

**Secretion of the cytoplasmic and high molecular weight β -galactosidase of
Paenibacillus wynnii with *Bacillus subtilis***

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Table S1: Oligonucleotides used in this study.

Name	Sequence (5'→3')
O1	ctagtgaaaaagatgttgatgtagctttacatttctttggcttgactatccatgtaggggg
O2	cgcgccccctacatggatagtcaaagccaaaagaaatgtaaaagctaacaatcaacatcttttca
P1	cgtctcacgcgcaggcgcgtaaaaaacttgtctattcacc
P2	ccttgctacaaaccccttaaaaacg
P3	tcgagtctctacggaaatagcg
P4	catcgataagctcaggcagtcaggatccg
P5	cctggaattcgccaaagctgtaatggctg
P6	gcactagtcattcctctcttacctataatgg
P7	cgtctcacgcgccgtaaaaaacttgtc
P8	gcctcgagcaccattctaatacgtaaadc

Table S2: Signal peptides used in this study.

Signal peptide	Amino acid sequence	Origin
YoaW	VKKMLMLAFTFLLALTIHVGAQA	<i>B. subtilis</i> 168
AprE	VRSKKLWISLLFALALIFTMAFGSTSSAQA	<i>B. subtilis</i> 168
PhoD	VAYDSRFDEWVQKLKEESFQNNTFDRRK FIQGAGKIALGLSLGLTIAQSASA	<i>B. subtilis</i> 168
GlmU	VDRRDNGGQYMDKRFAVVLA	<i>B. licheniformis</i>

Table S3: Plasmids used in this study.

Plasmid	Application
Bs_Pgeo_SPaprE_prom pMA	Provides modular cloning cassette
20AC44OP bGalPW_opt Bs_pMK-RQ	Provides optimized β -gal-Pw gene
pET20b - β Gal <i>P.wynnii</i> His6	Provides native β -gal-Pw gene
BNspeBif3	Vector backbone
pLF_P ₄₃ _YoaW	Negative control
pLF_P _{AprE} _AprE	Negative control
pLF_P ₄₃ _YoaW_ β -gal-Pw	β -gal-Pw expression
pLF_P ₄₃ _YoaW_ β -gal-Pw_opt	β -gal-Pw expression
pLF_P ₄₃ _AprE_ β -gal-Pw_opt	β -gal-Pw expression
pLF_P ₄₃ _PhoD_ β -gal-Pw_opt	β -gal-Pw expression
pLF_P ₄₃ _GlmU_ β -gal-Pw_opt	β -gal-Pw expression
pLF_P _{AprE} _YoaW_ β -gal-Pw	β -gal-Pw expression
pLF_P _{AprE} _YoaW_ β -gal-Pw_opt	β -gal-Pw expression
pLF_P _{AprE} _AprE_ β -gal-Pw_opt	β -gal-Pw expression
pLF_P _{AprE} _PhoD_ β -gal-Pw_opt	β -gal-Pw expression
pLF_P _{AprE} _GlmU_ β -gal-Pw_opt	β -gal-Pw expression

Table S4: Strains used in this study.

Strain	Genotype and properties	Source
<i>Escherichia coli</i> XL1 Blue	<i>endA1 gyrA96 (nal^R) thi-1 recA1 relA1 lac glnV44 F'[:Tn10 proAB+ lacIq Δ(lacZ)M15] hsdR17(rK - mK +)</i>	Bullock et al., 1987
<i>Bacillus subtilis</i> 168	<i>trpC2</i>	Burkholder & Giles, 1947
<i>B. subtilis</i> SCK6	Erm ^R , <i>his nprR2 nprE18 ΔaprA3 ΔeglS102 ΔbglIT bglSRV lacA::P_{xyIA} -comK</i>	Zhang & Zhang, 2011
BsAnc	<i>B. subtilis</i> SCK6 with plasmid pLF_P _{AprE} _AprE (negative control)	This work
BsAY1	<i>B. subtilis</i> SCK6 with plasmid pLF_P _{AprE} _YoaW_β-gal-Pw	This work
BsAY2	<i>B. subtilis</i> SCK6 with plasmid pLF_P _{AprE} _YoaW_β-gal-Pw_opt	This work
BsAP2	<i>B. subtilis</i> SCK6 with plasmid pLF_P _{AprE} _PhoD_β-gal-Pw_opt	This work
BsAG2	<i>B. subtilis</i> SCK6 with plasmid pLF_P _{AprE} _GlmU_β-gal-Pw_opt	This work
BsAA2	<i>B. subtilis</i> SCK6 with plasmid pLF_P _{AprE} _AprE_β-gal-Pw_opt	This work
Bs43nc	<i>B. subtilis</i> SCK6 with plasmid pLF_P ₄₃ _YoaW (negative control)	This work
Bs43Y1	<i>B. subtilis</i> SCK6 with plasmid pLF_P ₄₃ _YoaW_β-gal-Pw	This work
Bs43Y2	<i>B. subtilis</i> SCK6 with plasmid pLF_P ₄₃ _YoaW_β-gal-Pw_opt	This work
Bs43P2	<i>B. subtilis</i> SCK6 with plasmid pLF_P ₄₃ _PhoD_β-gal-Pw_opt	This work
Bs43G2	<i>B. subtilis</i> SCK6 with plasmid pLF_P ₄₃ _GlmU_β-gal-Pw_opt	This work
Bs43A2	<i>B. subtilis</i> SCK6 with plasmid pLF_P ₄₃ _AprE_β-gal-Pw_opt	This work

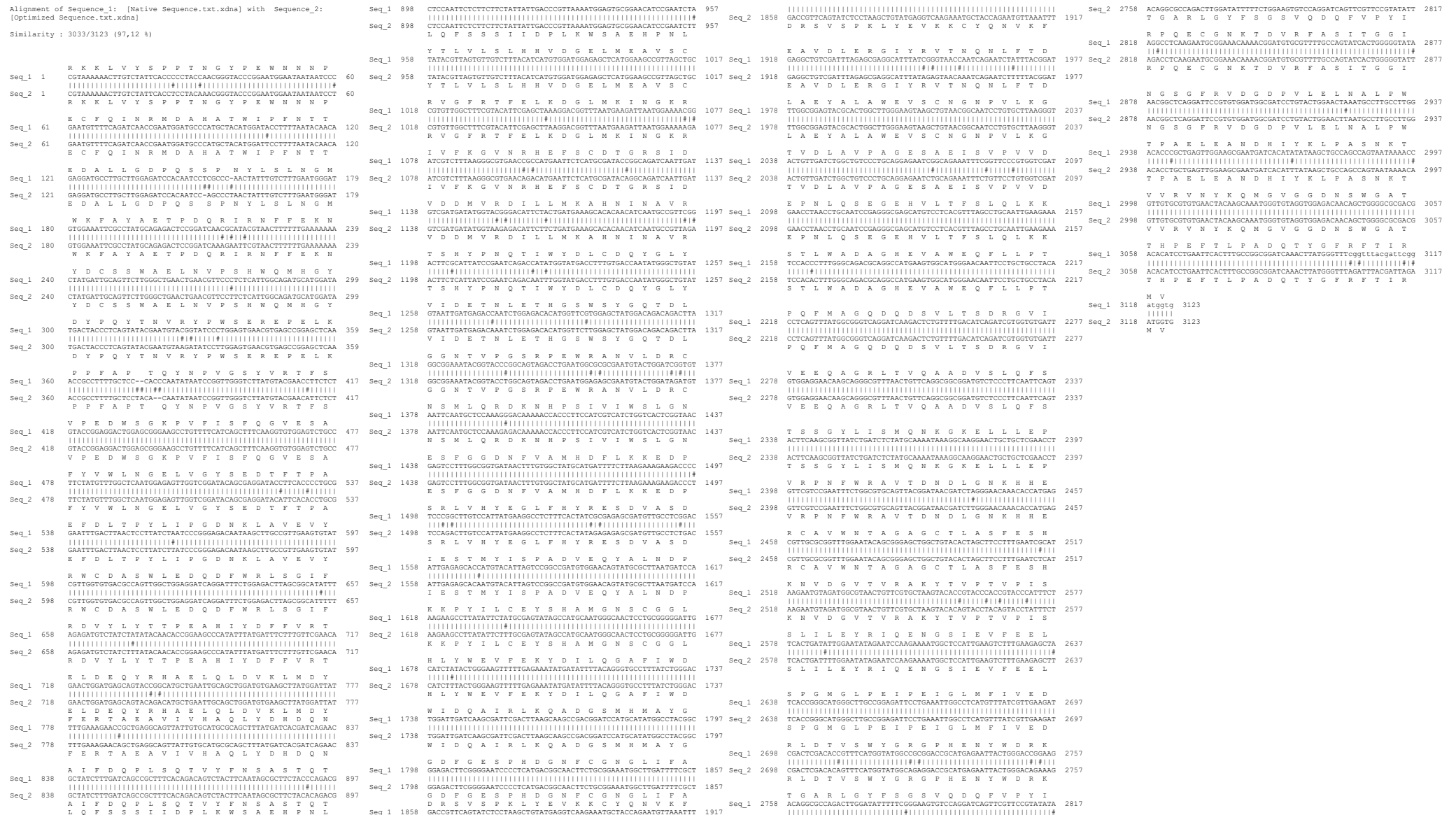


Figure S1: Alignment of native β -gal-Pw sequence (Seq1) and codon-optimized β -gal-Pw sequence (Seq2).

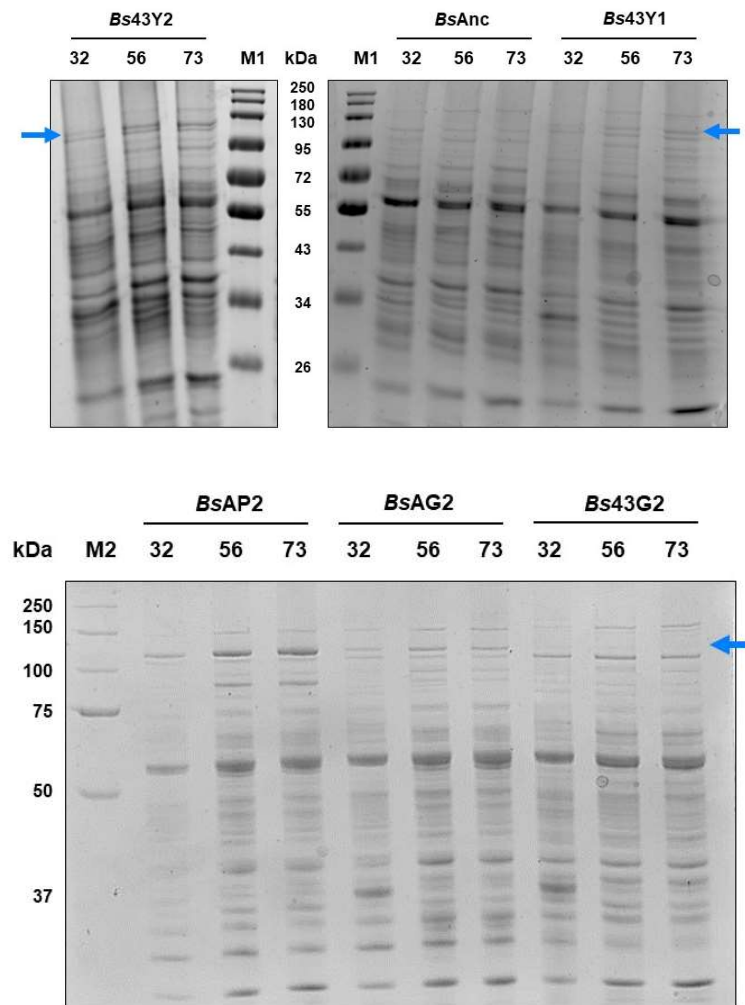


Figure S2: SDS PAGEs of the secretomes of the different *B. subtilis* strains during shake flask cultivation. The culture supernatant was analyzed after 32 h, 56 h and 73 h of cultivation. The blue arrow indicates the 120 kDa band corresponding to the size of the β -gal-Pw. An amount of 8 μ g of protein was loaded in each lane. M1=Biorad Precision Plus Protein™ Unstained Protein Standards; M2=NEB Color Prestained Protein Standard Broad Range (10-250 kDa)

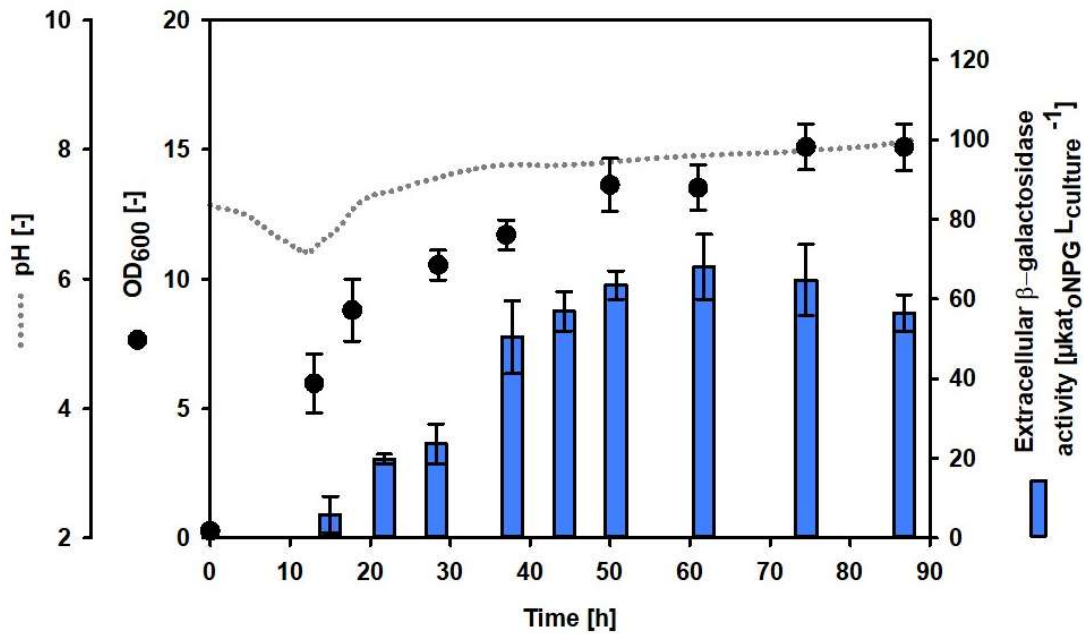


Figure S3: Repetition of the bioreactor cultivation of *BsAP2* for secretory β-gal-Pw production. Cultivation was done in duplicates at 30 °C, without pH control and with a working volume of 0.8 L.

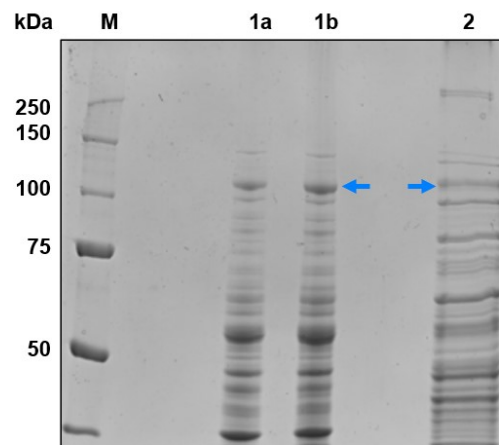


Figure S4: SDS PAGE of secretome (1) and intracellular proteome (2) of *BsAP2*. The bands (blue arrow) corresponding to a size of 120 kDa were analyzed by MS. Supernatant and cell free extract after 73 h of shake flask cultivation were analyzed. The supernatant sample was loaded twice (1a and b). An amount of 8 % SDS gel was used and 8 μg of protein was loaded. M = Marker

A

16 exclusive unique peptides, 18 exclusive unique spectra, 188 total spectra, 585/1107 amino acids (53% coverage)

VAYDSRFDEW	VQKLKEESFQ	NNTFDRRKFI	QGAGKIAGLS	LGLTIAQSAS	AAARRKKLVY	SPPTNGYPEW	NNNPECFQIN
RMDAHATWIP	FNTTTEALLG	DPQSSPNYLS	LNGMWHFAYA	ETPDQRIIRNF	FEKNYDCSSW	AELNVPSHWQ	MHGYDYPQYT
NVRYPWSERE	PELKPPFAPT	QYNPVGSYVR	TFSVPEDWSG	KPVFISFOGV	ESAFYVWLNQ	ELVGYS EDTF	TPAEFDLTPY
LIPGDNKLAV	EVYRWCDASW	LEDQDFWRLS	GIFRDVYLYT	TPEAHYDFF	VRTELDEQYR	HAELQLDVKL	MDYFERTAEA
VI VHAQLYDH	DQNAIFDQPL	SQT VYFNSAS	TQTLOFSSSI	IDPLKWSAEH	PNLYTLVLSSL	HHVDGELMEA	VSCRVGFRFTF
ELKDG LMKIN	GKRI VFKGVN	RHEFSCDTGR	SIDVDDMV RD	ILLMKAHNIN	AVRTSHYPNQ	TIWYDLCDQY	GLYVIDETNL
ETHGWSYSGQ	TDLGGNTVPG	SRPEWRANVL	DRCN SMLQRD	KNHPSIVIWS	LGNESFGGDN	FVAMHDFLKK	EDPSRLVHYE
GLFHYRES DV	ASDIESTMYI	SPADVEQYAL	NDPKKPYILC	EYSHAMGN SC	GGLHLYWEVF	EKYDILQGA F	IWDWIDQAIR
LKQADGSMHM	AYGGDFGES P	HDGNFCGNGL	IFADR SVSPK	LYEVKKCYQN	VKFEAVDLER	GIYRV TNQNL	FTDLAEYALA
WEVSCNGNPV	LKGTVDLAVP	AGESAEISVP	VVDEPNLQSE	GEHVLTFSLO	LKKSTLWADA	GHEVAWEQFL	LPTPQFMAGQ
DQDSVLTSDR	GVIVVEEQAGR	LTVQAADVSL	QFSTSSGYLI	SMQNK GKELL	LEPVRPNFWR	AVTDNDLG NK	HHERC AVWNT
AGAGCTLAS F	ESHKNVDGVT	VRAKYTVPTV	PISSLLILEYR	IQENGSI EVF	EELSPGMGLP	EIPEIGLMFI	VEDRLDTVSW
YGRGPHENYW	DRKTGARLG Y	FSGSVQDQFV	PYIRPQECGN	KTDVRFASIT	GGINGSGFRV	DGDPVLELNA	LPWTPAELEA
NDHIYKLPAS	NKTVVRVNYK	QMGVGGDN SW	GATTHPEFTL	PADQTYGFRF	TIRMVLEHHH	HHHHHHH	

B

3 exclusive unique peptides, 3 exclusive unique spectra, 173 total spectra, 516/1107 amino acids (47% coverage)

VAYDSRFDEW	VQKLKEESFQ	NNTFDRRKFI	QGAGKIAGLS	LGLTIAQSAS	AAARRKKLVY	SPPTNGYPEW	NNNPECFQIN
RMDAHATWIP	FNTTTEALLG	DPQSSPNYLS	LNGMWHFAYA	ETPDQRIIRNF	FEKNYDCSSW	AELNVPSHWQ	MHGYDYPQYT
NVRYPWSERE	PELKPPFAPT	QYNPVGSYVR	TFSVPEDWSG	KPVFISFOGV	ESAFYVWLNQ	ELVGYS EDTF	TPAEFDLTPY
LIPGDNKLAV	EVYRWCDASW	LEDQDFWRLS	GIFRDVYLYT	TPEAHYDFF	VRTELDEQYR	HAELQLDVKL	MDYFERTAEA
VI VHAQLYDH	DQNAIFDQPL	SQT VYFNSAS	TQTLOFSSSI	IDPLKWSAEH	PNLYTLVLSSL	HHVDGELMEA	VSCRVGFRFTF
ELKDG LMKIN	GKRI VFKGVN	RHEFSCDTGR	SIDVDDMV RD	ILLMKAHNIN	AVRTSHYPNQ	TIWYDLCDQY	GLYVIDETNL
ETHGWSYSGQ	TDLGGNTVPG	SRPEWRANVL	DRCN SMLQRD	KNHPSIVIWS	LGNESFGGDN	FVAMHDFLKK	EDPSRLVHYE
GLFHYRES DV	ASDIESTMYI	SPADVEQYAL	NDPKKPYILC	EYSHAMGN SC	GGLHLYWEVF	EKYDILQGA F	IWDWIDQAIR
LKQADGSMHM	AYGGDFGES P	HDGNFCGNGL	IFADR SVSPK	LYEVKKCYQN	VKFEAVDLER	GIYRV TNQNL	FTDLAEYALA
WEVSCNGNPV	LKGTVDLAVP	AGESAEISVP	VVDEPNLQSE	GEHVLTFSLO	LKKSTLWADA	GHEVAWEQFL	LPTPQFMAGQ
DQDSVLTSDR	GVIVVEEQAGR	LTVQAADVSL	QFSTSSGYLI	SMQNK GKELL	LEPVRPNFWR	AVTDNDLG NK	HHERC AVWNT
AGAGCTLAS F	ESHKNVDGVT	VRAKYTVPTV	PISSLLILEYR	IQENGSI EVF	EELSPGMGLP	EIPEIGLMFI	VEDRLDTVSW
YGRGPHENYW	DRKTGARLG Y	FSGSVQDQFV	PYIRPQECGN	KTDVRFASIT	GGINGSGFRV	DGDPVLELNA	LPWTPAELEA
NDHIYKLPAS	NKTVVRVNYK	QMGVGGDN SW	GATTHPEFTL	PADQTYGFRF	TIRMVLEHHH	HHHHHHH	

C

624 exclusive unique peptides, 973 exclusive unique spectra, 2487 total spectra, 1020/1107 amino acids (92% coverage)

VAYDSRFDEW	VQKLKEESFQ	NNTFDRRKFI	QGAGKIAGLS	LGLTIAQSAS	AAARRKKLVY	SPPTNGYPEW	NNNPECFQIN
RMDAHATWIP	FNTTTEALLG	DPQSSPNYLS	LNGMWHFAYA	ETPDQRIIRNF	FEKNYDCSSW	AELNVPSHWQ	MHGYDYPQYT
NVRYPWSERE	PELKPPFAPT	QYNPVGSYVR	TFSVPEDWSG	KPVFISFOGV	ESAFYVWLNQ	ELVGYS EDTF	TPAEFDLTPY
LIPGDNKLAV	EVYRWCDASW	LEDQDFWRLS	GIFRDVYLYT	TPEAHYDFF	VRTELDEQYR	HAELQLDVKL	MDYFERTAEA
VI VHAQLYDH	DQNAIFDQPL	SQT VYFNSAS	TQTLOFSSSI	IDPLKWSAEH	PNLYTLVLSSL	HHVDGELMEA	VSCRVGFRFTF
ELKDG LMKIN	GKRI VFKGVN	RHEFSCDTGR	SIDVDDMV RD	ILLMKAHNIN	AVRTSHYPNQ	TIWYDLCDQY	GLYVIDETNL
ETHGWSYSGQ	TDLGGNTVPG	SRPEWRANVL	DRCN SMLQRD	KNHPSIVIWS	LGNESFGGDN	FVAMHDFLKK	EDPSRLVHYE
GLFHYRES DV	ASDIESTMYI	SPADVEQYAL	NDPKKPYILC	EYSHAMGN SC	GGLHLYWEVF	EKYDILQGA F	IWDWIDQAIR
LKQADGSMHM	AYGGDFGES P	HDGNFCGNGL	IFADR SVSPK	LYEVKKCYQN	VKFEAVDLER	GIYRV TNQNL	FTDLAEYALA
WEVSCNGNPV	LKGTVDLAVP	AGESAEISVP	VVDEPNLQSE	GEHVLTFSLO	LKKSTLWADA	GHEVAWEQFL	LPTPQFMAGQ
DQDSVLTSDR	GVIVVEEQAGR	LTVQAADVSL	QFSTSSGYLI	SMQNK GKELL	LEPVRPNFWR	AVTDNDLG NK	HHERC AVWNT
AGAGCTLAS F	ESHKNVDGVT	VRAKYTVPTV	PISSLLILEYR	IQENGSI EVF	EELSPGMGLP	EIPEIGLMFI	VEDRLDTVSW
YGRGPHENYW	DRKTGARLG Y	FSGSVQDQFV	PYIRPQECGN	KTDVRFASIT	GGINGSGFRV	DGDPVLELNA	LPWTPAELEA
NDHIYKLPAS	NKTVVRVNYK	QMGVGGDN SW	GATTHPEFTL	PADQTYGFRF	TIRMVLEHHH	HHHHHHH	

Figure S5: MS analyses results of (A) intracellular and (B) extracellular β -gal-Pw (C) purified β -gal-Pw. The β -gal-Pw in the supernatant of the bioreactor cultivation of *BsAP* was purified.

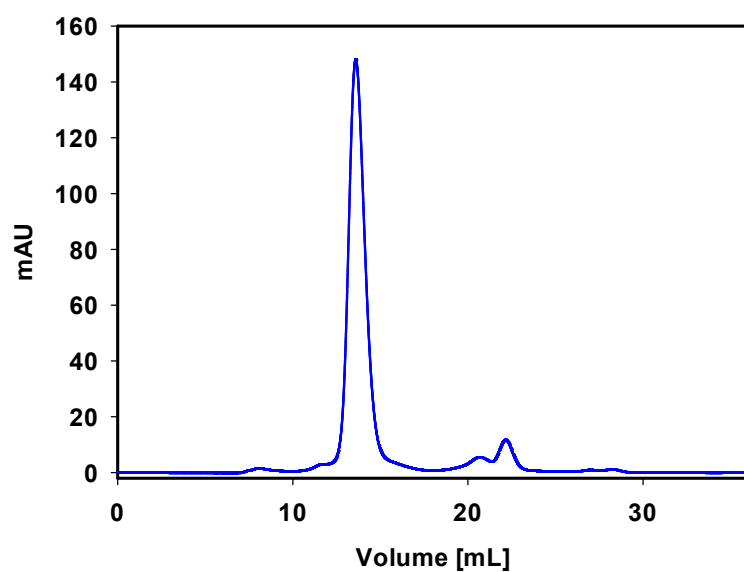
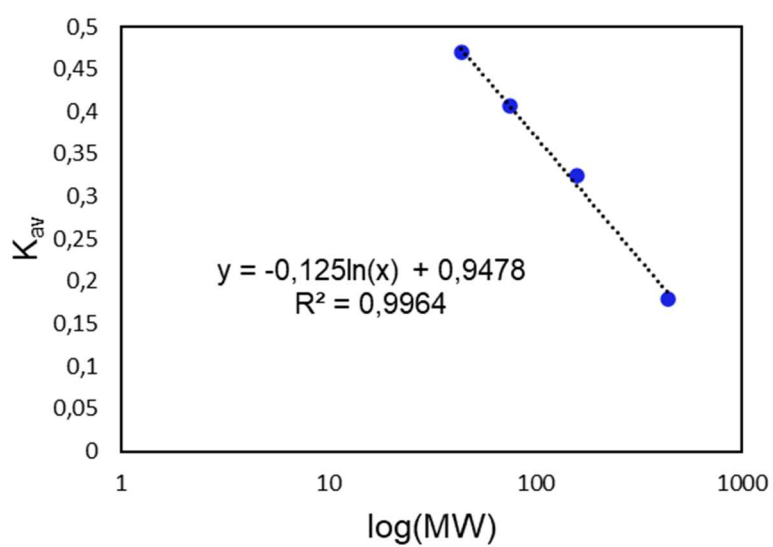
A**B**

Figure S6: Chromatogram of size exclusion chromatography of purified β -gal-Pw (A) and the calibration curve generated (B). The β -gal-Pw was purified from the supernatant of the bioreactor cultivation of *BsAP2*.

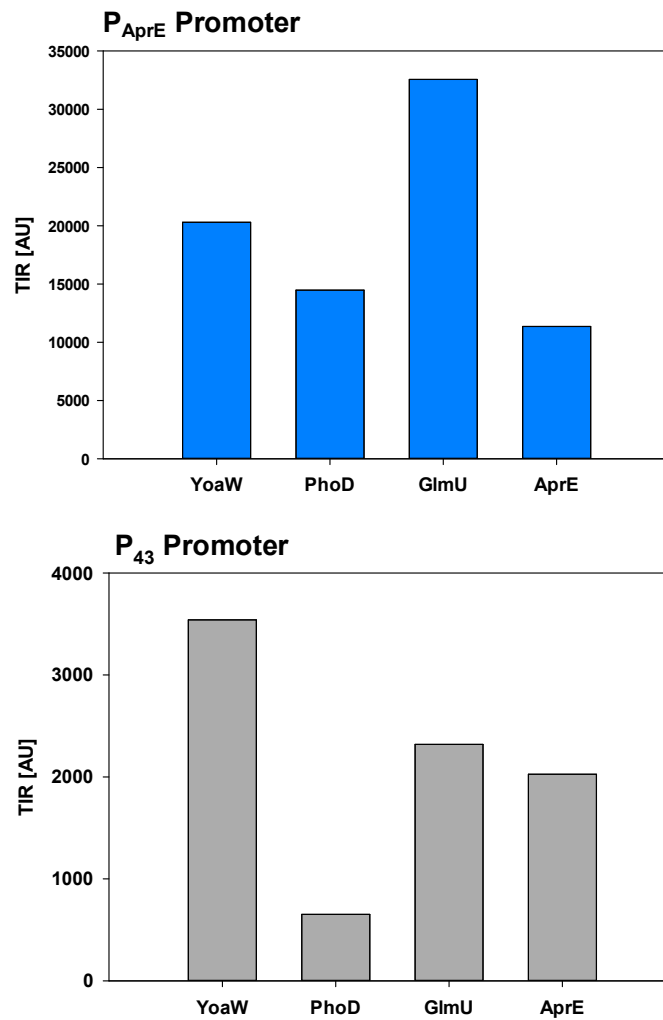
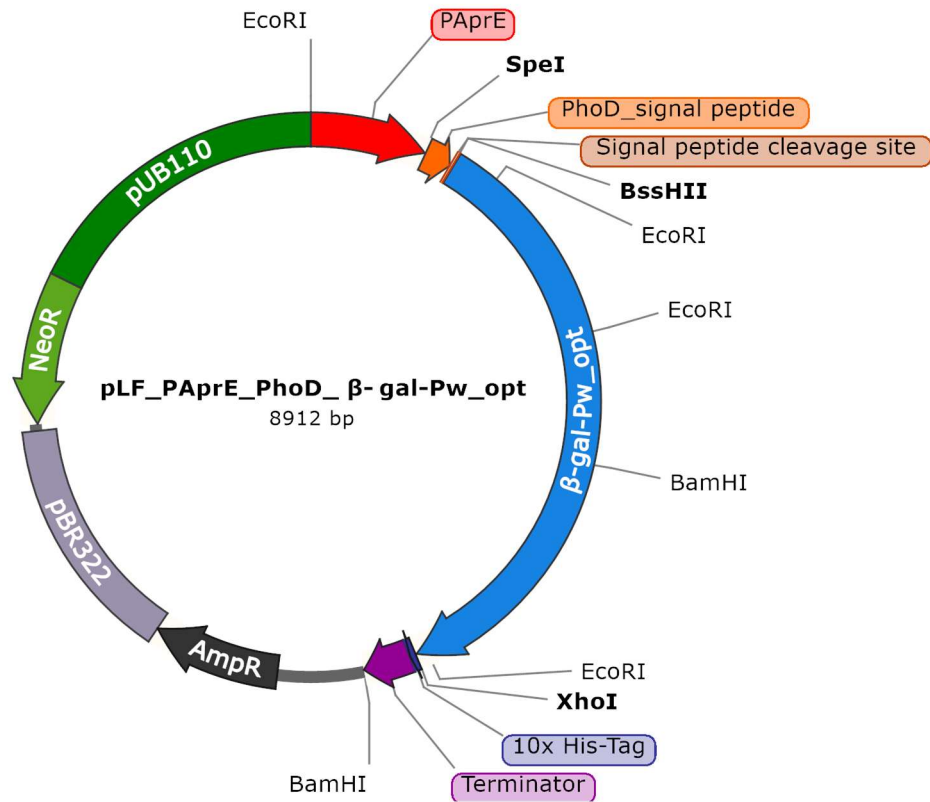


Figure S7: Translation initiation rates calculated with the RBS Calculator v2.1. for the different constructs. 100 nt upstream and 35 nt downstream of the start codon were considered. AU = Arbitrary units.

A



B

gaattcctccattttcttctgctatcaaaataacagactcgtgattttccaaacgagctttcaaaaaagcctctgccccttgc
 aaatcgatgacctgtctataaaattcccgatattggttaaacagcgccgcaatggcgccgcacatctgatgtctttgcttggcg
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Figure S8: Plasmid map (A) and DNA sequence (B) of plasmid pLF_P_{AprE}_PhoD_β-gal-Pw_opt.

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