

## Engineering of chimeric polyketide synthases using SYNZIP docking domains

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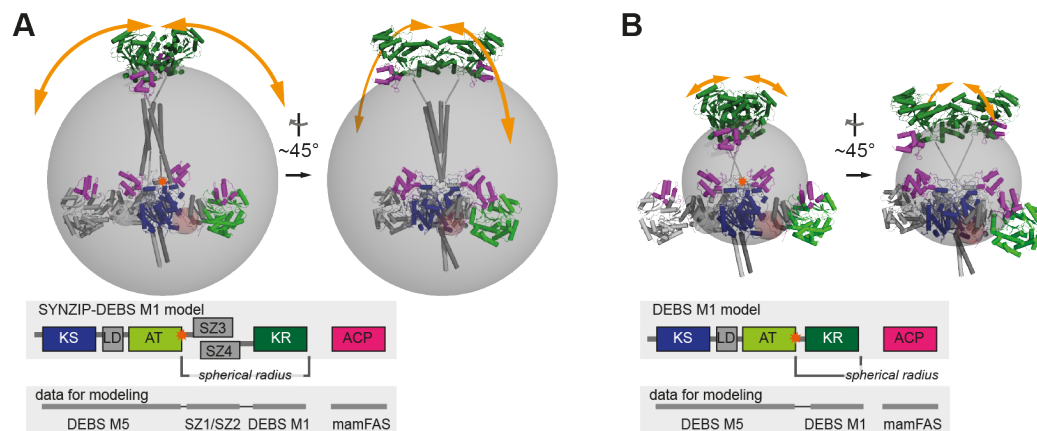
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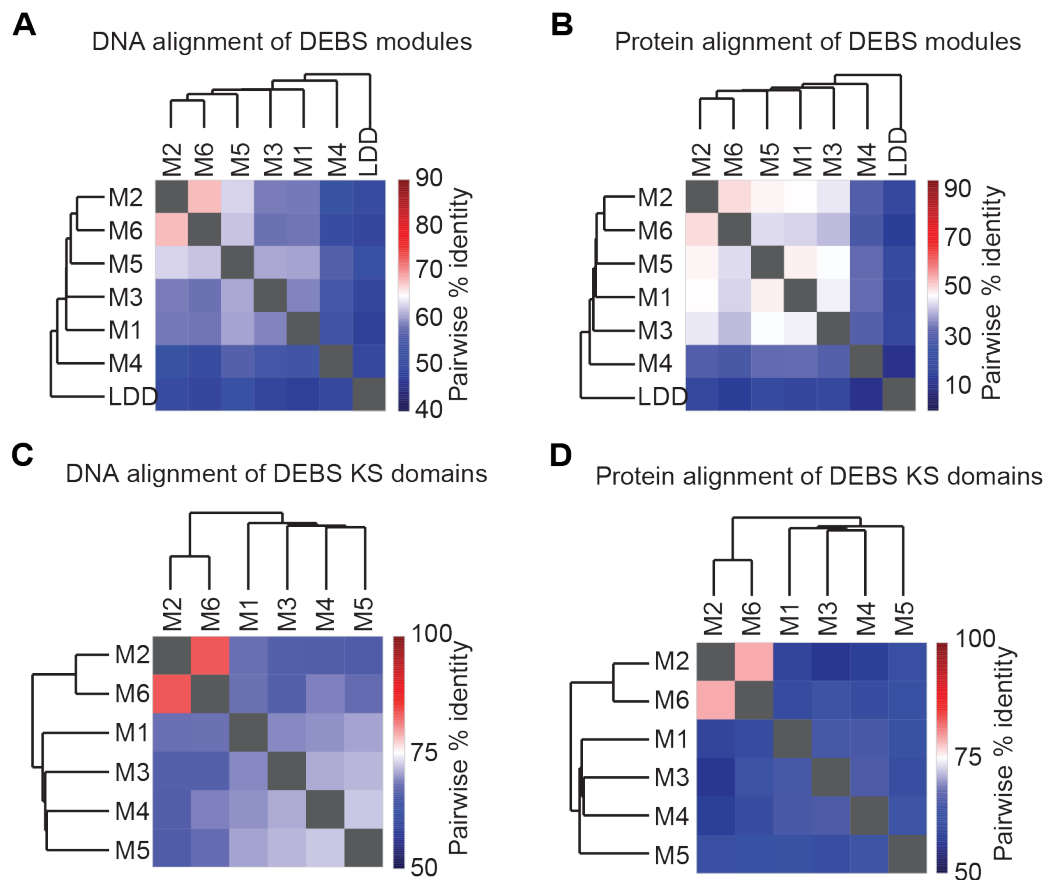
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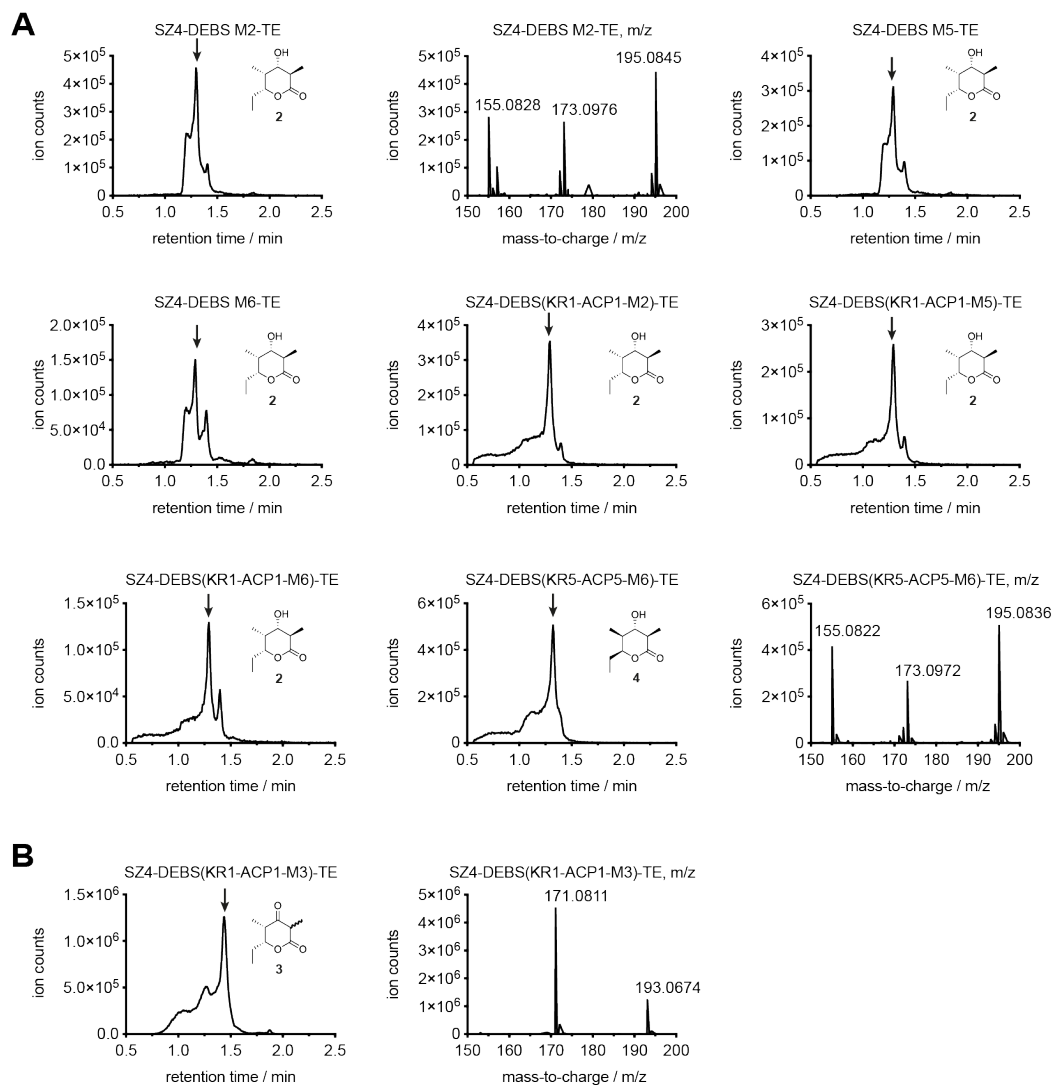
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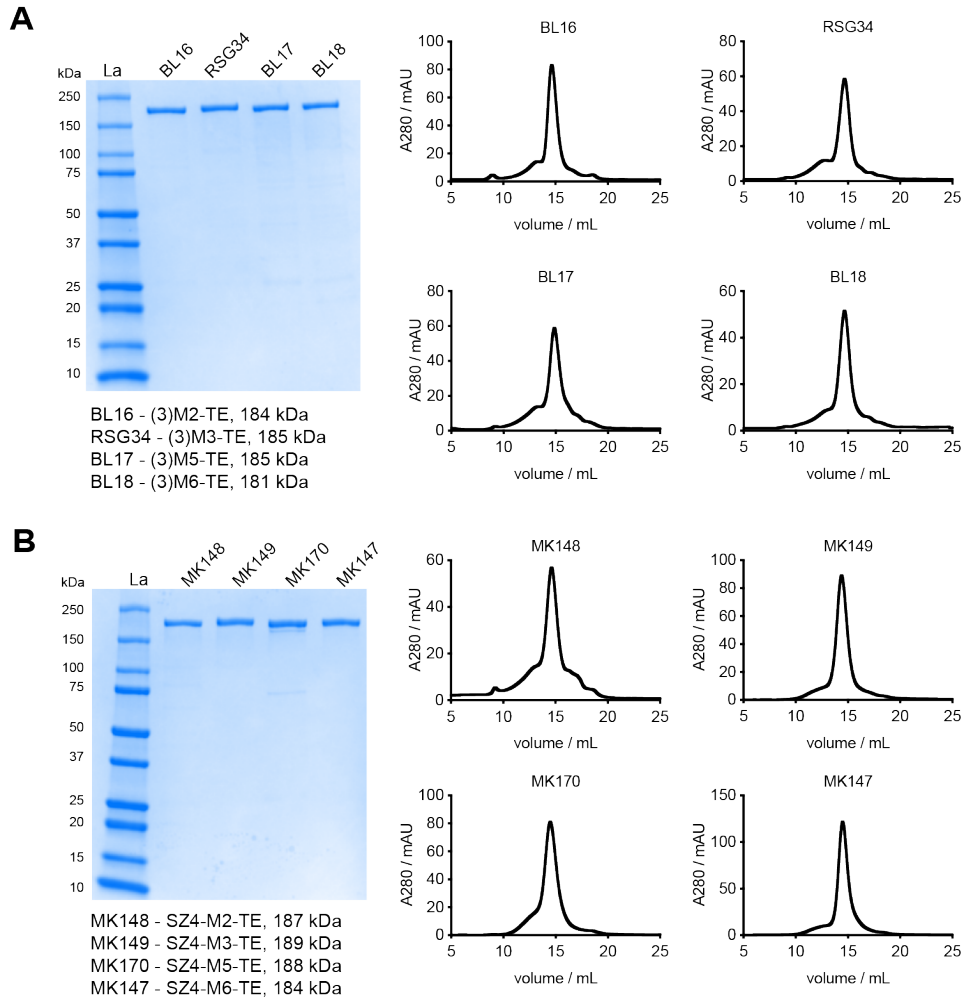
**Figure S1. Structural model of DEBS M1 with and without SYNZIP docking domains.** Structural models are based on X-ray crystallographic data of the KS-AT didomain of DEBS M5 (pdb 2HG4<sup>1</sup>), of the KR domain of DEBS M1 (pdb 2FR0<sup>2</sup>), and of the coiled-coil pair SYNZIP1:SYNZIP2 (pdb 3HE5<sup>3</sup>). The coiled-coil pair SYNZIP3:SYNZIP4 was modeled regarding data provided by Thompson *et al.*<sup>4</sup>. Linkers connecting the domains are not shown, but dashed lines indicate distances bridged by linkers (linkers lengths calculated with 3.6 Å per amino acid). ACP is shown in docking positions at KS, AT and KR as defined by Viegas *et al.* for mammalian FAS.<sup>5</sup> Please note that the model shows only the docked ACPs, but does not contain the ACP C-terminally attached to the KR. The relative orientation of domains bridged by linkers is not defined, and the positions and orientations of those domains were arbitrarily chosen. A) SYNZIP-bridged M1 model. The coiled-coil pair induces an elongated structure. The SYNZIP3:SYNZIP4-KR-ACP part is presumably conformationally highly flexible, because of flexible linkers and missing dimerizing elements (flexibility indicated by orange arrows). The grey sphere indicates the maximum conformational space of the C-terminal ACP (linked to KR, see Figure 2A and B). For illustration of the conformational space (shown for one protomer of the dimer), the distance between the attachment site of the coiled-coil pair at the AT domain and the attachment site of the ACP at the KR domain was used as the radius of a sphere (shown in grey; center of sphere indicated by orange star), notwithstanding more complex structural properties, as for example induced by the KS-AT didomain that constrains a free motion of the SYNZIP3:SYNZIP4-KR-ACP part. The structural model illustrates that the ACP can essentially reach any position of the KS-AT didomain in any orientation, including a “translocation site” revealed in a previously reported study<sup>6</sup>. The translocation site is highlighted by a red sphere (grey for other protomer). Docking at the translocation site may allow for direct transacylation of the acyl moiety from KS to ACP, which is discussed as side reaction. B) M1 model. The model has been designed as described above, including construct specific properties. According to the model, the conformational space of ACP is limited, and access to the translocation site prevented.



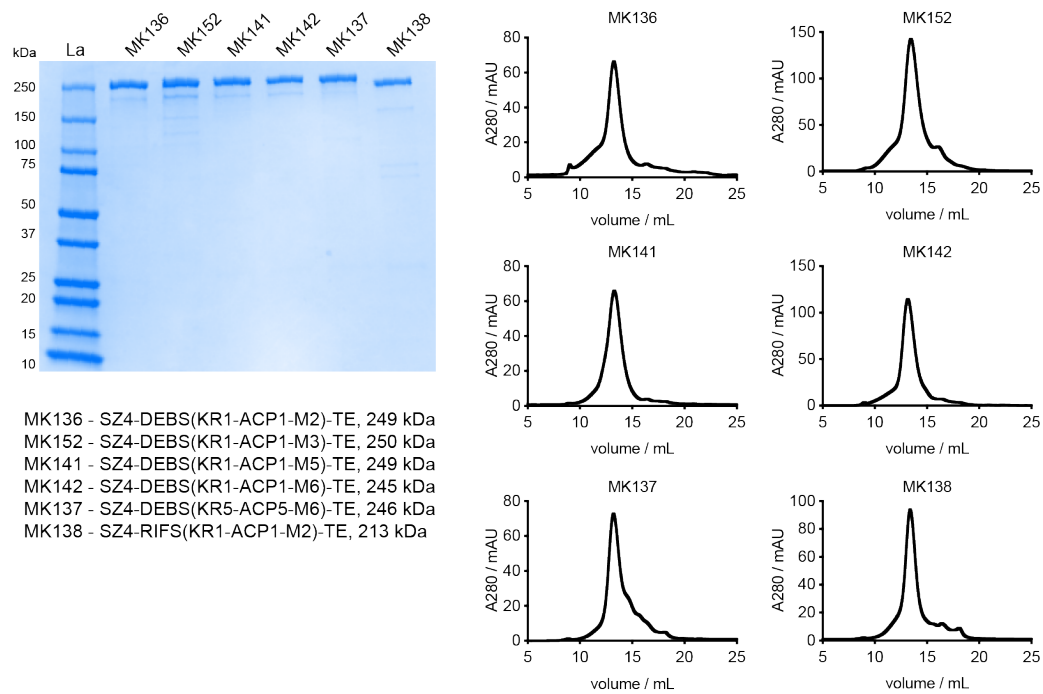
**Figure S2. Sequence similarity analysis of DEBS modules and KS domains.** Pairwise alignment of DNA and protein sequences of DEBS modules (A) and DEBS KS domains (B) are depicted as heatmaps.



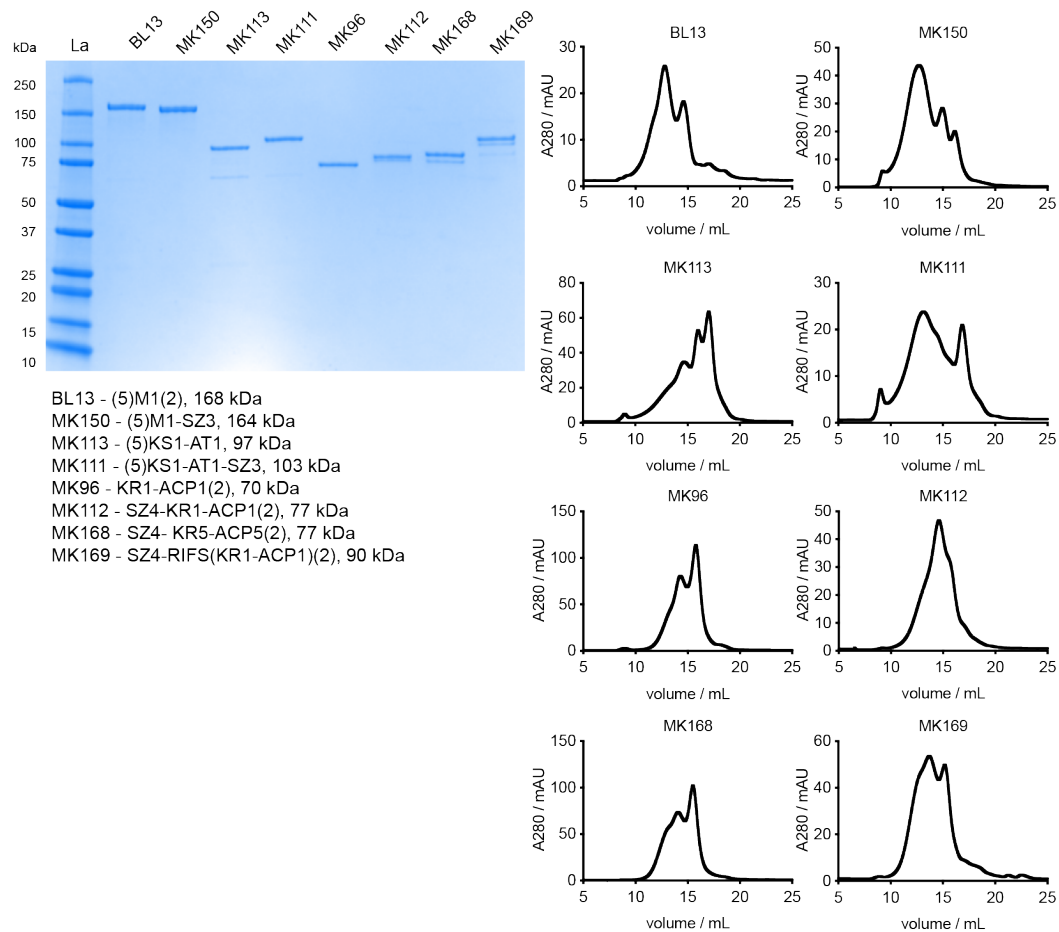
**Figure S3. LC-MS analysis of products produced by bimodular chimeric PKSs newly generated in this study.** A) Reduced triketide lactone products **2** and **4** ( $C_9H_{16}O_3$ , calculated MW 172.110) were detected in reaction mixtures containing SZ4-M2-TE, SZ4-M5-TE, SZ4-M6-TE, SZ4-KR1-ACP1-M2-TE, SZ4-KR1-ACP1-M5-TE, SZ4-KR1-ACP1-M6-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  $[M+H-H_2O]^+$ ,  $[M+H]^+$ , and  $[M+Na]^+$  ions. The peak of interest is marked with an arrow based on its mass spectrum.



**Figure S4. 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 S5. 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 S6. 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.

**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	CCGCGGGTGGGCGCGCTCGAGACCACCACCACCACCCTGAGATC			
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	CCGACGATCGCGATCGGGTCGACGGGGCCCGTGGTC	
pMK83 - ACP1-M2-TE, used to generate pADD03	Infusion	83_V1	P-MK250	GAGCCGATCGCGATCGTCGGCATGGCGT	pBL17
			P-MK251	GACACCGCGCGTGTGCGCGTCCG	
		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	CCGCGGGTGGGCGCGCTCGAGACCACCACCACCACCCTGAGATC			
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	GTGCAGCCCGTGATGTTGCGGGTCATGG	pBL13
			P-MK261	GTGGTGGTGGTGCTCGAGGCGGTAGCGCAGCGCGGAAACCTCGT	
		91_I2	P-MK229	CCATGACCGGAACATCACGGGCTGCAC	pBL13
			P-MK260	GAAGGAGATATACATATGAGCGGTGACAACGGCATGACCGAGGAAAA	



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pMK93 - KR1-ACP1-M6- TE, missing an Asp in ACP1- KS2 linker	Infusion	93_V	digestion of pMK81 with NdeI			pAYC59
		93_I	P-MK276	AAGGAGATATACATATGGACGAGGTTTCCGCGCTG		
			P-MK277	AGCGACGCCAGCATATGCGCGCCCACCCGCGGTTTC		
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	CTGGCACACAAAAGCTCGAGCACCACCACCAC		
		111_I	P-MK308	GGATCCGGTGGCGGATCCGGTAACGAAGTTACAACACTTGAGAATGAC		pfRSZ
			P-MK303	CTTTTGTGTGCCAGTCTATTTCTCAAT		
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	GAAGGAGATATACATATGAGCGGTGACAACGGCATGACCGAGGAAAA G		pMK91
			P-MK312	GAGCCAGACGCGCTCGC		
pADD02 - KR1-ACP1-M5- TE, missing an Asp in ACP1- KS2 linker	Infusion	ADD02_V	digestion of pMK80 with NdeI			pAYC59
		ADD02_I	P-MK276	AAGGAGATATACATATGGACGAGGTTTCCGCGCTG		
			P-MK277	AGCGACGCCAGCATATGCGCGCCCACCCGCGGTTTC		
pADD03 - KR1-ACP1-M2- TE - missing an Asp in ACP1- KS2 linker	Infusion	ADD03_V	digestion of pMK83 with NdeI			pAYC59
		ADD03_I	P-MK276	AAGGAGATATACATATGGACGAGGTTTCCGCGCTG		
			P-MK277	AGCGACGCCAGCATATGCGCGCCCACCCGCGGTTTC		
pMK133 - KR1-ACP1-M2- TE, complete ACP1-KS2 linker	Quickchan ge	133_QC	P-MK347	GCGACCACGGCCCCGTCGATGAGCCGATCGCGATCGTC		pADD03
			P-MK348	GACGATCGCGATCGGCTCATCGACGGGGGCCGTGGTTCG		

pMK134 - KR1-ACP1-M5- TE, complete ACP1-KS2 linker	Quickchan ge	134_QC	P-MK347	GCGACCACGGCCCCCGTCGATGAGCCGATCGCGATCGTC	pADD02
			P-MK348	GACGATCGCGATCGGCTCATCGACGGGGGCCGTGGTCGC	
pMK135 - KR1-ACP1-M6- TE, complete ACP1-KS2 linker	Quickchan ge	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	AGCGACGCCAGCATATGCGCGCCACCCGC	
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	GGCGGTGCCGATCTCGGCCGGCCGTTTCGCCCGGATCCGAAGAGCTT GGCGCGCAG	
pMK141 - SZ4-KR1-ACP1- M5-TE	Infusion	141_V	digestion of pMK134 with NdeI		
		136_I	P-MK351	GAAGGAGATATACATATGCAGAAAGTGGCTGAATTGAAAAAC	pMK112
			P-MK345	AGCGACGCCAGCATATGCGCGCCACCCGC	
pMK142 - SZ4-KR1-ACP1- M6-TE	Infusion	142_V	digestion of pMK135 with NdeI		
		136_I	P-MK351	GAAGGAGATATACATATGCAGAAAGTGGCTGAATTGAAAAAC	pMK112
			P-MK345	AGCGACGCCAGCATATGCGCGCCACCCGC	
pMK146 - SZ4-MCS-H6, intermediate vector for various cloning strategies	Infusion	146_all	P-MK386	TGCGGCCGCAAGCTTACCGGATCCGCCACCGG	pMK112
			P-MK387	AAGCTTGCGGCCGCACTC	
pMK147 -	Infusion	147_V	digestion of pMK146 with HindIII		

SZ4-M6-TE		147_I	P-MK388	CGGATCCGGTAAGCTTGACCCGATCGCGATCGTC	pMK137
			P-MK389	GTGCGGCCGCAAGCTTCGAATTCCTCCGCCAG	
pMK148 - SZ4-M2-TE	Infusion	148_V	digestion of pMK146 with HindIII		
		148_I	P-MK390	CGGATCCGGTAAGCTTGAGCCGATCGCGATCGTC	pMK136
			P-MK389	GTGCGGCCGCAAGCTTCGAATTCCTCCGCCAG	
pMK149 - SZ4-M3-TE	Infusion	149_V	digestion of pMK146 with HindIII		
		149_I	P-MK391	CGGATCCGGTAAGCTTGACCCGATCGCCATCGTC	pRSG34
			P-MK389	GTGCGGCCGCAAGCTTCGAATTCCTCCGCCAG	
pMK150 - (5)M1-SZ3	Infusion	150_V	P-MK394	ACGACCGCGACCGGTTTC	pMK111
			P-MK389	GTGCGGCCGCAAGCTTCGAATTCCTCCGCCAG	
		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	GAAGAGCTTGCGCGCAG	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	GTGCGGCCGCAAGCTTCGAATTCCTCCGCCAG	

References for plasmids constructed elsewhere: pCK7<sup>7</sup>; pBP130<sup>8</sup>; pAYC59<sup>9</sup>; pAJ20 and pAJ21<sup>10</sup>; pBL13, pBL16, pBL17, and pBL18<sup>11</sup>; pRSG34<sup>12</sup>; pFRSZ was a gift from Mislav Oreb, Goethe University Frankfurt. In addition pBL12 was used to produce LDD(4)<sup>11</sup>.

**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<sub>12</sub> is the ACP1-KS2 linker used to covalently fuse ACP1 to a heterologous acceptor module.

Construct	Amino acid sequence
MK96 KR1-ACP1-(2)	MDEVSAALRYRIEWRPTGAGEPARLDGTWLVAKYAGTADETSTAAREALESAGARVRELVVDARCGRDELAERLRSVGEV AGVLSLLAVDEAEPEEAPLALASLADTSLVQAMVSAELGCPLWVTESAVATGPFERVRNAAHGALWGVGRVIALENPA VWGGGLVDVPAGSVAELARHLAAVVSSGGAGEDQLALRADGVYGRRWVRAAAPATDDEWKPTGTVLVTGGTGGVGGQIA RWLARRGAPHLLLVSRSRGPADGAGELVAELEALGARTTVAACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVD TLTGERIERASRAKVLGARNLHELDTRELDLTAFLVLFSSFASAFGAPGLGGYAPGNAYLDGLAQRRSDGLPATAVAWGTW AGSGMAEGPVADRFRRHGVIEMPPETACRALQNALDRAEVCPIVIDVRWDRFLAYTAQRPTLRFDEIDDARRAAPQAAAE PRVGALASLPAPEREKALFELVRSHAAAVLGHASAERVPADQAFELGVDLSALELRNRLGAATGVRLPTTTVFDHPDVR TLAAHLAAELGTEVRGEAPSALAGLDALEAALPEVPATEREELVQRLERMLAALRPVAQAADASGTGANPSGDDLGEAGV DELLEALGRELDGDPNSSSSVDKLAALAEHHHHHH*
MK111 (5)KS1-AT1-L-SZ3	MSGDNGMTEEKLRRYLKRTVTELDSTARLREVEHHRAGEPVAVVAMACRLPGGVSTPEEFWELLSEGRDAVAGLPTDRG WDLDSLPHDPTRSGTAHQGGGFLTEATAFDPAFFGMSPREALAVDPQQRLMLELSWEVLERAGIPPTSLQASPTGVFVGL IPQEYGPRLAEGGEGVEGYLMTGTTTTSVASGRIAYTLGLEGPAISVDTACSSSLVAVHLACQSLRRGESSLAMAGGVTVMPT PGMLVDFSRMNSLAPDGRCKAFSAGANGFGMAEGAGMLLLERLSDARRNGHPVLA VLRGTA VNSDGASNGLSAPNGRAQ VRVIQALAESGLGPADIDAVEAHGTGTRLDGPPEARLFEAYGRDREQPLHLGSVKSNLGHQTQAAAGVAGVIKVMPLAMR AGTLPRTLHASERSKEIDWSSGAISLLDEPEPWAGARPRRAGVSSFGISGTNAHAIIEEAPQVVEGERVEAGDVPLVLSA SSAEGLRQAARLAAHLREHPGQDPRDIAYSLTAGRAALPHRAAFAPVDESAALRVLDGLATGNADGAAVGTSTRAQQRVAV FVFPQQGWQWAGMAVDLLDTSVPVFAAALRECADALEPHLDFEVIPFLRAEAARREQDAALSTERVDVVQVPMFAVMVSL ASMWRAHGVPEAAVIGHSQGEIAAACVAGALSDDAARVVALRSRVIATMPGNKGMASIAAPAGEVRARIGDRVEIAAVN GPRSVVVAGDSDELDRLVASCTTECIRAKRLAVDYASHSSHVETIRDALHAELGEDFHPLPGFVPPFFSTVTGRWTQPDELDA GYWYRNLRRTVRFADAVRALAEQGYRTFLEVSAPHILTAIEIEIGDGGSGADLSAIHSLRRGDGSLADFGAALSRAFAAGVA VDWESVHLGTGARRVPLPTYPFQRERVWLGSGGGSGNEVTTLENDAAFIENENAYLEKEIARLRKEKAALRNRLAHKKL EHHHHHH*
MK112 SZ4-L-KR1-ACP1(2)	MQKVAELKNRVAVKLNREQLKKNVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGDEVSALRYRIEWRPTG AGEPARLDGTWLVAKYAGTADETSTAAREALESAGARVRELVVDARCGRDELAERLRSVGEVAGVLSLLAVDEAEPEEAP LALASLADTSLVQAMVSAELGCPLWVTESAVATGPFERVRNAAHGALWGVGRVIALENPAVWGGGLVDVPAGSVAELA RHLAAVVSSGGAGEDQLALRADGVYGRRWVRAAAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHLLLVSRSR PDADGAGELVAELEALGARTTVAACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIERASRAKVLGA RNLHELDTRELDLTAFLVLFSSFASAFGAPGLGGYAPGNAYLDGLAQRRSDGLPATAVAWGTWAGSGMAEGPVADRFRRH GVIEMPPETACRALQNALDRAEVCPIVIDVRWDRFLAYTAQRPTLRFDEIDDARRAAPQAAAEPRVGALASLPAPEREKAL FELVRSHAAAVLGHASAERVPADQAFELGVDLSALELRNRLGAATGVRLPTTTVFDHPDVRTLAAHLAAELGTEVRGE APSALAGLDALEAALPEVPATEREELVQRLERMLAALRPVAQAADASGTGANPSGDDLGEAGVDELLEALGRELDGDPNS SSVDKLAALAEHHHHHH*
MK113 (5)KS1-AT1	MSGDNGMTEEKLRRYLKRTVTELDSTARLREVEHHRAGEPVAVVAMACRLPGGVSTPEEFWELLSEGRDAVAGLPTDRG WDLDSLPHDPTRSGTAHQGGGFLTEATAFDPAFFGMSPREALAVDPQQRLMLELSWEVLERAGIPPTSLQASPTGVFVGL IPQEYGPRLAEGGEGVEGYLMTGTTTTSVASGRIAYTLGLEGPAISVDTACSSSLVAVHLACQSLRRGESSLAMAGGVTVMPT PGMLVDFSRMNSLAPDGRCKAFSAGANGFGMAEGAGMLLLERLSDARRNGHPVLA VLRGTA VNSDGASNGLSAPNGRAQ

	<p>VRVIQQALAESGLPADIDAVEAHGTGTRLGDPIEARALFEAYGRDREQPLHLGSKVSNLGHGTQAAAGVAGVIKMLAMR  AGTLPRTLHASERSKEIDWSSGAISLLDEPEPWAGARPRRAGVSSFGISGTNAHAHIEEAPQVVEGERVEAGDVVAPWVLSA  SSAEGRLAQAARLAAHLREHPGQDPRDIAYSLATGRAALPHRAAFAPVDESAALRVL DGLATGNADGAAVGTSTRQQRAV  FVFPQGQWQWAGMAVDLLDTSPVFAAALRECADALEPHLDFEVIPFLRAEAARREQDAALSTERVDVVQPMFVAVMVS  ASMWRAHGVPEAAVIGHSQGEIAAACVAGALSDDAARVVALRSRVIAATMPGNKGMASIAAPAGEVRRARIGDRVEIAAVN  GPRS VVVAGDSDELDRLVASCTTECIRAKRLAVDYASHSSHVETIRDALHAELGEDFHPLPGFVPPFFSTVTGRWTQPELDA  GYWYRNLRRTVRFADAVRALAEQGYRTFLEVSAPILTAHIEEIGDGGADLSAIHSLRRGDGSLADFGAALSRAFAAGVA  VDWESVHLGTGARRVPLPTYPFQRERVWLEHHHHHHH*</p>
<p>MK136  SZ4-L-KR1-ACPI-  L12-M2-TE</p>	<p><b>MQKVAELKNRVAVKLNREQLKKNKVEELKNRNAYLKNELATLENEVARLENDVAE</b>GGSGGGSGDEVSAALRYRIEWRPTG  AGEPARLDGTWLVAKYAGTADETSTAAREALESAGARVREL VVDARCGRDELAERLRSVGEVAGVLSLLAVDEAEPEEAP  LALASLADTSLVQAMVSAELGCPLWTVTESAVATGPFERVRNAAHGALWGVGRVIALENPAVWGGLVDVPAGSVAELA  RHLAAVVSGGAGEDQLALRADGVYGRRWVRAAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHLVSRSG  PDADGAGELVAELEALGARTTVAACDVT DRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIERASRAKVLGA  RNLHEL TRELDLTAFVLFSSFASAFGAPGLGGYAPGNA YLDGLAQRRSDGLPATAVAWGTWAGSGMAEGPVADRFRRH  GVIEMPPETACRALQNALDRAEVCPIVIDVRWDRFLLAYTAQRPTLDFEIDDARRAAPQAAAEPVGAHMLASLPAPERE  KALFELVRSHAAAVLGHASAERVPADQAFaelGVDSLSALELRNRLGAATGVRLPTTTVFDHPDVRTLAAHLAAELGGAT  GAEQAAPATTAPVDEPIAIVGMACRLPGEVDSPERLWELITSGRDSAAEVPDDRGRWVPDELMA SDAAGTRRAHGNFMAGA  GDFDAAFFGISPREALAMDPQQRQALETTEWALESAGIPETLRGSDTGVFVGM SHQGYATGRPRPEDGVDTGNTAS  VASGRIAYVLGLEPALTVDTACSSSLVALHTACGSLRDGDCGLAVAGVSVMAGPEVTFEFSRQGALSPDGRCKPFSDEA  DGFLGEGSAFVVLQRLSDARREGRRVLGVVAGSAVNQDGASNGLSAPSGVAQQRVIRRAWARAGITGADVAVVEAHGT  GTRLDGPVEASALLATYGKSRGSSGPVLLGSKVSNIGHAQAAAGVAGVIKVLGLERGVPPMLCRGERSGLIDWSSGEIEL  ADGVREWSPAADGVRRAGVSAFGVSGTNAHVIIAEPPEPEPVQPRRMLPATGVVPPVLSARTGAALRAQAGRLADHLAA  HPGIAPADVSWTMARARQHFEERAAVLAADTAEAVHRLRAVADGAVVPGVVTGSASDGGSVFVFPQGGAQWEGMAREL  LPVPVFAESIAECDAVLSEVAGFSVSEVLEPRPDAPSLERVDVVQPVLFVAVMVS LARLWRACGAVPSAVIGHSQGEIAAAV  AGALSLEDGMRVVARRSRAVRAVAGRGSMLSVRGGRSDVEKLLADDSWTGRLEVA AVNGPDAVVVAGDAQAAREFLEY  CEGVGIRARAIPVDYASHTAHVEPVRDELVQALAGITPRRAEVPFFSTLTGDFLDGTELDAGYWYRNLRHPVEFHSAVQAL  TDQGYATFIEVSPHPVLASSVQETLDDAESDAAVLGTLERDAGDADRFLTALADAHTRGVAVDWEAVLGRAGLVDLPGYP  FQGRFWLLPDRTPRDEL DGFYRVDWTEVPRSEPAALRGRWLVVVEGHEEDGWTVEVRSALAEAGAEPEVTRGVGG  LVGDCAGVVSLLALEGDGAVQTLVLRVREDAEGIDAPLWTVTFGAVDAGSPVARPDQAKLWGLGQVASLERGPRWTGLV  DLPHMPDPPELRGRLTAVLAGSEDQAVRADAVRARRLSPAHTATSEYAVPGGTILVTGGTAGLGAELVARWLAGRGAEH  LALVSRGPDTEGVGDLTAE LTRLGARVSVHACDVSSREPVELVHGLIEQGDVVRGVVHAAGLPQQVAINDMDEAAFDE  VVAAKAGGAVHLDELCSDAELFLLFSSGAGVWGSARQGAYAAGNAFLDAFARHRRGRGLPATSVAWGLWAAGGMTGD  EEAVSFLRERGV RAMPVPRALAALDRVLASGETAVVVTDDVWPFAESYTAARPRPLLDRIVTTAPSERAGEPETESLRDR  LAGLPRAERTAELVRLVRTSTATV LGHDDPKAVRATTPFKELGFDSLAAVRLRNLLNAATGLRLPSTLVFDHPNASAVAGF  LTSELGSGTPAREASSALRDGYRQAGVSGRVRSYLDLLAGLSDFREHFHDGSDGFSLDL VDMADGPGEVTVICCACTAAISGP  HEFTRLAGALRGIAPVRAVPQPGYEEGEPLSSMAAAVA AVQADAVIRTQGD KPFVAVAGHSAGALMAYALATELLDRGHPP  RGVV LIDVYPPGHQDAMNAWLEELTATLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMPGPWPDSS  WKPTWPF EHDTVAVPGDHFTMVQEHADAIARHIDAWLGGGNSSSVDKLA AALEHHHHHHH*</p>
<p>MK137  SZ4-L-KR5-ACP5-</p>	<p><b>MQKVAELKNRVAVKLNREQLKKNKVEELKNRNAYLKNELATLENEVARLENDVAE</b>GGSGGGSGPIPTGGRARDEDDDW  RYQVVWREAEWESASLAGRVLLVTGPGVPSSELSDAIRSGLEQSGATVLTCDVESRSTIGTALEAADTDALSTVVSLSRDGE</p>

M6-TE	<p>AVDPSLDALALVQALGAAGVEAPLWVLTRNAVQVADGELVDPAQAMVGGLGRVVGIEQPGRWGGLVDLVDADAASIRS      LAAVLADPRGEEQVAIRADGIKVARLVPAPARAARTRWSRGTVLTGGTGGIGAHVARWLARSGAEHLVLLGRRGADAP      GASELREELTALGTGVTIAACDVADRARLEAVLAAERAEGRTVSVMHAAGVSTSTPLDDLTEAEFTEIADVVKVRGTVNL      ELCPLDADFVLFSSNAGVWVWSPGLASYAAANAFLDGFAARRRSEGAAPVTSIAWGLWAGQNMAGDEGGEYLRSQLRAMD      PDRAVEELHITLDHGQTSVSVVMDRRRFVELFTAARHRPLFDEIAGARAEARQSEEGPALAQRLAALSTAERREHLAHLIR      AEVA AVLGHGDDAAIDRDRAFRDLGFDSTAVDLRNRLAAVTGVREAATVVFDHPTITRLADHYLERLVGAAEAEQAPA      LVREVPKDADDPIAIVGMACRFPGGVHNPGELWEFIVGGGDAVTEMPTRDGRWDLDFDPDPQRHGTSYSRHGAFLDGAA      DFDAAFFGISPREALAMDPQQRQVLETTWELFENAGIDPHSLRGSSTGVFLGAAVYQGYGQDAVVPEDSEGILLTGNSAVV      SGRVAVVGLGEPVAVTVDACSSSLVALHSACGLRDGDCGLAVAGGVSVVMAGPEVFTFSRQGGGLAVDGRCKAFSAEAD      GFGFAEGVAVVLLQRLSDARRAGRQVLGVVAGSAINQDASNGLAAPSGVAQQRVIRKAWARAGITGADVAVVEAHGTG      TRLGDPVEASALLATYGKSRGSSGPVLLGSVKSNIHQAAGVAGVIKVVLLGLNRGLVPPMLCRGERSPLIEWSSGGVEL      AEAVSPWPPAADGVRRAGVSAFGVSGTNAHVIIAEPPEPEPLPEPGPVGLAAANSVPVLLSARTETALAAQARLLESVDD      SVPLTALASALATGRAHLPRRAALLAGDHEQLRGLRAVAEGVAAPGATTGTASAGGVVVFVPGQGAQWEGMARGLLSV      PVFAESIAECDAVLSEVAGFSASEVLEQRPDAPSLERVDVVQPVLFSVMVSLARLWGACGVSPSAVIGHSQGEIAAAVVAG      VLSLEDGVRVVALRAKALRALAGKGGMVSLAAPGERARALIAPWEDRISVAAVNSPSSVVVSGDPEALAEVVARCEDEGV      RAKTLPVDYASHSRHVEEIRETILADLDGISARRAAIPLYSTLHGERRDGMGPVRYWYDNLRSQVRFDEAVSAAVADGHA      TFVEMSPHPVLTAAVQEIAADAVAIGSLHRDTAEHLIAELARAHVHGVAVDWRNVFPAAPPVALPNYPFEPQRYWLAVEV      SDQLADSRVVDWRPLATTPVDLEGGFLVHGSAPESLTSAVEKAGGRVVPVASADREALAAALREVPGEVAGVLSVHTGA      ATHLALHQLGEGAVRPLWLVTSTRAVALGESEVPEQAMVWGLGRVMGLETPERWGGLVDLPAEPAPGDGEAFVACL      GADGHEDQVAIRDHARYGRRVLRAPLGTRESSWEPAGTALVTGGTALGGHVARHLARCGVEDLVLVSRRGVDPAGAAE      LEAELVALGAKTTITACDVADREQLSKLLEELRGQRPVVRTVVHTAGVPESRPLHEIGELESVCAAKVTGARLLDELCPDAE      TFVLFSSGAGVWGSANLGAYSAANAYLDALAHRRRAEGRAATSVAWGAWAGEGMATGDLEGLTRRGLRPMAPERAIRA      LHQALDNGDTCVSIADVDERFAVGFTAARPRLLDELVTPAVGAVPAVQAAPAREMTSQELLEFTSHVAAILGHSSPDA      VGQDQPFTELGFDSLTAVGLRNQLQATGLALPATLVFEHPTVRRADHIGQQLDSGTPAREASSALRDGYRQAGVSGRVR      SYDLLAGLSDFREHFDGSDGFSLDLVDMDGPGVETVICCAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYEEGEPLSS      MAVA AVQADAVIRTQGDKPFVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTATLFDRE      TVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPPDSWKPTWPFHDTVAVPGDHFTMVQEHADAIARH      IDAWLGGGNSSSVDKLAAALEHHHHHHH*</p>
<p>MK138  <b>SZ4-L-RIFS (KR1-          ACP1-M2)-TE</b></p>	<p><b>MQKVAELKNRVAVKLNREQLKNKVEELKNRNAYLKNELATLENEVARLENDVAE</b>GGSGGGSGEPAEPASAGDPLLGTV      VSTPGSDRLTAVAQWSRRAQPWAVDGLVPNAALVEAAIRLGDLAGTPVVGELVVDAPVVLPRRGSREVQLIVGEPGEQRR      RPIEVFSREADEPWTRHAHGTLPAAAAVPEPAAAGDATDVTVAGLRDADRYGIHPALLDAAVRTVVGDDLPSVWTGVS      LLASGATAVTVTPTATGLRLTDPAGQPVLTVESVRGTPFVAEQGTTDALFRVDWPEIPLTAETADFLPYEATSAEATLSAL      QAWLADPAETRLAVVTGDCTEPGAAIWLVRSAQSEHPGRIVLADLDDPAVLPVAVASGEPQVRVRNGVASVPRLTRVT      PRQDARPLDPEGTVLITGGTGLGALTARHLVTAHGVRHLVLSRRGEAPELQEELTALGASVAIAACDVADRAQLEAVLR      AIPAEHPLTAVIHTAGVLDGDDGVVTELPDRLATVRRPKVDAARLLDEL TREADLAAFVLFSSAAGVLGNPGQAGYAAANAE      LDALARQRNSLDLPAVSIWGYWATVSGMTEHLGDADLRRNQIRIGMSGLPADEGMALLDAAIATGGTLVAAKFDVAALR      ATAKAGGPVPLLRLGLAPLPRRAAAKTASLTERLAGLAETEQAALLDLVRRHAAEVLGHSGAESVHSGRTFKDAGFDSL      AVELRNRLAAATGLTSPAMIFDYPKPPALADHLRAKLFGSAANRPAEIGTAAAEPIAIVAMACRFPGGVHSPEDLWRLVA      DGADAVTEFPADRGWDTDRLYHEDPDHEGTTYVRHGAFLLDAAAGFDAAFFGISPNEALAMDPQQRLLLETSWELFERAAI      DPTTLAQDIGVFAGVNSHDYSMRMHRAAGVEGFRLTGGSSASVLSGRVAYHFGVEGPAVTVDTACSSSLVALHMAVQAL</p>

	<p>QRGECMALAGGVMVMTVETVFEFSRQRGLAPDGRCKAFADGADGTGWSEGVGLLLVERLSEAQRRGHQVLA VVRGS  AVNSDGASNGLTAPNGPSQQRVIRKALAAAGLSTSDVDAVEAHGTGTTLDGPIEAEALLATYQGNRETPLWLGSVKSNLG  HTQAAAGVAGVIKVMAMRHGVLPRTLHVDRPSSYVDWSAGAVELLTEARDWVSNGHPRRAGVSSFGIGGTNAHVLE  EVAAPITTPQPEAEFLVPVLSARTAAGLRGQAGRLAAFLGDRTDVRVPDAAYALATTRAQLDHRAVVLASDRAQLCAD  LAAFSGSVVTGTPVDGKLAVLFTGQGSQWAGMGRELAETFPVFRDAFEAAACEAVDTHLRERPLREVVFDDSDALLDQTMYT  QGALFAVETALFRLFESWGVPRGLLAGHSIGELAAHVSGVLDLADAGELVAARGRLMQALPAGGAMVA VQATEDEVAP  LLDGTVCVAAVNGPDSVVLSGTEAAVLAVADELAGRGRKTRRLAVSHAFHSPLMEPMLDDFRAVAERLTYRAGSLPVVST  LTGELAALDSPDYWVGQVRNAVRFSDAVTALGAQGASTFLELGPGGALAAALGTLGGPEQSCVATLRKNGAEVDPVLT  ALAEHVVRGVGVDTTTLVDEPATAVGTVLPTYAFQHQRFWVDVDETA AVSVTPPPAEPIVDRPVQDVLELVRESAAVVLG  HRDAGSFDLDRSFKDHGFDSL SAVKLRNRLRDFTGVELPSTLIFDYPNPAVLADHLRAELLSGTPAREASSALRDGYRQAGV  SGRVRSYLDLLAGLSDFREHFDFGSDGFSLDLVD MADGPGEVTVICCAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYEEG  EPLPSSMAAVAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTA  TLFDRETVRMDDTRLTALGAYDRLTGQWRPRETLPLTLLVSAGPEMGPWPDDSWKPTWPFHEHTVA VPGDHFTMVQEHA  DAIARHIDAWLGGGNSSSVDKLA AALEHHHHHHH*</p>
<p>MK141  SZ4-L-KR1-ACPI-  L12-M5-TE</p>	<p><b>MQKVAELKNRVAVKLNREQLKKNVEELKNRNAYLKNELATLENEVARLENDVAE</b>GGSGGGSGDEVSALRYRIEWRPTG  AGEPARLDGTWLVAKYAGTADETSTAAREALESAGARVREL VVDARCGRDELAERLRSVGEVAGVLSLLAVDEAEPEEAP  LALASLADTL SLVQAMVSAELGCPLWTVTESAVATGPFERVRNAAHGALWGVRVIALENPAVWGGLVDVPAGSVAELA  RHAAVVS GGAGEDQLALRADGVYGRWRVRAAAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHLLLVSRS  PDADGAGELVAEALGARTTVAACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIERASRAKVLGA  RNLHEL TRELDLTAFLVLFSSFASAFGAPGLGGYAPGNAYLDGLAQRRSDGLPATAVAWGTWAGSGMAEGPVADRFRRH  GVIEMPPETACRALQNALDRAEVCPIVIDVRWDRFLLAYTAQRPTRLFDEIDDARRAAPQAAAEPVGAHMLASLPAPERE  KALFELVRSHAAAVLGHASAERVPADQAFaelGVDSLSALELRNRLGAATGVRLPTTTVFDHPDVRTLAAHLAAELGGAT  <b>GAEQAAPATTAPVDEPIAIVGMACRFPGDVDSPEFWEFVSGGDAIAEAPADRGWEPDPDARLGGMLAAAGDFDAGFFGI</b>  SPREALAMPQQRIMLEISWEALERAGHDPVSLRGSATGVFTGVGTVDYGPRPDEAPDEV LGYVGTGTASSVASGRVAYCL  GLEGPAMTVDTACSSGLTALHLAMESLRRDECGLALAGGVTVMSSPGAFTEFRSQGGLAADGRCKPFSKAADGFGLAEGA  GVLVLQRLSAARREGRPVLA VLRGS AVNQDGASNGLTAPSGPAQQRVIRRALENAGVRAGVDYVEAHGTGTRLGDPIEV  HALLSTYGAERDPDDPLWIGSVKSNIGHTQAAAGVAGVMKAVLALRHGEMPRTLHFDEPSPQIEWDLGAVSVVSQARSWP  AGERPRRAGVSSFGISGTNAHVIVEEAPEADEPEPAPDSGPVPLVLSGRDEQAMRAQAGRLADHLAREPRNSLRDTGFTLAT  RRSAWEHRAVVVGDRDDALAGLRAVADGRIADRTATGQARTRRGVAMVFPGQGAQWQGMARDLLRESQVFADSIRDCE  RALAPHVDWSLTDLLSGARPLDRVDVVQPALFAMVSLAALWRSHGVPEAAVVGHSQGEIAAAHVAGALTLEDAAKLVA  VRSRVLRLGGQGMASFGLGTEQAERIGRFAGALSIVNGPRS VVVAGESGPLDELIAECEAEGITARRIPVDYASHSPQ  VESLREELLTELAGISPVADVALYSTTTGQPIDTATMDTAYWYANLREQVRFQDATRQLAEAGFD AFVEVSPHPVLTVGIE  ATLDSALPADAGACVVGTLRRDRGGLADFHTALGEAYAQGV EVDWSPAFADARPVELPVYPFQRQRYWLPIPTGGRARDE  DDDWRVYQVWREAEWESASLAGRVLLVTGPGVPSELSDAIRSGLEQSGATVLTCDVESRSTIGTALEAADTDALSTVVSL  SRDGEAVDPSLDALALVQALGAAGVEAPLWVLRNAVQVADGELVDP AQAMVGGGLGRVVGIEQPGRWGGVLDLVDADA  ASIRSLAAVLADPRGEEQVAIRADGIKVARLVPAPARAARTRWSPRGTVLVTGGTGGIGAHVARWLARSGAEHLVLLGRR  GADAPGASELREELTALGTGV TIAACDVADRARLEAVLAAERAEGRTVSAMMHAAGVSTSTPLDDLTEAEFTIADV KVRG  TVNLDELCPDLDAFVLFSSNAGVWSPGLASYAANAFLDGFARRRRSE GAPVTSIAWGLWAGQNMAGDEGGEYLR SQ  LRAMPDRAVEELHITLDHGQTSVSVVMDRRRFVELFTAARHRPLFDEIAGARAEARQSEEGPALAQR LAALSTAERREH  LAHLIRAEVAAVLGHGDDAAIDRDRAFRDLGFDSMTAVDLRNRLAAVTGVREAA TVVFDHPTITRLADHYLERLVSGTPA</p>

	REASSALRDGYRQAGVSGRVRSYDLLAGLSDFREHFDGSDGFSLDLVDMDADGPGEVTVICCAAGTAAISGPHEFTRLAGAL RGIAPVRAVPQPGYEEGEPLPSSMAAVAAVQADAVIRTQGDKPFVAVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYP PGHQDAMNAWLEELTATLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFHEH TVAVPGDHFTMVQEHADAIARHIDAWLGGGNSSSVDKLAAALEHHHHHH*
MK142 SZ4-L-KR1-ACPI- L12-M6-TE	MQKVAELKNRVAVKLNREQLKKNVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGDEVSALRYRIEWRPTG AGEPARLDGTWLVAKYAGTADETSTAAREALESAGARVRELVVDARCGRDELAERLRSVGEVAGVLSLLAVDEAEPEEAP LALASLADTSLVQAMVSAELGCPLWTVTESAVATGPFERVRNAAHGALWGVGRVIALENPAVWGGLVDVPAGSVAELA RHLAAVVS GGAGEDQLALRADGVYGRWRVRAAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHLLLVSRS PDADGAGELVAELEALGARTTVAACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIERASRAKVLGA RNLHEL TRELDLTAFLVLFSSFASAFGAPGLGGYAPGNAYLDGLAQRRSDGLPATAVAWGTWAGSGMAEGPVADRFRH GVIEMPPETACRALQNALDRAEVCPIVIDVRWDRFLAYTAQRPTLFDIIDDARRAAPQAAAEPVGAHMLASLPAPERE KALFELVRSHAAAVLGHASAERPADQAFaelGVDSLaleLRNRLGAATGVRLPTTTVFDHPDVRTLAAHLAAELGGAT GAEQAAPATTAPVDDPIAIVGMACRFPGGVHNPGELEWEIFVGGGDAVTEMPTDRGWLDLALFDPPQRHGTSYSRHGAFL DGAADFDAAFFGISPREALAMDPQQRQVLETTWELFENAGIDPHSLRGS DTGVFLGAA YQGYGQDAVVPEDSEGYLLTGN SSAVVSGRVAYVVLGLEGPAVTVDTACSSSLVALHSACGSLRDGDCGLAVAGGV SVMAGPEVFTEFSRQGLAVDGRCKAF SAEADGFGFAEGVAVVLLQRLSDARRAGRQVLGVVAGSAINQDGASNGLAAPSGVAQQRVIRKAWARAGITGADVAVVE AHGTGTRLDGPVEASALLATYGKSRGSSGPVLLGSVKSNIHQAAAGVAGVIKVV LGLNRGLVPPMLCRGERSPLIEWSS GGVELAEAVSPWPPAADGVRRAGVSAFGVSGTNAHVIIAEPPEPEPEPPEPGLAAANSVPVLLSARTETALAAQARLLE SAVDDSVPLTALASALATGRAHLPRRAALLAGDHEQLRGLRAVAEGVAAPGATTGTASAGGVVVFVFPQGAQWEGMAR GLLSVPVFAESIAECDAVLSEVAGFSASEVLEQRPDAPSLERVDVVPVLFVSVMSLARLWGACGVSPSAVIGHSQGEIAAA VVAGVLSLEDGVRVVALRAKALRALAGKGMVSLAAPGERARALIAPWEDRISVAAVNSPSSVVVSGDPEALAEVARCE DEGVRAKTLPVYASHSRHV EIRETILADLDGISARRAAIPLYSTLHGERRDGADMGPVRYWYDNLRSQVRFDEAVSAAVA DGHATFVEMSPHPVLTAAVQEIADAVAIGSLHRDTAEELHIAELARAHVHGVAVDWRNVFPAAPPVALPNYPFEPQRYW LAPEVSDQLADSRVVDWRPLATTPVDLEGGFLVHGSAPESLTSAVEKAGGRVVPVASADREALAAALREVPGEVAGVLS VHTGAATHLALHQLSLGEAGVRAPLWLVTSTRAVALGESEPVDPQAMVWGLGRVMGLETPERWGGVLDLPAEPAPGDGE AFVACL GADGHEDQVAIRDHARYGRRVLRAPLGTRESSWEPAGTALVTGGTGALGGHVARHLARCGVEDLVLSRRGVD APGAAELEAELVALGAKTTITACDVADREQLSKLLEELRGQGRPVRTVVHTAGVPESRPLHEIGELESVCAAKVTGARLLD ELCPDAETVLFSSGAGVWGSANLGAYSANAYLDALAHRRRAEGRAATSVAWGAWAGEGMATGDLEGLTRRGLRPM PERAIRALHQALDNGDTCVSIADV DWERFVAGFTAARPRLLDELVTPAVGAVPAVQAAPAREMTSQUELLEFTHSHVAAIL GHSSPDVAVGQDQPTELGFDSLTAVGLRNQLQATGLALPATLVFEHPTVRRADHIGQQQLDSGTPAREASSALRDGYRQA GVSGRVRSYDLLAGLSDFREHFDGSDGFSLDLVDMDADGPGEVTVICCAAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGY EGEPLPSSMAAVAAVQADAVIRTQGDKPFVAVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEEL TATLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFHEHTVAVPGDHFTMVQE HADAIARHIDAWLGGGNSSSVDKLAAALEHHHHHH*
MK147 SZ4-L-M6-TE	MQKVAELKNRVAVKLNREQLKKNVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGKLDPIAIVGMACRFPG GVHNPGELEWEIFVGGGDAVTEMPTDRGWLDLALFDPPQRHGTSYSRHGAFLDGAADFDAAFFGISPREALAMDPQQRQV LETTWELFENAGIDPHSLRGS DTGVFLGAA YQGYGQDAVVPEDSEGYLLTGNSSAVVSGRVAYVVLGLEGPAVTVDTACSS LVALHSACGSLRDGDCGLAVAGGV SVMAGPEVFTEFSRQGLAVDGRCKAFSAEADGFGFAEGVAVVLLQRLSDARRAG RQVLGVVAGSAINQDGASNGLAAPSGVAQQRVIRKAWARAGITGADVAVVEAHGTGTRLDGPVEASALLATYGKSRGSS GPVLLGSVKSNIHQAAAGVAGVIKVV LGLNRGLVPPMLCRGERSPLIEWSSGGVELAEAVSPWPPAADGVRRAGVSAF



	<p>GVSQTNAHVIIAEPPEPEPLPEPGPVGVLAANSVPVLLSARTETALAAQARLLESVDDSVPLTALASALATGRAHLPRRA  ALLAGDHEQLRQQLRAVAEGVAAPGATTGTASAGGVVFPFGQGAQWEGMARGLLSVPVFAESIAECDAVLSEVAGFSAS  EVLEQRPDAPSLERVDVVQPVLFSVMVSLARLWGACGVSPSAVIGHSQGEIAAAVVAGVLSLEDGVRVVALRAKALRALA  GKGGMVSLAAPGERARALIAPWEDRISVA AVNSPSSVVVSGDPEALAEVVARCEDEGVRAKTLPVVYASHSRHVEEIRETIL  ADLDGISARRAAIPLYSTLHGERRDGDADMGPVRYWYDNLRSQVRFDEAVSAAVADGHATFVEMSPHPVLTAAVQEIADA  AIGSLHRDTAEHLIAELARAHVHGVAVDWRNVFPAAPPVALPNYPFEPQRYWLAPEVSDQLADSRYRVDWRPLATTPVD  LEGGFLVHGSAPESLTSAVEKAGGRVVPVASADREALAAALREVPGEVAGVLSVHTGAATHLALHQSLEAGVRAPLWL  TSRAVALGESEPVDPQAMVWGLGRVMGLETPERWGGGLVDLPAEPAPGDGEAFVACLADGHEDQVAIRDHARYGRRLV  RAPLGTRESSWEPAGTALVTGGTGALGGHVARHLARCGVEDLVLSRRGVDAPGAAEAELEALVALGAKTTITACDVADRE  QLSKLLEELRQGRPVRTVVHTAGVPESRPLHEIGELESVCAAKVTGARLLDELCPDAETVFLFSSGAGVWGSANLGAYSA  ANAYLDALAHRRRAEGRATSVAWGAWAGEGMATGDLEGLTRRGLRPMAPERAIRALHQALDNGDTCVSIADVWERF  AVGFTAARPRLLDELVTPAVGAVPAVQAAPAREMTSQUELLEFTHSHVAAILGHSSPDAVGQDQPFTELGFDSLTA  VGLRNQLQATGLALPATLVFEHPTVRRADHIGQQLDSTPAREASSALRDGYRQAGVSGRVRSYLDLLAGLSDFREHFDGSDGF  SLDLVDMADGPGEVTVICCAAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYEEGEPLPSSMAAVAAVQADAVIRTQGD  KPFVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTATLFDRETVRMDDTRLTALGAYDRLTG  QWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFHDTVA VPGDHFTMVQEHADAIARHIDAWLGGGNSKLAAALEHHH  HHH*</p>
<p>MK148  SZ4-L-M2-TE</p>	<p><b>MQKVAELKNRVAVKLNREQLKNKVEELKNRNAYLKNELATLENEVARLENDVAE</b>GGSGGGSGKLEPIAIVGMACRLPG  EVDSPERLWELITSGRDSAAEVPDDRGWVPELMAASDAAGTRRAHGNFMAGAGDFDAFFGISPREALAMDPQORQALET  TWEALESAGIPPETLRGSDTG VFGMSHQYATGRPRPEDGVDGYLLTGNTASVASGRIAYVLGLEGPAITVDTACSSSLV  ALHTACGLRDGDCGLAVAGGVSMAGPEVTFESRQGALSPDGRCKPFSDEADGFGLEGSAFVVLQRLSDARREGRRV  LGVVAGSAVNQDGASNGLSAPSGVAQQRVIRRAWARAGITGADVAVVEAHGTGTRLGDPVEASALLATYGKSRGSSGPV  LLGSVKSNIHAQAAAGVAGVIKVLGLERGVVPPMLCRGERSGLIDWSSGEIELADGVREWSPAADGVRRAVSAFGVS  GTNAHVIIAEPPEPEPVQPRRMLPATGVVPPVLSARTGAALRAQAGRLADHLAAHPGIAPADVSWTMARARQHFEERAA  VLAADTAEAVHRLRAVADGAVVPGVVTGSASDGGSVFVFPFGQGAQWEGMARELLPVPVFAESIAECDAVLSEVAGFSVSE  VLEPRPDAPSLERVDVVQVLFVAVMVSLARLWRACGAVPSAVIGHSQGEIAAAVVAGALSLEDGMRVVARRSRAVRAVA  GRGSMLSVRGGRSVDEKLLADDSWTGRLEVA AVNGPDAVVVAGDAQAAREFLEYCEGVGIRARAIPVDYASHTAHVEPV  RDELVQALAGITPRRAEVPFFSTLTGDFLDGTELDAGYWYRNLRHPVEFHSVAVQALTDQGYATFIEVSPHPVLASSVQETLD  DAESDAAVLGTLERDAGDADRFLTALADAHTRGVAVDWEAVLGRAGLVDLPGYPFQGKRFWLLPDRTPRDELDTGWFYR  VDWTEVPRSEPAALRGRWL VVVPEGHEEDGWTVEVRSALAEAGAEPEVTRGVGGLVGDCAGVVSLLALEGDGA VQTLVL  VREDAEGIDAPLWTVTFGAVDAGSPVARPDQAKLWGLGQVASLERGPRWTGLVDLPHMPDPELRGRLTAVLAGSEDQV  AVRADAVRARRLSPAHTATSEYAVPGGTILVTGGTAGLGAEVARWLAGRGAEHLALVSRGPDTEGVGDLTAELTRLGA  RVSVHACDVSSREPVELVHGLIEQGDVVVRGVVHAAGLPQQVAINDMDEAAFDEVVAAKAGGAVHLDELCSDAELFLFS  SGAGVWGSARQGAYAAGNAFLDAFARHRRRGLPATSVAWGLWAAGGMTGDEEAVSFLRERGVRAAMPVPRALALDR  VLASGETAVVVTVDVWPAFAESYTAARPRLLDRIVTTAPSERAGEPETESLRDRLAGLPRAERTAELVRLVRTSTATVLGH  DDPKAVRATTPFKELGFDSLAAVRLRNLLNAATGLRPLSTLVFDHPNASAVAGFLTSELGSGTPAREASSALRDGYRQAGV  SGRVRSYLDLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVICCAAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYEEG  EPLPSSMAAVAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELT  ATLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFHDTVA VPGDHFTMVQEH  ADAIARHIDAWLGGGNSKLAAALEHHHHHHH*</p>

<p>MK149 SZ4-L-M3-TE</p>	<p>MQKVAELKNRVAVKLNREQLKKNKVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGKLDPIAIVSMACRLPG  GVNTPQRLWELLREGGETLSGFPTDRGWDLARLHHPDPNDPNTSYPVDKGGFLDDAAGFDAAEFFGVSPREAAAMDPQQRLL  LETSWELVENAGIDPHSLRGTATGVFLGVAKFGYGEDTAAAEDVEGYSVTGVAPAVASGRISYTMGLEGPSISVDTACSSSL  VALHLAVESLRKGESSMAVVGGAAVMATPGVFVDFSRQRALAADGRSKAFGAGADGFGFSEGVTLLVLLERLSEARRNGH  EVLAVVRGSALNQDGASNGLSAPSGPAQRRVIRQALESGLPEGDVDAVEAHGTGTALGDPIEANALLDITYGRDRDADRP  LWLGSVKSNIIGHTQAAAGVTGLLKVVLLALRNGELPATLHVEEPTPHVDWSSGGVALLAGNQPWRRGERTRRARVSAFGIS  GTNAHVIVEEAPEREHRETTAHDGRPVPLVVSARTTAALRAQAAQIAELLERPDADLAGVGLGLATTRARHEHRAAVVAST  REEAVRGLREIAAGAATADAVVEGVTEVDGRNVVFLFPGQGSQWAGMGAELLSSSPVFAGKIRACDESMAPMQDWKVS  VLRQAPGAPGLDRVDVVPVLFVAVMVSLAELWRSYGVPEAAVVGHSQGEIAAAHVAGALTLEDAAKLVVGRSRLMRSLS  GEGGMAAVALGEEAVRERLRPWQDRLSVAAVNGPRSVVVSVEGPGALRAFSEDCAAEGIRVRDIDVDYASHSPQIERVREE  LLETTGDIAPRPARVTFHSTVESRSMGTELDARYWYRNLRETVRFADAVTRLAESGYDAFIEVSPHPVVVQAVEEAVEEA  DGAEDAVVVGSLHRDGGDLAFLRSMATAHVSGVDIRWDVALPGAAPFALPTYPFQRKRYWLQPAAPAAASDELAYRVS  WTPIEKPESGNLDGDWLVVTPPLISPEWTEMLCEAINANGGRALRCEVDTSASRTEMAQAVAQAGTGFRGVLSLLSSDESAC  RPGVPAGAVGLLTLVQALGDAGVDAPVWCLTQGAVRTPADDDLARPAQTTAHGFAQVAGLELPGRWGGVVLDLPEVDD  AALRLLVAVLRGGGRAEDHLAVRDGRLHGRRVVRASLPQSGRSWTPHGTVLVTGAASPVGDQLVRWLADRGAERLVL  GACPGDDLLAAVEEAGASAVVCAQDAAALREALGDEPVTALVHAGTLTNFGSISEVAPEEFAETIAAKTALLAVLEL  RAVEREYVCSSVAGIWGGAGMAAYAAGSAYLDALAEHHRARGRSCTSVAWTPWALPGGAVDDGYLRERGLRSLSDRA  MRTWERVLAAGPVSVAADVDWPVLESEGFAATRPTALFAELAGRGGQAEAEPSGPTGEPAQRLAGLSPDEQQENLELV  ANAVAEVLGHESAAEINVRRAFSELGLDSLNAMALRKRLSASTGLRLPASLVFDHPTVTLAQLHLSQLDSGTPAREASSAL  RDGYRQAGVSGRVRSYLDLLAGLSDFREHFDGSDGFSLDLVDMDGPGEVTVICCAGTAAISGPHEFTRLAGALRGIAPVR  AVPQPGYEEGEPLPSSMAA VAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPPRGVVLDVYPPGHQDA  MNAWLEELTATLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPPDSWKPTWPFHDTVAVPG  DHFTMVQEHADAIARHIDAWLGGGNSKLAALAEHHHHHHH*</p>
<p>MK150 (5)M1-L-SZ3</p>	<p>MSGDNGMTEEKLRRYLKRTVTELDVSTARLREVEHRAGEPVAVAMACRLPGGVSTPEEFWELLSEGRDAVAGLPTDRG  WLDLSLFHPDPTRSGTAHQGGGFLTEATAFDPAFFGMSPREALAVDPQQRMLLELSWEVLERAGIPPTSLOASPTGVFVGL  IPQEYGPRLAEGGEGVEGYLMTGTTTASVAGRIAYTLGLEGPAISVDTACSSSLVAVHLACQSLRRGESSLAMAGGVTVMPT  PGMLVDFSRMNSLAPDGRCKAFSAGANGFGMAEGAGMLLLERLSDARRNGHPVLAVLRGTAVNSDGASNGLSAPNGRAQ  VRVIQALAESGLPADIDAVEAHGTGTRLGDPIEARALFEAYGRDREQLHLGVSXSNLGHGTQAAAGVAGVIKMLAMR  AGTLPRTLHASERSKEIDWSSGAISLLDEPEPWPAGARPRRAGVSSFGISGTNAHAHIEEAPQVVEGERVEAGDVVAPWVLSA  SSAEGLRQAARLAAHLREHPGQDPRDIAYSLATGRAALPHRAAFAPVDESAALRVLDGLATGNADGAAVGTSAQQRAV  FVFPQGWQWAGMAVDLLDTSPVFAAALRECADALEPHLDFEVIPFLRAEAARREQDAALSTERVDVVQPMFVAVMVS  ASMWRAHGVPEAAVIGHSQGEIAAACVAGALSLDDAARVVALRSRVIAATMPGNKGMASIAAPAGEVRARIGDRVEIAAVN  GPRSVVVAGDSDELDRLVASCTTECIRAKRLAVDYASHSSHVETIRDALHAELGEDFHPLPGFVPPFFSTVTGRWTQPELDA  GYWYRNLRRTVRFADAVRALAEQGYRTFLEVSAPILTAHIEEIGDGGADLSAIHSLRRGDGSLADFGAALSRAFAAGVA  VDWESVHLGTGARRVPLPTYPFQRERVWLEPKPVARRSTEVDEVSALRYRIEWRPTGAGEPARLDGTWLVAKYAGTADET  STAAREALESAGARVRELVVDARCGRDELAERLRSVGEVAGVLSLLAVDEAEPEEAPLALASLADTSLVQAMVSAELGCP  LWTVTESAVATGPFERVRNAAHGALWGVRVIALENPAVWGGGLVDVPAGSVAELARHLAAVVS GGAGEDQLALRADGV  YGRRWVRAAAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHLLVSRSGPDADGAGELVAEALGARTTVA  ACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIERASRAKVLGARNLHEL TRELDLTAFLVLFSSFAAF  GAPGLGGYAPGNAYLDGLAQRRSDGLPATAVAWGTWAGSGMAEGPVADRFRRHGVIEMPPETACRALQNALDRAEVC</p>

	<p>PIVIDVRWDRFLLAYTAQRPTLRFDEIDDARRAAPQAAAEPVVGALASLPAPERKALFELVRSAAAFLGHASAERVPAD  QAFaelGVDSLSaleLRNRLGAATGVRLPTTTVFDHPDVRTLAAHLAAELGGGSGGGSGNEVTTLENDAAFIENENAYLEK  EIARLRKEKAALRNRLAHKKLEHHHHHH*</p>
<p>MK152  SZ4-L-KR1-ACP1-  L12-M3-TE</p>	<p>MQKVAELKNRVAVKLNREQLKKNVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGDEVSALRYRIEWRPTG  AGEPARLDGTWLVAKYAGTADETSTAAREALESAGARVREL VVDARCGRDELAERLRSVGEVAGVLSLLAVDEAEPEEAP  LALASLADTSLVQAMVSAELGCPLWTVTESAVATGPFERVRNAAHGALWGVGRVIALENPAVWGGLVDVPAGSVAELA  RHLAAVVSGGAGEDQLALRADGVYGRRWVRAAAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHLLLVSRS  PDADGAGELVAELEALGARTTVAACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIERASRAKVLGA  RNLHEL TRELDLTAFLVLFSSFASAFGAPGLGGYAPGNAYLDGLAQRRSDGLPATAVAWGTWAGSGMAEGPVADRFRH  GVIEMPPETACRALQNALDRAEVCPIVIDVRWDRFLLAYTAQRPTLRFDEIDDARRAAPQAAAEPVVGALASLPAPER  KALFELVRSAAAFLGHASAERVPADQAFaelGVDSLSaleLRNRLGAATGVRLPTTTVFDHPDVRTLAAHLAAELGGAT  GAEQAAPATTAPVDDPIAIVSMACRLPGGVNTPQRLWELLREGGETLSGFPTDRGWDLARLHHPDPDPNGTYSYVDKGGFLD  DAAGFDAEFFGVSPREAAAMPDQQRLLLETSWELVENAGIDPHSLRGTATGVFLGVAKFGYGEDTAAAEDEVEGYSVTGVA  PAVASGRISYTMGLEGPSISVDTACSSSLVALHLAVESLRKGESSMAVVGGAAVMATPGVFVDFSRQRALAADGRSKAFGA  GADGFGFSEGVTLVLLERLSEARRNGHEVLA VVRGSALNQDGASNGLSAPSGPAQRRVIRQALESGLPEGDVDAVEAHGT  GTALGDPIEANALLD TYGRDRADRPLWLGSVKSNIGHTQAAAGVTGLLKVV LALRNGELPATLHVEEPTPHVDWSSGGV  ALLAGNQPWRRGERTRRARVSAFGISGTNAHVIVEEAPEREHRETTAHDGRPVPLVVSARTTAALRAQAQIAELLERPD  DLAGVGLGLATTRARHEHRAAVVASTREEAVRGLREAAGAATADAVVEGVTEVDGRNVVFLFPGQGSQWAGMGAEELS  SSPVFAGKIRACDESMAPMQDWKVS DVL RQAPGAPGLDRVDVQPVLFVVMVSLAELWRSYGVPEAAVVGHSQGEIAAA  HVAGALTLEDAAKLVVGRSRLMRSLSGEGMAAVALGEAAVRERLRPWQDRLSVAAVNGPRSVVSGEPGALRAFSEDC  AAEGIRVRDIDVDYASHSPQIERVREELLETTGDIAPRPARVTFHSTVESRSMDGTELDARYWYRNLRETVRFADAVTRLAE  SGYDAFIEVSPHPVVVQAVEEAVEEADGAEDAVVVGSLHRDGGDLAFLRSMATAHVSGVDIRWDVALPGAAPFALPTYP  FQRKRYWLQPAAPAAASDELAYRVS WTPIEKPESGNLDGDWL VVTPLISPEWTEMLCEAINANGGRALRCEVDTSASRTE  MAQAVAQAGTGFRGVLSLLSSDESACRPGVPAGAVGLLTLVQALGDAGVDAPVWCLTQGAVRTPADDDLARPAQTTAHG  FAQVAGLELPGRWGGVVDLPESVDDAALRLLVAVLRGGGRAEDHLAVRDGRLHGRRVRASLPQSGSRSWTPHGTVLVT  GAASPVGDQLVRWLADRGAERLVLGACPGDDLLAAVEEAGASAVVCAQDAAALREALGDEPVTALVHAGTLTNFGSIS  EVAPEEFAETIAAKTALLAVLDEVLGDRAVEREVYCSSVAGIWWGAGMAAYAAGSAYLDALAEHHRARGRSCTSVAWTP  WALPGGAVDDGYLRERGLRSLSADRAMRTWERVLAAGPVSVAVADVDPVLPVLESEGFAATRPTALFAELAGRGGQAEAE  DSGPTGEPAQRLAGLSPDEQENLLELVANAVAEVLGHESAAEINVRRAFSELGLDSLNAMALRKRLSASTGLRPLASL VFD  HPTVTALAQHLSQLDSGTPAREASSALRDGYRQAGVSGR VRSYDLLAGLSDFREHFDGSDGFSLDL VDMADGPGEVTVI  CCAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYEEGELPSSMAA VAVQADAVIRTQGD KPFV VAGHSAGALMAYAL  ATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTATLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAG  EPMGPWPDSSWKPTWPFHDTVA VPGDHFTMVQEHADAIARHIDAWLGGGNSSSVDKLAAALEHHHHHHH*</p>
<p>MK168  SZ4-L-KR5-ACP5(2)</p>	<p>MQKVAELKNRVAVKLNREQLKKNVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGPIPTGGRARDEDDDW  RYQVVWREA EWESASLAGRVLLVTGPGVPSSELSDAIRSGLEQSGATVLTCDVESRSTIGTAL EAADTDALSTVVSLLSRDGE  AVDPSLDALALVQALGAAGVEAPLWVLRNAVQVADGELVDPAQAMVGGGLGRVVGIEQPGRWGGGLVDLVDADAASIRS  LAAVLADPRGEEQVAIRADGIKVARLVPAPARAARTRWSPRGTVLVTGGTGGIGAHVARWLARSGAEHLVLLGRRGADAP  GASELREELTALGTGVTIAACDVADRARLEAVLAAERAEGRTVSAMHAAAGVSTSTPLDDLTEAEFTEIADV KVRGTVNLD  ELCPDLDAFVLFSSNAGVWGSPLASYAAAANAFLDGFAARRRSE GAPVTSIAWGLWAGQNMAGDEGGEYLR SQGLRAMD  PDRAVEELHITLDHGQTSVSVVDMDRRRFVELFTAARHRPLFDEIAGARAEARQSEEGPALAQRLAALSTAERREHLAHLIR</p>

	<p>AEVAAVLGHGDDAAIDRDRAFRDLGFDSMTAVDLRNRLAAVTGVREAATVVFHDPTITRLADHYLERLVGTEVRGEAPSA LAGLDALEAALPEVPATEREELVQRLERMLAALRPVAQAADASGTGANPSGDDLGEAGVDELLEALGRELDGDPNSSSSVD KLA AALEHHHHHHH*</p>
<p>MK169 SZ4-L-RIFS(KR1- ACP)(2)</p>	<p>MQKVAELKNRVAVKLNREQLKKNVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGGEPAPASAGDPLLGTV VSTPGSDRLTAVAQWSRRAQPWAVDGLVPNAALVEAIRLGDLAGTPVVGELVVDAPVVLPRRGSREVQLIVGEPGEQRR RPIEVFSREADEPWTRHAHGTLPAAAAVPEPAAAGDATDVTVAGLRDADRYGIHPALLDAAVRTVVGDDLLPSVWTGVS LLASGATAVTVTPTATGLRLTDPAGQPVLTVESVRGTPFVAEQGTTDALFRVDWPEIPLPTAETADFLPYEATSAEATLSAL QAWLADPAETRLAVVTGDCTEPGAAAIWGLVRSQAQSEHPGRIVLADLDDPAVLPVAVASGEPQVRVRNGVASVPRLTRVT PRQDARPLDPEGTVLITGGTGLGALTARHLVTAHGVRHLVLSRRGEAPELQEELTALGASVAIAACDVADRAQLEAVLR AIPAEHPLTAVIHTAGVLDDGVVTELTDPRLATVRRPKVDAARLLDEL TREADLA AFVLFSSAAGVLGNPQGAGYAAANAE LDALARQRNSLDLPAVSIAWGYWATVSGMTEHLGDADLRRNQIRIGMSGLPADEGMALLDAAIATGGTLVAAKFDVAALR ATAKAGGPVPLLRLGLAPLPRRAAAKTASLTERLAGLAETEQAALLDLVRRHAAEVLGHSGAESVHSGRTFKDAGFDSL AVELRNRLAAATGLTSPAMIFDYPKPPALADHLRAKLFGTEVRGEAPSA LAGLDALEAALPEVPATEREELVQRLERMLA ALRPVAQAADASGTGANPSGDDLGEAGVDELLEALGRELDGDPNSSSSVDKLA AALEHHHHHHH*</p>
<p>MK170 SZ4-L-M5-TE</p>	<p>MQKVAELKNRVAVKLNREQLKKNVEELKNRNAYLKNELATLENEVARLENDVAEGGSGGGSGKLEPIAIVGMACRFPG DVDSPEFWEFVSGGDAIAEAPADRGWEPDPDARLGGMLAAAGDFDAGFFGISPREALAMDPQQRIMLEISWEALERAG HDPVSLRGSATGVFTGVGTVDYGPRPDEAPDEVLYGVGTGTASSVASGRVAYCLGLEGPAMTVDTACSSGLTALHLAMES LRRDECGLLAGGVTVMSSPGAFTEFRSQGGLAADGRCKPFSKAADGFGLAEGAGVVLQRLSARREGRPVLAVLRGSA VNQDGASNGLTAPSGPAQQRVIRRALENAGVRAGDVYVEAHGTGTRLGDPVHALLSTYGAERDPPDPLWIGSVKSNIG HTQAAAGVAGVMKAVLALRHGEMPRTLHFDEPSPQIEWDLGAVSVVSQARSVPAGERPRRAGVSSFGISGTNAHVIVEEA PEADEPEPAPDSGPVPLVLSGRDEQAMRAQAGRLADHLAREPRNSLRDTGFTLATRRSAWEHRAVVVGDRDDALAGLRAV ADGRIADRTATGQARTRRGVAMVFPQGGAQWQGMARDLLRESQVFADSIRD CERALAPHVDWSLTDLLSGARPLDRVDV VQPALFAMVSLAALWRSHGVEPAAVVGHSQGEIAAAHVAGALTLEDAAKLVAVRSRVLRRGGQGGMASFGLGTEQA AERIGRFAGALSIVNGPRSVVAGESGPLDELIAECEAEGITARRIPVDYASHSPQVESLREELLTELAGISPVSAVALYST TTGQPIDTATMDTAYWYANLREQVRFQDATRQLAEAGFDFVEVSPHPVLTVGIEATLDSALPADAGACVVGTLRRDRGG LADFHTALGEAYAQGVVDWSPAFADARPVELPVYFQRQRYWLPIPTGGRARDEDDDWRYQVWVWREAEWESASLAGR VLLVTGPGVPSSELSAIRSGLEQSGATVLTCDVESRSTIGTALAAADTDALSTVVSLLSRDGEAVDPSLDALALVQALGAAG VEAPLWVLTRNAVQVADGELVDPAQAMVGGGLR VVGIEQPGRWGGGLVDLVDADAASIRSLAAVLADPRGEEQVAIRADG IKVARLVPAPARAARTRWSPRGTVLVTGGTGGIGAHVARWLARSGAEHLVLLGRRGADAPGASELREELTALGTGVTIAA CDVADRARLEAVLAAERAEGRTVSAVMHAAGVSTSTPLDDLTEAEFTEIADVKVRGTVNLDELCPDLDAFVLFSSNAGVW GSPGLASYAAANAFLDGFARRRRSEGAPVTSIAWGLWAGQNMAGDEGGEYLSQGLRAMDPDRAVEELHITLDHGQTSV SVVDMDRRRFVELFTAARHRPLFDEIAGARAEARQSEEGPALAQLAALSTAERREHLAHLIRA EVA AVLGHGDDAAIDRD RAFRDLGFDSMTAVDLRNRLAAVTGVREAATVVFHDPTITRLADHYLERLVSGTPAREASSALRDGYRQAGVSGR VRSYL DLLAGLSDFREHFDGSDGFSLDLVD MADGPGEVTVICCAAGTAAISGPHEFTRLGALRGIAPVRAVPQGYEEGEPLPSSMA AVAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTATLFDRETV RMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEMGPWPDDSWKPTWPFEHDTVA VPGDHFTMVQEHADAIARHID AWLGGGNSKLA AALEHHHHHHH*</p>

**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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