Engineering of chimeric polyketide synthases using SYNZIP docking domains

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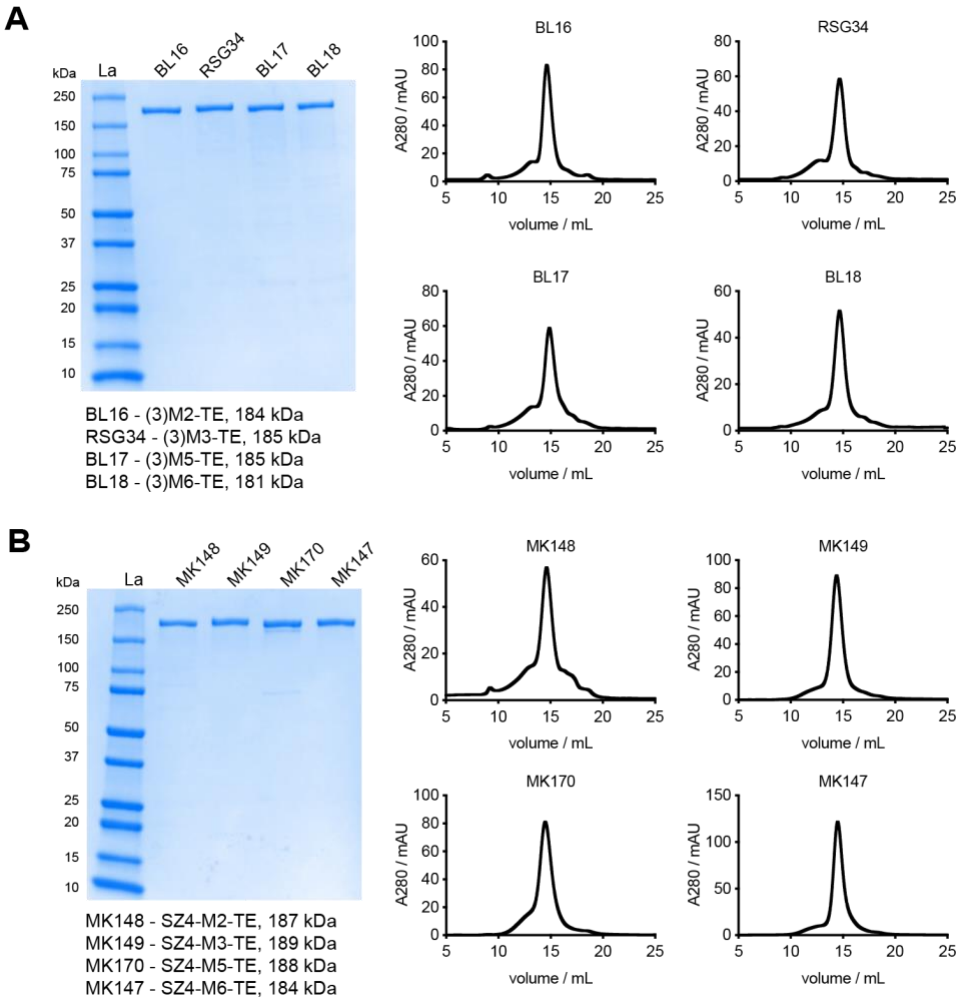

Figure S1. Analysis of protein purity by SDS-PAGE and SEC – single module acceptors. Acceptor proteins harboring a DEBS docking domain (A), and in comparison, a SZ domain (B). Protein abbreviations and their molecular weights (MW) are indicated. All proteins are pure and eluted in a predominately single peak from SEC.

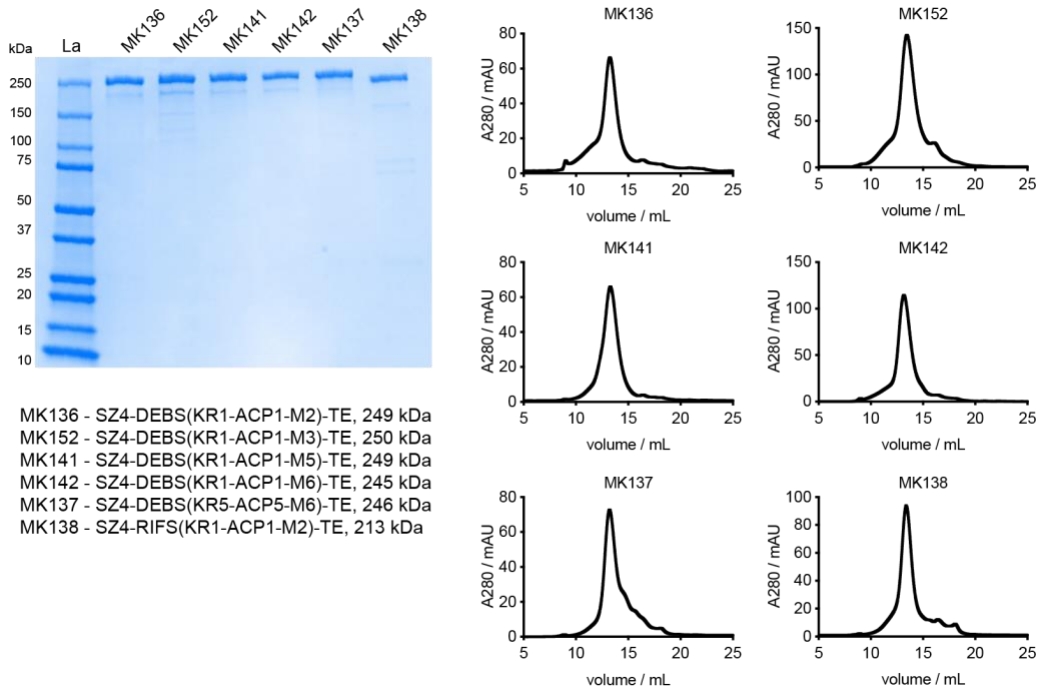

Figure S2. Analysis of protein purity by SDS-PAGE and SEC – covalent fusion acceptors. Acceptor proteins in which a KR-ACP fragment was fused to the acceptor module. Protein abbreviations and their MW are indicated. All proteins are pure and eluted in a predominately single peak from SEC.

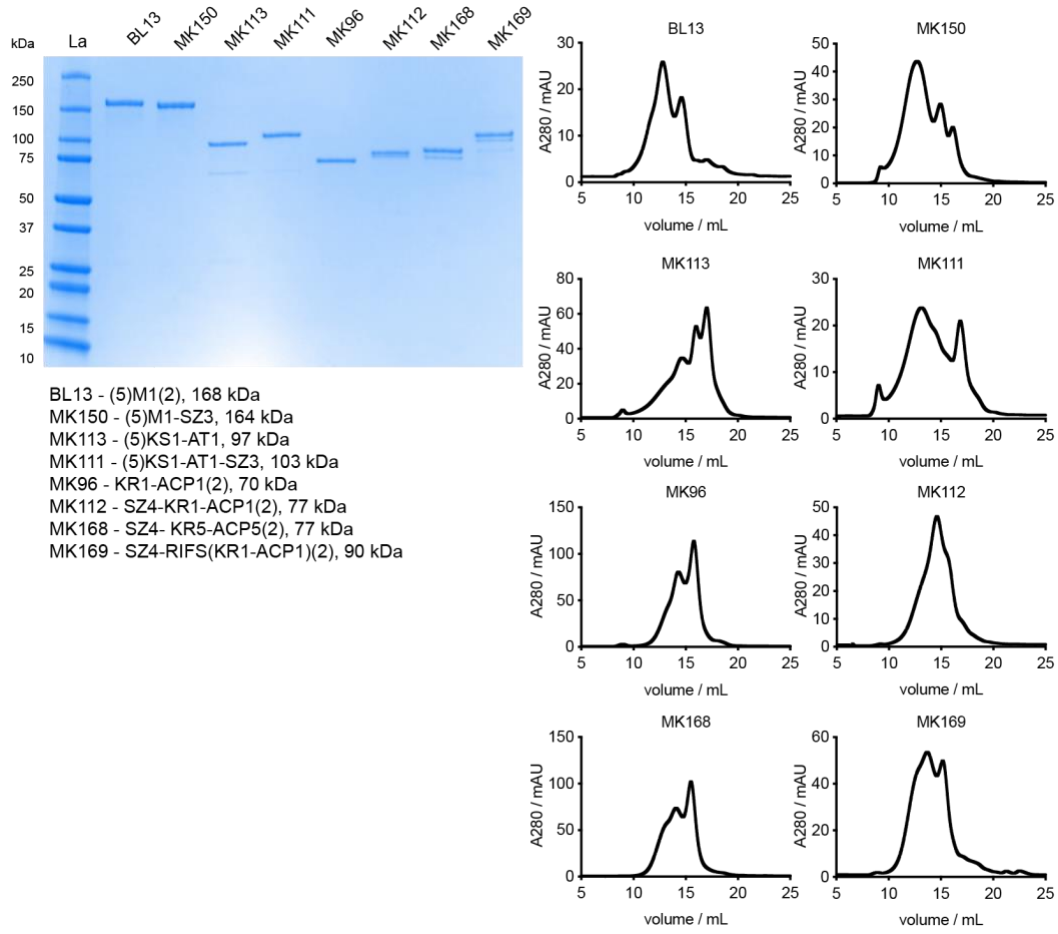

Figure S3. Analysis of protein purity by SDS-PAGE and SEC – DEBS M1 and its derivatives. DEBS M1 and its derivatives/fragments used in this study. If no indication is given the PKS domain/modules are derived from DEBS. Protein abbreviations and their MW are indicated. All proteins are pure, yet they appear as multiple oligomeric species based on SEC.

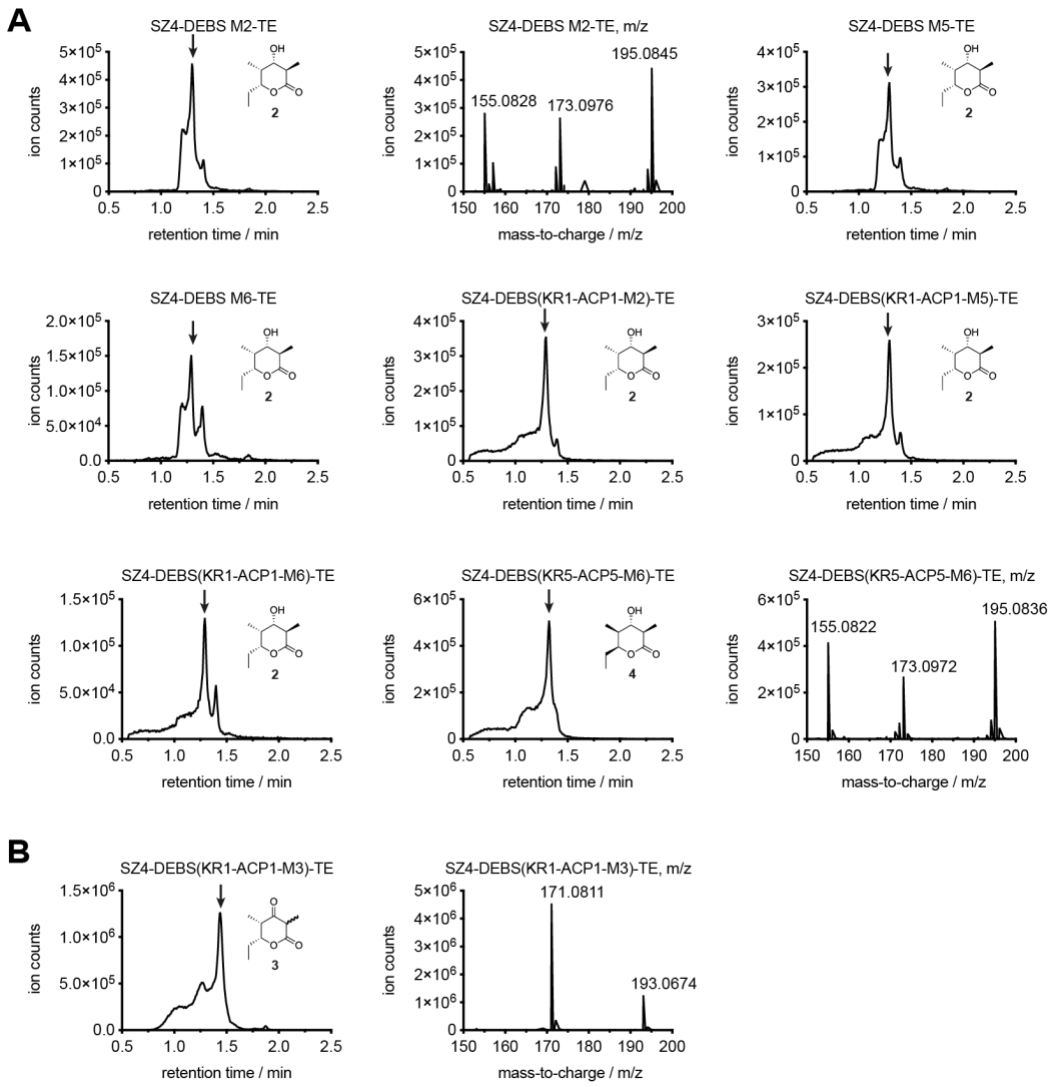

Figure S4. LC-MS analysis of products produced by bimodular chimeric PKSs newly generated in this study. A) Reduced triketide lactone products **2** and **4** ($C_9H_{16}O_3$, calculated MW 172.110) were detected in reaction mixtures containing SZ4-M2-TE, SZ4-M5-TE, SZ4-M6-TE, SZ4-KR1-ACP1-M2-TE, SZ4-KR1-ACP1-M5-TE, SZ4-KR1-ACP1-M5-TE, and SZ4-KR5-ACP5-M6-TE. B) Ketolactone **3** ($C_9H_{14}O_3$, calculated MW 170.090) was detected in reaction mixtures containing SZ4-KR1-ACP1-M3-TE. All PKS domain/modules are derived from DEBS. For all systems the extracted ion chromatograms were obtained by extraction of the $[M+Na]^+$ species and one chromatogram per compound is shown as an example. Labeled peaks from left to right correspond to $[M+H-H2O]^+$, $[M+H]^+$, and [M+Na]+ ions. The peak of interest is marked with an arrow based on its mass spectrum.

Table S1: Plasmids and primers used in this study. The cloning strategy is indicated for each construct. Some plasmids were only generated to function as intermediate constructs of the given cloning strategy and were not used for protein purification. If no indication is given the PKS domain/modules are derived from DEBS.

Plasmid Encoded Protein	Cloning Method	Cloning Fragments	Primer Name	Primer Sequence 5'-3'	Template
pMK80 - ACP1-M5-TE, used to generate pADD02	Infusion	80_V1	P-MK254	CGCCTGGCTGGGCGGAGGG	pBL17
			P-MK239	CATATGTATATCTCCTTCTTAAAGTTAAACAAAATTA	
		80_V2	P-MK250	GAGCCGATCGCGATCGTCGGCATGGCGT	pBL17
			P-MK255	CACGCCCTGCGCGTACGCCTCGCC	
		80_V3	P-MK256	GCGTACGCGCAGGGCGTG	pBL17
			P-MK253	CCCTCCGCCCAGCCAGGCG	
		80_I	P-MK236	AAGAAGGAGATATACATATGCTGGCGTCGCTGCCCG	pCK7
			P-MK242	CCGCGGGTGGGCGCGCTCGAGCACCACCACCACCACCACTGAGATC	
pMK81 - ACP1-M6-TE, used to generate pMK93	Infusion	81_V1	P-MK257	GACCCGATCGCGATCGTCGGCATGGC	pBL18
			P-MK258	CACGCCGTGCACGTGCGCCCGG	
		81_V2	P-MK249	GCGCACGTGCACGGCGTG	pBL18
			P-MK239	CATATGTATATCTCCTTCTTAAAGTTAAACAAAATTA	
		81_I	P-MK236	AAGAAGGAGATATACATATGCTGGCGTCGCTGCCCG	pCK7
			P-MK246	CCGACGATCGCGATCGGGTCGACGGGGGCCGTGGTC	
pMK83 - ACP1-M2-TE, used to generate pADD03	Infusion	83_V1	P-MK250	GAGCCGATCGCGATCGTCGGCATGGCGT	pBL17
			P-MK251	GACACCGCGCGTGTGCGCGTCGG	
		83_V2	P-MK252	CGCACACGCGCGGTGTC	pBL16
			P-MK253	CCCTCCGCCCAGCCAGGCG	
		83_V3	P-MK254	CGCCTGGCTGGGCGGAGGG	pBL16
			P-MK239	CATATGTATATCTCCTTCTTAAAGTTAAACAAAATTA	
		80_I	P-MK236	AAGAAGGAGATATACATATGCTGGCGTCGCTGCCCG	pCK7
			P-MK242	CCGCGGGTGGGCGCGCTCGAGCACCACCACCACCACCACTGAGATC	
pMK91-(5)KS1-AT1, used as a template for other cloning strategies	Infusion	91_V	P-MK239	CATATGTATATCTCCTTCTTAAAGTTAAACAAAATTA	pBL13
			P-MK262	TTTCCGCGCTGCGCTACCGCCTCGAGCACCACCACCAC	
		91_I1	P-MK228	GTGCAGCCCGTGATGTTCGCGGTCATGG	pBL13
			P-MK261	GTGGTGGTGGTGCTCGAGGCGGTAGCGCAGCGCGGAAACCTCGT	
		91_I2	P-MK229	CCATGACCGCGAACATCACGGGCTGCAC	pBL13

			P-MK260	GAAGGAGATATACATATGAGCGGTGACAACGGCATGACCGAGGAAAAG	
pMK93 - KR1-ACP1-M6-TE, missing an Asp in ACP1-KS2 linker	Infusion	93_V	digestion of pMK81 with NdeI		
		93_I	P-MK276	AAGGAGATATACATATGGACGAGGTTTCCGCGCTG	pAYC59
			P-MK277	AGCGACGCCAGCATATGCGCGCCCACCCGCGGTTC	
pMK96 - KR1-ACP1(2)	Infusion	96_V	P-MK239	CATATGTATATCTCCTTCTTAAAGTTAAACAAAATTA	pBL13
			P-MK62	GGCACCGAGGTCCGGG	
		96_I	P-MK276	AAGGAGATATACATATGGACGAGGTTTCCGCGCTG	pBL13
			P-MK280	CCGGACCTCGGTGCCGAGTTCGGCGGCCAGGT	
pMK111 - (5)KS1-AT1-SZ3	Infusion	111_V	P-MK309	TCCGCCACCGGATCCGCCGAGCCAGACGCGCTCGC	pMK91
			P-MK304	CTGGCACACAAAAAGCTCGAGCACCACCACCAC	
		111_I	P-MK308	GGATCCGGTGGCGGATCCGGTAACGAAGTTACAACACTTGAGAATGAC	pfRSZ
			P-MK303	CTTTTTGTGTGCCAGTCTATTTCTCAAT	
pMK112 - SZ4-KR1-ACP1(2)	Infusion	112_V	P-MK239	CATATGTATATCTCCTTCTTAAAGTTAAACAAAATTA	pMK96
			P-MK311	TCCGGTGGCGGATCCGGTGACGAGGTTTCCGCGCTG	
		112_I	P-MK305	GGAGATATACATATGCAGAAAGTGGCTGAATTGAAAAACAGA	pfRSZ
			P-MK310	GGATCCGCCACCGGATCCGCCTTCAGCAACATCGTTCTCCAATCTG	
pMK113 - (5)KS1-AT1 (shorter than pMK91)	Infusion	113_V	P-MK239	CATATGTATATCTCCTTCTTAAAGTTAAACAAAATTA	pMK91
			P-MK313	GAGCGCGTCTGGCTCCTCGAGCACCACCACCAC	
		113_I	P-MK260	GAAGGAGATATACATATGAGCGGTGACAACGGCATGACCGAGGAAAAG	pMK91
			P-MK312	GAGCCAGACGCGCTCGC	
pADD02 - KR1-ACP1-M5-TE, missing an Asp in ACP1-KS2 linker	Infusion	ADD02_V	digestion of pMK80 with NdeI		
		ADD02_I	P-MK276	AAGGAGATATACATATGGACGAGGTTTCCGCGCTG	pAYC59
			P-MK277	AGCGACGCCAGCATATGCGCGCCCACCCGCGGTTC	
pADD03 - KR1-ACP1-M2-TE - missing an Asp in ACP1-KS2 linker	Infusion	ADD03_V	digestion of pMK83 with NdeI		
		ADD03_I	P-MK276	AAGGAGATATACATATGGACGAGGTTTCCGCGCTG	pAYC59
			P-MK277	AGCGACGCCAGCATATGCGCGCCCACCCGCGGTTC	
pMK133 - KR1-ACP1-M2-	Quickchange	133_QC	P-MK347	GCGACCACGGCCCCCGTCGATGAGCCGATCGCGATCGTC	pADD03
			P-MK348	GACGATCGCGATCGGCTCATCGACGGGGGCCGTGGTCGC	

TE, complete ACP1-KS2 linker					
pMK134 - KR1-ACP1-M5-TE, complete ACP1-KS2 linker	Quickchange	134_QC	P-MK347	GCGACCACGGCCCCCGTCGATGAGCCGATCGCGATCGTC	pADD02
			P-MK348	GACGATCGCGATCGGCTCATCGACGGGGGCCGTGGTCGC	
pMK135 - KR1-ACP1-M6-TE, complete ACP1-KS2 linker	Quickchange	135_QC	P-MK349	GCGACCACGGCCCCCGTCGATGACCCGATCGCGATCGTC	pMK93
			P-MK350	GACGATCGCGATCGGGTCATCGACGGGGGCCGTGGTCGC	
pMK136 - SZ4-KR1-ACP1-M2-TE	Infusion	136_V	digestion of pMK133 with NdeI		
		136_I	P-MK351	GAAGGAGATATACATATGCAGAAAGTGGCTGAATTGAAAAAC	pMK112
			P-MK345	AGCGACGCCAGCATATGCGCGCCCACCCGC	
pMK137 - SZ4-KR5-ACP5-M6)-TE	Infusion	137_V	P-MK247	GACCCGATCGCGATCGTC	pMK93
			P-MK239	CATATGTATATCTCCTTCTTAAAGTTAAACAAAATTA	
		137_I1	P-MK351	GAAGGAGATATACATATGCAGAAAGTGGCTGAATTGAAAAAC	pMK112
			P-MK352	GCCGGTGGGGATGGGACCGGATCCGCCACCG	
		137_I2	P-MK353	CCCATCCCCACCGGCG	pBL130
			P-MK354	GATCGCGATCGGGTCGTCGGCATCCTTCGGCAC	
pMK138 - SZ4-RIFS(KR1-ACP1-M2)-TE	Infusion	138_V	P-MK358	GAGATCGGCACCGCCGCGGCCGAGGAGCCGATCGCGATCGTC	pAJ21
			P-MK239	CATATGTATATCTCCTTCTTAAAGTTAAACAAAATTA	
		138_I1	P-MK351	GAAGGAGATATACATATGCAGAAAGTGGCTGAATTGAAAAAC	pMK112
			P-MK355	GGGCTCGGCGGGCTCACCGGATCCGCCACCG	
		138_I2	P-MK356	GAGCCCGCCGAGCCC	pAJ20
			P-MK357	GGCGGTGCCGATCTCGGCCGGCCGGTTCGCCGCCGATCCGAAGAGCTTGGCGCGCAG	
pMK141 - SZ4-KR1-ACP1-M5-TE	Infusion	141_V	digestion of pMK134 with NdeI		
		136_I	P-MK351	GAAGGAGATATACATATGCAGAAAGTGGCTGAATTGAAAAAC	pMK112
			P-MK345	AGCGACGCCAGCATATGCGCGCCCACCCGC	
pMK142 - SZ4-KR1-ACP1-M6-TE	Infusion	142_V	digestion of pMK135 with NdeI		
		136_I	P-MK351	GAAGGAGATATACATATGCAGAAAGTGGCTGAATTGAAAAAC	pMK112
			P-MK345	AGCGACGCCAGCATATGCGCGCCCACCCGC	
pMK146 - SZ4-MCS-H6, intermediate	Infusion	146_all	P-MK386	TGCGGCCGCAAGCTTACCGGATCCGCCACCGG	pMK112
			P-MK387	AAGCTTGCGGCCGCACTC	

vector for various cloning strategies					
pMK147 - SZ4-M6-TE	Infusion	147_V	digestion of pMK146 with HindIII		
		147_I	P-MK388	CGGATCCGGTAAGCTTGACCCGATCGCGATCGTC	pMK137
			P-MK389	GTGCGGCCGCAAGCTTCGAATTCCCTCCGCCCAG	
pMK148 - SZ4-M2-TE	Infusion	148_V	digestion of pMK146 with HindIII		
		148_I	P-MK390	CGGATCCGGTAAGCTTGAGCCGATCGCGATCGTC	pMK136
			P-MK389	GTGCGGCCGCAAGCTTCGAATTCCCTCCGCCCAG	
pMK149 - SZ4-M3-TE	Infusion	149_V	digestion of pMK146 with HindIII		
		149_I	P-MK391	CGGATCCGGTAAGCTTGACCCGATCGCCATCGTC	pRSG34
			P-MK389	GTGCGGCCGCAAGCTTCGAATTCCCTCCGCCCAG	
pMK150 - (5)M1-SZ3	Infusion	150_V	P-MK394	ACGACCGCGACCGGTTC	pMK111
			P-MK389	GTGCGGCCGCAAGCTTCGAATTCCCTCCGCCCAG	
		150_I	P-MK392	GAACCGGTCGCGGTCGT	pBL13
			P-MK393	GCCGAGTTCGGCGGCC	
pMK152 - SZ4-KR1-ACP1-M3-TE	Infusion	152_V	P-MK478	GATGGCGATCGGGTCATCGACGGGGGCCGTGG	pMK142
			P-MK153	AGCGGGACTCCCGCCC	
		152_I	P-MK398	GACCCGATCGCCATCGTC	pRSG34
			P-MK399	GTCGAGCTGACTAGTGTGCTG	
pMK168 - SZ4-KR5-ACP5(2)	Infusion	168_V	P-MK402	GACGAGCCGCTCCAGGTA	pMK137
			P-MK291	TCGAGCTCCGTCGACAAGCT	
		168_I	P-MK457	CTGGAGCGGCTCGTCGGCACCGAGGTCCGGG	pMK112
			P-MK458	GTCGACGGAGCTCGAATTCGGATCGCCGTCGAGC	
pMK169 - SZ4-RIFS(KR1-ACP1)(2)	Infusion	169_V	P-MK459	GAAGAGCTTGGCGCGCAG	pMK138
			P-MK291	TCGAGCTCCGTCGACAAGCT	
		169_I	P-MK460	CGCGCCAAGCTCTTCGGCACCGAGGTCCGGG	pMK112
			P-MK458	GTCGACGGAGCTCGAATTCGGATCGCCGTCGAGC	
pMK170 - SZ4-M5-TE	Infusion	170_V	digestion of pMK146 with HindIII		
		170_I	P-MK390	CGGATCCGGTAAGCTTGAGCCGATCGCGATCGTC	pBL17
			P-MK389	GTGCGGCCGCAAGCTTCGAATTCCCTCCGCCCAG	

References for plasmids constructed elsewhere: pCK7[1]; pBP130[2]; pAYC59[3]; pAJ20 and pAJ21[4]; pBL13, pBL16, pBL17,and pBL18[5]; pRSG34[6]; pfRSZ was a gift from Mislav Oreb, Goethe University Frankfurt. In addition pBL12 was used to produce LDD(4)[5].

Table S2: Amino acid sequences of proteins used in this study. If no indication is given the PKS domain/modules are derived from DEBS. SZ domains are shown in red, docking domains in green, and linker regions in gray. L_{12} is the ACP1-KS2 linker used to covalently fuse ACP1 to a heterologous acceptor module.

Construct	Amino acid sequence
MK96 KR1-ACP1-(2)	MDEVSALRYRIEWRPTGAGEPARLDGTWLVAKYAGTADETSTAAREALESAGARVRELVVDARCGRDELAERLRSVGEV AGVLSLLAVDEAEPEEAPLALASLADTLSLVQAMVSAELGCPLWTVTESAVATGPFERVRNAAHGALWGVGRVIALENPA VWGGLVDVPAGSVAELARHLAAVVSGGAGEDQLALRADGVYGRRWVRAAAPATDDEWKPTGTVLVTGGTGGVGGQIA RWLARRGAPHLLLVSRSGPDADGAGELVAELEALGARTTVAACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVD TLTGERIERASRAKVLGARNLHELTRELDLTAFVLFSSFASAFGAPGLGGYAPGNAYLDGLAQQRRSDGLPATAVAWGTW AGSGMAEGPVADRFRRHGVIEMPPETACRALQNALDRAEVCPIVIDVRWDRFLLAYTAQRPTRLFDEIDDARRAAPQAAAE PRVGALASLPAPEREKALFELVRSHAAAVLGHASAERVPADQAFAELGVDSLSALELRNRLGAATGVRLPTTTVFDHPDVR TLAAHLAAELGTEVRGEAPSALAGLDALEAALPEVPATEREELVQRLERMLAALRPVAQAADASGTGANPSGDDLGEAGV DELLEALGRELDGDPNSSSVDKLAAALEHHHHHH*
MK111 (5)KS1-AT1-L-SZ3	MSGDNGMTEEKLRRYLKRTVTELDSVTARLREVEHRAGEPVAVVAMACRLPGGVSTPEEFWELLSEGRDAVAGLPTDRG WDLDSLFHPDPTRSGTAHQRGGGFLTEATAFDPAFFGMSPREALAVDPQQRLMLELSWEVLERAGIPPTSLQASPTGVFVGL IPQEYGPRLAEGGEGVEGYLMTGTTTSVASGRIAYTLGLEGPAISVDTACSSSLVAVHLACQSLRRGESSLAMAGGVTVMPT PGMLVDFSRMNSLAPDGRCKAFSAGANGFGMAEGAGMLLLERLSDARRNGHPVLAVLRGTAVNSDGASNGLSAPNGRAQ VRVIQQALAESGLGPADIDAVEAHGTGTRLGDPIEARALFEAYGRDREQPLHLGSVKSNLGHTQAAAGVAGVIKMVLAMR AGTLPRTLHASERSKEIDWSSGAISLLDEPEPWPAGARPRRAGVSSFGISGTNAHAIIEEAPQVVEGERVEAGDVVAPWVLSA SSAEGLRAQAARLAAHLREHPGQDPRDIAYSLATGRAALPHRAAFAPVDESAALRVLDGLATGNADGAAVGTSRAQQRAV FVFPGQGWQWAGMAVDLLDTSPVFAAALRECADALEPHLDFEVIPFLRAEAARREQDAALSTERVDVVQPVMFAVMVSL ASMWRAHGVEPAAVIGHSQGEIAAACVAGALSLDDAARVVALRSRVIATMPGNKGMASIAAPAGEVRARIGDRVEIAAVN GPRSVVVAGDSDELDRLVASCTTECIRAKRLAVDYASHSSHVETIRDALHAELGEDFHPLPGFVPFFSTVTGRWTQPDELDA GYWYRNLRRTVRFADAVRALAEQGYRTFLEVSAHPILTAAIEEIGDGSGADLSAIHSLRRGDGSLADFGEALSRAFAAGVA VDWESVHLGTGARRVPLPTYPFQRERVWLGGSGGGSGNEVTTLENDAAFIENENAYLEKEIARLRKEKAALRNRLAHKKL EHHHHHH*
MK112 SZ4-L-KR1-ACP1(2)	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGDEVSALRYRIEWRPTG AGEPARLDGTWLVAKYAGTADETSTAAREALESAGARVRELVVDARCGRDELAERLRSVGEVAGVLSLLAVDEAEPEEAP LALASLADTLSLVQAMVSAELGCPLWTVTESAVATGPFERVRNAAHGALWGVGRVIALENPAVWGGLVDVPAGSVAELA RHLAAVVSGGAGEDQLALRADGVYGRRWVRAAAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHLLLVSRSG PDADGAGELVAELEALGARTTVAACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIERASRAKVLGA RNLHELTRELDLTAFVLFSSFASAFGAPGLGGYAPGNAYLDGLAQQRRSDGLPATAVAWGTWAGSGMAEGPVADRFRRH GVIEMPPETACRALQNALDRAEVCPIVIDVRWDRFLLAYTAQRPTRLFDEIDDARRAAPQAAAEPRVGALASLPAPEREKAL FELVRSHAAAVLGHASAERVPADQAFAELGVDSLSALELRNRLGAATGVRLPTTTVFDHPDVRTLAAHLAAELGTEVRGE APSALAGLDALEAALPEVPATEREELVQRLERMLAALRPVAQAADASGTGANPSGDDLGEAGVDELLEALGRELDGDPNS SSVDKLAAALEHHHHHH*
MK113 (5)KS1-AT1	MSGDNGMTEEKLRRYLKRTVTELDSVTARLREVEHRAGEPVAVVAMACRLPGGVSTPEEFWELLSEGRDAVAGLPTDRG WDLDSLFHPDPTRSGTAHQRGGGFLTEATAFDPAFFGMSPREALAVDPQQRLMLELSWEVLERAGIPPTSLQASPTGVFVGL IPQEYGPRLAEGGEGVEGYLMTGTTTSVASGRIAYTLGLEGPAISVDTACSSSLVAVHLACQSLRRGESSLAMAGGVTVMPT PGMLVDFSRMNSLAPDGRCKAFSAGANGFGMAEGAGMLLLERLSDARRNGHPVLAVLRGTAVNSDGASNGLSAPNGRAQ

	VRVIQQALAESGLGPADIDAVEAHGTGTRLGDPIEARALFEAYGRDREQPLHLGSVKSNLGHTQAAAGVAGVIKMVLAMR AGTLPRTLHASERSKEIDWSSGAISLLDEPEPWPAGARPRRAGVSSFGISGTNAHAIIEEAPQVVEGERVEAGDVVAPWVLSA SSAEGLRAQAARLAAHLREHPGQDPRDIAYSLATGRAALPHRAAFAPVDESAALRVLDGLATGNADGAAVGTSRAQQRAV FVFPGQGWQWAGMAVDLLDTSPVFAAALRECADALEPHLDFEVIPFLRAEAARREQDAALSTERVDVVQPVMFAVMVSL ASMWRAHGVEPAAVIGHSQGEIAAACVAGALSLDDAARVVALRSRVIATMPGNKGMASIAAPAGEVRARIGDRVEIAAVN GPRSVVVAGDSDELDRLVASCTTECIRAKRLAVDYASHSSHVETIRDALHAELGEDFHPLPGFVPFFSTVTGRWTQPDELDA GYWYRNLRRTVRFADAVRALAEQGYRTFLEVSAHPILTAAIEEIGDGSGADLSAIHSLRRGDGSLADFGEALSRAFAAGVA VDWESVHLGTGARRVPLPTYPFQRERVWLLEHHHHHH*
MK136 SZ4-L-KR1-ACP1- L_{12}-M2-TE	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGDEVSALRYRIEWRPTG AGEPARLDGTWLVAKYAGTADETSTAAREALESAGARVRELVVDARCGRDELAERLRSVGEVAGVLSLLAVDEAEPEEAP LALASLADTLSLVQAMVSAELGCPLWTVTESAVATGPFERVRNAAHGALWGVGRVIALENPAVWGGLVDVPAGSVAELA RHLAAVVSGGAGEDQLALRADGVYGRRWVRAAAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHLLLVSRSG PDADGAGELVAELEALGARTTVAACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIERASRAKVLGA RNLHELTRELDLTAFVLFSSFASAFGAPGLGGYAPGNAYLDGLAQQRRSDGLPATAVAWGTWAGSGMAEGPVADRFRRH GVIEMPPETACRALQNALDRAEVCPIVIDVRWDRFLLAYTAQRPTRLFDEIDDARRAAPQAAAEPRVGAHMLASLPAPERE KALFELVRSHAAAVLGHASAERVPADQAFAELGVDSLSALELRNRLGAATGVRLPTTTVFDHPDVRTLAAHLAAELGGAT GAEQAAPATTAPVDEPIAIVGMACRLPGEVDSPERLWELITSGRDSAAEVPDDRGWVPDELMASDAAGTRRAHGNFMAGA GDFDAAFFGISPREALAMDPQQRQALETTWEALESAGIPPETLRGSDTGVFVGMSHQGYATGRPRPEDGVDGYLLTGNTAS VASGRIAYVLGLEGPALTVDTACSSSLVALHTACGSLRDGDCGLAVAGGVSVMAGPEVFTEFSRQGALSPDGRCKPFSDEA DGFGLGEGSAFVVLQRLSDARREGRRVLGVVAGSAVNQDGASNGLSAPSGVAQQRVIRRAWARAGITGADVAVVEAHGT GTRLGDPVEASALLATYGKSRGSSGPVLLGSVKSNIGHAQAAAGVAGVIKVLLGLERGVVPPMLCRGERSGLIDWSSGEIEL ADGVREWSPAADGVRRAGVSAFGVSGTNAHVIIAEPPEPEPVPQPRRMLPATGVVPVVLSARTGAALRAQAGRLADHLAA HPGIAPADVSWTMARARQHFEERAAVLAADTAEAVHRLRAVADGAVVPGVVTGSASDGGSVFVFPGQGAQWEGMAREL LPVPVFAESIAECDAVLSEVAGFSVSEVLEPRPDAPSLERVDVVQPVLFAVMVSLARLWRACGAVPSAVIGHSQGEIAAAVV AGALSLEDGMRVVARRSRAVRAVAGRGSMLSVRGGRSDVEKLLADDSWTGRLEVAAVNGPDAVVVAGDAQAAREFLEY CEGVGIRARAIPVDYASHTAHVEPVRDELVQALAGITPRRAEVPFFSTLTGDFLDGTELDAGYWYRNLRHPVEFHSAVQAL TDQGYATFIEVSPHPVLASSVQETLDDAESDAAVLGTLERDAGDADRFLTALADAHTRGVAVDWEAVLGRAGLVDLPGYP FQGKRFWLLPDRTTPRDELDGWFYRVDWTEVPRSEPAALRGRWLVVVPEGHEEDGWTVEVRSALAEAGAEPEVTRGVGG LVGDCAGVVSLLALEGDGAVQTLVLVRELDAEGIDAPLWTVTFGAVDAGSPVARPDQAKLWGLGQVASLERGPRWTGLV DLPHMPDPELRGRLTAVLAGSEDQVAVRADAVRARRLSPAHVTATSEYAVPGGTILVTGGTAGLGAEVARWLAGRGAEH LALVSRRGPDTEGVGDLTAELTRLGARVSVHACDVSSREPVRELVHGLIEQGDVVRGVVHAAGLPQQVAINDMDEAAFDE VVAAKAGGAVHLDELCSDAELFLLFSSGAGVWGSARQGAYAAGNAFLDAFARHRRGRGLPATSVAWGLWAAGGMTGD EEAVSFLRERGVRAMPVPRALAALDRVLASGETAVVVTDVDWPAFAESYTAARPRPLLDRIVTTAPSERAGEPETESLRDR LAGLPRAERTAELVRLVRTSTATVLGHDDPKAVRATTPFKELGFDSLAAVRLRNLLNAATGLRLPSTLVFDHPNASAVAGF LTSELGSGTPAREASSALRDGYRQAGVSGRVRSYLDLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVICCAGTAAISGP HEFTRLAGALRGIAPVRAVPQPGYEEGEPLPSSMAAVAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPP RGVVLIDVYPPGHQDAMNAWLEELTATLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDS WKPTWPFEHDTVAVPGDHFTMVQEHADAIARHIDAWLGGGNSSSVDKLAAALEHHHHHH*

MK137 SZ4-L-KR5-ACP5-M6-TE	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGPIPTGGRARDEDDDW RYQVVWREAEWESASLAGRVLLVTGPGVPSELSDAIRSGLEQSGATVLTCDVESRSTIGTALEAADTDALSTVVSLLSRDGE AVDPSLDALALVQALGAAGVEAPLWVLTRNAVQVADGELVDPAQAMVGGLGRVVGIEQPGRWGGLVDLVDADAASIRS LAAVLADPRGEEQVAIRADGIKVARLVPAPARAARTRWSPRGTVLVTGGTGGIGAHVARWLARSGAEHLVLLGRRGADAP GASELREELTALGTGVTIAACDVADRARLEAVLAAERAEGRTVSAVMHAAGVSTSTPLDDLTEAEFTEIADVKVRGTVNLD ELCPDLDAFVLFSSNAGVWGSPGLASYAAANAFLDGFARRRRSEGAPVTSIAWGLWAGQNMAGDEGGEYLRSQGLRAMD PDRAVEELHITLDHGQTSVSVVDMDRRRFVELFTAARHRPLFDEIAGARAEARQSEEGPALAQRLAALSTAERREHLAHLIR AEVAAVLGHGDDAAIDRDRAFRDLGFDSMTAVDLRNRLAAVTGVREAATVVFDHPTITRLADHYLERLVGAAEAEQAPA LVREVPKDADDPIAIVGMACRFPGGVHNPGELWEFIVGGGDAVTEMPTDRGWDLDALFDPDPQRHGTSYSRHGAFLDGAA DFDAAFFGISPREALAMDPQQRQVLETTWELFENAGIDPHSLRGSDTGVFLGAAYQGYGQDAVVPEDSEGYLLTGNSSAVV SGRVAYVLGLEGPAVTVDTACSSSLVALHSACGSLRDGDCGLAVAGGVSVMAGPEVFTEFSRQGGLAVDGRCKAFSAEAD GFGFAEGVAVVLLQRLSDARRAGRQVLGVVAGSAINQDGASNGLAAPSGVAQQRVIRKAWARAGITGADVAVVEAHGTG TRLGDPVEASALLATYGKSRGSSGPVLLGSVKSNIGHAQAAAGVAGVIKVVLGLNRGLVPPMLCRGERSPLIEWSSGGVEL AEAVSPWPPAADGVRRAGVSAFGVSGTNAHVIIAEPPEPEPLPEPGPVGVLAAANSVPVLLSARTETALAAQARLLESAVDD SVPLTALASALATGRAHLPRRAALLAGDHEQLRGQLRAVAEGVAAPGATTGTASAGGVVFVFPGQGAQWEGMARGLLSV PVFAESIAECDAVLSEVAGFSASEVLEQRPDAPSLERVDVVQPVLFSVMVSLARLWGACGVSPSAVIGHSQGEIAAAVVAG VLSLEDGVRVVALRAKALRALAGKGGMVSLAAPGERARALIAPWEDRISVAAVNSPSSVVVSGDPEALAELVARCEDEGV RAKTLPVDYASHSRHVEEIRETILADLDGISARRAAIPLYSTLHGERRDGADMGPRYWYDNLRSQVRFDEAVSAAVADGHA TFVEMSPHPVLTAAVQEIAADAVAIGSLHRDTAEEHLIAELARAHVHGVAVDWRNVFPAAPPVALPNYPFEPQRYWLAPEV SDQLADSRYRVDWRPLATTPVDLEGGFLVHGSAPESLTSAVEKAGGRVVPVASADREALAAALREVPGEVAGVLSVHTGA ATHLALHQSLGEAGVRAPLWLVTSRAVALGESEPVDPEQAMVWGLGRVMGLETPERWGGLVDLPAEPAPGDGEAFVACL GADGHEDQVAIRDHARYGRRLVRAPLGTRESSWEPAGTALVTGGTGALGGHVARHLARCGVEDLVLVSRRGVDAPGAAE LEAELVALGAKTTITACDVADREQLSKLLEELRGQGRPVRTVVHTAGVPESRPLHEIGELESVCAAKVTGARLLDELCPDAE TFVLFSSGAGVWGSANLGAYSAANAYLDALAHRRRAEGRAATSVAWGAWAGEGMATGDLEGLTRRGLRPMAPERAIRA LHQALDNGDTCVSIADVDWERFAVGFTAARPRPLLDELVTPAVGAVPAVQAAPAREMTSQELLEFTHSHVAAILGHSSPDA VGQDQPFTELGFDSLTAVGLRNQLQQATGLALPATLVFEHPTVRRLADHIGQQLDSGTPAREASSALRDGYRQAGVSGRVR SYLDLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVICCAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYEEGEPLPSS MAAVAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTATLFDRE TVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFEHDTVAVPGDHFTMVQEHADAIARH IDAWLGGGNSSSVDKLAAALEHHHHHH*
MK138 SZ4-L-RIFS (KR1-ACP1-M2)-TE	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGEPAEPASAGDPLLGTV VSTPGSDRLTAVAQWSRRAQPWAVDGLVPNAALVEAAIRLGDLAGTPVVGELVVDAPVVLPRRGSREVQLIVGEPGEQRR RPIEVFSREADEPWTRHAHGTLAPAAAAVPEPAAAGDATDVTVAGLRDADRYGIHPALLDAAVRTVVGDDLLPSVWTGVS LLASGATAVTVTPTATGLRLTDPAGQPVLTVESVRGTPFVAEQGTTDALFRVDWPEIPLPTAETADFLPYEATSAEATLSAL QAWLADPAETRLAVVTGDCTEPGAAAIWGLVRSAQSEHPGRIVLADLDDPAVLPAVVASGEPQVRVRNGVASVPRLTRVT PRQDARPLDPEGTVLITGGTGTLGALTARHLVTAHGVRHLVLVSRRGEAPELQEELTALGASVAIAACDVADRAQLEAVLR AIPAEHPLTAVIHTAGVLDDGVVTELTPDRLATVRRPKVDAARLLDELTREADLAAFVLFSSAAGVLGNPGQAGYAAANAE LDALARQRNSLDLPAVSIAWGYWATVSGMTEHLGDADLRRNQRIGMSGLPADEGMALLDAAIATGGTLVAAKFDVAALR ATAKAGGPVPPLLRGLAPLPRRAAAKTASLTERLAGLAETEQAAALLDLVRRHAAEVLGHSGAESVHSGRTFKDAGFDSLT AVELRNRLAAATGLTLSPAMIFDYPKPPALADHLRAKLFGSAANRPAEIGTAAAEEPIAIVAMACRFPGGVHSPEDLWRLVA

	DGADAVTEFPADRGWDTDRLYHEDPDHEGTTYVRHGAFLDDAAGFDAAFFGISPNEALAMDPQQRLLLETSWELFERAAI DPTTLAGQDIGVFAGVNSHDYSMRMHRAAGVEGFRLTGGSASVLSGRVAYHFGVEGPAVTVDTACSSSLVALHMAVQAL QRGECSMALAGGVMVMGTVETFVEFSRQRGLAPDGRCKAFADGADGTGWSEGVGLLLVERLSEAQRRGHQVLAVVRGS AVNSDGASNGLTAPNGPSQQRVIRKALAAAGLSTSDVDAVEAHGTGTTLGDPIEAEALLATYGQNRETPLWLGSVKSNLG HTQAAAGVAGVIKMVMAMRHGVLPRTLHVDRPSSYVDWSAGAVELLTEARDWVSNGHPRRAGVSSFGIGGTNAHVVLE EVAAPITTPQPEPAEFLVPVLVSARTAAGLRGQAGRLAAFLGDRTDVRVPDAAYALATTRAQLDHRAVVLASDRAQLCAD LAAFGSGVVTGTPVDGKLAVLFTGQGSQWAGMGRELAETFPVFRDAFEAACEAVDTHLRERPLREVVFDDSALLDQTMYT QGALFAVETALFRLFESWGVRPGLLAGHSIGELAAAHVSGVLDLADAGELVAARGRLMQALPAGGAMVAVQATEDEVAP LLDGTVCVAAVNGPDSVVLSGTEAAVLAVADELAGRGRKTRRLAVSHAFHSPLMEPMLDDFRAVAERLTYRAGSLPVVST LTGELAALDSPDYWVGQVRNAVRFSDAVTALGAQGASTFLELGPGGALAAMALGTLGGPEQSCVATLRKNGAEVPDVLT ALAELHVRGVGVDWTTVLDEPATAVGTVLPTYAFQHQRFWVDVDETAAVSVTPPPAEPIVDRPVQDVLELVRESAAVVLG HRDAGSFDLDRSFKDHGFDSLSAVKLRNRLRDFTGVELPSTLIFDYPNPAVLADHLRAELLSGTPAREASSALRDGYRQAGV SGRVRSYLDLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVICCAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYEEG EPLPSSMAAVAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTA TLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFEHDTVAVPGDHFTMVQEHA DAIARHIDAWLGGGNSSSVDKLAAALEHHHHHH*
MK141 SZ4-L-KR1-ACP1- L_{12}-M5-TE	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGDEVSALRYRIEWRPTG AGEPARLDGTWLVAKYAGTADETSTAAREALESAGARVRELVVDARCGRDELAERLRSVGEVAGVLSLLAVDEAEPEEAP LALASLADTLSLVQAMVSAELGCPLWTVTESAVATGPFERVRNAAHGALWGVGRVIALENPAVWGGLVDVPAGSVAELA RHLAAVVSGGAGEDQLALRADGVYGRRWVRAAAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHLLLVSRSG PDADGAGELVAELEALGARTTVAACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIERASRAKVLGA RNLHELTRELDLTAFVLFSSFASAFGAPGLGGYAPGNAYLDGLAQQRRSDGLPATAVAWGTWAGSGMAEGPVADRFRRH GVIEMPPETACRALQNALDRAEVCPIVIDVRWDRFLLAYTAQRPTRLFDEIDDARRAAPQAAAEPRVGAHMLASLPAPERE KALFELVRSHAAAVLGHASAERVPADQAFAELGVDSLSALELRNRLGAATGVRLPTTTVFDHPDVRTLAAHLAAELGGAT GAEQAAPATTAPVDEPIAIVGMACRFPGDVDSPESFWEFVSGGGDAIAEAPADRGWEPDPDARLGGMLAAAGDFDAGFFGI SPREALAMDPQQRIMLEISWEALERAGHDPVSLRGSATGVFTGVGTVDYGPRPDEAPDEVLGYVGTGTASSVASGRVAYCL GLEGPAMTVDTACSSGLTALHLAMESLRRDECGLALAGGVTVMSSPGAFTEFRSQGGLAADGRCKPFSKAADGFGLAEGA GVLVLQRLSAARREGRPVLAVLRGSAVNQDGASNGLTAPSGPAQQRVIRRALENAGVRAGDVDYVEAHGTGTRLGDPIEV HALLSTYGAERDPDDPLWIGSVKSNIGHTQAAAGVAGVMKAVLALRHGEMPRTLHFDEPSPQIEWDLGAVSVVSQARSWP AGERPRRAGVSSFGISGTNAHVIVEEAPEADEPEPAPDSGPVPLVLSGRDEQAMRAQAGRLADHLAREPRNSLRDTGFTLAT RRSAWEHRAVVVGDRDDALAGLRAVADGRIADRTATGQARTRRGVAMVFPGQGAQWQGMARDLLRESQVFADSIRDCE RALAPHVDWSLTDLLSGARPLDRVDVVQPALFAVMVSLAALWRSHGVEPAAVVGHSQGEIAAAHVAGALTLEDAAKLVA VRSRVLRRLGGQGGMASFGLGTEQAAERIGRFAGALSIASVNGPRSVVVAGESGPLDELIAECEAEGITARRIPVDYASHSPQ VESLREELLTELAGISPVSADVALYSTTTGQPIDTATMDTAYWYANLREQVRFQDATRQLAEAGFDAFVEVSPHPVLTVGIE ATLDSALPADAGACVVGTLRRDRGGLADFHTALGEAYAQGVEVDWSPAFADARPVELPVYPFQRQRYWLPIPTGGRARDE DDDWRYQVVWREAEWESASLAGRVLLVTGPGVPSELSDAIRSGLEQSGATVLTCDVESRSTIGTALEAADTDALSTVVSLL SRDGEAVDPSLDALALVQALGAAGVEAPLWVLTRNAVQVADGELVDPAQAMVGGLGRVVGIEQPGRWGGLVDLVDADA ASIRSLAAVLADPRGEEQVAIRADGIKVARLVPAPARAARTRWSPRGTVLVTGGTGGIGAHVARWLARSGAEHLVLLGRR GADAPGASELREELTALGTGVTIAACDVADRARLEAVLAAERAEGRTVSAVMHAAGVSTSTPLDDLTEAEFTEIADVKVRG TVNLDELCPDLDAFVLFSSNAGVWGSPGLASYAAANAFLDGFARRRRSEGAPVTSIAWGLWAGQNMAGDEGGEYLRSQG

	LRAMDPDRAVEELHITLDHGQTSVSVVDMDRRRFVELFTAARHRPLFDEIAGARAEARQSEEGPALAQRLAALSTAERREH LAHLIRAEVAAVLGHGDDAAIDRDRAFRDLGFDSMTAVDLRNRLAAVTGVREAATVVFDHPTITRLADHYLERLVSGTPA REASSALRDGYRQAGVSGRVRSYLDLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVICCAGTAAISGPHEFTRLAGAL RGIAPVRAVPQPGYEEGEPLPSSMAAVAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYP PGHQDAMNAWLEELTATLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFEHD TVAVPGDHFTMVQEHADAIARHIDAWLGGGNSSSVDKLAAALEHHHHHH*
MK142 SZ4-L-KR1-ACP1- L_{12}-M6-TE	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGDEVSALRYRIEWRPTG AGEPARLDGTWLVAKYAGTADETSTAAREALESAGARVRELVVDARCGRDELAERLRSVGEVAGVLSLLAVDEAEPEEAP LALASLADTLSLVQAMVSAELGCPLWTVTESAVATGPFERVRNAAHGALWGVGRVIALENPAVWGGLVDVPAGSVAELA RHLAAVVSGGAGEDQLALRADGVYGRRWVRAAAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHLLLVSRSG PDADGAGELVAELEALGARTTVAACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIERASRAKVLGA RNLHELTRELDLTAFVLFSSFASAFGAPGLGGYAPGNAYLDGLAQQRRSDGLPATAVAWGTWAGSGMAEGPVADRFRRH GVIEMPPETACRALQNALDRAEVCPIVIDVRWDRFLLAYTAQRPTRLFDEIDDARRAAPQAAAEPRVGAHMLASLPAPERE KALFELVRSHAAAVLGHASAERVPADQAFAELGVDSLSALELRNRLGAATGVRLPTTTVFDHPDVRTLAAHLAAELGGAT GAEQAAPATTAPVDDPIAIVGMACRFPGGVHNPGELWEFIVGGGDAVTEMPTDRGWDLDALFDPDPQRHGTSYSRHGAFL DGAADFDAAFFGISPREALAMDPQQRQVLETTWELFENAGIDPHSLRGSDTGVFLGAAYQGYGQDAVVPEDSEGYLLTGN SSAVVSGRVAYVLGLEGPAVTVDTACSSSLVALHSACGSLRDGDCGLAVAGGVSVMAGPEVFTEFSRQGGLAVDGRCKAF SAEADGFGFAEGVAVVLLQRLSDARRAGRQVLGVVAGSAINQDGASNGLAAPSGVAQQRVIRKAWARAGITGADVAVVE AHGTGTRLGDPVEASALLATYGKSRGSSGPVLLGSVKSNIGHAQAAAGVAGVIKVVLGLNRGLVPPMLCRGERSPLIEWSS GGVELAEAVSPWPPAADGVRRAGVSAFGVSGTNAHVIIAEPPEPEPLPEPGPVGVLAAANSVPVLLSARTETALAAQARLLE SAVDDSVPLTALASALATGRAHLPRRAALLAGDHEQLRGQLRAVAEGVAAPGATTGTASAGGVVFVFPGQGAQWEGMAR GLLSVPVFAESIAECDAVLSEVAGFSASEVLEQRPDAPSLERVDVVQPVLFSVMVSLARLWGACGVSPSAVIGHSQGEIAAA VVAGVLSLEDGVRVVALRAKALRALAGKGGMVSLAAPGERARALIAPWEDRISVAAVNSPSSVVVSGDPEALAELVARCE DEGVRAKTLPVDYASHSRHVEEIRETILADLDGISARRAAIPLYSTLHGERRDGADMGPRYWYDNLRSQVRFDEAVSAAVA DGHATFVEMSPHPVLTAAVQEIAADAVAIGSLHRDTAEEHLIAELARAHVHGVAVDWRNVFPAAPPVALPNYPFEPQRYW LAPEVSDQLADSRYRVDWRPLATTPVDLEGGFLVHGSAPESLTSAVEKAGGRVVPVASADREALAAALREVPGEVAGVLS VHTGAATHLALHQSLGEAGVRAPLWLVTSRAVALGESEPVDPEQAMVWGLGRVMGLETPERWGGLVDLPAEPAPGDGE AFVACLGADGHEDQVAIRDHARYGRRLVRAPLGTRESSWEPAGTALVTGGTGALGGHVARHLARCGVEDLVLVSRRGVD APGAAELEAELVALGAKTTITACDVADREQLSKLLEELRGQGRPVRTVVHTAGVPESRPLHEIGELESVCAAKVTGARLLD ELCPDAETFVLFSSGAGVWGSANLGAYSAANAYLDALAHRRRAEGRAATSVAWGAWAGEGMATGDLEGLTRRGLRPMA PERAIRALHQALDNGDTCVSIADVDWERFAVGFTAARPRPLLDELVTPAVGAVPAVQAAPAREMTSQELLEFTHSHVAAIL GHSSPDAVGQDQPFTELGFDSLTAVGLRNQLQQATGLALPATLVFEHPTVRRLADHIGQQLDSGTPAREASSALRDGYRQA GVSGRVRSYLDLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVICCAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYE EGEPLPSSMAAVAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEEL TATLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFEHDTVAVPGDHFTMVQE HADAIARHIDAWLGGGNSSSVDKLAAALEHHHHHH*
MK147 SZ4-L-M6-TE	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGKLDPIAIVGMACRFPG GVHNPGELWEFIVGGGDAVTEMPTDRGWDLDALFDPDPQRHGTSYSRHGAFLDGAADFDAAFFGISPREALAMDPQQRQV LETTWELFENAGIDPHSLRGSDTGVFLGAAYQGYGQDAVVPEDSEGYLLTGNSSAVVSGRVAYVLGLEGPAVTVDTACSSS LVALHSACGSLRDGDCGLAVAGGVSVMAGPEVFTEFSRQGGLAVDGRCKAFSAEADGFGFAEGVAVVLLQRLSDARRAG

	RQVLGVVAGSAINQDGASNGLAAPSGVAQQRVIRKAWARAGITGADVAVVEAHGTGTRLGDPVEASALLATYGKSRGSS GPVLLGSVKSNIGHAQAAAGVAGVIKVVLGLNRGLVPPMLCRGERSPLIEWSSGGVELAEAVSPWPPAADGVRRAGVSAF GVSGTNAHVIIAEPPEPEPLPEPGPVGVLAAANSVPVLLSARTETALAAQARLLESAVDDSVPLTALASALATGRAHLPRRA ALLAGDHEQLRGQLRAVAEGVAAPGATTGTASAGGVVFVFPGQGAQWEGMARGLLSVPVFAESIAECDAVLSEVAGFSAS EVLEQRPDAPSLERVDVVQPVLFSVMVSLARLWGACGVSPSAVIGHSQGEIAAAVVAGVLSLEDGVRVVALRAKALRALA GKGGMVSLAAPGERARALIAPWEDRISVAAVNSPSSVVVSGDPEALAELVARCEDEGVRAKTLPVDYASHSRHVEEIRETIL ADLDGISARRAAIPLYSTLHGERRDGADMGPRYWYDNLRSQVRFDEAVSAAVADGHATFVEMSPHPVLTAAVQEIAADAV AIGSLHRDTAEEHLIAELARAHVHGVAVDWRNVFPAAPPVALPNYPFEPQRYWLAPEVSDQLADSRYRVDWRPLATTPVD LEGGFLVHGSAPESLTSAVEKAGGRVVPVASADREALAAALREVPGEVAGVLSVHTGAATHLALHQSLGEAGVRAPLWLV TSRAVALGESEPVDPEQAMVWGLGRVMGLETPERWGGLVDLPAEPAPGDGEAFVACLGADGHEDQVAIRDHARYGRRLV RAPLGTRESSWEPAGTALVTGGTGALGGHVARHLARCGVEDLVLVSRRGVDAPGAAELEAELVALGAKTTITACDVADRE QLSKLLEELRGQGRPVRTVVHTAGVPESRPLHEIGELESVCAAKVTGARLLDELCPDAETFVLFSSGAGVWGSANLGAYSA ANAYLDALAHRRRAEGRAATSVAWGAWAGEGMATGDLEGLTRRGLRPMAPERAIRALHQALDNGDTCVSIADVDWERF AVGFTAARPRPLLDELVTPAVGAVPAVQAAPAREMTSQELLEFTHSHVAAILGHSSPDAVGQDQPFTELGFDSLTAVGLRN QLQQATGLALPATLVFEHPTVRRLADHIGQQLDSGTPAREASSALRDGYRQAGVSGRVRSYLDLLAGLSDFREHFDGSDGF SLDLVDMADGPGEVTVICCAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYEEGEPLPSSMAAVAAVQADAVIRTQGDKP FVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTATLFDRETVRMDDTRLTALGAYDRLTG QWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFEHDTVAVPGDHFTMVQEHADAIARHIDAWLGGGNSKLAAALEHHH HHH*
MK148 SZ4-L-M2-TE	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGKLEPIAIVGMACRLPG EVDSPERLWELITSGRDSAAEVPDDRGWVPDELMASDAAGTRRAHGNFMAGAGDFDAAFFGISPREALAMDPQQRQALET TWEALESAGIPPETLRGSDTGVFVGMSHQGYATGRPRPEDGVDGYLLTGNTASVASGRIAYVLGLEGPALTVDTACSSSLV ALHTACGSLRDGDCGLAVAGGVSVMAGPEVFTEFSRQGALSPDGRCKPFSDEADGFGLGEGSAFVVLQRLSDARREGRRV LGVVAGSAVNQDGASNGLSAPSGVAQQRVIRRAWARAGITGADVAVVEAHGTGTRLGDPVEASALLATYGKSRGSSGPV LLGSVKSNIGHAQAAAGVAGVIKVLLGLERGVVPPMLCRGERSGLIDWSSGEIELADGVREWSPAADGVRRAGVSAFGVS GTNAHVIIAEPPEPEPVPQPRRMLPATGVVPVVLSARTGAALRAQAGRLADHLAAHPGIAPADVSWTMARARQHFEERAA VLAADTAEAVHRLRAVADGAVVPGVVTGSASDGGSVFVFPGQGAQWEGMARELLPVPVFAESIAECDAVLSEVAGFSVSE VLEPRPDAPSLERVDVVQPVLFAVMVSLARLWRACGAVPSAVIGHSQGEIAAAVVAGALSLEDGMRVVARRSRAVRAVA GRGSMLSVRGGRSDVEKLLADDSWTGRLEVAAVNGPDAVVVAGDAQAAREFLEYCEGVGIRARAIPVDYASHTAHVEPV RDELVQALAGITPRRAEVPFFSTLTGDFLDGTELDAGYWYRNLRHPVEFHSAVQALTDQGYATFIEVSPHPVLASSVQETLD DAESDAAVLGTLERDAGDADRFLTALADAHTRGVAVDWEAVLGRAGLVDLPGYPFQGKRFWLLPDRTTPRDELDGWFYR VDWTEVPRSEPAALRGRWLVVVPEGHEEDGWTVEVRSALAEAGAEPEVTRGVGGLVGDCAGVVSLLALEGDGAVQTLVL VRELDAEGIDAPLWTVTFGAVDAGSPVARPDQAKLWGLGQVASLERGPRWTGLVDLPHMPDPELRGRLTAVLAGSEDQV AVRADAVRARRLSPAHVTATSEYAVPGGTILVTGGTAGLGAEVARWLAGRGAEHLALVSRRGPDTEGVGDLTAELTRLGA RVSVHACDVSSREPVRELVHGLIEQGDVVRGVVHAAGLPQQVAINDMDEAAFDEVVAAKAGGAVHLDELCSDAELFLLFS SGAGVWGSARQGAYAAGNAFLDAFARHRRGRGLPATSVAWGLWAAGGMTGDEEAVSFLRERGVRAMPVPRALAALDR VLASGETAVVVTDVDWPAFAESYTAARPRPLLDRIVTTAPSERAGEPETESLRDRLAGLPRAERTAELVRLVRTSTATVLGH DDPKAVRATTPFKELGFDSLAAVRLRNLLNAATGLRLPSTLVFDHPNASAVAGFLTSELGSGTPAREASSALRDGYRQAGV SGRVRSYLDLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVICCAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYEEG EPLPSSMAAVAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTA

	TLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFEHDTVAVPGDHFTMVQEHA DAIARHIDAWLGGGNSKLAAALEHHHHHH*
MK149 SZ4-L-M3-TE	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGKLDPIAIVSMACRLPG GVNTPQRLWELLREGGETLSGFPTDRGWDLARLHHPDPDNPGTSYVDKGGFLDDAAGFDAEFFGVSPREAAAMDPQQRLL LETSWELVENAGIDPHSLRGTATGVFLGVAKFGYGEDTAAAEDVEGYSVTGVAPAVASGRISYTMGLEGPSISVDTACSSSL VALHLAVESLRKGESSMAVVGGAAVMATPGVFVDFSRQRALAADGRSKAFGAGADGFGFSEGVTLVLLERLSEARRNGH EVLAVVRGSALNQDGASNGLSAPSGPAQRRVIRQALESCGLEPGDVDAVEAHGTGTALGDPIEANALLDTYGRDRDADRP LWLGSVKSNIGHTQAAAGVTGLLKVVLALRNGELPATLHVEEPTPHVDWSSGGVALLAGNQPWRRGERTRRARVSAFGIS GTNAHVIVEEAPEREHRETTAHDGRPVPLVVSARTTAALRAQAAQIAELLERPDADLAGVGLGLATTRARHEHRAAVVAST REEAVRGLREIAAGAATADAVVEGVTEVDGRNVVFLFPGQGSQWAGMGAELLSSSPVFAGKIRACDESMAPMQDWKVSD VLRQAPGAPGLDRVDVVQPVLFAVMVSLAELWRSYGVEPAAVVGHSQGEIAAAHVAGALTLEDAAKLVVGRSRLMRSLS GEGGMAAVALGEAAVRERLRPWQDRLSVAAVNGPRSVVVSGEPGALRAFSEDCAAEGIRVRDIDVDYASHSPQIERVREE LLETTGDIAPRPARVTFHSTVESRSMDGTELDARYWYRNLRETVRFADAVTRLAESGYDAFIEVSPHPVVVQAVEEAVEEA DGAEDAVVVGSLHRDGGDLSAFLRSMATAHVSGVDIRWDVALPGAAPFALPTYPFQRKRYWLQPAAPAAASDELAYRVS WTPIEKPESGNLDGDWLVVTPLISPEWTEMLCEAINANGGRALRCEVDTSASRTEMAQAVAQAGTGFRGVLSLLSSDESAC RPGVPAGAVGLLTLVQALGDAGVDAPVWCLTQGAVRTPADDDLARPAQTTAHGFAQVAGLELPGRWGGVVDLPESVDD AALRLLVAVLRGGGRAEDHLAVRDGRLHGRRVVRASLPQSGSRSWTPHGTVLVTGAASPVGDQLVRWLADRGAERLVLA GACPGDDLLAAVEEAGASAVVCAQDAAALREALGDEPVTALVHAGTLTNFGSISEVAPEEFAETIAAKTALLAVLDEVLGD RAVEREVYCSSVAGIWGGAGMAAYAAGSAYLDALAEHHRARGRSCTSVAWTPWALPGGAVDDGYLRERGLRSLSADRA MRTWERVLAAGPVSVAVADVDWPVLSEGFAATRPTALFAELAGRGGQAEAEPDSGPTGEPAQRLAGLSPDEQQENLLELV ANAVAEVLGHESAAEINVRRAFSELGLDSLNAMALRKRLSASTGLRLPASLVFDHPTVTALAQHLTSQLDSGTPAREASSAL RDGYRQAGVSGRVRSYLDLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVICCAGTAAISGPHEFTRLAGALRGIAPVR AVPQPGYEEGEPLPSSMAAVAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDA MNAWLEELTATLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFEHDTVAVPG DHFTMVQEHADAIARHIDAWLGGGNSKLAAALEHHHHHH*
MK150 (5)M1-L-SZ3	MSGDNGMTEEKLRRYLKRTVTELDSVTARLREVEHRAGEPVAVVAMACRLPGGVSTPEEFWELLSEGRDAVAGLPTDRG WDLDSLFHPDPTRSGTAHQRGGGFLTEATAFDPAFFGMSPREALAVDPQQRLMLELSWEVLERAGIPPTSLQASPTGVFVGL IPQEYGPRLAEGGEGVEGYLMTGTTTSVASGRIAYTLGLEGPAISVDTACSSSLVAVHLACQSLRRGESSLAMAGGVTVMPT PGMLVDFSRMNSLAPDGRCKAFSAGANGFGMAEGAGMLLLERLSDARRNGHPVLAVLRGTAVNSDGASNGLSAPNGRAQ VRVIQQALAESGLGPADIDAVEAHGTGTRLGDPIEARALFEAYGRDREQPLHLGSVKSNLGHTQAAAGVAGVIKMVLAMR AGTLPRTLHASERSKEIDWSSGAISLLDEPEPWPAGARPRRAGVSSFGISGTNAHAIIEEAPQVVEGERVEAGDVVAPWVLSA SSAEGLRAQAARLAAHLREHPGQDPRDIAYSLATGRAALPHRAAFAPVDESAALRVLDGLATGNADGAAVGTSRAQQRAV FVFPGQGWQWAGMAVDLLDTSPVFAAALRECADALEPHLDFEVIPFLRAEAARREQDAALSTERVDVVQPVMFAVMVSL ASMWRAHGVEPAAVIGHSQGEIAAACVAGALSLDDAARVVALRSRVIATMPGNKGMASIAAPAGEVRARIGDRVEIAAVN GPRSVVVAGDSDELDRLVASCTTECIRAKRLAVDYASHSSHVETIRDALHAELGEDFHPLPGFVPFFSTVTGRWTQPDELDA GYWYRNLRRTVRFADAVRALAEQGYRTFLEVSAHPILTAAIEEIGDGSGADLSAIHSLRRGDGSLADFGEALSRAFAAGVA VDWESVHLGTGARRVPLPTYPFQRERVWLEPKPVARRSTEVDEVSALRYRIEWRPTGAGEPARLDGTWLVAKYAGTADET STAAREALESAGARVRELVVDARCGRDELAERLRSVGEVAGVLSLLAVDEAEPEEAPLALASLADTLSLVQAMVSAELGCP LWTVTESAVATGPFERVRNAAHGALWGVGRVIALENPAVWGGLVDVPAGSVAELARHLAAVVSGGAGEDQLALRADGV YGRRWVRAAAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHLLLVSRSGPDADGAGELVAELEALGARTTVA

	ACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIERASRAKVLGARNLHELTRELDLTAFVLFSSFASAF GAPGLGGYAPGNAYLDGLAQQRRSDGLPATAVAWGTWAGSGMAEGPVADRFRRHGVIEMPPETACRALQNALDRAEVC PIVIDVRWDRFLLAYTAQRPTRLFDEIDDARRAAPQAAAEPRVGALASLPAPEREKALFELVRSHAAAVLGHASAERVPAD QAFAELGVDSLSALELRNRLGAATGVRLPTTTVFDHPDVRTLAAHLAAELGGGSGGGSGNEVTTLENDAAFIENENAYLEK EIARLRKEKAALRNRLAHKKLEHHHHHH*
MK152 SZ4-L-KR1-ACP1-L_{12}-M3-TE	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGDEVSALRYRIEWRPTG AGEPARLDGTWLVAKYAGTADETSTAAREALESAGARVRELVVDARCGRDELAERLRSVGEVAGVLSLLAVDEAEPEEAP LALASLADTLSLVQAMVSAELGCPLWTVTESAVATGPFERVRNAAHGALWGVGRVIALENPAVWGGLVDVPAGSVAELA RHLAAVVSGGAGEDQLALRADGVYGRRWVRAAAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHLLLVSRSG PDADGAGELVAELEALGARTTVAACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIERASRAKVLGA RNLHELTRELDLTAFVLFSSFASAFGAPGLGGYAPGNAYLDGLAQQRRSDGLPATAVAWGTWAGSGMAEGPVADRFRRH GVIEMPPETACRALQNALDRAEVCPIVIDVRWDRFLLAYTAQRPTRLFDEIDDARRAAPQAAAEPRVGAHMLASLPAPERE KALFELVRSHAAAVLGHASAERVPADQAFAELGVDSLSALELRNRLGAATGVRLPTTTVFDHPDVRTLAAHLAAELGGAT GAEQAAPATTAPVDDPIAIVSMACRLPGGVNTPQRLWELLREGGETLSGFPTDRGWDLARLHHPDPDNPGTSYVDKGGFLD DAAGFDAEFFGVSPREAAAMDPQQRLLLETSWELVENAGIDPHSLRGTATGVFLGVAKFGYGEDTAAAEDVEGYSVTGVA PAVASGRISYTMGLEGPSISVDTACSSSLVALHLAVESLRKGESSMAVVGGAAVMATPGVFVDFSRQRALAADGRSKAFGA GADGFGFSEGVTLVLLERLSEARRNGHEVLAVVRGSALNQDGASNGLSAPSGPAQRRVIRQALESCGLEPGDVDAVEAHGT GTALGDPIEANALLDTYGRDRDADRPLWLGSVKSNIGHTQAAAGVTGLLKVVLALRNGELPATLHVEEPTPHVDWSSGGV ALLAGNQPWRRGERTRRARVSAFGISGTNAHVIVEEAPEREHRETTAHDGRPVPLVVSARTTAALRAQAAQIAELLERPDA DLAGVGLGLATTRARHEHRAAVVASTREEAVRGLREIAAGAATADAVVEGVTEVDGRNVVFLFPGQGSQWAGMGAELLS SSPVFAGKIRACDESMAPMQDWKVSDVLRQAPGAPGLDRVDVVQPVLFAVMVSLAELWRSYGVEPAAVVGHSQGEIAAA HVAGALTLEDAAKLVVGRSRLMRSLSGEGGMAAVALGEAAVRERLRPWQDRLSVAAVNGPRSVVVSGEPGALRAFSEDC AAEGIRVRDIDVDYASHSPQIERVREELLETTGDIAPRPARVTFHSTVESRSMDGTELDARYWYRNLRETVRFADAVTRLAE SGYDAFIEVSPHPVVVQAVEEAVEEADGAEDAVVVGSLHRDGGDLSAFLRSMATAHVSGVDIRWDVALPGAAPFALPTYP FQRKRYWLQPAAPAAASDELAYRVSWTPIEKPESGNLDGDWLVVTPLISPEWTEMLCEAINANGGRALRCEVDTSASRTE MAQAVAQAGTGFRGVLSLLSSDESACRPGVPAGAVGLLTLVQALGDAGVDAPVWCLTQGAVRTPADDDLARPAQTTAHG FAQVAGLELPGRWGGVVDLPESVDDAALRLLVAVLRGGGRAEDHLAVRDGRLHGRRVVRASLPQSGSRSWTPHGTVLVT GAASPVGDQLVRWLADRGAERLVLAGACPGDDLLAAVEEAGASAVVCAQDAAALREALGDEPVTALVHAGTLTNFGSIS EVAPEEFAETIAAKTALLAVLDEVLGDRAVEREVYCSSVAGIWGGAGMAAYAAGSAYLDALAEHHRARGRSCTSVAWTP WALPGGAVDDGYLRERGLRSLSADRAMRTWERVLAAGPVSVAVADVDWPVLSEGFAATRPTALFAELAGRGGQAEAEP DSGPTGEPAQRLAGLSPDEQQENLLELVANAVAEVLGHESAAEINVRRAFSELGLDSLNAMALRKRLSASTGLRLPASLVFD HPTVTALAQHLTSQLDSGTPAREASSALRDGYRQAGVSGRVRSYLDLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVI CCAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYEEGEPLPSSMAAVAAVQADAVIRTQGDKPFVVAGHSAGALMAYAL ATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTATLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAG EPMGPWPDDSWKPTWPFEHDTVAVPGDHFTMVQEHADAIARHIDAWLGGGNSSSVDKLAAALEHHHHHH*
MK168 SZ4-L-KR5-ACP5(2)	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGPIPTGGRARDEDDDW RYQVVWREAEWESASLAGRVLLVTGPGVPSELSDAIRSGLEQSGATVLTCDVESRSTIGTALEAADTDALSTVVSLLSRDGE AVDPSLDALALVQALGAAGVEAPLWVLTRNAVQVADGELVDPAQAMVGGLGRVVGIEQPGRWGGLVDLVDADAASIRS LAAVLADPRGEEQVAIRADGIKVARLVPAPARAARTRWSPRGTVLVTGGTGGIGAHVARWLARSGAEHLVLLGRRGADAP GASELREELTALGTGVTIAACDVADRARLEAVLAAERAEGRTVSAVMHAAGVSTSTPLDDLTEAEFTEIADVKVRGTVNLD

	ELCPDLDAFVLFSSNAGVWGSPGLASYAAANAFLDGFARRRRSEGAPVTSIAWGLWAGQNMAGDEGGEYLRSQGLRAMD PDRAVEELHITLDHGQTSVSVVDMDRRRFVELFTAARHRPLFDEIAGARAEARQSEEGPALAQRLAALSTAERREHLAHLIR AEVAAVLGHGDDAAIDRDRAFRDLGFDSMTAVDLRNRLAAVTGVREAATVVFDHPTITRLADHYLERLVGTEVRGEAPSA LAGLDALEAALPEVPATEREELVQRLERMLAALRPVAQAADASGTGANPSGDDLGEAGVDELLEALGRELDGDPNSSSVD KLAAALEHHHHHH*
MK169 SZ4-L-RIFS(KR1-ACP)(2)	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGEPAEPASAGDPLLGTV VSTPGSDRLTAVAQWSRRAQPWAVDGLVPNAALVEAAIRLGDLAGTPVVGELVVDAPVVLPRRGSREVQLIVGEPGEQRR RPIEVFSREADEPWTRHAHGTLAPAAAAVPEPAAAGDATDVTVAGLRDADRYGIHPALLDAAVRTVVGDDLLPSVWTGVS LLASGATAVTVTPTATGLRLTDPAGQPVLTVESVRGTPFVAEQGTTDALFRVDWPEIPLPTAETADFLPYEATSAEATLSAL QAWLADPAETRLAVVTGDCTEPGAAAIWGLVRSAQSEHPGRIVLADLDDPAVLPAVVASGEPQVRVRNGVASVPRLTRVT PRQDARPLDPEGTVLITGGTGTLGALTARHLVTAHGVRHLVLVSRRGEAPELQEELTALGASVAIAACDVADRAQLEAVLR AIPAEHPLTAVIHTAGVLDDGVVTELTPDRLATVRRPKVDAARLLDELTREADLAAFVLFSSAAGVLGNPGQAGYAAANAE LDALARQRNSLDLPAVSIAWGYWATVSGMTEHLGDADLRRNQRIGMSGLPADEGMALLDAAIATGGTLVAAKFDVAALR ATAKAGGPVPPLLRGLAPLPRRAAAKTASLTERLAGLAETEQAAALLDLVRRHAAEVLGHSGAESVHSGRTFKDAGFDSLT AVELRNRLAAATGLTLSPAMIFDYPKPPALADHLRAKLFGTEVRGEAPSALAGLDALEAALPEVPATEREELVQRLERMLA ALRPVAQAADASGTGANPSGDDLGEAGVDELLEALGRELDGDPNSSSVDKLAAALEHHHHHH*
MK170 SZ4-L-M5-TE	MQKVAELKNRVAVKLNRNEQLKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGKLEPIAIVGMACRFPG DVDSPESFWEFVSGGGDAIAEAPADRGWEPDPDARLGGMLAAAGDFDAGFFGISPREALAMDPQQRIMLEISWEALERAG HDPVSLRGSATGVFTGVGTVDYGPRPDEAPDEVLGYVGTGTASSVASGRVAYCLGLEGPAMTVDTACSSGLTALHLAMES LRRDECGLALAGGVTVMSSPGAFTEFRSQGGLAADGRCKPFSKAADGFGLAEGAGVLVLQRLSAARREGRPVLAVLRGSA VNQDGASNGLTAPSGPAQQRVIRRALENAGVRAGDVDYVEAHGTGTRLGDPIEVHALLSTYGAERDPDDPLWIGSVKSNIG HTQAAAGVAGVMKAVLALRHGEMPRTLHFDEPSPQIEWDLGAVSVVSQARSWPAGERPRRAGVSSFGISGTNAHVIVEEA PEADEPEPAPDSGPVPLVLSGRDEQAMRAQAGRLADHLAREPRNSLRDTGFTLATRRSAWEHRAVVVGDRDDALAGLRAV ADGRIADRTATGQARTRRGVAMVFPGQGAQWQGMARDLLRESQVFADSIRDCERALAPHVDWSLTDLLSGARPLDRVDV VQPALFAVMVSLAALWRSHGVEPAAVVGHSQGEIAAAHVAGALTLEDAAKLVAVRSRVLRRLGGQGGMASFGLGTEQA AERIGRFAGALSIASVNGPRSVVVAGESGPLDELIAECEAEGITARRIPVDYASHSPQVESLREELLTELAGISPVSADVALYST TTGQPIDTATMDTAYWYANLREQVRFQDATRQLAEAGFDAFVEVSPHPVLTVGIEATLDSALPADAGACVVGTLRRDRGG LADFHTALGEAYAQGVEVDWSPAFADARPVELPVYPFQRQRYWLPIPTGGRARDEDDDWRYQVVWREAEWESASLAGR VLLVTGPGVPSELSDAIRSGLEQSGATVLTCDVESRSTIGTALEAADTDALSTVVSLLSRDGEAVDPSLDALALVQALGAAG VEAPLWVLTRNAVQVADGELVDPAQAMVGGLGRVVGIEQPGRWGGLVDLVDADAASIRSLAAVLADPRGEEQVAIRADG IKVARLVPAPARAARTRWSPRGTVLVTGGTGGIGAHVARWLARSGAEHLVLLGRRGADAPGASELREELTALGTGVTIAA CDVADRARLEAVLAAERAEGRTVSAVMHAAGVSTSTPLDDLTEAEFTEIADVKVRGTVNLDELCPDLDAFVLFSSNAGVW GSPGLASYAAANAFLDGFARRRRSEGAPVTSIAWGLWAGQNMAGDEGGEYLRSQGLRAMDPDRAVEELHITLDHGQTSV SVVDMDRRRFVELFTAARHRPLFDEIAGARAEARQSEEGPALAQRLAALSTAERREHLAHLIRAEVAAVLGHGDDAAIDRD RAFRDLGFDSMTAVDLRNRLAAVTGVREAATVVFDHPTITRLADHYLERLVSGTPAREASSALRDGYRQAGVSGRVRSYL DLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVICCAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYEEGEPLPSSMA AVAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTATLFDRETV RMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFEHDTVAVPGDHFTMVQEHADAIARHID AWLGGGNSKLAAALEHHHHHH*

Table S3: Yields of proteins used in this study. If no indication is given the PKS domain/modules are derived from DEBS. Typical yields are presented.

Construct	Protein	Yield /mg/L of culture
MK96	KR1-ACP1(2)	8.6
MK111	(5)KS1-AT1-SZ3	1.3
MK112	SZ4-KR1-ACP1(2)	7.9
MK113	(5)KS1-AT1	1.1
MK136	SZ4-KR1-ACP1-M2-TE	0.9
MK137	SZ4-KR5-ACP5-M6-TE	2.1
MK138	SZ4-KR1-ACP1-M2-TE	3.4
MK141	SZ4-KR1-ACP1-M5-TE	1.6
MK142	SZ4-KR1-ACP1-M6-TE	1.4
MK147	SZ4-M6-TE	7.9
MK148	SZ4-M2-TE	1.5
MK149	SZ4-M3-TE	3.8
MK150	(5)M1-SZ3	15.3
MK152	SZ4-KR1-ACP1-M3-TE	3.6
MK168	SZ4-KR5-ACP5(2)	2.3
MK169	SZ4-RIFS(KR1-ACP1)(2)	9.8
MK170	SZ4-M5-TE	3.3
BL12	LDD(4)	6.7
BL13	(5)M1(2)	2.4
BL16	(3)M2-TE	1.6
BL17	(3)M5-TE	0.8
BL18	(3)M6-TE	4.9
RSG34	(3)M3-TE	9.4

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