sapiens_3_oxoacyl_ACP_synth    LACYYQKLPPTLNLDCSEPEFDLNYVPLK----------------AQEWKTEKRFIGLTN
Glycine_max_beta_ketoacyl_synth     KAITTGWLHPTINQFNPEPAVDFDTVANV----------------KQQHEIN---VAISN
Streptomyces_coelicolor_act         LALEHGVVPPTANLRTSDPECDLDYVPLE----------------ARERKLR---SVLTV
Streptomyces_avermitilis_pks9       LAIDAGLIPPTANLHEPDPELGLDYVPLS----------------ARQADLR---TVLKV
Bacillus_subtilis_pksK_mod2         MSLYHQELAPSVNYKEPNPNTDLAS--SPFYVVDQKKTLS---------REIKTHRAALS
Bacillus_subtilis_pksK_mod3         LQMKHKTLVKSLHCETLNPYLQLTD--SPFYIVQEKQEWK-SVTDRDGNE--LPRRAGIS
Bacillus_subtilis_pksL_mod1         LQLHHQKLVPSLHSEELNPYVDFEK--SPFYVQHETETWKQPVIKENGEDVPYPRRAGIS
Bacillus_subtilis_pksL_mod2         LQMKYRHVAPSLHSNVLNPNIDFLN--SPFKVQQELEEWKRPIISVNGKDIELPRIAGVS
Bacillus_subtilis_pksL_mod3         LCMNHKTLVPTLNFTTPNEHFEFEH--SPLYVNTELKPWE----TADGK----PRRACVS
Bac_subtilis_mycA_pks1_mod2         LMLNHKKIPPLAHFNKPNPLIPFHS--SPFYVNQEVMDFTPE---------DRPLRGGIS
Microcystis_aruginosa_mycE          LILQQGEIPPHLHFQSPNPLINWQD--HPIEIPTQNIPWPNNNK------V--P-IAGVS
Microcystis_aruginosa_mycG          LALKYRVIPPTLHFQNPNPQINFSQ--TPFYINNEAISWT----TKQDKSEKLPRRAGVN
Mycobacterium_leprae_pksE           LALQHAYIPRNVHFTQWNPAIDAST--TRLFVPTESAPWPA-IP------G--PRRGAVS
Mycobacterium_tuberculosis_mas      LSLRHGVVPPLLHFNRLPDELSDVE--TGLFVPQAVTPWPNGND------HT-PKRVAVS
Mycobacterium_tuberculosis_ppsC     LAVHNGYIPRHLNFHQLTPHASEAA--SRLRIAADGIDWPT-TG------R--PRRAGVS
Mycobacterium_tuberculosis_ppsD     LAVQRGHIPRNLHFTRWNPAIDASA--TRLFVPTESAPWPA-AA------G--PRRAAVS
Mycobacterium_tuberculosis_ppsE     LCLKNKALPATLHYTSPNPELRLDQ--SPFVVQSKYGPWE----CD------GVRRAGVS
Myxococcus_xanthus_ta1_mod2         LSLRQGEVPPTLHVTQVNPKLELTD--SPFVIADRLAPWP---------SLPGPRRAAVS
Nostoc_sp_nosB                      LALQNKMLPPSLHFETPNPKIDFAN--SPFYVNTTLTEWR----T-----NTTPRRAGVS
Pseudomonas_syringae_cfa6           MALRTGTLPRSLHITAPSTEVDWST--GAIELLSERRPWPNVAD------R--PRRAGIS
Pseudomonas_syringae_cfa7           MALNQGVLPKTLHAQEPSRKIDWSE--QTVRLLHRARPWP-ETD------Q--PRRAGVS
Sorangium_cellulosum_epoA_mod1      LSLQHGQIPAHLHAQALNPRISWGD--LRLTVTRARTPWPDWNT---------PRRAGVS
Sorangium_cellulosum_epoC_mod2      LALEHRQLPPSLNFESPNPSIDFAS--SPFYVNTSLKDWN----T-----GSTPRRAGVS
Sorangium_cellulosum_epoF_mod9      LALHHESIPRNLHFHTLNPRIRIEG--TALALATEPVPWP-RAG------R--PRFAGVS
Stigmatella_aurantiaca_mxaB2_B1     LSLQHKEIPPHLHFRTPNPHVEWDR--IPARVPVERVPWPAHEG---------RRIAGVS
Stigmatella_aurantiaca_mxaC1        LAMRHQSIPPHLHLKQVNPRIQLEG--SALTIPTRLTPWKASG-------Q--PRRAGVS
Stigmatella_aurantiaca_mxaC2        LALRHEAIPKHLHFKALNPRITIED--TPFVIPTQMQPWPVSQ-------R--RRYAAVS
Stigmatella_aurantiaca_mxaC3        LAHRHGVVPPHLHLKKLNPHIELNG--FPLDIPTQVTPWPERAR---------PRIAGIS
Stigmatella_aurantiaca_mxaD         LALRNETIPPNLHFKRLNPDIVLDG--APVVVPTEPRSWPRAEQ---------PRFAGVS
Stigmatella_aurantiaca_mxaE         LSMQHGAVPPIAHFQRLNPRIDFAG--ESITIPTALHPWPAREE------R--KRRGAIS
Stigmatella_aurantiaca_mxaF         LSIKNRALPPSLHFETPNPLIPFED--LRLEVQRTLSDWPEPD-------R--KLVAGVS
Streptomyces_natalensis_PimS0       LALRHGVLPQTLHVDAPSAKVDWSA--GSVRLLTEARPWPRESG------R--TRRAGVS
Streptomyces_natalensis_PimS2_mod3  LALRNGQLPRTLHADTPSSHIDWTP--GTVSLLTEPTDWP-EGE------R--PRRCAVS
Streptomyces_natalensis_PimS2_mod4  MAMRHAAVPRSLHIDRPSSHVDWSS--GAIQLLTEPLPWP-ATG------H--PRRAGVS
S_viridochromogenes_aviM            LALDEDRIPASLLDGDPNPEIDWAG--LDIRLATRALPWPER-P------H--PRRAAVS
Xanthomonas_albilineans_xabB_mod2   LMLKHGEQAGTRHFSTLNPLIDLRG--TSFEVVAQHRAWPSQVGI---HGTLLPRRAGIS
Xanthomonas_albilineans_xabB_mod3   LQFRHGELVPSLNAFPLNPYIEF----GRFQVQQQPAPWPR-----RGAQ---PRRAGLS

[                                    481        487]
Bf_PKS7                             ......
Aspergillus_terreus_at1             NFGASG
Aspergillus_terreus_at4             NFSAAG
Aspergillus_terreus_at5             NFGASG
Gm_PKS5                             ......
Ch_PKS9                             SFGYGG
Ch_PKS8                             SFGYGG
Gz_PKS2                             SFGVGG
Gm_PKS2                             SFGFGG
Ch_PKS10                            SFGISG
Ch_PKS5                             SFGVGG
Ch_PKS7                             SFGYGG
Ch_PKS1                             SFGYGG
Didymella_maydis_PKS1               SFGYGG
Gz_PKS4                             GFGMGG
Gz_PKS7                             CFGFGG
Gm_PKS7                             C.....
Ch_PKS6                             SFGFGG
Gz_PKS1                             ......
Ch_PKS4                             STGYGG
Gm_PKS6                             SFGYGG
Nc_PKS1                             NFGFGG
Bf_PKS8                             NFGFGG
Nc_PKS2                             NFGFSG
Ch_PKS2                             NYGFGG
Aspergillus_terreus_lovF            NFGFGG
Penicillium_citrinum_mlcB           NFGFGG
Ch_PKS3                             NFGYGG
Nc_PKS3                             NFGYGG
Bf_PKS2                             SFGYGG
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Gz_PKS5                             SFGYGG
Gm_PKS1_CAC44633                    SFGFGG
Gm_PKS1                             SFGFGG
Bf_PKS5                             SFGFGG
Gm_PKS9                             SFGFGG
Aspergillus_terreus_lovB            SFGFGG
Penicillium_citrinum_mlcA           SFGFGG
Gz_PKS9                             ......
Ch_PKS16                            NFGFGG
Bf_PKS6                             SFGFGG
Bf_PKS3                             SFGFGG
Ch_PKS17                            SFGYVF
Gz_PKS10                            SFGFGG
Gm_PKS10                            SFGFGG
Nc_PKS4                             SFGFGG
Bf_PKS4                             SFGFGG
Gz_PKS11                            ......
Ch_PKS14                            SFGLGG
Ch_PKS12                            NFGIGG
Gm_PKS12                            SFGIGG
Ch_PKS13_pseudogene                 SFRVGG
Ch_PKS11_FUM1                       SFGIGG
Gm_FUM1_AAD43562                    SFGIGG
Gm_FUM1                             SFGIGG
Ch_PKS15                            SFGIGG
Nc_PKS5                             SFGYGG
Gm_PKS15                            SFGYGG
Nc_PKS6                             SFGYGG
Gm_PKS14                            SFGYGG
Bf_PKS9                             SFGYGG
Gm_PKS13                            SLGIGG
Bf_PKS10                            SFGYGG
Bf_PKS11                            SFGYGG
Penicillium_patulum_6MSAS           SYGYGG
Byssochlamys_nivea_6MSAS            SYGYGG
Aspergillus_terreus_pksM            SYGYGG
Aspergillus_parasiticus_pksL2       SYGYGG
Penicillium_griseofulvum_pks2       SYGYSG
Ch_PKS25                            SHSYGG
Nc_PKS7                             NFSAAG
Colletotrichum_lagenarium_pks1      NFSAAG
Nodulisporium_sp_PKS1               NFSAAG
Xylaria_sp_PKS12                    NFSAAG
Bf_PKS12                            NFSAAG
Glarea_lozoyensis_PKS1              NFSAAG
Monascus_purpureus_PKS1             NFSAAG
Bf_PKS13                            NFSAAG
Ch_PKS18                            NFSAAG
Bf_PKS14                            NFGAAG
Ch_PKS20                            SFGAHG
Aspergillus_nidulans_wA             NFSAAG
Aspergillus_fumigatus_alb1          NFSAAG
Gz_PK12                             NFSAAG
Gm_PKS3_CAC88775                    NFSAAG
Gm_PKS3                             NFSAAG
Gz_PKS12                            NFSAAG
Gm_PKS4_CAC92399                    NFSAAG
Gm_PKS4                             NFSAAG
Aspergillus_parasiticus_pksL1       NFSAAG
Aspergillus_nidulans_pksST          NFSAAG
Gz_PKS13                            NFDAAV
Bf_PKS15                            SFDAAG
Bf_PSK19                            SHGAAG
Ch_PKS22                            SYGAAG
Bf_PKS16                            SYGAAG
Ch_PKS19                            NFGAAG
Ch_PKS23                            NYGAAG
Ch_PKS21                            NYGASG
Bf_PKS17                            ......
Bf_PKS18                            NYGASG
Bf_PKS20                            NFGASG
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Homo_sapiens_FAS                    SFGFGG
Gallus_gallus_FAS                   SFGFGG
Caenorhabditis_elegans_FAS          SFGFGG
Bombyx_mori_FAS_p270                SFGFGG
Ch_9497_PKS24_3p_of_nps7            AFGIGG
Nc_3_oxoacyl_ACP_synthetase         SFGXGG
Homo_sapiens_3_oxoacyl_ACP_synth    SFGFGG
Glycine_max_beta_ketoacyl_synth     SFGFGG
Streptomyces_coelicolor_act         GSGFGG
Streptomyces_avermitilis_pks9       GSGFGG
Bacillus_subtilis_pksK_mod2         SFGLGG
Bacillus_subtilis_pksK_mod3         SFGIGG
Bacillus_subtilis_pksL_mod1         SFGATG
Bacillus_subtilis_pksL_mod2         SFGAGG
Bacillus_subtilis_pksL_mod3         SFGYSG
Bac_subtilis_mycA_pks1_mod2         SFGFSG
Microcystis_aruginosa_mycE          SFGFSG
Microcystis_aruginosa_mycG          SLGIGG
Mycobacterium_leprae_pksE           SFGLSG
Mycobacterium_tuberculosis_mas      SFGMSG
Mycobacterium_tuberculosis_ppsC     SFGVSG
Mycobacterium_tuberculosis_ppsD     SFGLSG
Mycobacterium_tuberculosis_ppsE     SFGVGG
Myxococcus_xanthus_ta1_mod2         AFGLGG
Nostoc_sp_nosB                      SFGIGG
Pseudomonas_syringae_cfa6           SFGVSG
Pseudomonas_syringae_cfa7           SFGFSG
Sorangium_cellulosum_epoA_mod1      SFGMSG
Sorangium_cellulosum_epoC_mod2      SFGIGG
Sorangium_cellulosum_epoF_mod9      AFGLSG
Stigmatella_aurantiaca_mxaB2_B1     SFGLSG
Stigmatella_aurantiaca_mxaC1        SFGISG
Stigmatella_aurantiaca_mxaC2        SFGISG
Stigmatella_aurantiaca_mxaC3        AFGLSG
Stigmatella_aurantiaca_mxaD         AFGISG
Stigmatella_aurantiaca_mxaE         SFGISG
Stigmatella_aurantiaca_mxaF         SFGFGG
Streptomyces_natalensis_PimS0       SFGLTG
Streptomyces_natalensis_PimS2_mod3  SFGISG
Streptomyces_natalensis_PimS2_mod4  SFGLSG
S_viridochromogenes_aviM            GFGYGG
Xanthomonas_albilineans_xabB_mod2   SFGFGG
Xanthomonas_albilineans_xabB_mod3   AFGAGG
```

Bf, *Botrytis fuckeliana*; Ch, *Cochliobolus heterostrophus*; Gm, *Gibberella moniliformis*; Gz, *Gibberella zeae;* Nc, *Neurospora crassa*.

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Table 3. Type I *PKS* genes annotated from the genomes of eight ascomycete fungi

Fungus	*PKS* gene*	Domain structure of the PKS protein[†]	
Schizosaccharomyces pombe	None		
Schizosaccharomycetes;			
Schizosaccharomycetales;			
Schizosaccharomycetaceae			
Saccharomyces cerevisiae	None		
Saccharomycotina;			
Saccharomycetes;			
Saccharomycetales;			
Saccharomycetaceae			
Eremothecium (*Ashbya*) *gossypii*	None		
Saccharomycotina;			
Saccharomycetes;			
Saccharomycetales;			
Eremotheciaceae			
Botryotinia fuckeliana (*Botrytis cinerea*)	(reducing PKS clade I) *BfPKS1*-[‡]M58U	(KS-AT-DH-(ME)-ER-KR-PP) KS-AT-DH-ME -ER-KR-PP	
Pezizomycotina;	*BfPKS2*-M37H	KS-AT-DH-ME -ER-KR-PP	

Leotiomycetes; Helotiales; Sclerotiniaceae	(reducing PKS clade II) *BfPKS3*-M4H5 *BfPKS4*-M4CL	(KS-AT-DH-(ME) -KR-PP- -(CON)-(AMP-PP) KS-AT-DH -KR-PP -CON-AMP-PP KS-AT-DH-ME -KR-PP	
	BfPKS5-M40A	KS-AT-DH-ME -KR-PP -CON-AMP-PP	
	BfPKS6-M39G	KS-AT-DH-ME -KR-PP	
	***BfPKS7*-M2TQ	[§]KS-AT-DH-ME -KR-PP -CON-AMP-PP	
	(reducing PKS clade III) *BfPKS8*-M58P	(KS-AT-DH -ER-KR-PP-(PP)) KS-AT-DH -ER-KR-PP-PP	
	(reducing PKS clade IV) *BfPKS9*-M4RN	(KS-AT-DH-(ME)-ER-KR-PP) KS-AT-DH -ER-KR-PP	
	BfPKS10-M5VH	KS-AT-DH -ER-KR-PP	
	BfPKS11-M48U	KS-AT-DH-ME -ER-KR-PP	
	(nonreducing PKS clade II) *BfPKS12*-M5QUb	(KS-AT -PP-(PP) -CYC) KS-AT -PP-PP -CYC	
	BfPKS13-M2WM	KS-AT -PP-PP -CYC	
	(nonreducing PKSs basal to clades I and II) *BfPKS14*-M5DE	(KS-AT -PP-(PP) -(CYC)) KS-AT -PP-PP	
	BfPKS15-M304	KS-AT -PP-PP -CYC	
	(nonreducing PKS clade III) *BfPKS16*-M3R8	(KS-AT -PP-(PP)-ME-(CYC)) KS-AT -PP-PP -ME	
	BfPKS17-M3N0	KS-AT -PP -ME	
	BfPKS18-M5QUa	KS-AT -PP -ME	
	BfPKS19-M34F	KS-AT- -PP -ME	
	BfPKS20-M5PH	KS-AT- -PP-PP -ME-CYC	
Cochliobolus heterostrophus	(reducing PKS clade I) *ChPKS1*-[‡]M4FP	(KS-AT-DH-(ME)-ER-KR-PP) KS-AT-DH -ER-KR-PP	

(*Bipolaris maydis*)	*ChPKS3*-M3FUa	KS-AT-DH-ME-ER-KR-PP	
Pezizomycotina;	*ChPKS4*-M3FUb	KS-AT-DH-ME-ER-KR-PP	
Dothideomycetes;	*ChPKS5*-M4EG	KS-AT-DH-ME-ER-KR-PP	
Pleosporales;	*ChPKS6*-M578	KS-AT-DH-ME-ER-KR-PP	
Pleosporaceae	*ChPKS7*-M584	KS-AT-DH -ER-KR-PP	
	ChPKS8-M4VU	KS-AT-DH-ME-ER-KR-PP	
	ChPKS9-M4U9	KS-AT-DH -ER-KR-PP	
	ChPKS10-M43G (reducing PKS clade II) *ChPKS16*-M4GJ *ChPKS17*-M3HR (reducing PKS clade III) *ChPKS2*-M4LU	KS-AT-DH -ER-KR-PP (KS-AT-DH-(ME) -KR-PP -(CON)-(AMP-PP)) KS-AT-DH-ME -KR-PP KS-AT-DH-ME -KR-PP -CON (KS-AT-DH -ER-KR-PP-(PP)) KS-AT-DH -ER-KR-PP-PP	
	(reducing PKS clade IV) *ChPKS11*-M55H	(KS-AT-DH-(ME)-ER-KR-PP) KS-AT-DH-ME-ER-KR-PP	
	ChPKS12-M3U6	KS-AT-DH-ME-ER-KR-PP	
	[¶]*ChPKS13*-M3SM	KS-AT-DH-ME-ER-KR-PP	
	ChPKS14-M3SV	KS-AT-DH-ME-ER-KR-PP	
	ChPKS15-M356b	KS-AT-DH-ME-ER-KR-PP	
	(nonreducing PKS clade II) *ChPKS18*-M5CW	(KS-AT -PP-(PP) -CYC) KS-AT -PP -CYC	
	(nonreducing PKSs basal to clades I and II) *ChPKS19*-M4H3	(KS-AT -PP-(PP) -(CYC)) KS-AT -PP	
	ChPKS20-M5KW	KS-AT -PP-PP	
	(nonreducing PKS clade III) *ChPKS21*-M3FU	(KS-AT -PP-(PP) -ME-(CYC)) KS-AT -PP -ME	

	ChPKS22-M3QM	KS-AT -PP-PP-PP-ME	
	ChPKS23-M4MK	KS-AT -PP-PP -ME	
	(fungal NRPS/PKS clade) *ChPKS24*-M356a	(AMP-PP-KS-AT-DH -KR-PP -DHG) AMP-PP-KS-AT-DH -KR-PP -DHG	
	(fungal 6MSAS clade) *ChPKS25*-M3HB	(KS-AT-DH -KR-PP) KS-AT-DH -KR-PP	
Gibberella moniliformis (*Fusarium verticillioides*)	(reducing PKS clade I) *GmPKS2*-[‡]MOWT	(KS-AT-DH-(ME)-ER-KR-PP) KS-AT-DH-ME-ER-KR-PP	
Pezizomycotina; Sordariomycetes;	*GmPKS5*-MOQ4 *GmPKS6*-M232b	KS-AT-DH-ME-ER-KR-PP KS-AT-DH -ER-KR-PP	
Hypocreales;	*GmPKS7*-M1NB	KS-AT-DH -ER-KR-PP	
Nectriaceae	(reducing PKS clade II) *GmPKS1*-M232a	(KS-AT-DH-(ME) -KR-PP -(CON)-(AMP-PP)) KS-AT-DH-ME -KR-PP -CON-AMP-PP	
	GmPKS8-MODGb	KS-AT-DH-ME -KR-PP	
	GmPKS9-M2SJ	KS-AT-DH-ME -KR-PP -CON-AMP-PP	
	GmPKS10-M3ED	KS-AT-DH-ME -KR-PP -CON-AMP-PP	
	(reducing PKS clade IV) *GmPKS11*-M2VE	(KS-AT-DH-(ME) -ER-KR-PP) KS-AT-DH-ME-ER-KR –PP	
	GmPKS12-MOUB	KS-AT-DH-ME-ER-KR –PP	
	GmPKS13-MODGa	KS-AT-DH-ME-ER-KR –PP	
	GmPKS14-M2DH	KS-AT-DH -ER-KR –PP	
	GmPKS15-M2KJ	KS-AT-DH-ME-ER-KR –PP	
	(nonreducing PKS clade I) *GmPKS3*-MOS2	(KS-AT -PP-(PP) -CYC) KS-AT -PP-PP	
	GmPKS4-MYKP	KS-AT PP -CYC	

Gibberella zeae (*Fusarium graminearum*)	(reducing clade I) *GzPKS1*-[‖]9490+18265	(KS-AT-DH-(ME) -ER-KR-PP) [§]KS-AT-DH-ME-ER-KR-PP	
Pezizomycotina;	*GzPKS2*-17858	[§]KS-AT-DH-ME-ER-KR-PP	
Sordariomycetes;	*GzPKS4*-10828	[§]KS-AT-DH -ER-KR-PP	
Hypocreales;	*GzPKS5*-11130	[§]KS-AT-DH-ME-ER-KR-PP	
Nectriaceae;	*GzPKS7*-8578	[§]KS-AT-DH-ME -ER-KR-PP	
	[**]*GzPKS8*-12692	[§]KS-AT-DH-ME-ER-KR-PP	
	(reducing PKS clade II) *GzPKS9*-5148	(KS-AT-DH-(ME) -KR-PP -(CON)-(AMP-PP)) [§]KS-AT-DH -KR-PP	
	GzPKS10-7224	[§]KS-AT-DH -KR-PP -CON-AMP-PP	
	(reducing PKS clade IV) [**]*GzPKS6*-4447 *GzPKS11*-3270	(KS-AT-DH-(ME) -ER-KR-PP) [§]KS-AT-DH-ME-ER-KR-PP [§]KS-AT-DH-ME-ER-KR-PP	
	(nonreducing PKS clade I) *GzPKS3*-8340+6005 *GzPKS12*-8340+6550	(KS-AT -PP-(PP) -CYC) [§]KS-AT -PP -CYC [§]KS-AT -PP-TE	
	(nonreducing PKSs basal to clades I and II) *GzPKS13*-7923	(KS-AT -PP-(PP) -(CYC)) [§]KS-AT -PP	
	GzPKS14-15081+19966	[§]KS-AT -PP	
	(nonreducing PKS clade III)	(KS-AT -PP-(PP)-ME -(CYC))	
	GzPKS15-13158	[§]KS-AT -PP	
	[**]*GzPKS16*-18966	[§]KS-AT -PP -ME	

Neurospora crassa	(reducing PKS clade I)	(KS-AT-DH-(ME) -ER-KR-PP)	
Pezizomycotina;	*NcPKS3*-NCUO4865.1	KS-AT-DH-ME-ER-KR-PP	
Sordariomycetes;	(reducing PKS clade II)	(KS-AT-DH-(ME) -KR-PP -(CON)-(AMP-PP))	
Sordariales;	*NcPKS4*-NCU08399.1	KS-AT-DH-ME-ER-KR-PP	
Sordariaceae;	(reducing PKS clade III	(KS-AT-DH -ER-KR-PP-(PP))	
	NcPKS1-NCUO6013.1	KS-AT-DH -ER-KR-PP	
	NcPKS2-NCUO5011.1	KS-AT-DH -ER-KR-PP	
	(reducing PKS clade IV)	(KS-AT-DH-(ME) -ER-KR-PP)	
	NcPKS5-NCUO9638.1	KS-AT-DH -ER-KR-PP	
	NcPKS6-NCU02918.1	KS-AT-DH-ME-ER-KR-PP	
	(nonreducing PKS clade II)	(KS-AT -PP-(PP) -CYC)	
	NcPKS7-NCU03584.1	KS-AT- PP-PP -CYC	

*Genes within a species are listed by their subclades as they appear in the protein genealogy in Fig. 1.

[†] KS, ketoacyl synthetase [PKS-associated domain pfam00109.6 (N-terminal) + pfam2801.6 (C-terminal)]; AT, acyl transferase (PKS-associated domain pfam 00698.6); DH, dehydratase (PKS-associated domain, C terminus of COG3321.1, which includes KS and AT domains); ER, enoyl reductase (PKS-associated domain ~COG0604.1);, KR, ketoreductase (PKS-associated domain ~COG1028.1); PP, acyl carrier protein of PKSs and thiolation of NPSs (attachment cite of phosphopantetheine, pfam 00550.6); ME, methyltransferase (PKS-associated domain COG2226.1); CYC, Claisen-type cyclase; AMP, adenylation (NPS-associated domain COG1020.1); CON, condensation (NPS -associated domain pfam 00668.6); DHG, dehydrogenase (NPS-associated domain COG3320.1).

[‡] Celera/TMRI assembly metacontig numbers from 5× coverage of *B. fuckeliana*, *C. heterostrophus*, and *G. moniliformis* genomes.

[§] Modular construction is predicted, based on placement of the gene fragment in the protein genealogy; prediction is identical to its orthologs when they occur or includes all possible domains for those genes without an orthologous match in the genealogy.

[¶] Pseudogene with domain residues punctuated by stop codons.

[||] TMRI assembly contig numbers from 2× coverage of the *G. zeae* genome.

**Gene drawn onto gene genealogy and marked with a single asterisk in Fig. 1, as available sequence is a C-terminal fragment of the KS domain (alignment used for phylogenetic analysis includes only N-terminal fragments).

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