

# Electronic Supporting Information

## Challenges and advances in genetic manipulation of filamentous actinomycetes – the remarkable producers of specialized metabolites

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**Table S1: List of plasmids according to the *Streptomyces/E. coli* replicon, transposon elements and functions. Selected examples are reported with their properties**

1. Integrating shuttle plasmids				
E. coli replicon	Plasmid	Features	Comments	References
pUC18	pIJ8600	8.1 kb, <i>oriT</i> RK2, <i>int</i> $\Phi$ C31, <i>attP</i> $\Phi$ C31, $P_{tipA}$ , <i>t0</i> (terminator from phage $\lambda$ ), <i>tsr</i> , <i>acc(3)IV</i>	expression vector (gene expression under the control of the thiostrepton-inducible $P_{tipA}$ )	<sup>1</sup>
pUC18	pIJ8630 and pIJ8660	7.7 kb, <i>int</i> $\Phi$ C31, <i>acc(3)IV</i> , <i>oriT</i> RK2, <i>egfp</i>	pIJ8600-derivatives, in which the $P_{tipA}$ promoter was deleted and <i>egfp</i> was inserted to be used as indicator	<sup>1; 2, 3</sup>
pIC20R	pKT02	6.078 kb, <i>int</i> VWB, <i>attP</i> (VWB), <i>tsr</i> , <i>bla</i>	- integrating vector derived from phage VWB from <i>S. venezuelae</i> - integration into the tRNA <sup>Arg</sup>	<sup>4; 5</sup>
pUC18	pMT3226	8.4 kb, <i>oriT</i> RK2, <i>attP</i> $\Phi$ C31, <i>int</i> $\Phi$ C31, <i>gylR</i> , <i>xylE</i> , <i>fdt</i> , <i>bla</i>	- integrating expression vector, <i>gylR</i> -cassette for glycerol - inducible gene expression	<sup>6</sup>
pUC18	pSET152	5.5 kb, <i>oriT</i> RK2, <i>attP</i> ( $\Phi$ C31), <i>int</i> $\Phi$ C31, <i>lacZα</i> , MCS, <i>oriT</i> ,	derived from $\Phi$ C31 phage	<sup>7; 8</sup>
pBR322	pOJ436	11.1 kb, <i>oriT</i> RK2, <i>acc(3)IV</i> , <i>attP</i> ( $\Phi$ C31), <i>int</i> $\Phi$ C31, $P_{T7}$ / $T3$ (promoters), <i>cos</i> sites,	derived from $\Phi$ C31 phage	<sup>7; 9; 10; 11</sup>
pBR327	pIJ4201 pIJ4210	8.1 kb, <i>IS117</i> derivatives, <i>tsr</i> , <i>aphII</i> , <i>orf1</i> , <i>orf2,3</i> only in pIJ4210, <i>attM</i> , <i>bla</i>	- integrate into specific sites - transposable elements (derived from <i>IS117</i> from <i>S. coelicolor</i> ) - pIJ4201 and pIJ4210 differ in the orientation of the resistance genes - the <i>aphII</i> gene from Tn5 lacks its own promoter	<sup>12; 13</sup>
pBR322	pIJ4696, pIJ4698 pIJ4700	pIJ4696: 7.5 kb; pIJ4698: 10.7 kb and pIJ4700: 7.8 kb, <i>IS117</i> derivatives, <i>bla</i> , <i>orf1</i> , <i>orf2,3</i> , <i>attM</i> , <i>hphR</i> in pIJ4696, <i>aadA</i> , <i>tsr</i> and <i>aphII</i> , only in pIJ4698	- for gene expression - pIJ4698 can be used as positive selection replacement vector	<sup>14; 15; 16; 17; 18</sup>
pUC18	pSET151	6.2 kb, <i>tsr</i> , <i>xylE</i> , <i>oriT</i> , <i>lacZα</i> , MCS, <i>aac(3)IV</i>	- non-replicating vector, integration of DNA fragments into specific sites in the chromosome, can be used for reversible integration - derived from pHJL401 by deleting the SCP2* replicon on a Bell fragment and inserting a cassette containing <i>oriT</i> and the <i>xylE</i> structural gene driven	<sup>7; 19; 20</sup>

			by $P_{ermE}$	
<b>2. Plasmids grouped according to <i>Streptomyces</i> replicon</b>				
<b>pJ101</b>		8.8 kb, <i>rep</i> , <i>ori</i> (ds origin for RCR (rolling circle replication), <i>rep</i> , <i>sti</i> , <i>tra</i> , <i>clt</i> , <i>korA</i> , <i>kilA</i> , <i>spdAB</i> , <i>kilB</i> , <i>korB</i> , <i>orf56</i> (unknown function)	- replicative plasmid (RCP), approx. 300 copies per chromosome - pock formation in <i>S. lividans</i> and <i>S. coelicolor</i>	21; 22
	pJ699	9.5 kb, <i>ori</i> pA15 ( <i>E. coli</i> replicon), <i>Ptet</i> (Promoter), <i>vph</i> , <i>aphII</i> , <i>ter</i> (terminator sequence), <i>ter</i> , <i>tsr</i>	- positive selection vector - replicative plasmid, which can be used for gene expression - the pA15 replicon is removed during the cloning procedure and the obtained hybrid plasmids replicate only in actinomycetes (mainly <i>Streptomyces</i> ) - selection on neomycin/kanamycin is only possible in <i>E. coli</i> not in actinomycetes - Self-religation after removing the „stuffer“ fragment leads to the generation of a fragment with a perfect palindrome from the inverted <i>fd</i> ter sequence, rendering the plasmid “invisible”	23
	pJ702	5.65 kb, $\Delta traB$	- cloning vector	21; 24
	pJ486 pJ487	6.2 kb, $\Delta traB$	- cloning vector (the two vectors differ for the MCS orientation) - is lost spontaneously	25; 26
	pJ303	$\Delta traB$ deleted	- ts, (lost at 37°C)	27; 28;
	pMT660	5.6 kb, $\Delta traB$	- ts, derivative of pJ702	29
	pWHM3	7.2 kb, $\Delta traB$ , <i>ori</i> pU18	- vector for knockouts - unstable replicon	30; 31
	pHZ1351 and pHZ1358	8.0 kb, $\Delta traB$ 10 kb, deletion of the stability region	- vector for knockouts - pJ101 with deleted region between <i>sti</i> and <i>rep</i>	6; 32
	pANT1200-1202	pANT1200: 8 kp, pANT1201: 6.6 kb, pANT1202: 6.3 kb <i>ori</i> (pUC), <i>rep</i> (pJ101), resistance gene(s), <i>ter</i> sequences, <i>snpA</i> promoter, <i>snpR</i> gene	- expression vectors - pANT1200: <i>bla</i> and <i>tsr</i> - pANT1201: <i>aphII</i> (kanamycin resistance gene under the control of the <i>acc(3)IV</i> promoter) - pANT1202: <i>acc(3)IV</i>	6; 33
<b>pSG5</b>		12.2 kb replicative, conjugative plasmid, naturally temperature sensitive (ts) plasmid (replication stops above 34°C)	- expression vectors - multicopy plasmid (copy number 20-50) - wide range within <i>Streptomyces</i>	34; 35; 36
	pSG5 derivatives pCZA185, pKC1139, pGM series	contain only <i>rep</i> gene and ds <i>ori</i> of pSG5	- pSG5 derivatives are extremely useful for transposon delivery, for gene description and gene replacement by including homologous regions - in most cases replicative vectors	- pGM series <sup>34; 35; 36</sup> - pKC1139 <sup>7; 37</sup> - pCZA185 1994 <sup>38</sup>

	pHZ132	10.1 kb cosmid, <i>ori</i> (pAT153), <i>vph</i> , <i>cos</i> site, <i>oriT</i> ), <i>tsr</i> , <i>bla</i>	- bifunctional pSG5 derivative (shuttle plasmid) - for gene expression	
<b>SCP2*</b>		31.4 kb transposase-like protein, regions for replication ( <i>rep</i> ), stability and transfer	- low copy number plasmid	39; 40; 41; 42; 43; 44
	pSCP103	24.5 kb SCP2*-derivative with deleted fragment of approx. 4 kb (PstI-A + B fragments circularised in their native configuration)	- lack of partition function (instable, do not contain stability region)	45; 41; 42
	pIJ922	24.0 kb, <i>tsr</i> , <i>traA</i>	- pSCP103 derivative	46; 42; 47
	pIJ698	29.9 kb, pSCP103 derivative <i>aphII</i> , <i>vph</i> , pA15, <i>ter</i> , <i>tsr/hph<sup>R</sup></i> cassette	- shuttle vector (replication in <i>E. coli</i> , p15A) - derived from pSCP103	42; 23
	pIJ80	pSCP103 derivative, <i>aphI</i>		6
	pKC505	18.7 kb pSCP103 derivative, SCP2* replication and fertility function, <i>ori</i> ( <i>E. coli</i> ), acc(3)IV	- shuttle cosmid vector - can be conjugally transferred between different streptomycetes	48
	pMT603	18.7 kb pSCP103 derivative <i>tsr</i> , <i>mel</i> gene (melanin production)	- cloning vector (pMT603) based on the low copy number plasmid SCP2* - pMT603 is unstable because it lacks the SCP2* stability region	49
	pRM5	pSCP103 derivative, transfer and stability region were deleted, includes pBR327 parts, <i>tsr</i>	- designed for cloning (and expression) polyketide biosynthetic gene clusters (combinatorial biosynthesis)	50
	pHJL401	5.9 kb, higher copy number pSCP103-derivative <i>E. coli</i> replicon (pUC19)	- shuttle vectors - the region around the replication origin of pSCP103 was used for construction of pHJL401, which resulted in an increased copy number vector (10 copies)	20
	pKC1064	10 kb, <i>ori</i> (SPC2*), <i>lacZα</i> (MCS), P <sub><i>tipA</i></sub> , <i>tfd</i> ( <i>ter</i> ), <i>ori</i> (pUC vector), <i>bla</i> , <i>oriT</i> (RK4)	- cloning and expression vector - gene expression under the control of the inducible <i>tipA</i> promoter	51
	pKC1218	5.8 kb, <i>ori</i> (SPC2*), <i>lacZα</i> (MCS), <i>ori</i> (pUC18), acc(3)IV, <i>oriT</i> (RK2)	- replicates autonomously in actinomycetes ( <i>Streptomyces</i> ) - for gene expression	7
	pIJ4231	pSCP103 derivative (see below, pSCP103), IS117 integration site, <i>vph</i> , <i>hph<sup>R</sup></i>	- transfer-proficient SCP2* derivative containing a cloned IS117 <i>attB</i> site - used for gene expression	52
<b>SLP1</b>		17.2 kb	- SLP1 plasmids found in <i>Streptomyces lividans</i> after mating with <i>S. coelicolor</i> strain A3(2) originate as deletion mutants of a 17 kb segment of the <i>S. coelicolor</i> chromosome - integrates into specific, highly conserved chromosomal tRNA gene (40 bp copy of the 3' end of the respective tRNA <sup>Tyr</sup> gene) - deletion mutants of SLP1 resulted in formation of autonomously replicating, conjugative, pock-forming CCC plasmids	53

	pCAO106	21.1 kb, SLP1 derivative, <i>bla</i> , transfer and replication function, <i>attP</i> , Kan <sup>R</sup> , <i>ori</i> (p15A)	-integrate into <i>S. lividans</i> chromosome via <i>attP</i> site, is transfer-proficient and forms pocks	<sup>6</sup>
	pCAO170	SLP1/ derivative, pCAO106 containing <i>tsr</i>	-integrate into <i>S. lividans</i> chromosome via <i>attP</i> site, is transfer proficient and forms pocks	<sup>6</sup>
<b>3. Plasmids containing transposable elements</b>				
	plJ4201, plJ4210, plJ4696, plJ4698, plJ4700	see 1. Integrating shuttle plasmids		
	pCZA163	5.8 kb, <i>ori</i> (pUC19), <i>bla</i> <i>orfA</i> upstream and <i>orfB</i> downstream of the <i>acc(3)IV</i> , <i>P<sub>lac</sub></i> upstream of the Tn5096	- transposon mutagenesis - shuttle vector	<sup>54</sup>
	pOJ446	10.4 kb cosmid, <i>ori</i> (SCP2*), ( <i>cos</i> ) <sup>3λ</sup> , <i>rep</i> (pUC), <i>oriT</i> RK2, <i>acc(3)IV</i>	- cloning vectors (derived from pKC505) for the conjugal transfer of DNA from <i>E. coli</i> to actinomycetes - autonomous replication, or site-specific integration at the bacteriophage ΦC31 attachment site	<sup>7; 55</sup>
	pCZA258	6.9 kb, <i>ori</i> (ColEI), <i>P<sub>lac</sub></i> , MCS, <i>hph<sup>R</sup></i> , Tn5099-10, <i>orfA</i> upstream and <i>orfB</i> downstream-PstI and SphI sites, <i>oriT</i> (RK2), <i>bla</i>	- transposon integration - shuttle vector	<sup>38</sup>
	pCZA276	7 kb, <i>ori</i> (pUC19), <i>P<sub>lac</sub></i> , MCS, <i>hph<sup>R</sup></i> , Tn5100-4, <i>orfA</i> upstream and <i>orfB</i> downstream-PstI and SphI sites ( <i>orfA</i> - <i>orfB</i> are in the opposite direction compared to pCZA258), <i>oriT</i> (RK2), <i>bla</i>	- shuttle vector - the ORFA-ORFB is in the opposite direction compared to pCZA258	<sup>38</sup>
<b>4. λ cosmid vectors</b>				
	pOJ446	10.4 kb cosmid, <i>ori</i> (SCP2*), ( <i>cos</i> ) <sup>3λ</sup> , <i>rep</i> (pUC), <i>oriT</i> RK2, <i>acc(3)IV</i>		
	SuperCos1 or pSuperCos1	- 8 kb cosmid, <i>ori</i> (SV40), ( <i>cos</i> )2 sites, MCS, <i>bla</i> , <i>ori</i> (ColEI), <i>aphII</i>	- selection on kanamycin - size limitation: 36-53 kb insert (allowing packaging into λ head)	<sup>56; 57</sup>
	pOJ436	see 1. Integrating shuttle plasmids		
	pHZ1358	see, 2. plJ101 derivatives		
	pKC505	see 2. SCP2* derivatives		
<b>5. Phage-derived integrating plasmids</b>				
pSAM2		11-kb, <i>attP</i> , <i>int</i> , <i>ds</i> origin of replication, <i>rep</i> operon (replication), <i>xis</i> , <i>tra</i> , <i>spd</i> , <i>kor</i> , <i>pra</i> and <i>orf131</i> (regulatory genes)	- phage-derived integrative, conjugative vector - integrates into specific, highly conserved chromosomal tRNA gene (40 bp copy of the 3' end of the respective tRNA <sub>Pro</sub> gene) - the plasmid can reintegrate from the genome	<sup>58; 59</sup>
	pPM927	integrative vectors (integration in non-tRNA sequence)	- mostly conjugative and integrative plasmids, which can be used for gene	<sup>60; 6; 61,62</sup>

		possible)	expression - wide host range	
<b>ΦC31 phage</b>	ΦC31-derived vectors	phage-derived integrating vectors	- mostly conjugative and integrative plasmids, which can be used for gene expression - integrate more efficiently compared to pSAM2 vectors	63; 64; 65; 66; 67; 68; 69; 70; 71; 72; 73; 74; 75; 76; 77; 78; 7
	pJ8600	see 1. Integrating shuttle plasmids		
	pJ8630 and pJ8660	see 1. Integrating shuttle plasmids		
	pOJ446	see 3. Plasmids containing transposable elements		
	KC515	-38.3 kb, $\Delta attP$ , phage ΦC31-based cloning vectors - <i>vph</i> gene (promoterless viomycin phosphotransferase gene conferring resistance), <i>tsr</i>	- phage KC515-derived systems are used for gene disruption and replacement - contains single sites for the enzymes <i>BamHI</i> , <i>BgIII</i> , <i>PstI</i> , <i>PvuII</i> , <i>SstI</i> (two sites) and <i>XbaI</i> , available for the insertion of DNA of up to 4 kb	79; 80
	KC516	38.3 kb, $\Delta attP$ , phage ΦC31-based cloning vectors <i>vph</i> gene, <i>tsr</i>	allows DNA insert of up to 4-4.5 kb	79
	KC857	40.1 kb, $\Delta attP$ , phage ΦC31-based cloning vectors <i>vph</i> gene, <i>tsr</i> , <i>xylE</i> reporter gene, <i>ter(fd)</i> ( <i>ter</i> )	- allows DNA insert of up to 2.2 kb - useful for <i>in situ</i> fusion to <i>xylE</i>	6
	PM8	39.0 kb, $\Delta attP$ , phage ΦC31-based cloning vectors <i>hphR</i> , <i>tsr</i> , <i>xylE</i> reporter gene, <i>ter(fd)</i> ( <i>ter</i> )	- allows insertion of up to 3.3 kb	6
<b>6. Expression vectors</b>				
	pJ8600, pMT3226	see 1. Integrating shuttle plasmids		
	pANT1200-1202	see 2. pJ101 derivatives		
	pCZA185	see 2. pSG5 derivatives		
	pKC1064	see 2. SCP2* derivatives		
	pRM5	see 2. SCP2* derivatives		
	pANT849-851	5.3-5.8 kb, <i>ori</i> (pJ101), <i>tsr</i> , <i>PsnpA</i> (small neutral protease SnpA promoter) upstream of the MCS, <i>snpR</i> (SnpA-regulator gene), <i>rep</i> (pJ101) in pANT850-851, <i>aphL</i> gene	- for gene expression - reporter protein levels up to 50-fold higher compared to <i>melC1</i> promoter	81; 82; 83; 84, 85
	pJ4123 and pJ6021	9.2 kb (pJ4123) and 7.8 kb (pJ6021) pJ4123 and pJ6021 differ in MCS pJ4123 contains a N-terminal His-Tag <i>ori</i> (pJ101), <i>tsr</i> , <i>KanR</i> gene under the control of <i>PtipA</i> and <i>t0</i> , <i>ter</i> , <i>ori</i> (pJ101)	- thiostrepton inducible <i>PtipA</i> - <i>E. coli</i> - <i>Streptomyces</i> shuttle vectors for gene expression	86
	pHZ1271-1272	10.2 kb (pHZ1272) and 11.7 kb (pHZ1271) pHZ1271 and pHZ1272 differ in the MCS pHZ1271 contains a N-terminal His-Tag	- high copy number - structurally stable in <i>E. coli</i> and <i>Streptomyces lividans</i> - pJ4123 and pJ6021 derivatives	87

		<i>ori</i> (pIJ101), <i>tsr</i> , Kan <sup>R</sup> gene under the control of P <sub>tpA</sub> and <i>t0</i> , <i>ter</i> , <i>ori</i> (pBR322), <i>bla</i>	- <i>E. coli</i> -Streptomyces shuttle vectors for gene expression	
	pCJR24	4.6 kb, <i>ori</i> (pUC19), <i>tsr</i> , <i>actII-ORF4</i> with downstream actinorhodin promoters ( <i>PactI</i> and <i>PactIII</i> ), <i>bla</i>	- <i>E. coli</i> -Streptomyces shuttle vectors for regulated gene expression of antibiotic biosynthesis genes	88
<b>pJV1</b>		11.1 kb, transfer region similar to pSN22	- wide host range - several cloning vectors were derived from pJV1 (e.g. pB series or the cosmid vector pFD666) - multicopy plasmid (replicative plasmid)	89; 90; 30

## 7. Unstable and temperature sensitive plasmids

	pHZ1351, pHZ1358, and pMT660	see 2.2 pIJ101 derivatives		
	pCZA185	see 2. pSG5 derivatives		
	pCZA185 and pKC1139	see 2. pSG5 derivatives		
	pIJ80 and pIJ4680	see 2. SCP2* derivatives		
	pHZ132	see 2. pSG5 derivatives		
	pGM9	6.2 kb, <i>rep</i> (pSG5), <i>ori</i> (pSG5), <i>ts</i> , <i>tsr</i> , Ble <sup>R</sup> , <i>aphII</i>	- naturally <i>ts</i> for replication - for gene expression	34; 91; 35; 36
	pGM11	5.3 kb, <i>rep</i> (pSG5), <i>ts</i> , <i>ori</i> (pSG5), <i>aphII</i> , <i>ter</i>	- naturally <i>ts</i> for replication - for gene expression - <i>aacC1</i> not expressed (lacks promoter)	34; 91; 35; 36
	pGM16-17	pGM16 (5.1 kb) and pGM17 (6.8 kb) contain different selection markers, <i>rep</i> (pSG5), <i>ori</i> (pSG5), <i>ts</i> pGM16: <i>tsr</i> , Ble <sup>R</sup> with an upstream promoter of <i>aphII</i> from Tn5 and MCS pGM17: <i>tsr</i> was replaced by <i>cat</i> , ble <sup>R</sup> and <i>aphII</i>	- naturally <i>ts</i> for replication - for gene expression	34; 92
	pGM160	- approx. 7.8 kb, <i>ori</i> (pSG5), <i>rep</i> (pSG5), <i>ts</i> , <i>aacC1</i> , Ble <sup>R</sup> .	- <i>E. coli</i> -Streptomyces shuttle vector (bifunctional pSG5-derived vector) - naturally <i>ts</i> for replication - can be used for gene expression (at 28°C-30°C) and for integration into the genome (at 37°C-39°C and without selection)	34; 92; 93

## 8. Examples of CRISPR-vectors

<b>pSG5-derivative, pJVD52.1</b>	pCRISP omyces	11.4 kb, <i>oriT</i> , <i>rpsL</i> promoter, <i>cas9</i> , <i>gapdh</i> promoter, <i>lacZα</i> cloning site, P <sub>T7/T3</sub> promoter, gRNA site, <i>ori</i> , <i>bla</i> , <i>rep</i> (pSG5)	- multiplex genome editing of <i>Streptomyces</i> species - <i>Streptomyces</i> codon-optimized <i>cas9</i> gene	94; 95
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<b>pSG5-derivative, pGM1190</b>	pCRISPR-Cas9	11.2 kb, the <i>S. coelicolor</i> -codon optimized <i>cas9</i> gene was cloned into the vector pGM1190 pGM1190: <i>ts</i> , <i>tsr</i> , <i>aac(3)IV</i> , <i>oriT</i> , <i>t0</i> ter, RBS, <i>P<sub>tipA</sub></i> , <i>fd</i> ter	- multiplex genome editing of <i>Streptomyces</i> species - <i>S. coelicolor</i> -codon optimized <i>cas9</i> gene	34; 92; 93; 96
<b>9. Other plasmids/vectors</b>				
SLP1		see, 1.5 SLP1 derivatives for SLP1 plasmid		
	pIJ61	15.7 kb, <i>attP</i> was replaced by <i>aphII</i> , <i>tsr</i>	- bifunctional plasmid ( <i>E. coli</i> - <i>Streptomyces</i> shuttle vector) - non-integrating, autonomous conjugative, self-transmissible, pock-forming CCC plasmid, with a copy number of 4-5	97; 98; 99
pBR327	pBR327 derivatives	3.2 kb, derived from pBR322 <i>ori</i> , <i>bla</i> , <i>Tet<sup>R</sup></i>	parts of the vector were used for the construction of hybrid vectors (e.g. <i>E. coli</i> - <i>Streptomyces</i> shuttle vector)	100; 101; 102; 103; 104; 105; 106;
	pGUS derivatives based on pKCLP2, pKC1139	<i>gusA</i> as reporter system	mostly used for knock-in/knock-outs	107; 108; 109, 110

Abbreviations: *aacC1*= gentamicin resistance gene, *aadA*= aminoglycoside resistance gene, *acc(3)IV*= apramycin resistance gene, *aphI*= kanamycin resistance gene, *aphII*= neomycin resistance, *att*= attachment site, *bla*= ampicillin resistance gene, *Ble<sup>R</sup>*= bleomycin resistance, *cat*= chloramphenicol resistance gene, *cIt*= cis-acting transfer function (*oriT*-related), *egfp*= gene encoding recombinant Green Fluorescence Protein, *fd*= transcriptional terminator, *gyrR*= cassette for glycerol inducible gene expression, *gusA*= GusA directs conversion of X-Gluc into coloured 5,5'-dibromo-4,4'-dichloroindigo, *hphR*= hygromycin resistance, *int*= integrase, *Kan<sup>R</sup>*= kanamycin resistance, *kilA*= promoter and amino-terminal region of *tra* (lethality in the absence of the KorA repressor), *kilB*= lethality in the absence of KorB, KorA=kil override (repressor for *tra* and the *korA* expression), KorB= regulator for *kilB*, *LacZα*= β-galactosidase (first 59 residues), the α-peptide, MCS= Multiple Cloning Sites, *orf*= open reading frame, *ori*= origin of replication, *P<sub>tipA</sub>*= thiostrepton inducible promoter, *P<sub>T7/T3</sub>*= T7/T3 promoters, *rep*= replicon region, RBS= Ribosome Binding Site, *snpR*= SnpA-regulator gene, *snpAp*= protease promoter, *spd*= spreading pock-formation, *spdAB*= spread genes, *sti*= strong incompatibility, *Tet<sup>R</sup>*= tetracycline resistance, *ter*= terminator, *ts*= temperature sensitive plasmid, *tra*= transfer gene, *tsr*= thiostrepton resistance gene, *vph*= viomycin resistance gene, *xylE*= reporter gene encoding catechol 2,3-dioxygenase,

## References

1. J. Sun, G. H. Kelemen, J. M. Fernandez-Abalos and M. J. Bibb, *Microbiology*, 1999, **145 ( Pt 9)**, 2221-2227.
2. D. Claessen, H. A. Wosten, G. van Keulen, O. G. Faber, A. M. Alves, W. G. Meijer and L. Dijkhuizen, *Mol Microbiol*, 2002, **44**, 1483-1492.
3. A. Sola-Landa, A. Rodriguez-Garcia, E. Franco-Dominguez and J. F. Martin, *Mol Microbiol*, 2005, **56**, 1373-1385.
4. J. L. Marsh, M. Erfle and E. J. Wykes, *Gene*, 1984, **32**, 481-485.
5. L. Van Mellaert, L. Mei, E. Lammertyn, S. Schacht and J. Anne, *Microbiology*, 1998, **144 ( Pt 12)**, 3351-3358.
6. T. Kieser, M. J. Bibb, M. J. Buttner, K. F. Chater and D. A. Hopwood, *John Innes Foundation, Norwich, U.K.*, 2000.
7. M. Bierman, R. Logan, K. O'Brien, E. T. Seno, R. N. Rao and B. E. Schoner, *Gene*, 1992, **116**, 43-49.
8. C. J. Wilkinson, Z. A. Hughes-Thomas, C. J. Martin, I. Bohm, T. Mironenko, M. Deacon, M. Wheatcroft, G. Wirtz, J. Staunton and P. F. Leadlay, *J Mol Microbiol Biotechnol*, 2002, **4**, 417-426.
9. P. Matsushima and R. H. Baltz, *Microbiology* 1994, **140**, 139-143.
10. P. Matsushima and R. H. Baltz, *Microbiology*, 1996, **142 ( Pt 2)**, 261-267.
11. D. Kallifidas, G. Jiang, Y. Ding and H. Luesch, *Microb Cell Fact*, 2018, **17**, 25.
12. D. J. Lydiate, H. Ikeda and D. A. Hopwood, *Mol Gen Genet*, 1986, **203**, 79-88.
13. D. J. Lydiate, A. M. Ashby, D. H. Henderson, H. M. Kieser and D. A. Hopwood, *Microbiology*, 1989, **4**, 941-955.
14. A. Bhatt and T. Kieser, *Microbiology*, 1999, **145 ( Pt 5)**, 1201-1207.
15. A. Bhatt, H. M. Kieser, R. E. Melton and T. Kieser, *Mol Microbiol*, 2002, **43**, 135-146.
16. T. Smokvina, D. J. Henderson, R. E. Melton, D. F. Brolle, T. Kieser and D. A. Hopwood, *Mol Microbiol*, 1994, **12**, 459-468.
17. H. Motamedi, A. Shafiee and S. J. Cai, *Gene*, 1995, **160**, 25-31.
18. M. S. Paget, G. Hintermann and C. P. Smith, *Gene*, 1994, **146**, 105-110.
19. M. J. Bibb, G. R. Janssen and J. M. Ward, *Gene*, 1985, **38**, 215-226.
20. J. L. Larson and C. L. Hershberger, *Plasmid*, 1986, **15**, 199-209.
21. T. Kieser, D. A. Hopwood, H. M. Wright and C. J. Thompson, *Mol Gen Genet*, 1982, **185**, 223-228.
22. K. J. Kendall and S. N. Cohen, *J Bacteriol*, 1988, **170**, 4634-4651.
23. T. Kieser and R. E. Melton, *Gene*, 1988, **65**, 83-91.
24. Y. Murooka, T. Ishizaki, O. Nimi and N. Maekawa, *Appl Environ Microbiol*, 1986, **52**, 1382-1385.
25. J. M. Ward, G. R. Janssen, T. Kieser, M. J. Bibb, M. J. Buttner and M. J. Bibb, *Mol Gen Genet*, 1986, **203**, 468-478.
26. S. Herai, Y. Hashimoto, H. Higashibata, H. Maseda, H. Ikeda, S. Omura and M. Kobayashi, *Proc Natl Acad Sci U S A*, 2004, **101**, 14031-14035.
27. F. Rafii and D. L. Crawford, *Appl Environ Microbiol*, 1988, **54**, 1334-1340.
28. C. A. Wrigley-Jones, H. Richards, C. R. Thomas and J. Ward, *Biotechnol Bioeng*, 1993, **41**, 148-155.
29. A. W. Birch and J. Cullum, *J Gen Microbiol*, 1985, **131**, 1299-1303.
30. J. Vara, M. Lewandowska-Skarbek, Y. G. Wang, S. Donadio and C. R. Hutchinson, *J Bacteriol*, 1989, **171**, 5872-5881.
31. V. Mohrle, U. Roos and C. Bormann, *Mol Microbiol*, 1995, **15**, 561-571.
32. S. Banos, R. Perez-Redondo, B. Koekman and P. Liras, *Appl Environ Microbiol*, 2009, **75**, 2991-2995.

33. J. Nikodinovic and N. D. Priestley, *Plasmid*, 2006, **56**, 223-227.
34. G. Muth, B. Nußbaumer, W. Wohlleben and A. Pühler, *Mol Gen Genet* 1989, **219**, 341–348.
35. G. Muth, M. Farr, V. Hartmann and W. Wohlleben, *Plasmid*, 1995, **33**, 113-126.
36. R. M. Maas, J. Gotz, W. Wohlleben and G. Muth, *Microbiology*, 1998, **144 ( Pt 10)**, 2809-2817.
37. D. Du, L. Wang, Y. Tian, H. Liu, H. Tan and G. Niu, *Sci Rep*, 2015, **5**, 8740.
38. P. J. Solenberg and R. H. Baltz, *Gene*, 1994, **147**, 47-54.
39. H. Schrempf, H. Bujard, D. A. Hopwood and W. Goebel, *J Bacteriol*, 1975, **121**, 416-421.
40. M. J. Bibb, R. F. Freeman and D. A. Hopwood, *Mol Gen Genet*, 1977, **154**, 155–166.
41. M. J. Bibb and D. A. Hopwood, *J Gen Microbiol*, 1981, **126**, 427–442.
42. D. J. Lydiate, F. Malpartida and D. A. Hopwood, *Gene*, 1985, **35**, 223-235.
43. H. Kinashi, M. Shimaji-Murayama and T. Hanafusa, *Plasmid*, 1991, **26**, 123-130.
44. I. Haug, A. Weissenborn, D. Brolle, S. Bentley, T. Kieser and J. Altenbuchner, *Microbiology*, 2003, **149**, 505-513.
45. M. Bibb, J. L. Schottel and S. N. Cohen, *Nature*, 1980, **284**, 526-531.
46. F. Malpartida and D. A. Hopwood, *Nature*, 1984, **309**, 462-464.
47. B. Price, T. Adamidis, R. Kong and W. Champness, *J Bacteriol*, 1999, **181**, 6142-6151.
48. M. A. Richardson, S. Kuhstoss, P. Solenberg, N. A. Schaus and R. N. Rao, *Gene*, 1987, **61**, 231-241.
49. K. Kendall and J. Cullum, *Genet Res*, 1988, **51**, 71-74.
50. R. McDaniel, S. Ebert-Khosla, D. A. Hopwood and C. Khosla, *Science*, 1993, **262**, 1546-1550.
51. S. Kuhstoss and R. N. Rao, *J Mol Biol*, 1991, **222**, 897-908.
52. D. J. Henderson, D. F. Brolle, T. Kieser, R. E. Melton and D. A. Hopwood, *Mol Gen Genet*, 1990, **224**, 65-71.
53. C. A. Omer and S. N. Cohen, *Mol Gen Genet*, 1984, **196**, 429-438.
54. P. J. Solenberg and S. G. Burgett, *J Bacteriol*, 1989, **171**, 4807-4813.
55. R. N. Rao, M. A. Richardson and S. Kuhstoss, *Methods Enzymol*, 1987, **153**, 166-198.
56. M. Redenbach, H. M. Kieser, D. Denapaite, A. Eichner, J. Cullum, H. Kinashi and D. A. Hopwood, *Mol Microbiol*, 1996, **21**, 77-96.
57. G. A. Evans, K. Lewis and B. E. Rothenberg, *Gene*, 1989, **79**, 9-20.
58. J. L. Pernodet, J. M. Simonet and M. Guerineau, *Mol Gen Genet*, 1984, **198**, 35-41.
59. F. Boccard, T. Smokvina, J. L. Pernodet, A. Friedmann and M. Guerineau, *EMBO J*, 1989, **8**, 973-980.
60. S. Clerc and P. Simonet, *FEMS Microbiology Ecology*, 1996, **21**, 157–165.
61. C. Possoz, C. Ribard, J. Gagnat, J. L. Pernodet and M. Guerineau, *Mol Microbiol*, 2001, **42**, 159-166.
62. T. Smokvina, P. Mazodier, F. Boccard, C. J. Thompson and M. Guerineau, *Gene*, 1990, **94**, 53-59.
63. M. C. Smith, R. N. Burns, S. E. Wilson and M. A. Gregory, *Nucleic Acids Res*, 1999, **27**, 2145-2155.
64. C. J. Bruton, E. P. Guthrie and K. F. Chater, *Biotechnology (N Y)*, 1991, **9**, 652-656.
65. K. F. Chater, C. J. Bruton, W. Springer and J. E. Suarez, *Gene*, 1981, **15**, 249-256.
66. K. F. Chater, C. J. Bruton and J. E. Suarez, *Gene*, 1981, **14**, 183-194.
67. R. W. Hendrix, M. C. Smith, R. N. Burns, M. E. Ford and G. F. Hatfull, *Proc Natl Acad Sci U S A*, 1999, **96**, 2192-2197.
68. C. W. Howe and M. C. Smith, *J Bacteriol*, 1996, **178**, 2127-2130.
69. C. W. Howe and M. C. Smith, *Microbiology*, 1996, **142 ( Pt 6)**, 1357-1367.
70. C. J. Ingham, H. J. Crombie, C. J. Bruton, K. F. Chater, N. M. Hartley, G. J. Murphy and M. C. Smith, *Mol Microbiol*, 1993, **9**, 1267-1274.
71. C. J. Ingham, C. E. Owen, S. E. Wilson, I. S. Hunter and M. C. Smith, *Nucleic Acids Res*, 1994, **22**, 821-827.
72. C. J. Ingham, I. S. Hunter and M. C. Smith, *Nucleic Acids Res*, 1995, **23**, 370-376.
73. C. J. Ingham and M. C. Smith, *Gene*, 1992, **122**, 77-84.

74. M. C. Smith and C. E. Owen, *Mol Microbiol*, 1991, **5**, 2833-2844.
75. M. C. Smith, C. J. Ingham, C. E. Owen and N. T. Wood, *Gene*, 1992, **115**, 43-48.
76. H. M. Thorpe and M. C. Smith, *Proc Natl Acad Sci U S A*, 1998, **95**, 5505-5510.
77. S. E. Wilson, C. J. Ingham, I. S. Hunter and M. C. Smith, *Mol Microbiol*, 1995, **16**, 131-143.
78. S. E. Wilson and M. C. Smith, *Nucleic Acids Res*, 1998, **26**, 2457-2463.
79. M. R. Rodicio, C. J. Bruton and K. F. Chater, *Gene*, 1985, **34**, 283-292.
80. M. Carmody, B. Byrne, B. Murphy, C. Breen, S. Lynch, E. Flood, S. Finnane and P. Caffrey, *Gene*, 2004, **343**, 107-115.
81. J. S. Lampel, J. S. Aphale, K. A. Lampel and W. R. Strohl, *J Bacteriol*, 1992, **174**, 2797-2808.
82. M. L. Dickens and W. R. Strohl, *J Bacteriol*, 1996, **178**, 3389-3395.
83. M. L. Dickens, J. Ye and W. R. Strohl, *J Bacteriol*, 1996, **178**, 3384-3388.
84. M. L. Dickens, N. D. Priestley and W. R. Strohl, *J Bacteriol*, 1997, **179**, 2641-2650.
85. C. L. DeSanti and W. R. Strohl, *Appl Environ Microbiol*, 2003, **69**, 1647-1654.
86. E. Takano, J. White, C. J. Thompson and M. J. Bibb, *Gene*, 1995, **166**, 133-137.
87. R. Yang, Z. Hu, Z. Deng and J. Li, *Chin J Biotechnol*, 1998, **14**, 1-8.
88. C. J. Rowe, J. Cortes, S. Gaisser, J. Staunton and P. F. Leadlay, *Gene*, 1998, **216**, 215-223.
89. M. Kataoka, T. Seki and T. Yoshida, *J Bacteriol*, 1991, **173**, 4220-4228.
90. M. Kataoka, Y. M. Kiyose, Y. Michisugi, T. Horiguchi, T. Seki and T. Yoshida, *Plasmid*, 1994, **32**, 55-69.
91. M. Roth, C. Hoffmeier, R. Geuther, G. Muth and W. Wohlleben, *Biotechnol Lett*, 1994, **16**, 1225-1230.
92. W. Wohlleben, V. Hartmann, D. Hillemann, K. Krey, G. Muth, B. Nussbaumer and S. Pelzer, *Acta Microbiol Immunol Hung*, 1994, **41**, 381-389.
93. G. Muth, *Appl Microbiol Biotechnol*, 2018, **102**, 9067-9080.
94. J. A. Blodgett, P. M. Thomas, G. Li, J. E. Velasquez, W. A. van der Donk, N. L. Kelleher and W. W. Metcalf, *Nat Chem Biol*, 2007, **3**, 480-485.
95. R. E. Cobb, Y. Wang and H. Zhao, *ACS Synth Biol*, 2015, **4**, 723-728.
96. Y. Tong, P. Charusanti, L. Zhang, T. Weber and S. Y. Lee, *ACS Synth Biol*, 2015, **4**, 1020-1029.
97. C. J. Thompson, T. Kieser, J. M. Ward and D. A. Hopwood, *Gene*, 1982, **20**, 51-62.
98. T. Kieser, *Plasmid*, 1984, **12**, 19-36.
99. E. Strauch, W. Wohlleben and A. Puhler, *J Basic Microbiol*, 1987, **27**, 449-455.
100. J. G. Sutcliffe, *Cold Spring Harb Symp Quant Biol*, 1979, **43 Pt 1**, 77-90.
101. F. Bolivar, R. L. Rodriguez, M. C. Betlach and H. W. Boyer, *Gene*, 1977, **2**, 75-93.
102. F. Bolivar, R. L. Rodriguez, P. J. Greene, M. C. Betlach, H. L. Heyneker, H. W. Boyer, J. H. Crosa and S. Falkow, *Gene*, 1977, **2**, 95-113.
103. X. Soberon, L. Covarrubias and F. Bolivar, *Gene*, 1980, **9**, 287-305.
104. L. Y. Fuchs, L. Covarrubias, L. Escalante, S. Sanchez and F. Bolivar, *Gene*, 1980, **10**, 39-46.
105. L. Covarrubias, L. Cervantes, A. Covarrubias, X. Soberon, I. Vichido, A. Blanco, Y. M. Kupersztoch-Portnoy and F. Bolivar, *Gene*, 1981, **13**, 25-35.
106. D. A. Hopwood, G. Hintermann, T. Kieser and H. M. Wright, *Plasmid*, 1984, **11**, 1-16.
107. M. Myronovskyy, E. Welle, V. Fedorenko and A. Luzhetsky, *Appl Environ Microbiol*, 2011, **77**, 5370-5383.
108. R. A. Jefferson, *Nature*, 1989, **342**, 837-838.
109. R. A. Jefferson, T. A. Kavanagh and M. W. Bevan, *EMBO J*, 1987, **6**, 3901-3907.
110. T. Siegl and A. Luzhetsky, *Antonie Van Leeuwenhoek*, 2012, **102**, 503-516.