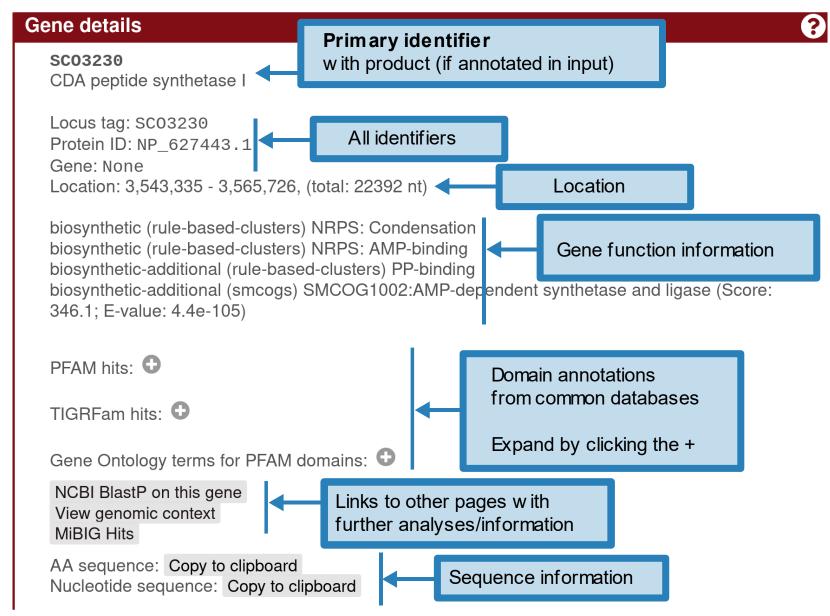


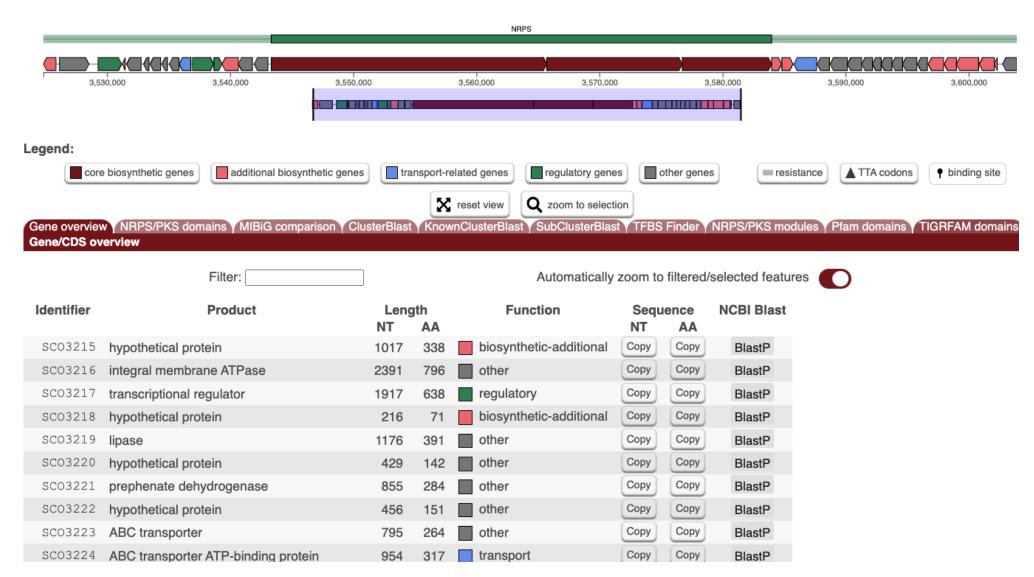
antiSMASH – results: Gene details



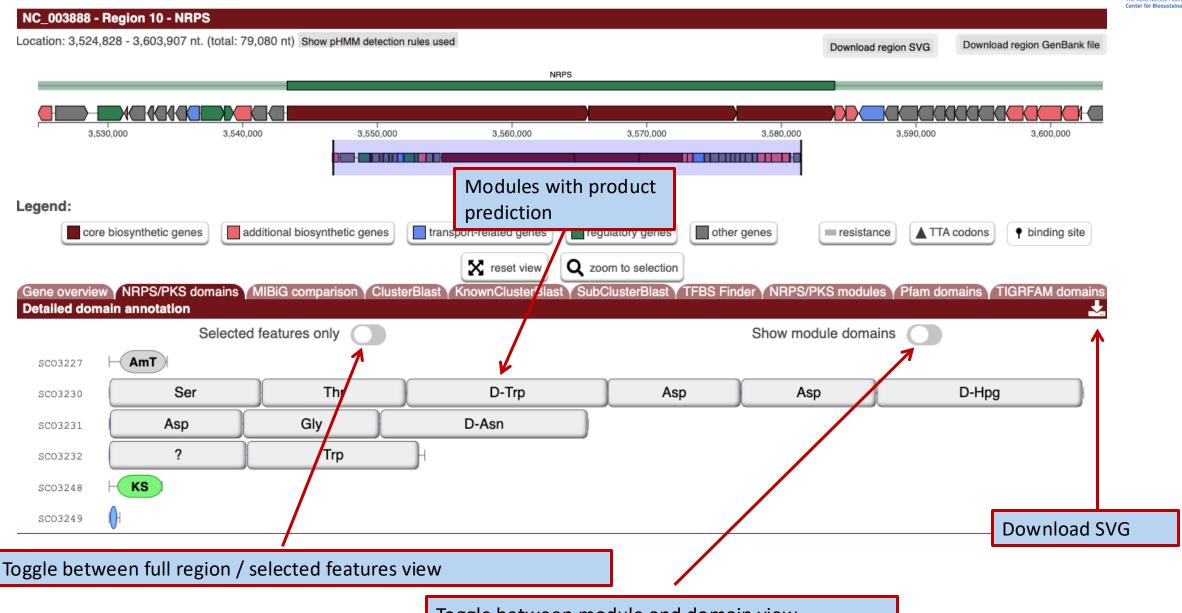


antiSMASH results- Gene Overview



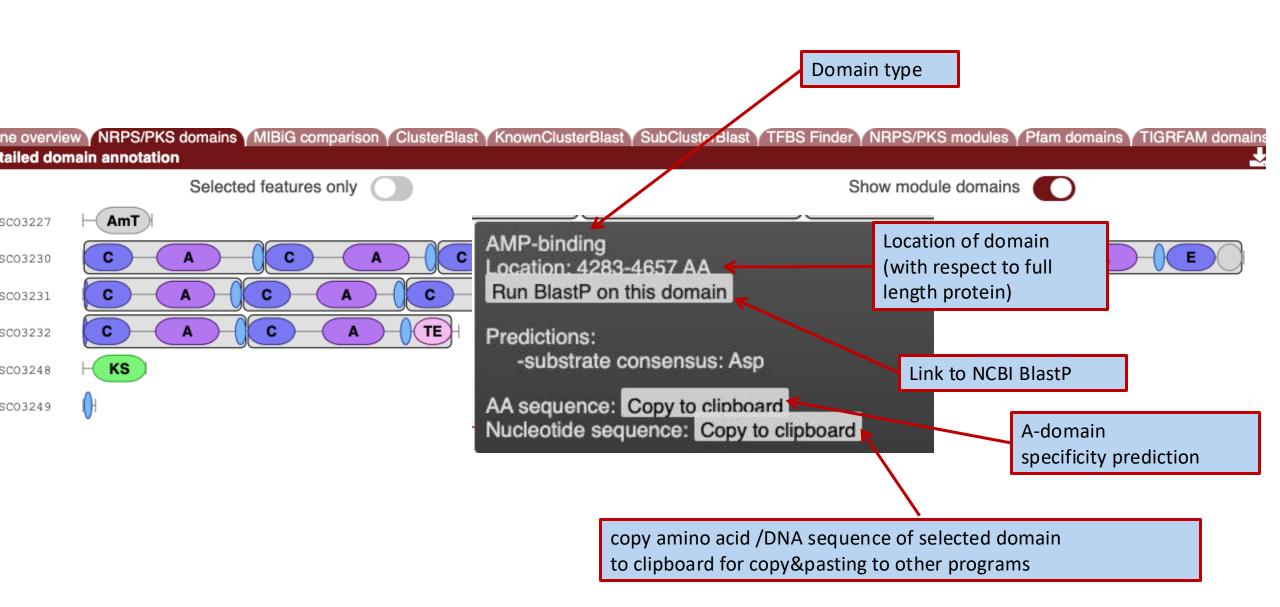






Toggle between module and domain view





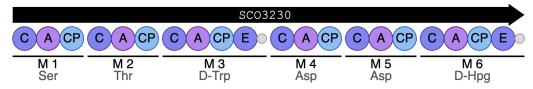
PKS/NRPS modules view

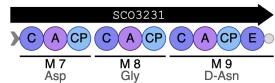


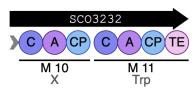
Gene overview NRPS/PKS domains MIBiG comparison ClusterBlast KnownClusterBlast SubClusterBlast TFBS Finder NRPS/PKS modules Pfam domains TIGRFAM domains

Module view

Candidate 10 (3524827 - 3603907): single NRPS ~







Legend



Special domain (e.g. trans-AT docking domains)

Domain in an incomplete module or outside modules

N-terminal docking domains

C-terminal docking domains

Marks domains that are predicted to be inactive

The gene/CDS feature containing the domains

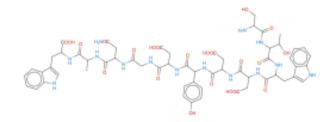
M# The extent of a module, with the module number and the predicted monomer for that module

Module extents when predicted to be iterative



NRPS/PKS products NRPS/PKS monomers TFBS Finder Predicted core structure(s)

For candidate cluster 10, location 3524827 - 3603907:



core structure prediction

Rough prediction of core scaffold based on assumed PKS/NRPS colinearity; tailoring reactions not taken into account

Polymer prediction:

Direct lookup in NORINE database: strict ☑ or relaxed ☑

Link to NORINE database query form □

Link to NORINE NRP database (for NRPs)

prediction of the monomer sequence



```
NRPS/PKS products NRPS/PKS monomers TFBS Finder
NRPS/PKS monomer predictions
sco3230: Ser - Thr - Trp - Asp - Asp - Hpa
     Search NORINE for peptide: strict ☑ or relaxed ☑
     AMP-binding (475..883): Ser
       Stachelhaus: Ser
        Stachelhaus lookup: serine
        10 AA signature DVWHFSLVDK
      NRPSPredictor2: ser
        SVM prediction details:
           Predicted physicochemical class:
              hydrophobic-aliphatic
           Large clusters prediction:
                                                   prediction details for the PKS/NRPS domains
              ser, thr, dhpg, hpg
            Small clusters prediction:
            Single AA prediction:
        Stachelhaus prediction details:
            Stachelhaus sequence:
              DVWHFSLVDK
            Nearest Stachelhaus code:
            Stachelhaus code match:
              100% (strong)
     AMP-binding (1674..2097): Thr
     AMP-binding (2759..3160): Trp
     AMP-binding (4283..4657): Asp
                                                     Click "+" to unfold
     AMP-binding (5323..5697): Asp
     AMP-binding (6360..6777): Hpg
SC03231: Asp - Gly - Asn
sco3232: X - Trp
```

antiSMASH – results: ClusterBlast



Similar gene clusters	
All hits	Download graphic
Query sequence	
NC_003888_c10: Streptomyces coelicolor A3(2) chromosome, complete genome (100% of genes show simil	ilarity), nrps
NZ_CP009124_c17: Streptomyces lividans TK24, complete genome (94% of genes show similarity), nrps	
NZ_LT629768_c10: Streptomyces sp. 2114.2 genome assembly, chromosome: I (94% of genes show simila	arity), nrps
NZ_JOCT01000040_c25: Streptomyces sp. NRRL S-455 contig40.1, whole genome sho (62% of genes sho	ow similarity), nı
NZ_JOCE01000054_c25: Streptomyces violaceoruber strain NRRL S-12 contig54.1, (100% of genes show	v similarity), nrp
NZ_JOCE01000043_c22: Streptomyces violaceoruber strain NRRL S-12 contig43.1, (79% of genes show s	similarity), nrps
NZ_JOCG01000010_c14: Streptomyces sp. NRRL WC-3795 contig10.1, whole genome s (88% of genes sh	how similarity), r
NZ_KB911613_c24: Streptomyces canus 299MFChir4.1 H293DRAFT scaffold00032.32, (38% of genes sho	now similarity), la
NZ_CP015098_c21: Streptomyces sp. S10(2016), complete genome (32% of genes show similarity), nrps	4 00 00-43333 0 4
NZ_JOCG01000031_c23: Streptomyces sp. NRRL WC-3795 contig31.1, whole genome s (66% of genes sh	how similarity), r

→ Identification of similar biosynthetic pathways in other strains

antiSMASH – results: SubClusterBlast

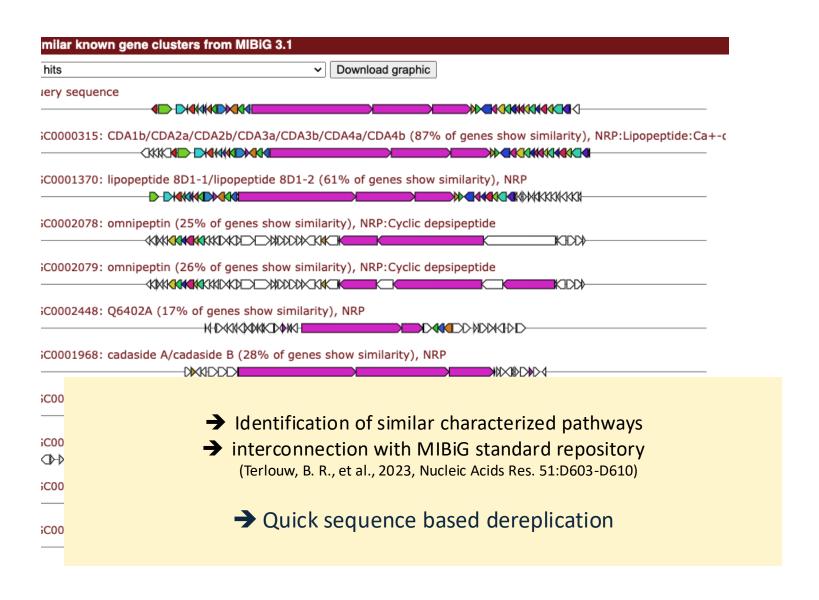


Similar subclusters	
All hits	Download graphic
Query sequence	
AF386507_c1: complestatin hydroxyphenylglycine (100% of ger	nes show similarity), HPG
Y16952_c2: balhimycin hydroxyphenylglycine (100% of genes s	show similarity), HPG
HE589771_c2: vancomycin hydroxyphenylglycine (100% of gen	es show similarity), HPG
AJ632270_c2: teicoplanin hydroxyphenylglycine (66% of genes	show similarity), HPG
AL939125_c1: prodigiosin 2-undecylpyrrole (25% of genes show	w similarity), 2-undecylpyrrole

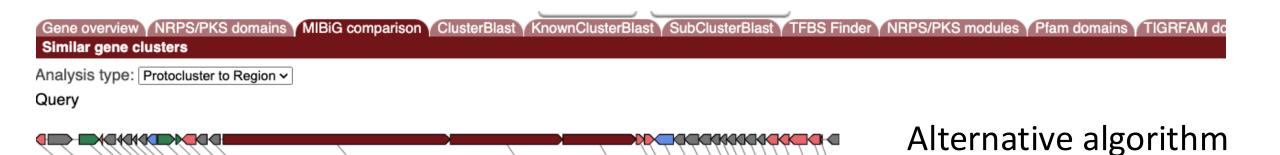
→ Identification of genes within the gene cluster encoding pathways for precursor building-blocks

antiSMASH – results: KnownClusterBlast





antiSMASH MIBiG comparison

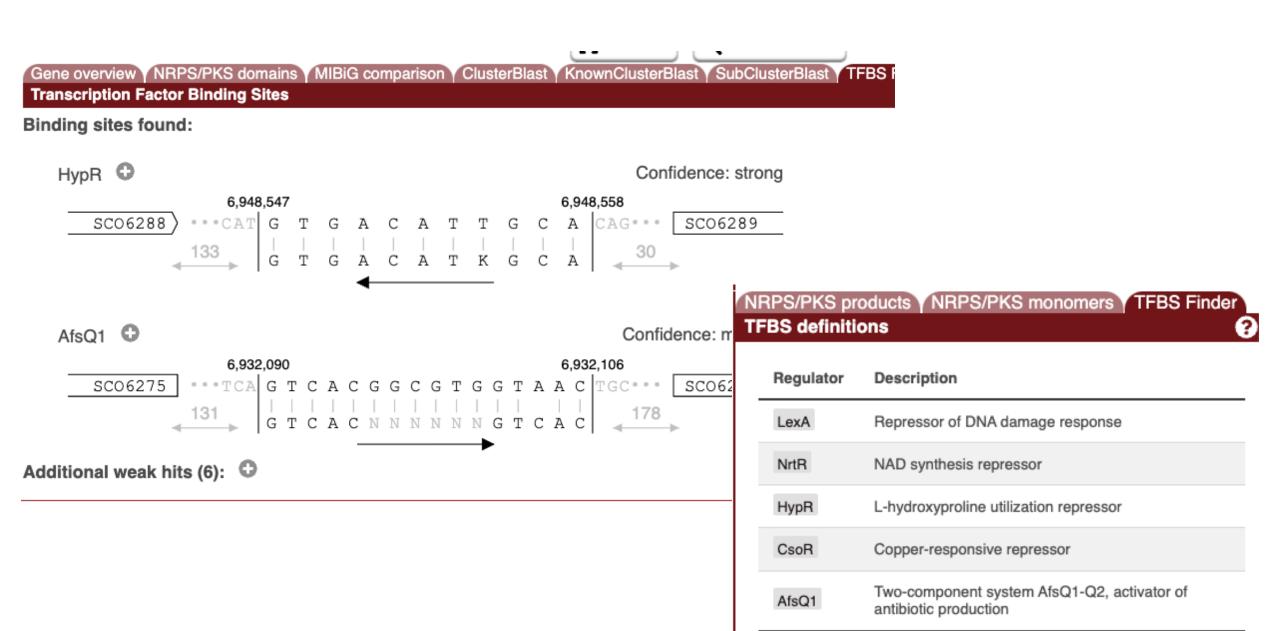


to KnownClusterBlast

Reference: BGC0000315: 0-82872

Reference	NRPS Similarity score	Туре	Compound(s)	Organism
BGC0000315	0.95	NRP	CDA1b, CDA2a, CDA2b, CDA3a, CDA3b, CDA4a, CDA4b	Streptomyces coelicolor A3(2)
BGC0001133	0.45	NRP	taxIllaid A	Xenorhabdus bovienii SS-2004
BGC0001370	0.44	NRP	lipopeptide 8D1-1, lipopeptide 8D1-2	Streptomyces rochei
BGC0001050	0.38	NRP, Polyketide	thalassospiramide A	Tistrella bauzanensis
BGC0002071	0.37	NRP	virginiafactin A, virginiafactin B, virginiafactin C, virginiafactin D	Pseudomonas sp. QS1027
BGC0002017	0.36	NRP	potensibactin	Nocardiopsis potens DSM 45234
BGC0001185	0.35	NRP	bacillibactin	Bacillus velezensis FZB42
BGC0001844	0.35	NRP	holrhizin	Paraburkholderia rhizoxinica HKI 454
BGC0001758	0.35	NRP	rhizomide A, rhizomide B, rhizomide C	Paraburkholderia rhizoxinica HKI 454
BGC0000417	0.35	NRP	rhodochelin	Rhodococcus jostii RHA1

Transcription Factor Binding Site prediction (for *Streptomyces sp.*)



Downloading results



