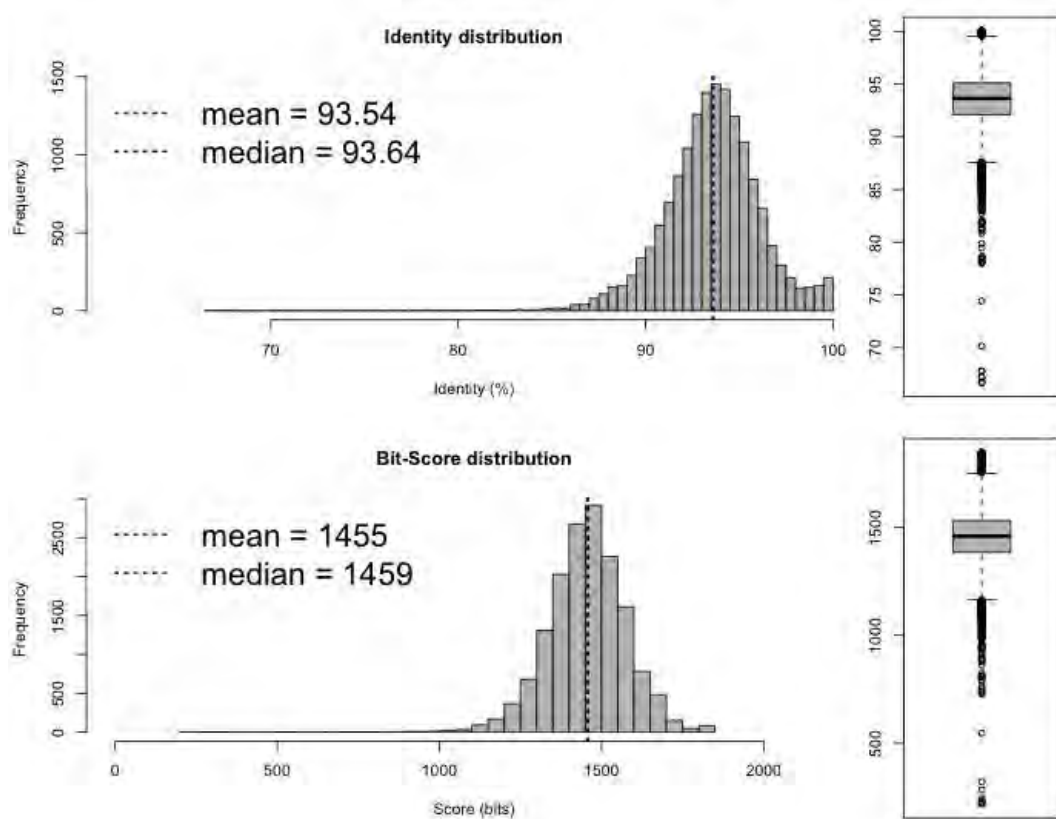


ゲノムによる当該菌株の同定

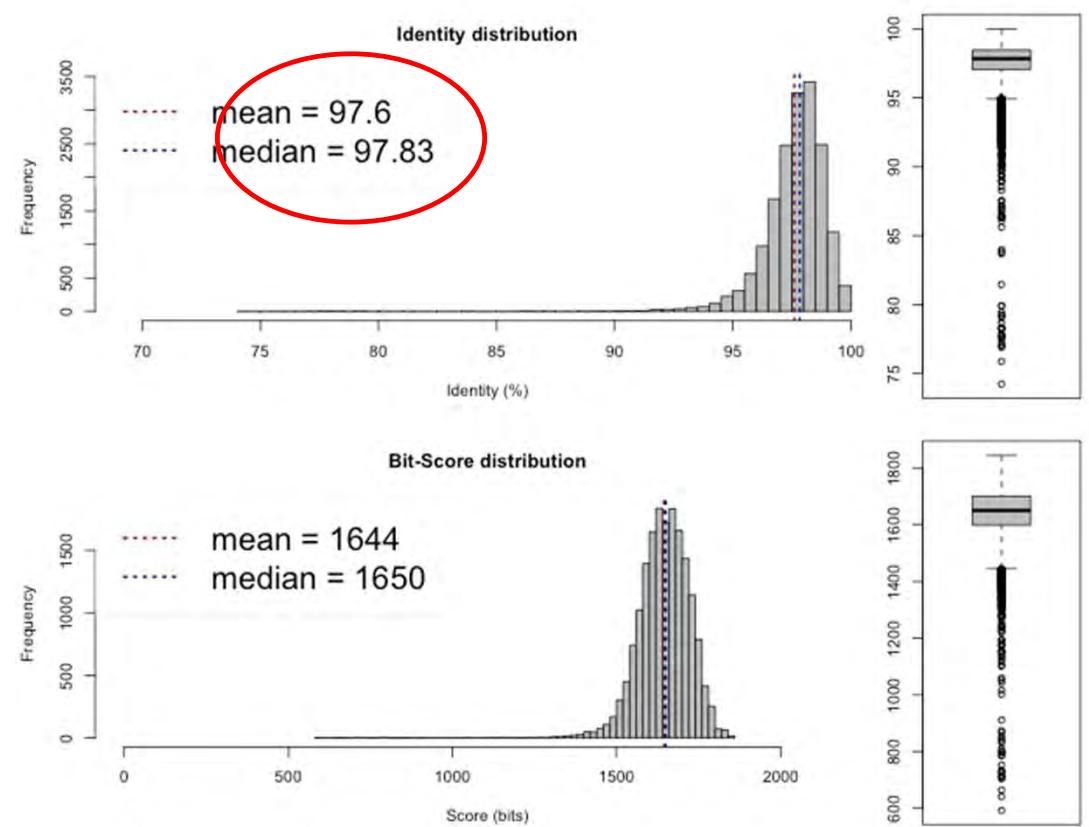
Average Nucleotide Identity (ANI) 解析

ANI解析は、対照株のゲノム配列をコンピュータ上で1,020 bpに断片化し、比較株のゲノム配列に対して各断片の相同性検索を行い、それらの相同値の平均値からゲノム配列間のANI値を求める。ANI値が95%以上であれば同種、95%未満であれば別種（新種）と判定する。

VS *B. amyloliquefaciens*^{ts} BSM7

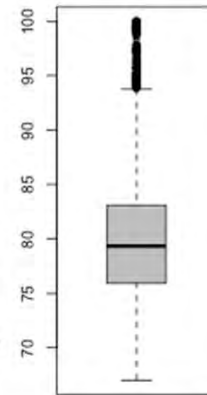
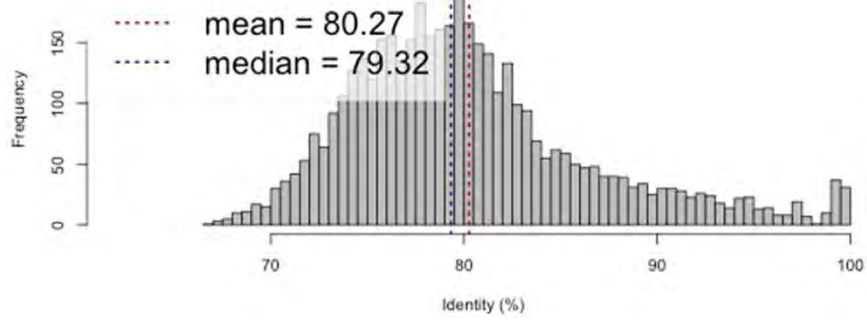


VS *B. velezensis*^{ts} FZB42

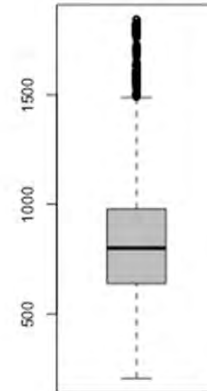
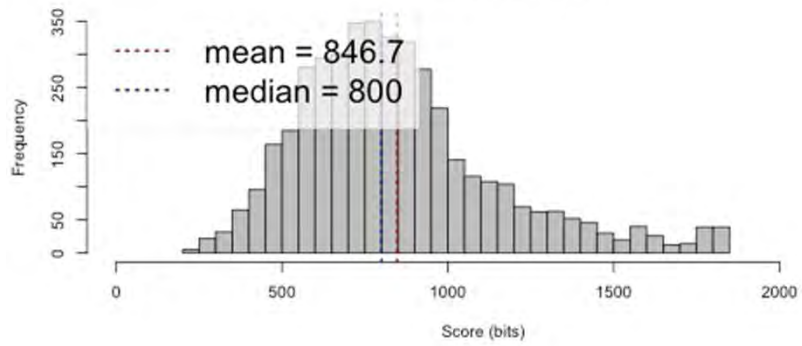


VS *B. subtilis*^{ts}

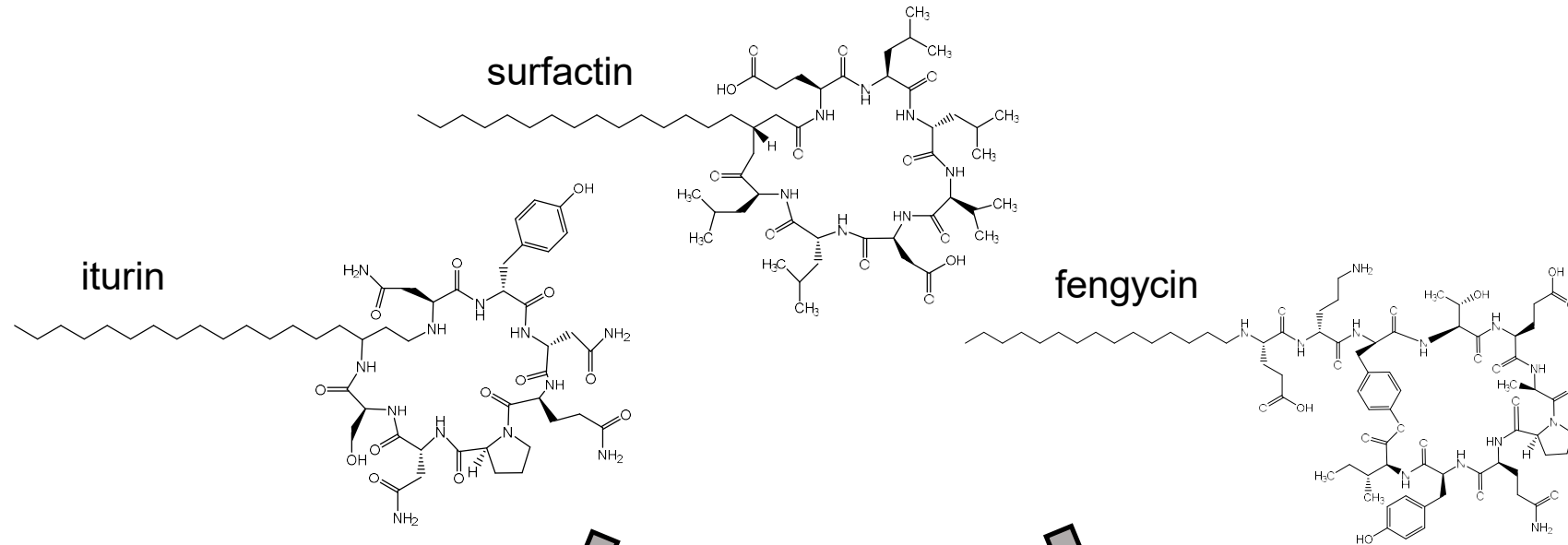
Identity distribution



Bit-Score distribution



Cyclic lipopeptide(cLP) produced by *Bacillus* species



植物病原菌殺菌作用



Antimicrobial activity against plant pathogen

植物の病害抵抗性付与



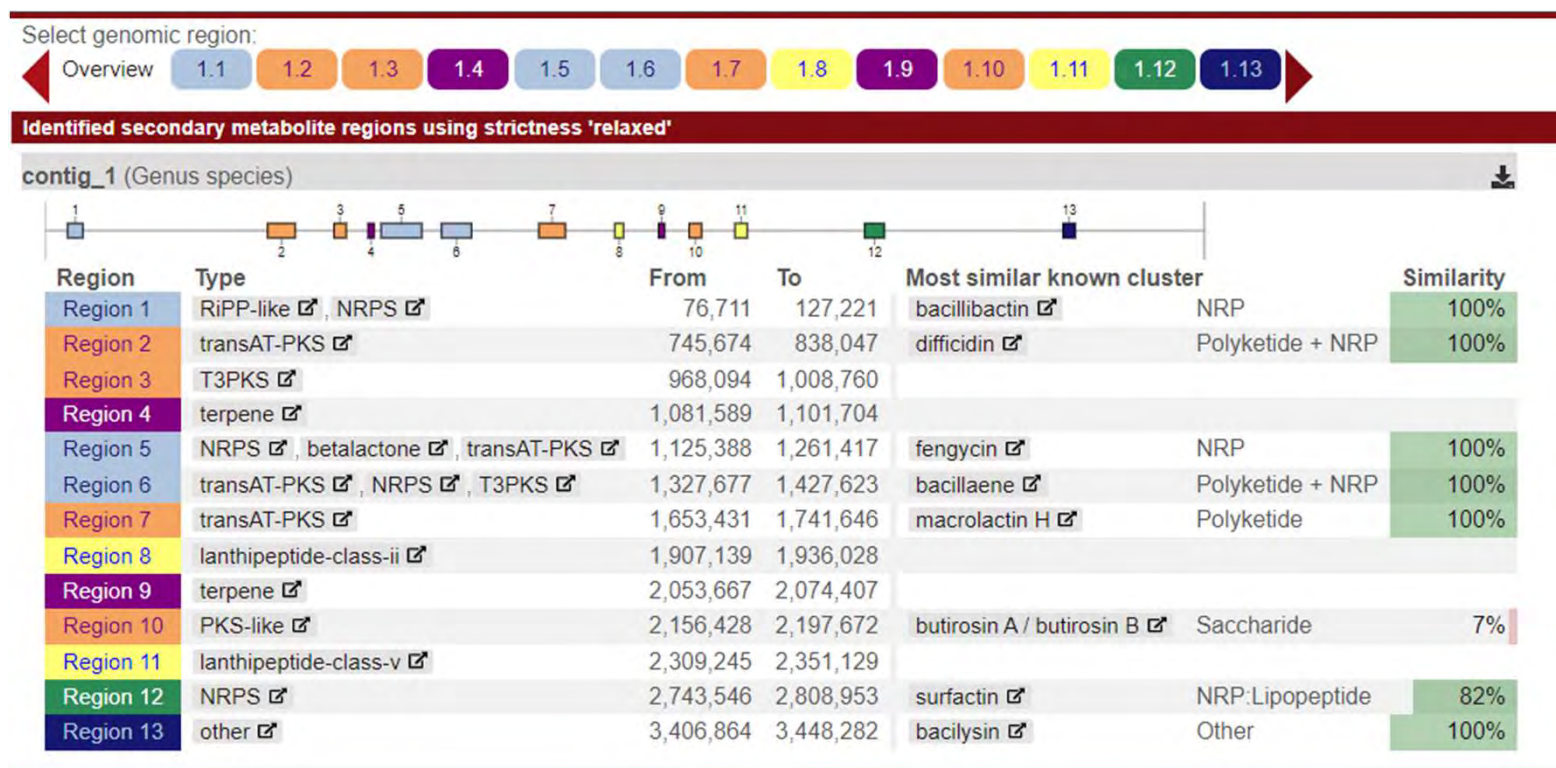
Induction of disease resistance on host plants

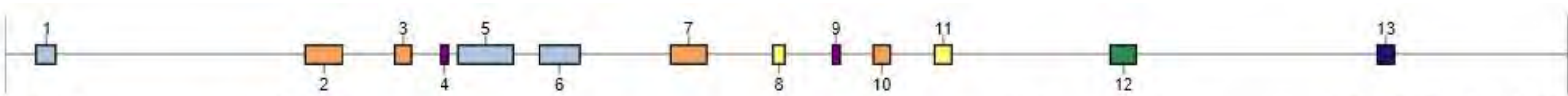


Identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial genomes

二次代謝物
合成遺伝子

antiSMASH 6.0: improving cluster detection and comparison capabilities
Kai Blin, Simon Shaw, Alexander M Kloosterman, Zach Charlop-Powers, Gilles P van Weezel, Marnix H Medema, & Tilmann Weber
Nucleic Acids Research (2021) doi: 10.1093/nar/gkab335.





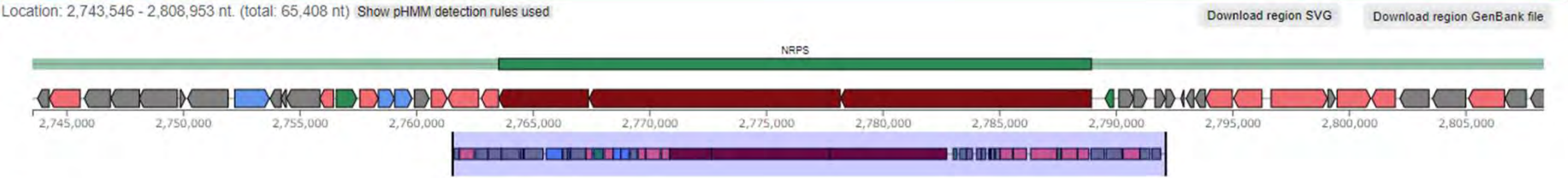
領域	タイプ	から	に	最も類似した既知のクラスター	類似性
リージョン 1	RiPP様 ☑、 NRPS ☑	76,711	127,221	バシリバクチン ☑ NRP	100%
リージョン 2	transAT-PKS ☑	745,674	838,047	ディフィシジン ☑ ポリケチド + NRP	100%
リージョン 3	T3PKS ☑	968,094	1,008,760		
リージョン 4	テルペン ☑	1,081,589	1,101,704	fengycin & iturin	
リージョン 5	NRPS ☑、 ベータラクトン、 transAT ☑ -PKS ☑	1,125,388	1,261,417	フェンギシン ☑ NRP	100%
リージョン 6	transAT-PKS ☑、 NRPS ☑、 T3PKS ☑	1,327,677	1,427,623	バシレン ☑ ポリケチド + NRP	100%
リージョン 7	transAT-PKS ☑	1,653,431	1,741,646	マクロラクチンH ☑ ポリケチド	100%
リージョン 8	ランチペプチドクラスII ☑	1,907,139	1,936,028		
リージョン 9	テルペン ☑	2,053,667	2,074,407		
リージョン 10	PKS様 ☑	2,156,428	2,197,672	ブチロシンA/ブチロシンB ☑ 糖類	7%
リージョン 11	lanthipeptide-class-v ☑	2,309,245	2,351,129		
リージョン 12	NRPS ☑	2,743,546	2,808,953	サーファクチン ☑ NRP:リポペプチド	82%
リージョン 13	他の ☑	3,406,864	3,448,282	バシリシン ☑ 他の	100%



SrfA operon



contig_1 - Region 12 - NRPS



Legend:

core biosynthetic genes
 additional biosynthetic genes
 transport-related genes
 regulatory genes
 other genes
 resistance

NRPS/PKS domains [KnownClusterBlast](#) [SubClusterBlast](#) [NRPS/PKS modules](#)

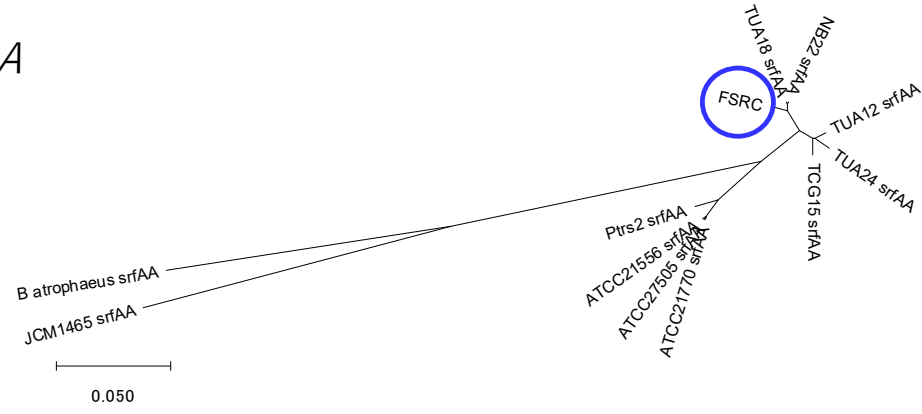
Detailed domain annotation

Selected features only Show module domains

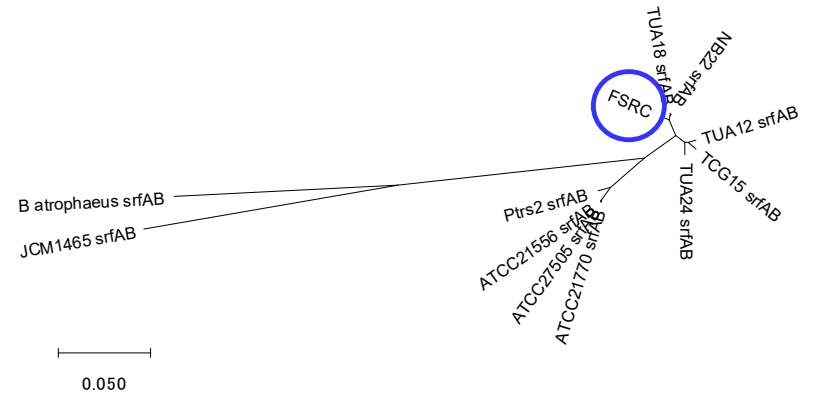
FSRC201_02742	-----○-----		
FSRC201_02743	-----AmT-----		
FSRC201_02744	-----TE-----		
FSRC201_02745	-----leu-----		
FSRC201_02746	-----val-----	-----asp-----	-----D-leu-----
FSRC201_02747	-----glu-----	-----leu-----	-----D-leu-----

Name	Peptide moiety
Surfactin A	L-Glu-L-Leu-D-Leu-L-Val-L-Asp-D-Leu-L-Leu

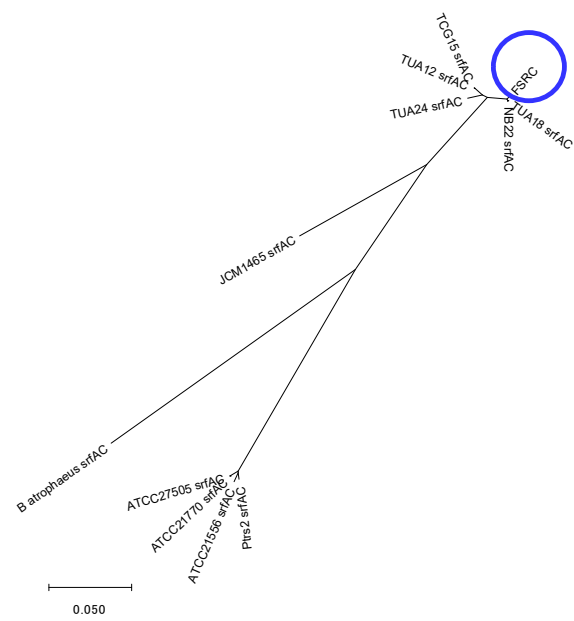
srfAA



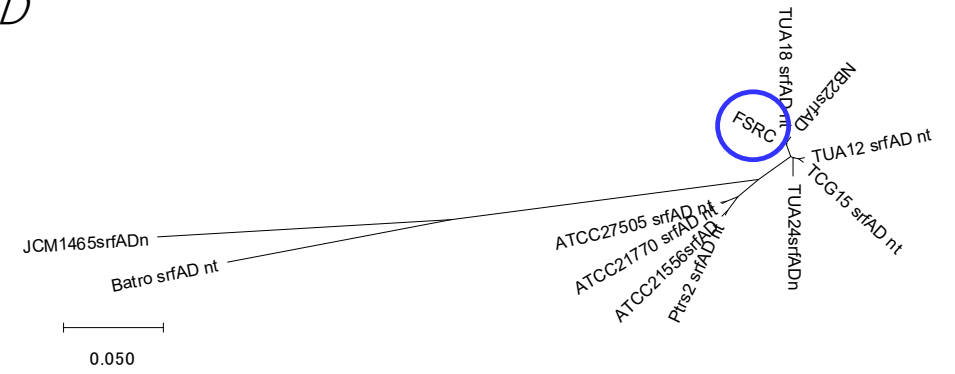
srfAB



srfAC



srfAD



contig_1 - Region 5 - NRPS,betalactone,transAT-PKS

Location: 1,125,388 - 1,261,417 nt. (total: 136,030 nt) Show pHMM detection rules used

[Download region SVG](#)

[Download region GenBank file](#)



Legend:

■ core biosynthetic genes

■ additional biosynthetic genes

■ transport-related genes

■ regulatory genes

■ other genes

■ resistance

pps Operon for fengycin

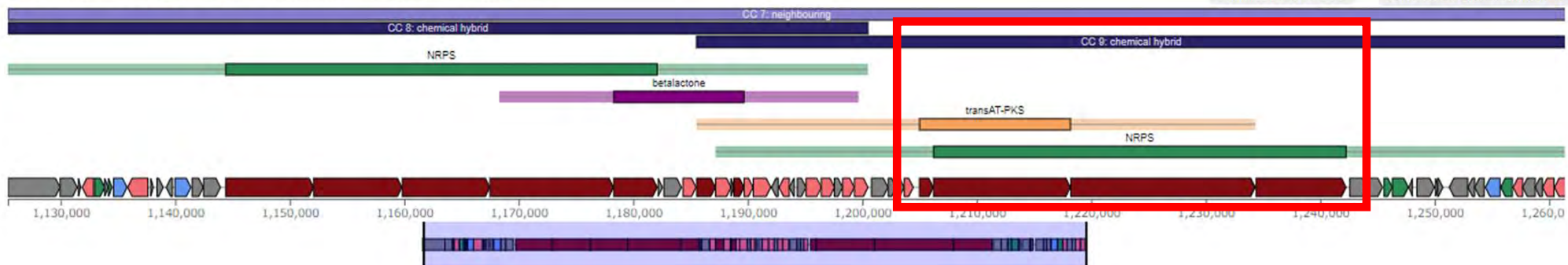
itu operon for iturin

contig_1 - Region 5 - NRPS,betalactone,transAT-PKS

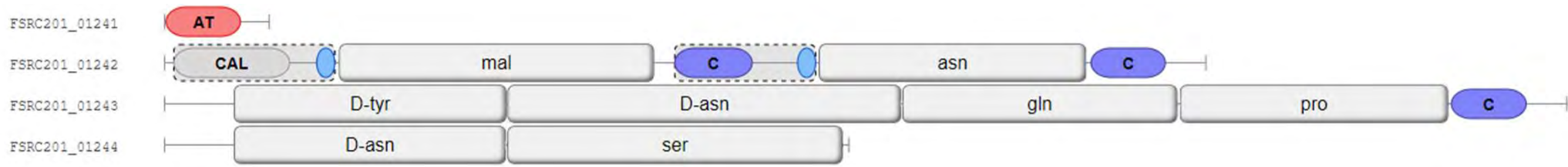
Location: 1,125,388 - 1,261,417 nt. (total: 136,030 nt) Show pHMM detection rules used

Download region SVG

Download region GenBank file



Legend:



Iturin family	Heptapeptide closed by a lactam ring with the β -NH ₂ group of the acid chain	β -NH ₂ fatty acids	
Bacillomycin D	L-Asn-D-Tyr-D-Asn-L-Pro-L-Glu-D-Ser-L-Thr	<i>n</i> C ₁₄ , <i>i</i> C ₁₅ , <i>a</i> C ₁₅	Peypoux et al. 1981
Bacillomycin F	L-Asn-D-Tyr-D-Asn-L-Gln-L-Pro-D-Asn-L-Thr	<i>n</i> C ₁₆ , <i>i</i> C ₁₇ , <i>a</i> C ₁₇	Peypoux et al. 1985
Bacillomycin L or L ^a	L-Asn-D-Tyr-D-Asn-L-Ser-L-Gln-D-Ser-L-Thr	<i>n</i> C ₁₄ , <i>i</i> C ₁₅ , <i>a</i> C ₁₅	Velzen et al. 2007
Iturin A	L-Asn-D-Tyr-D-Asn-L-Gln-L-Pro-D-Asn-L-Ser	<i>n</i>C₁₄, <i>i</i>C₁₅, <i>a</i>C₁₅	Peypoux 1978
Iturin A_L	L-Asn-D-Tyr-D-Asn-L-Gln-L-Pro-D-Asn-L-Ser	<i>n</i>C₁₆, <i>i</i>C₁₆	Winkelmann et al. 1985
Iturin C	L-Asp-D-Tyr-D-Asn-L-Gln-L-Pro-D-Asn-L-Ser	<i>n</i> C ₁₄ , <i>i</i> C ₁₅ , <i>a</i> C ₁₅	Peypoux et al. 1986
Mycosubtilin	L-Asn-D-Tyr-D-Asn-L-Gln-L-Pro-D-Ser-L-Asn	<i>n</i> C ₁₆ , <i>i</i> C ₁₆ , <i>a</i> C ₁₇	Peypoux et al. 1986

contig_1 - Region 5 - NRPS,betalactone,transAT-PKS

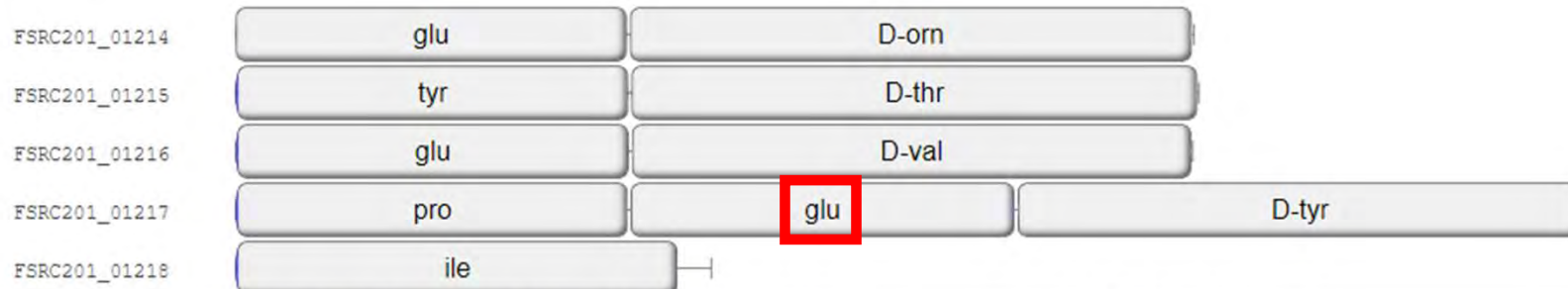
Location: 1,125,388 - 1,261,417 nt. (total: 136,030 nt) Show pHMM detection rules used

Download region SVG

Download region GenBank file



Legend:



Fengycin family

Decapeptide with a lactone ring between carboxy-terminal group of Ile₁₀ and OH group of Tyr₃

β-OH fatty acids

- Fengycin A
- Fengycin B
- Plipastatin A
- Plipastatin B

L-Glu-D-Orn-D-**Tyr**-D-a Thr-L-Glu-D-**Ala**-L-Pro-L-**Gln**-L-Tyr-L-Ile
 L-Glu-D-Orn-D-**Tyr**-D-a Thr-L-Glu-D-**Val**-L-Pro-L-**Gln**-L-Tyr-L-Ile
 L-Glu-D-Orn-D-**Tyr**-D-a Thr-L-Glu-D-**Ala**-L-Pro-L-**Gln**-L-Tyr-L-Ile
 L-Glu-D-Orn-D-**Tyr**-D-a Thr-L-Glu-D-**Val**-L-Pro-L-**Gln**-L-Tyr-L-Ile

*a*C₁₅, *i*C₁₆, *n*C₁₆
*a*C₁₅, *i*C₁₆, *n*C₁₆, C₁₇
*n*C₁₆, *a*C₁₇
*n*C₁₆, *a*C₁₇

Schneider et al. 1999
 Schneider et al. 1999
 Nishikiori et al. 1986
 Nishikiori et al. 1986