Table S1. Primers used in the construction of mutants of *P. protegens* Pf-5

Target gene and primers	Sequence 5'-3'
FpvZ (PFL_4092)	
4092UpFBam	CACACCATCAGGATCCACAACACCGACTGACCCCTTT
4092DnFFRT-1	AGGAACTTCAAGATCCCCAATTCGATGCCGGAGCCATCTATGA
4092UpRFRT	TCAGAGCGCTTTTGAAGCTAATTCGATGTTCTGGTCATCCATGCGC
4092DnRBam-1	CTCTGCTTCTGGATCCTGTAGATGGTGTTCTGGCCA
FpvW (PFL_2293)	
2293UpFHind	GTGGTTGTGGAAGCTTTTCACAAGTCGAAGTTGGCC
2293DnFFRT	AGGAACTTCAAGATCCCCAATTCGCCGACGACAGCTACTACGAAA
2293UpRFRT	TCAGAGCGCTTTTGAAGCTAATTCGTCTCCATCACCTGGTCAATG
2293DnRHind	GACGAAGACGAAGCTTAGTTGTCACTCTGGGCGTTGA
FpvX (PFL_3315)	
3315UpFBam	GTTGTGCTGAGGATCCCAAACGGTGACGGTGATCA
3315DnFFRT-1	AGGAACTTCAAGATCCCCAATTCGTGGTCTACGACCTCAACGACA
3315UpRFRT	TCAGAGCGCTTTTGAAGCTAATTCGTGAAGTACATCGGGAAGCC
3315DnRBam-1	GAGAAGGAGAGGATCCGAAGCCGGTGCTGAAATTG
FpvV (PFL_2527)	
2527UpFBam	GTGTGGTAGTGGATCCTGCACCGTAGTTACCGTAGGA
2527DnFFRT	AGGAACTTCAAGATCCCCAATTCGTTGCGGATCAGGTTGATGGT
2527UpRFRT	TCAGAGCGCTTTTGAAGCTAATTCGTACACCAGCATCTTCAACCCC
2527DnRBam	CACACCATCAGGATCCGCGCACATTTTGCTGTCCTA
FpvU (PFL_2391)	
2391UpFBam	CTCTGCTTCTGGATCCACAGGTTCTGGGTGATCTGGT
2391DnFFRT	AGGAACTTCAAGATCCCCAATTCGTTCTTGCGCACCAGGTTGAT
2391UpRFRT	TCAGAGCGCTTTTGAAGCTAATTCGAAGGACAGCAAGCTGCTCAAC
2391DnRBam	GAGAAGGAGAGGATCCAACTGAGTACCCAGAGCGGTT
FpvY (PFL_3485)	
3485UpFBam	GAGAAGGAGAGGATCCCGGGCTATCGGGGTAATACA
3485DnFFRT1	AGGAACTTCAAGATCCCCAATTCGCCTACTTCGAGGTGCATGA
3485UpRFRT	TCAGAGCGCTTTTGAAGCTAATTCGTCGAGGATGCCGTAGTAGA
3485DnRBam	GTGAGTTGCTGGATCCCCTTGCCGTAGTTGCTGAGTA
PFL_2772	
2772UpFHind	CAGCACGAAGCTTCGGTTTTCACCGCCAGCTTC
2772UpR	GGCGTGATGGCGCTCCAGCAATTCATAGGGC
2772DnF	TTGCTGGAGCGCCATCACGCCTTACGAACT
2772DnRHind	CTCCTCGAAGCTTAGGAGTACCTGGTGATACGC

Table S2. Primers used to amplify *pvdD* of *P. fluorescens* A506, WCS374, and SBW25

Target gene and primers	Sequence 5'-3'
PflA506_3090 (*pvdD* of A506)	
PflA506_3090 F	AGTACCTGTTCAACGGCTATG
PflA506_3090 M1	TGCCGACGCATTTGATGTTC
PflA506_3090 M2	CGAAGACGACCATGTGTTG
PflA506_3090 R	CCAGAAGTGCTACCACCATTTC
PFLU_2544 (*pvdD* of SBW25)	
PFLU_2544 F1	CTACCTGTTCAACGGCTAC
PFLU_2544 R1	CAACTGCTCCTTGATCTGCT
PFLU_2544 F2	CTCAAGCAGATCAAGGAGCA
PFLU_2544 R2	GCCAACGACCATTTCAATCG

Table S3. Growth of Fpv$^-$ mutants of Pf-5 on an iron-limited medium in the presence of crossfeeding strains of *Pseudomonas* spp.

Crossfeeding Strain	**Growth of Pf-5 Deletion Mutant**[a]					
	fpvZ	*fpvU*	*fpvY*	*fpvW*	*fpvX*	*fpvV*
P. protegens Pf-5	-	+	+	+	+	+
P. aeruginosa PAO1	+	-	+	+	+	+
P. fluorescens SBW25	+	-	+	+	+	+
P. fluorescens ATCC 13525	+	-	+	+	+	+
P. chlororaphis ATCC 9446	+	-	+	+	+	+
P. rhodesiae CFML 92-104	+	+	-	+	+	+
P. fluorescens B10	+	+	+	-	+	+
P. putida CS111	+	+	+	+	-	+
P. putida BN7	+	+	+	+	+	-
P. fluorescens A506	+	+	+	+	+	+
P. fluorescens WCS374	+	+	+	+	+	+
P. aeruginosa LESB58	+	+	+	+	+	+

[a] Growth of Fpv$^-$ mutants in a Δ*pvdI-pchA* background of Pf-5 on an iron-limited medium (KMB amended with 600 μM 2,2'-dipyridyl) in the presence of the crossfeeding strain: +, growth; –, no growth. The Δ*pvdI-pchA* mutant of Pf-5 did not grow on the iron-limited medium in isolation, but did grow in the presence of all crossfeeding strains listed.

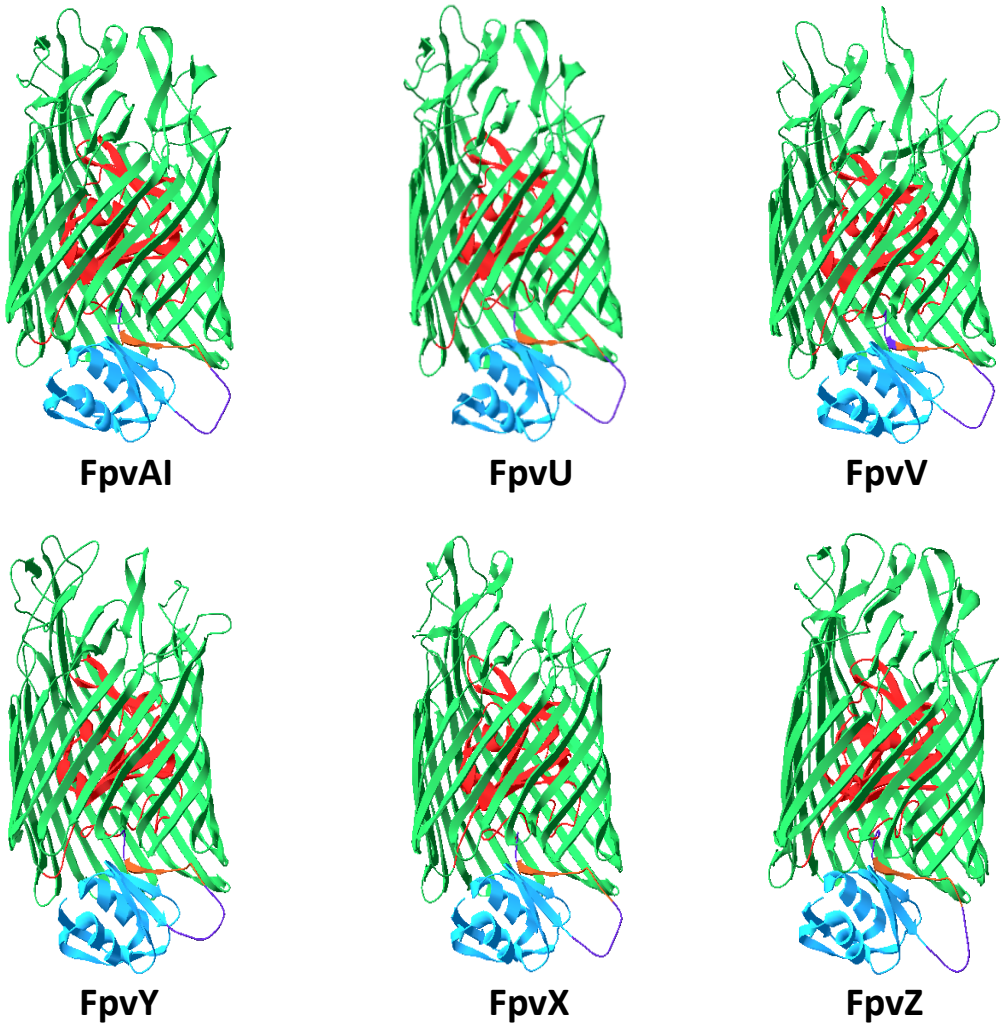
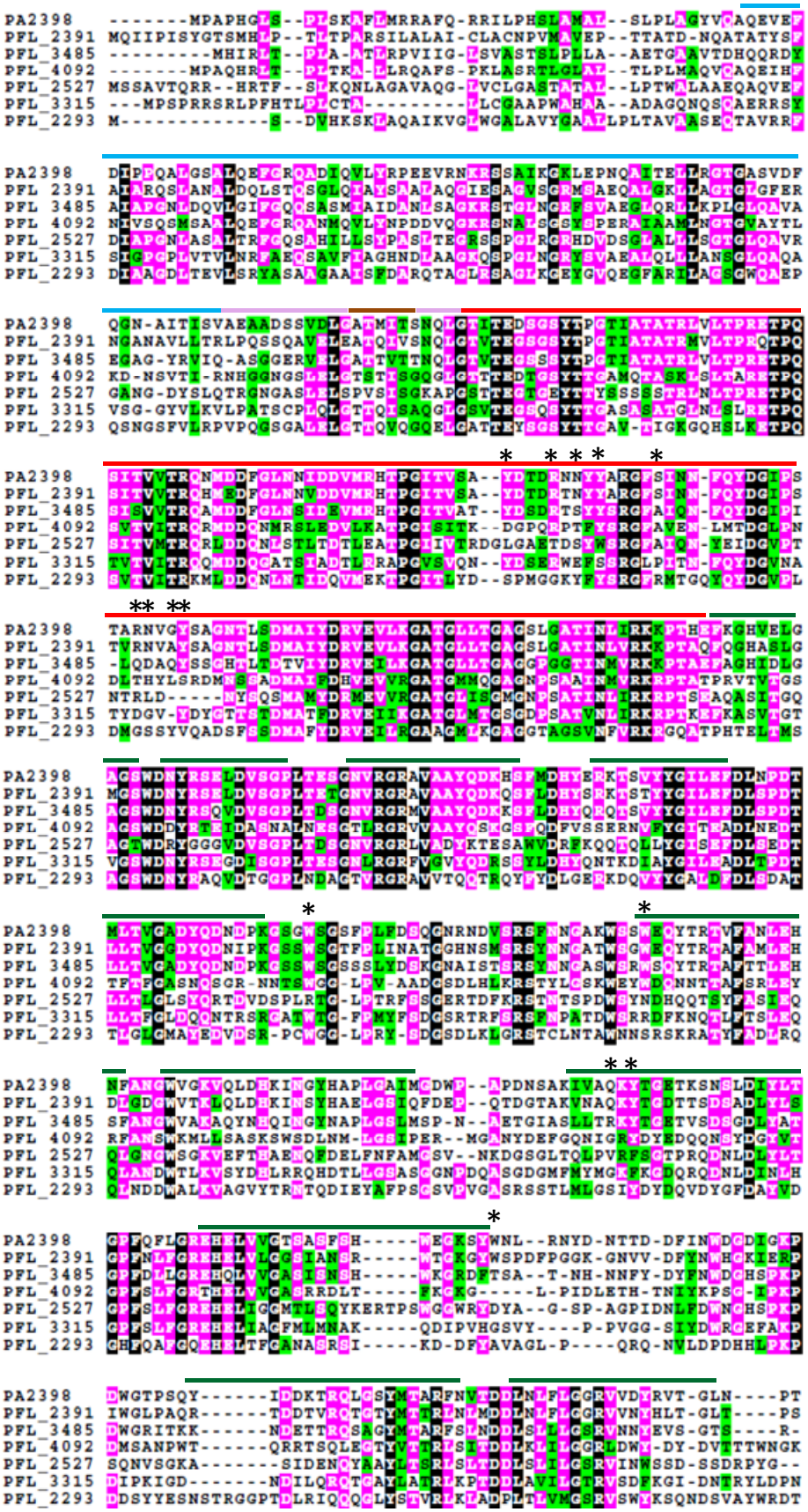


Fig. S1. Homology models of FpvAI of *P. aeruginosa* PAO1 and five proteins (FpvU, FpvY, FpvZ; FpvV; FpvX) of *P. protegens* Pf-5. Structural components of Fpvs, with the β-barrel in green, plug in red, N-terminal signaling domain in blue, connecting loop in purple, and TonB box in brown. The homology models were constructed using a structure-based sequence alignment with the crystal structure of FpvAI from *P. aeruginosa* PAO1 (3) as a template. Locus tags corresponding to Fpvs of Pf-5 are FpvU (PFL_2391), FpvV (PFL_2527), FpvW (PFL_2293), FpvX (PFL_3315), FpvY (PFL_3485), and FpvZ (PFL_4092).


PA2398
PFL_2391
PFL_3485
PFL_4092
PFL_2527
PFL_3315
PFL_2293

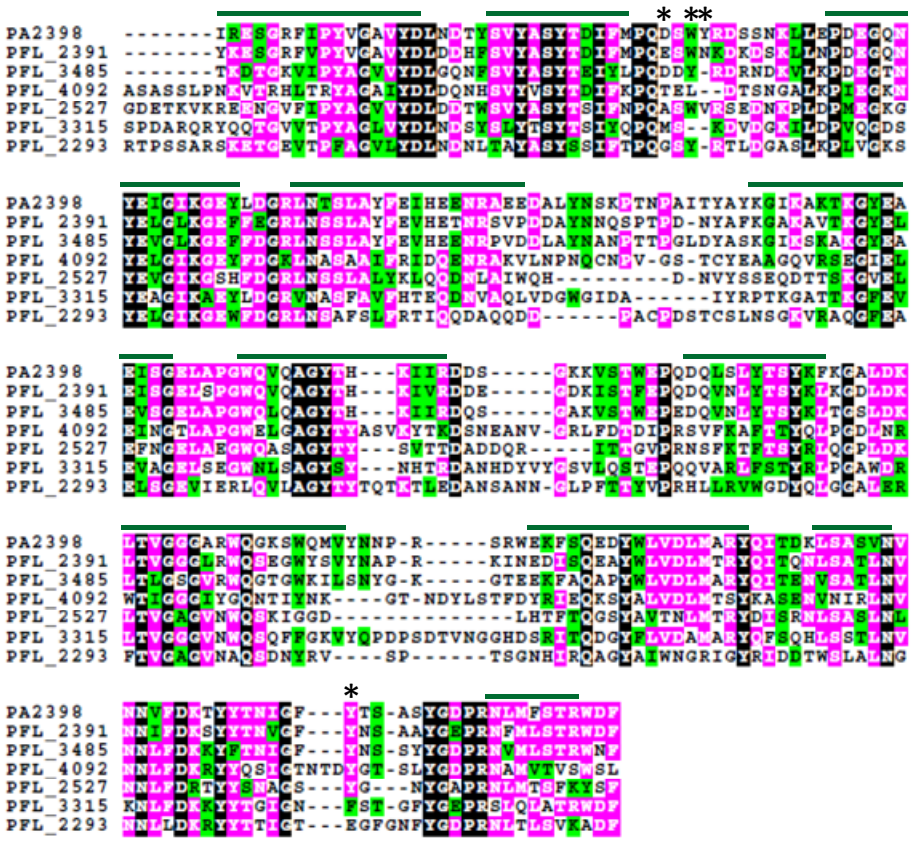


Fig. S2. Alignment of PA2398 (FpvAI) from *P. aeruginosa* PAO1 with the six Fpv outer-membrane proteins from Pf-5. The colored lines above the alignment delineate domains and conserved regions based on the characterized residues of FpvAI: N-terminal signaling domain, blue; connecting loop, purple; TonB box, brown; plug domain, red; and β-strands of the β-barrel, green. Amino acid residues of FpvAI (PA2398) involved in pyoverdine binding are indicated with an asterisk. Residues are highlighted to show levels of similarity: identical residues present in all proteins, black; identical residues present in a subset of proteins, pink; similar residues, green. Locus tags correspond to FpvU (PFL_2391), FpvV (PFL_2527), FpvW (PFL_2293), FpvX (PFL_3315), FpvY (PFL_3485), and FpvZ (PFL_4092).

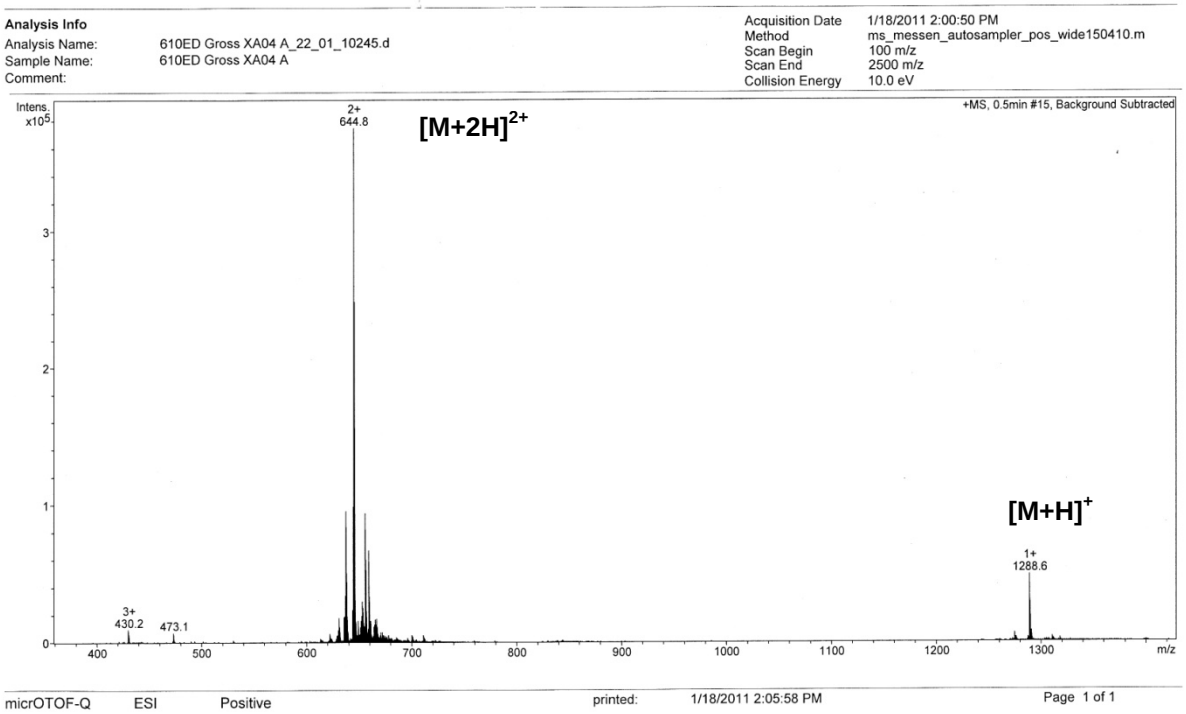


Fig. S3. Low-Res-ESI-MS spectrum of the pyoverdine of *P.protegens* Pf-5.

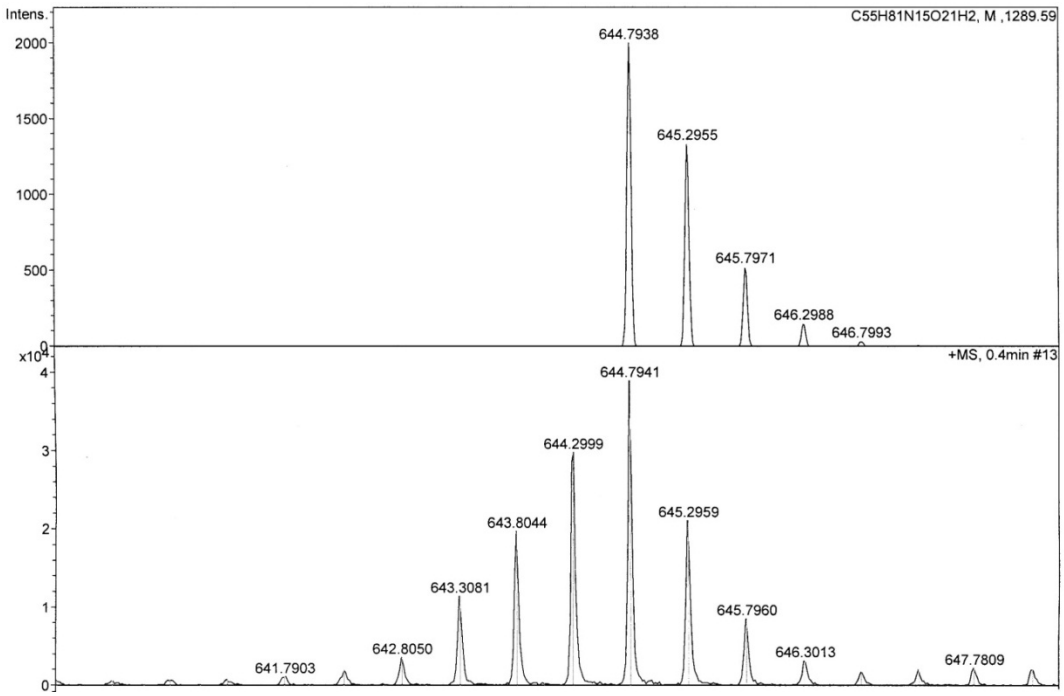


Fig. S4. HR-ESI-MS spectrum of the pyoverdine of *P.protegens* Pf-5.

Text S1. Identification of purified pyoverdines including co-occuring isoforms by high resolution electron spray ionization mass spectroscopy (HR-ESI-MS). HR-ESI-MS analysis of the pyoverdines of *P. aeruginosa* PAO1 yielded $[M+H]^+$ ions at *m/z* 1334.5938 and 1362.5906, which agrees with values obtained in previous studies (5) and the molecular formula of pyoverdine D ($[M+H]^+$: $C_{55}H_{84}N_{17}O_{22}$, *m/z* 1334.5971) and C ($[M+H]^+$: $C_{56}H_{84}N_{17}O_{23}$, *m/z* 1362.5920), respectively (1). The mass difference (Δ 28 Da) corresponds to the side chains α-ketoglutaric acid in pyoverdine C and succinic acid in pyoverdine D. Mass analysis of free pyoverdines of *P. fluorescens* B10 gave quasi molecular ions $[M+H]^+$ at *m/z* 1035.4381, 1019.4475 and 990.4166. The latter ion is consistent with the formula of pseudobactin ($[M+H]^+$: $C_{42}H_{60}N_{11}O_{17}$, *m/z* 990.4163), which is known to be produced by *P. fluorescens* B10 (7). The occurrence of the other two pyoverdines was reported (5-6) but, to the best of our knowledge, their structures have not been described previously. Empirically, the pyoverdines of one strain differ most likely in the nature of the dicarboxylic acid side chain bound via the amino group of the chromophore or in the chromophore itself. Therefore, we suggest that the derivative with M=1018 Da possibly represents the glutamate isoform of pseudobactin ($[M+H]^+$: $C_{43}H_{63}N_{12}O_{17}$, *m/z* 1019.4429). The remaining derivative with M=1034 shows a difference of 16 Da to B10-1018 which points towards a hydroxylated congener of B10-1018 (e.g. OH-glutamate, 5-OH-chromophore, exchange of Ala with Ser). HR-MS analysis of the pyoverdines of *P. putida* Bn7 revealed three isoforms with $[M+H]^+$ ions at *m/z* 1163.4956, 1047.441 and 1134.4751. The structures of these pyoverdines are currently unknown and further structure elucidation was not attempted. However, the mass difference of 29 mass units between Bn7-1133 and Bn7-1162 might be attributable to an exchange of succinic acid with glutamic acid regarding the acyl side chain. In the pyoverdine fractions of *Pseudomonas* sp. SB8.3 and *P. rhodesiae* CFML92-104, isoforms were absent and only one major pyoverdine was detectable. Peaks at *m/z* 1047.4787 and 1438.6061 confirmed the known pyoverdines of *P. putida* SB83 (Suc-Chr-Ala-Lys-Thr-Ser-AcOHOrn-cOHOrn; $[M+H]^+$: $C_{45}H_{67}N_{12}O_{17}$, *m/z* 1047. 4742)[1] and *P. rhodesiae* CFML92-104 (Mal-Chr-Ser–Lys–FOHOrn–Ser–Ser–Gly–(Lys–FOHOrn–Ser–Ser)[2]; $C_{58}H_{88}N_{17}O_{26}$, *m/z* 1438.6081), respectively (2, 4).

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[1] Underline denotes D-configurated amino acids. [2] Absolute configuration unknown.

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