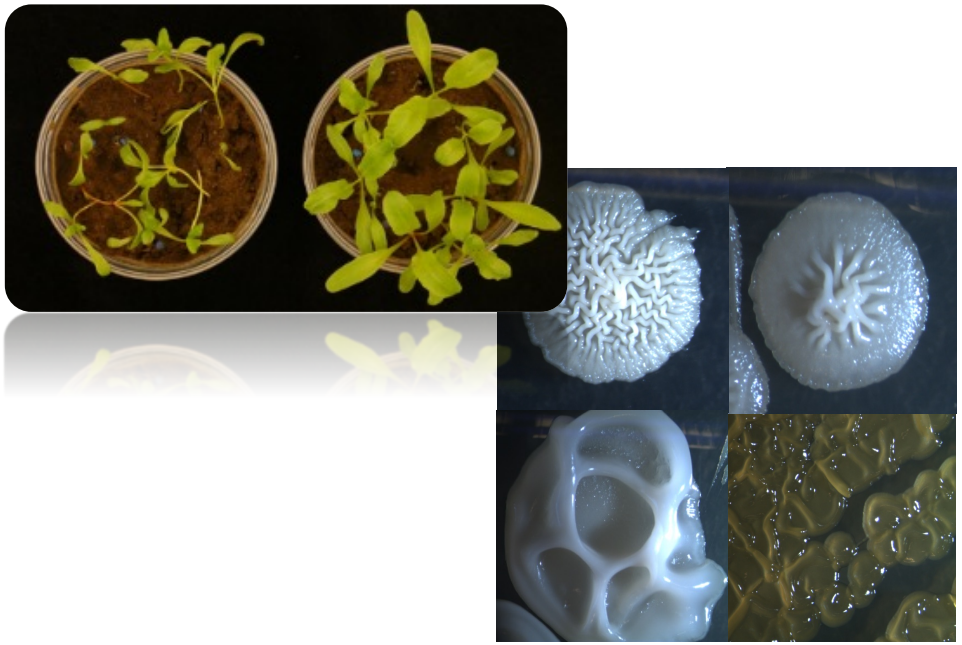
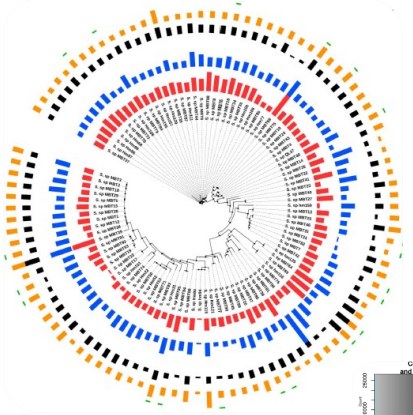
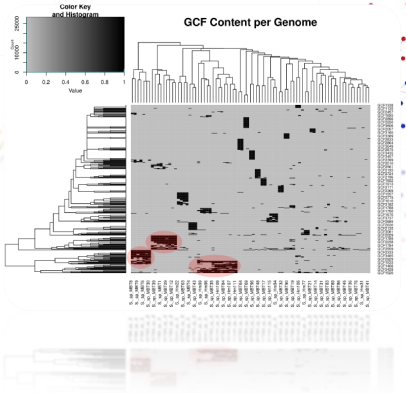
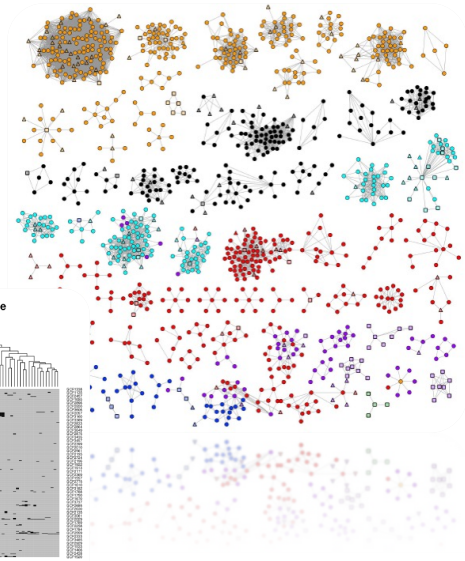
ANNOTATION TOOLS

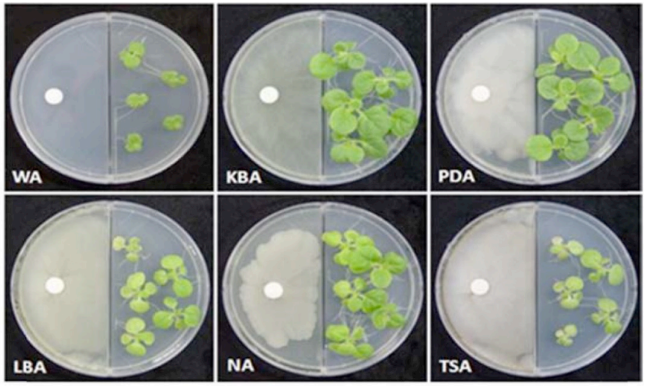


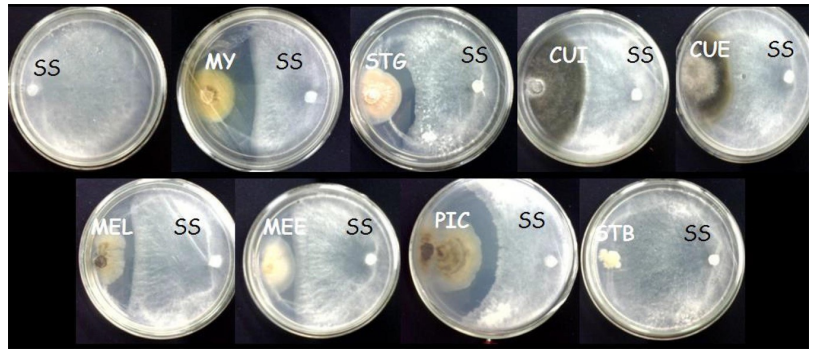






Victor J **Carrión**
v.j.carrion.bravo@biology.leidenuniv.nl
@VCarryOn1





DNA reads

Quality control

FastQC

Filtered DNA reads

Genome assembly

Velvet

SPAdes

MEGAHIT

MEGAHIT

(meta)Genome

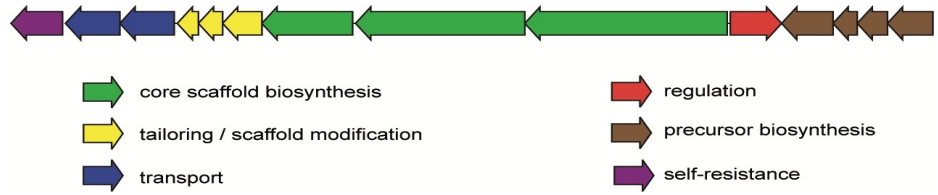
Quast

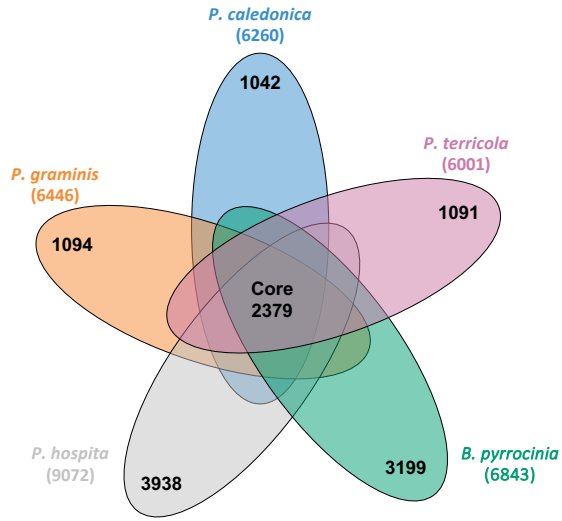
Quality Assessment Tool for Genome Assemblies

CheckM

Annotation

Comp. Genomics

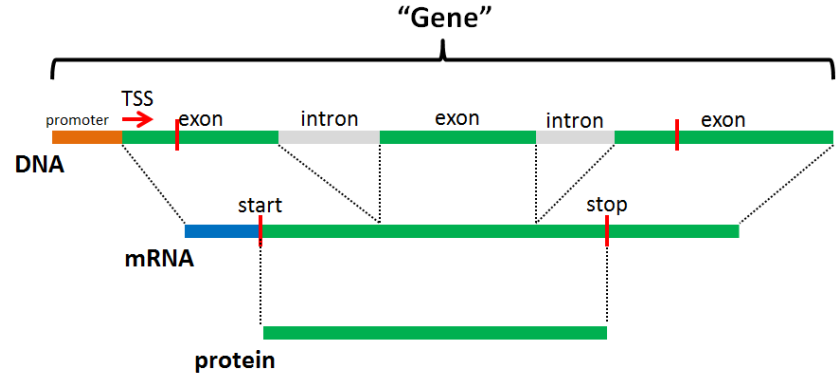




WHAT IS GENOME ANNOTATION?

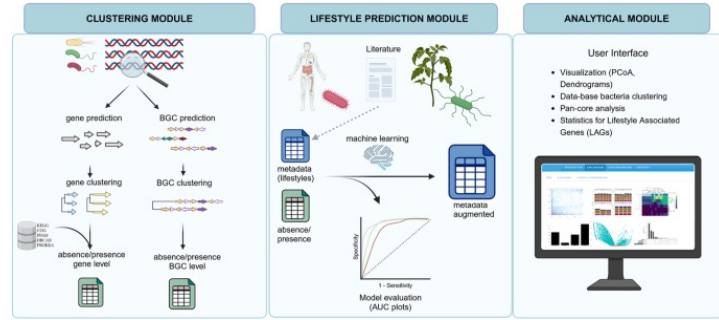
Genome annotation involves identifying genes, their structures, and functions in a genome.

- **Structural annotation**: Identifies coding regions and regulatory elements (Prodigal).



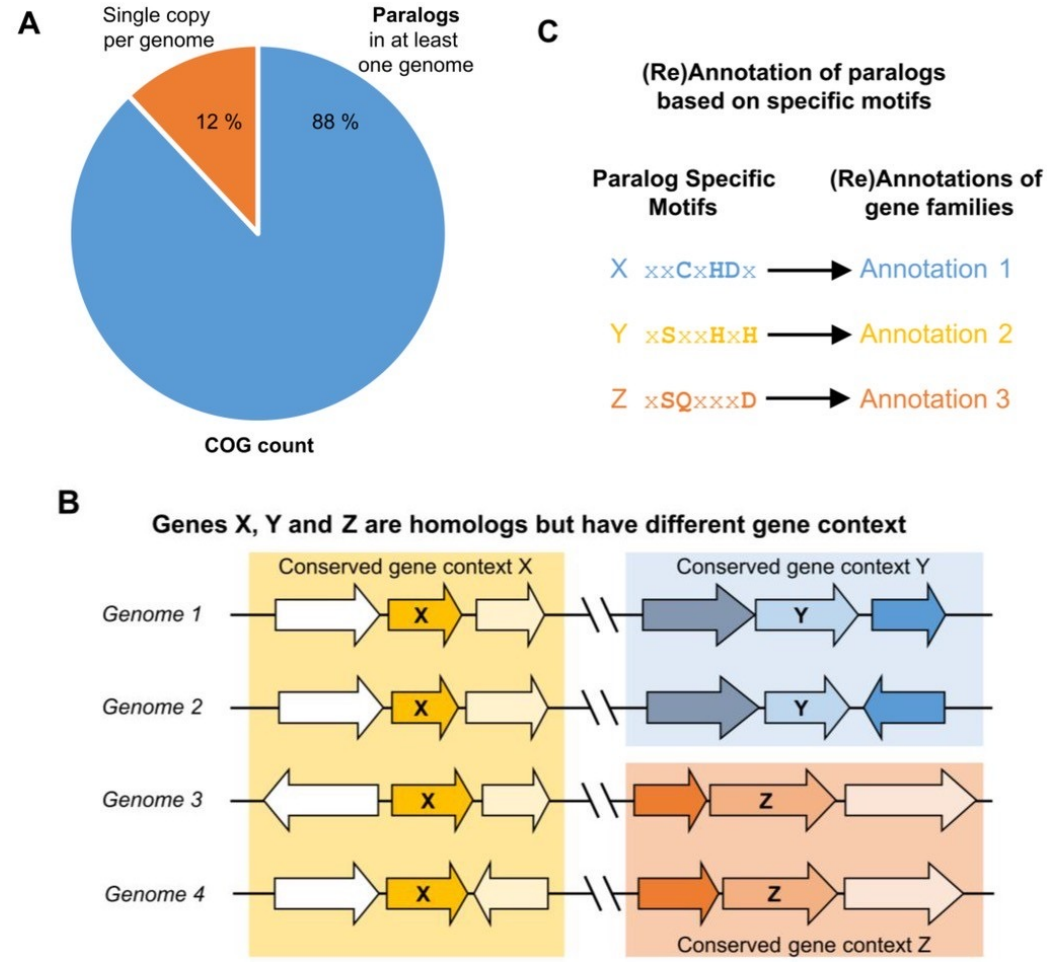
- **Functional annotation**: Assigns functions to genes based on homology and pathways.

- **Comparative annotation**: Analyzes evolutionary relationships and gene orthology.



LESSON 1: NEVER TRUST AN ANNOTATION

- Functional annotations provide a first hint ***but are often wrong***
- Often based on the protein with the best BLAST hit in some database, which may not be that closely related
- Errors are easily propagated
- To draw strong conclusions, manual validation is necessary, by looking at (conservation of) gene context, active-site motifs, etc.



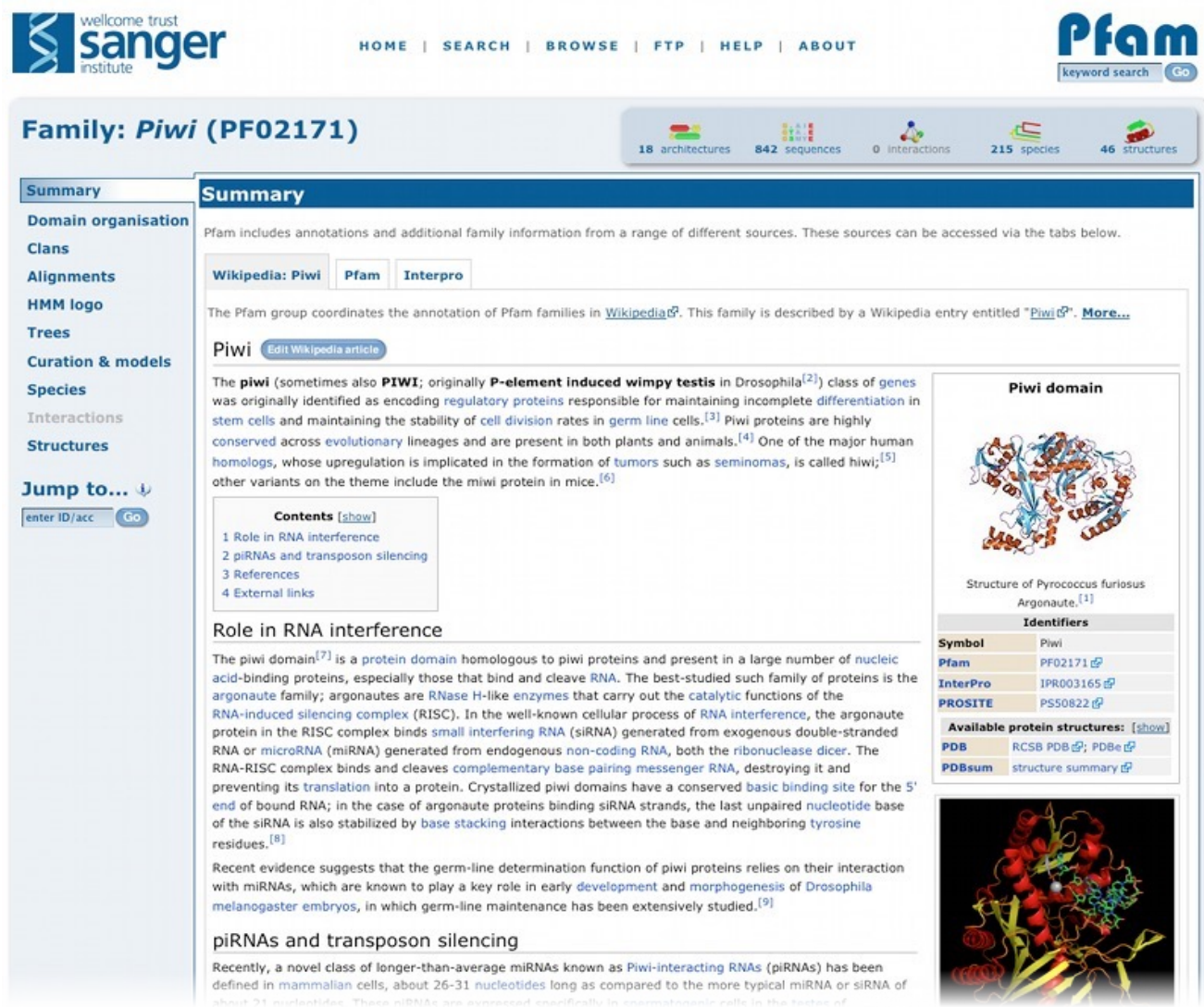
GENERAL FUNCTIONAL ANNOTATION TOOLS

PFAM CAN BE USED TO RAPIDLY PROVIDE A HIGH-CONFIDENCE INITIAL ANNOTATION OF GENE FUNCTIONS

HMMER

http://www.ebi.ac.uk/Tools/hmmer/

http://pfam.xfam.org/



HMMER

Biosequence analysis using profile hidden Markov Models

Quick search

Paste in your sequence or use the example

Enter your sequence

Reference Proteomes | UniProtKB | SwissProt | Pfam

Submit | Reset | Clean

Alternative search options

The HMMER web server: fast and sensitive homology searches. This site has been designed to provide near **interactive searches** for most queries, coupled with **intuitive and interactive results** visualisations.

Quickstart tutorial

Online documentation

Historia de los Hidden Markov Models (HMMs)

• Propuestos por Leonard E. Baum y sus colaboradores en la década de 1960.

• Inicialmente diseñados para **aplicaciones matemáticas y teóricas.**

• Permiten modelar sistemas complejos donde los estados internos no son directamente observables.

• Su capacidad de **inferencia probabilística** los hizo ideales para la biología computacional.

• Introducción en análisis de secuencias biológicas en los años 1990.

• Herramientas como HMMER utilizan HMMs para detectar familias de proteínas y regiones funcionales en ADN.

Historia de los Hidden Markov Models (HMMs)

Otras aplicaciones:

- **Reconocimiento de voz** 🎤 (los sonidos que escuchamos provienen de estados ocultos en las cuerdas vocales).

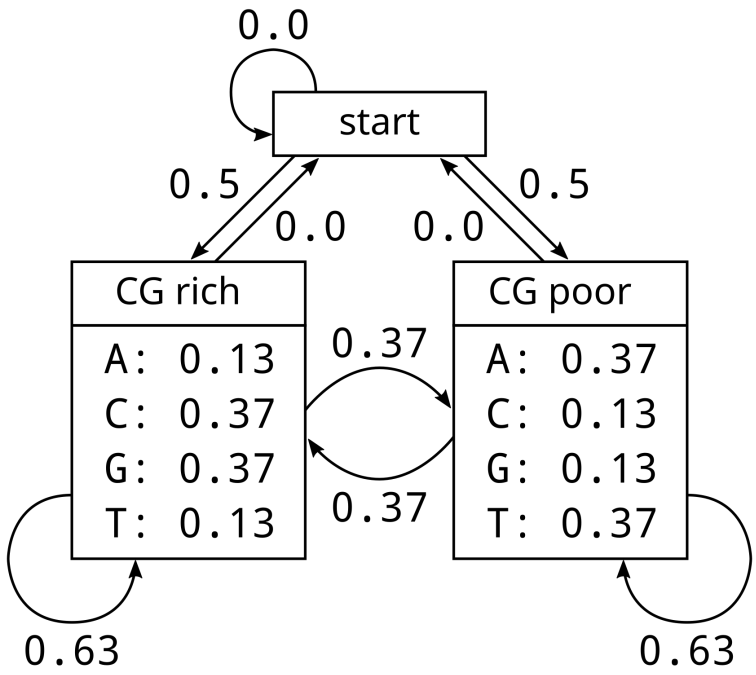
- **Finanzas** 📈 (inferir tendencias del mercado).

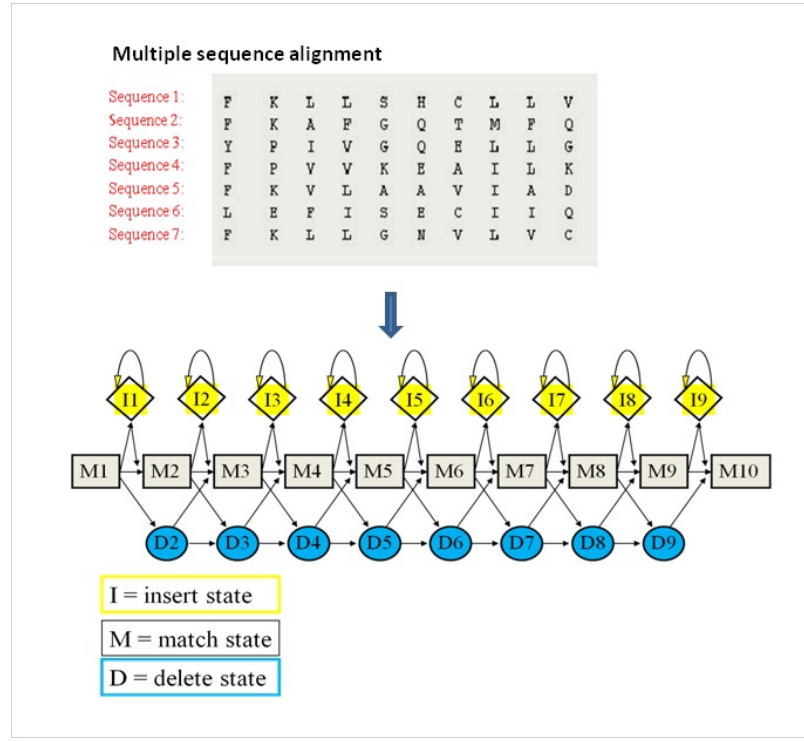
- **Análisis de ADN** 🧬 (detectar genes según patrones en la secuencia).

Modelos estadísticos que describen sistemas con estados ocultos.

En bioinformática: se usan para analizar secuencias de ADN.

- **Estados ocultos:** Ej. regiones codificantes (exones) y no codificantes (intrones).
- **Observaciones:** Bases nucleotídicas (A, T, C, G).
- **Probabilidades de transición:** Ej. paso de intrón a exón.
- **Probabilidades de emisión:** Probabilidad de observar una base en un estado específico.





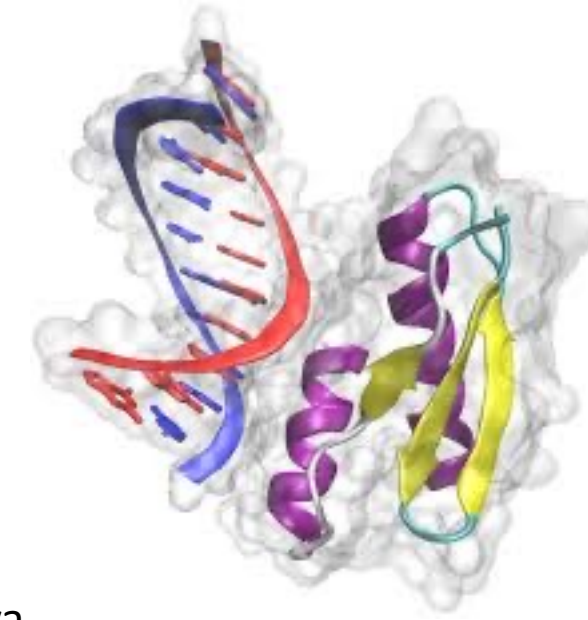
Imagine you are a detective living in Santiago trying to infer the weather in a La Serena, but you can only see how people dress.

Hidden States: Weather (Sunny ☀️, Rainy 🌧️)

Observations: Clothing (T-shirt 👕, Coat 🧥, Umbrella ☂️)

Clasificación de Proteínas con HMMs: protein quinasas

Estado Dominio Quinasa:
P(Ser) = 0.25, P(Thr) = 0.20, P(Lys) = 0.15, P(Asp) = 0.15, P(Otros) = 0.25



HMMs pueden ser entrenados con una base de datos de proteínas ya clasificadas y luego utilizados para analizar nuevas proteínas.

HIDDEN MARKOV MODELS (HMMs)

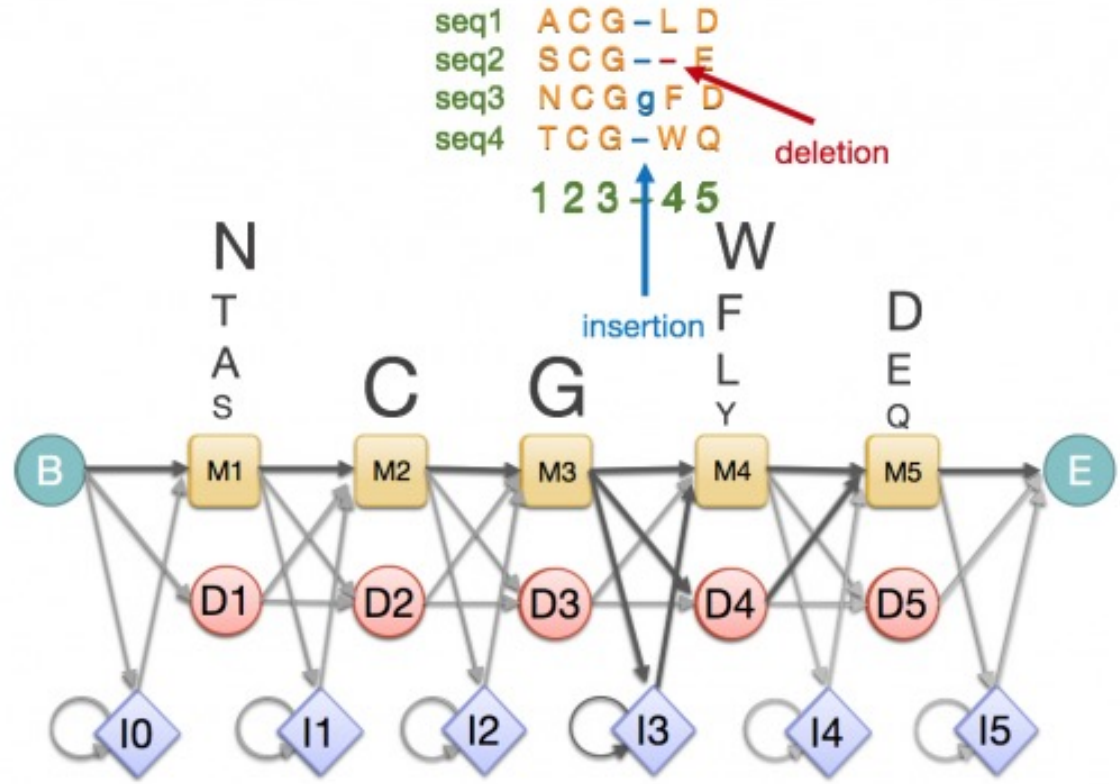
One of the computational algorithms used for predicting protein structure and function, identifies significant protein sequence similarities allowing the detection of homologs and consequently the transfer of information.

Start with a multiple sequence alignment

Insertions / deletions can be modelled

Occupancy and amino acid frequency at each position in the alignment are encoded

Profile created



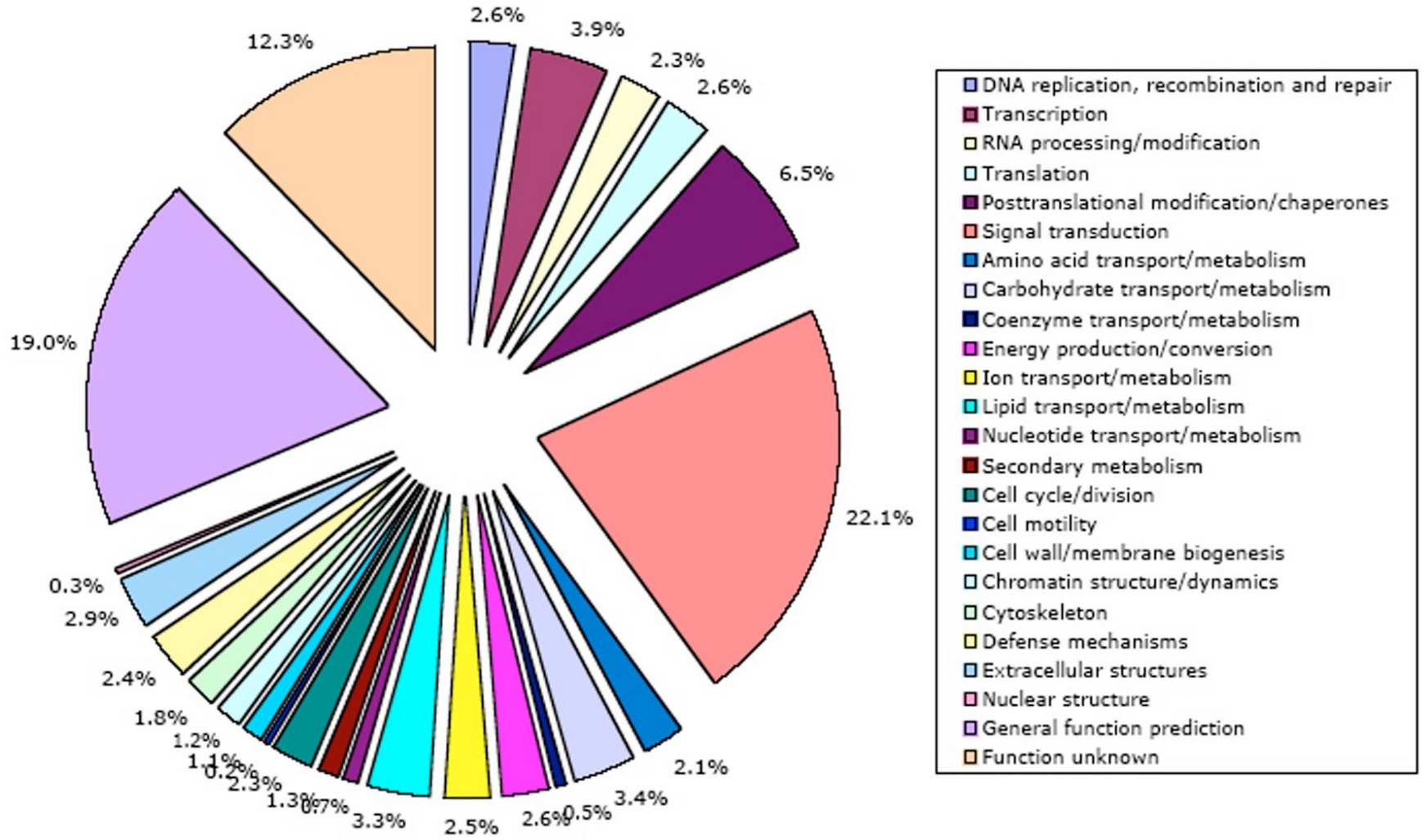
THE COG (CLUSTERS OF ORTHOLOGOUS GROUPS) DATABASE

- The protein database of Clusters of Orthologous Groups (COGs) is an attempt to phylogenetically classify the complete complement of proteins (both predicted and characterized) encoded by complete genomes.

- Each COG is a group of three or more proteins, i.e., they are direct evolutionary counterparts.

Proteínas ortólogas son aquellas que comparten una función y secuencia similar porque han evolucionado de un gen ancestral común mediante especiación

THE COG DATABASE CAN BE USED TO CLASSIFY LARGE SETS OF GENES INTO FUNCTIONAL CATEGORIES



https://www.ncbi.nlm.nih.gov/research/cog

KEGG: KYOTO ENCYCLOPEDIA OF GENES AND GENOMES

- KEGG is a collection of biological information compiled from published material curated database.

- Includes information on genes, proteins, metabolic pathways, molecular interactions, and biochemical reactions associated with specific organisms

- Provides a relationship (map) for how these components are organized in a cellular structure or reaction pathway.

KEGG PATHWAY Database

Wiring diagrams of molecular interactions, reactions and relations

Select prefix map Organism

Enter keywords Go Help

[New pathway maps | Update history]

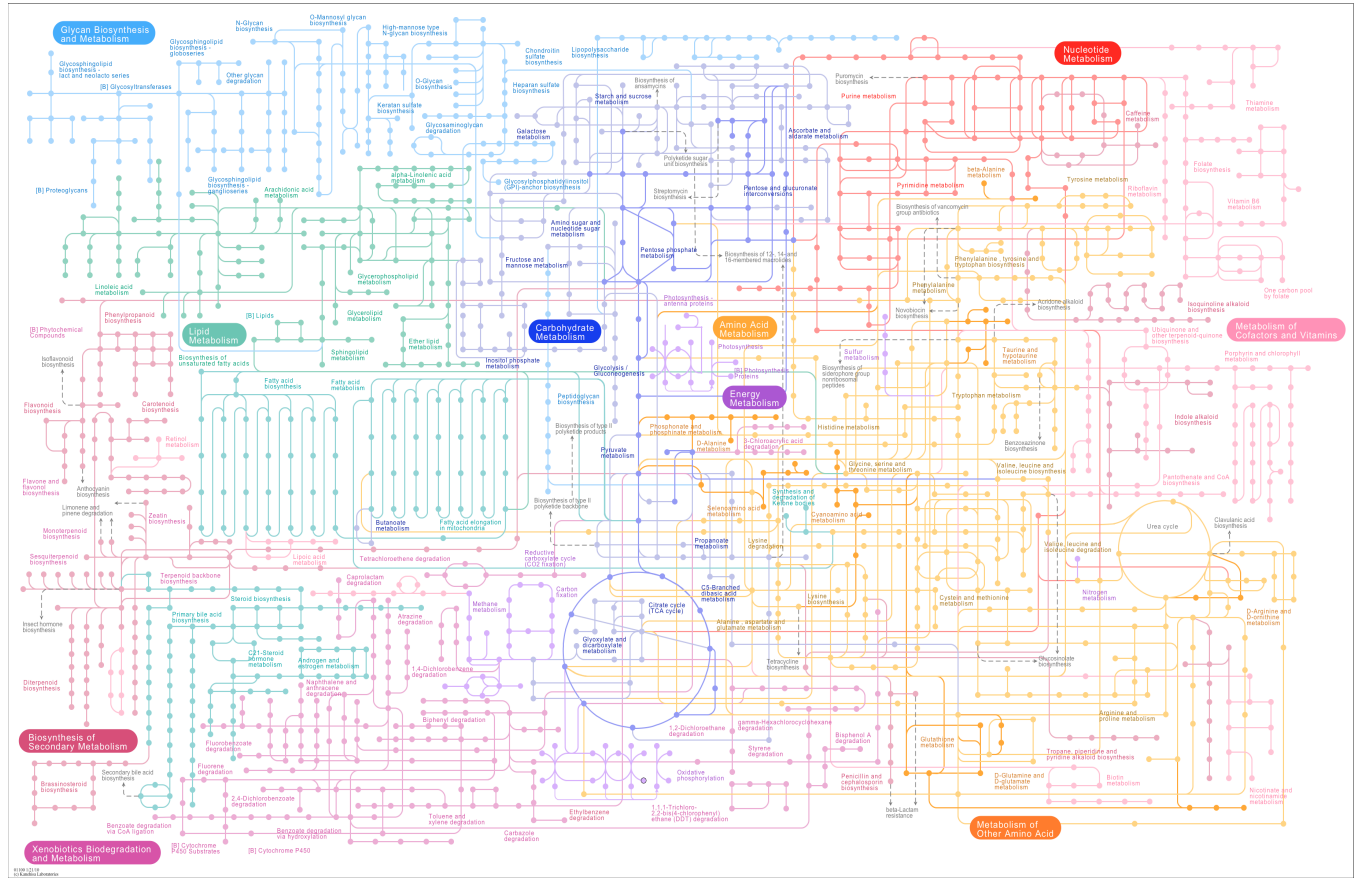
Pathway Maps

KEGG PATHWAY is a collection of manually drawn pathway maps representing our knowledge of the molecular interaction, reaction and relation networks for:

1. **Metabolism**
   Global/overview Carbohydrate Energy Lipid Nucleotide Amino acid Other amino Glycan
   Cofactor/vitamin Terpenoid/PK Other secondary metabolite Xenobiotics Chemical structure
2. **Genetic Information Processing**
3. **Environmental Information Processing**
4. **Cellular Processes**
5. **Organismal Systems**
6. **Human Diseases**
7. **Drug Development**

The pathway map viewer linked from this page contains features of KEGG mapping, especially for coloring map objects as described here.

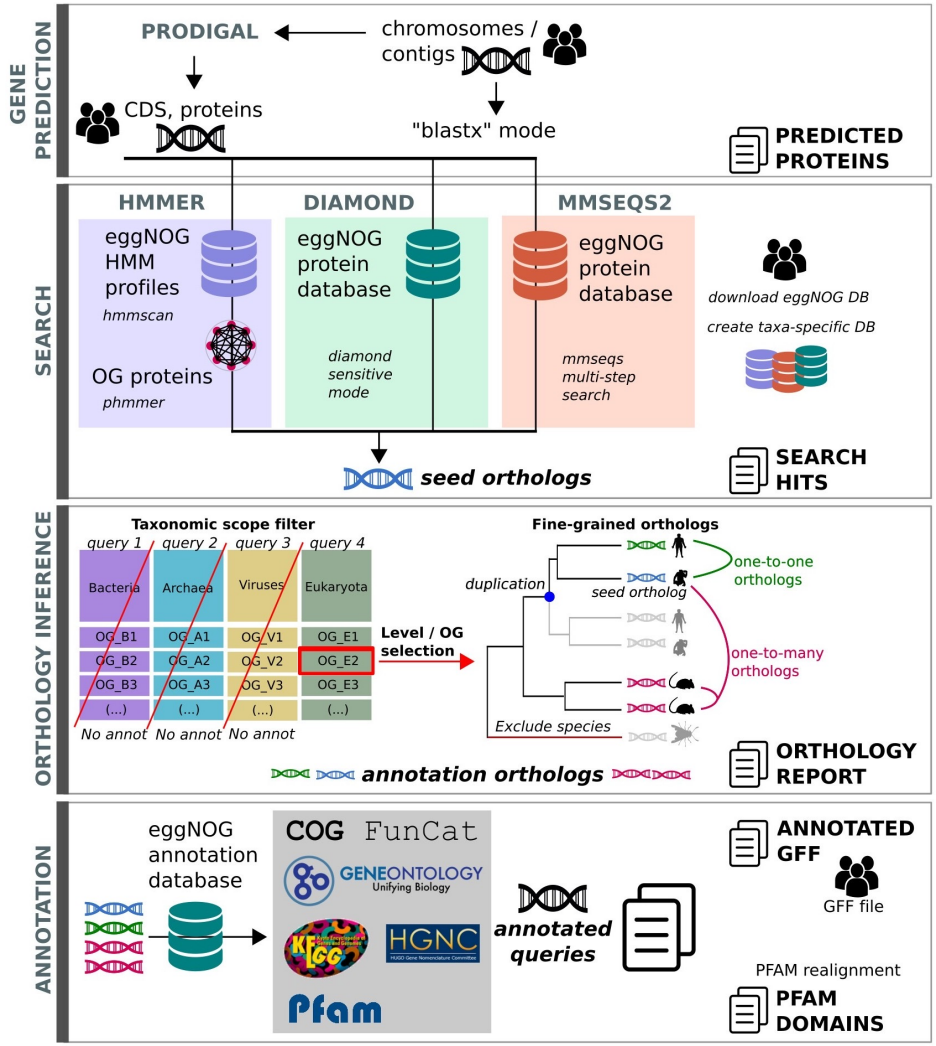
KEGG: A BROAD OVERVIEW OF KNOWN METABOLIC PATHWAYS

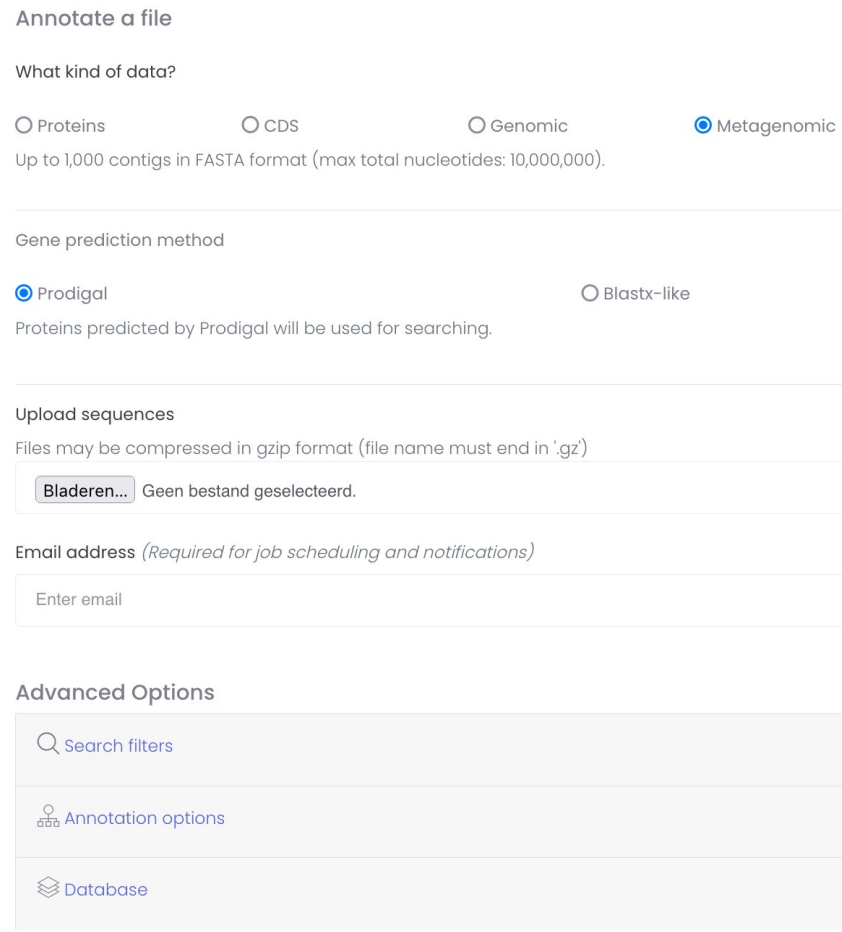


Very good for common (primary metabolic) pathways, often incomplete for specialized primary and secondary metabolism

https://www.genome.jp/kegg/

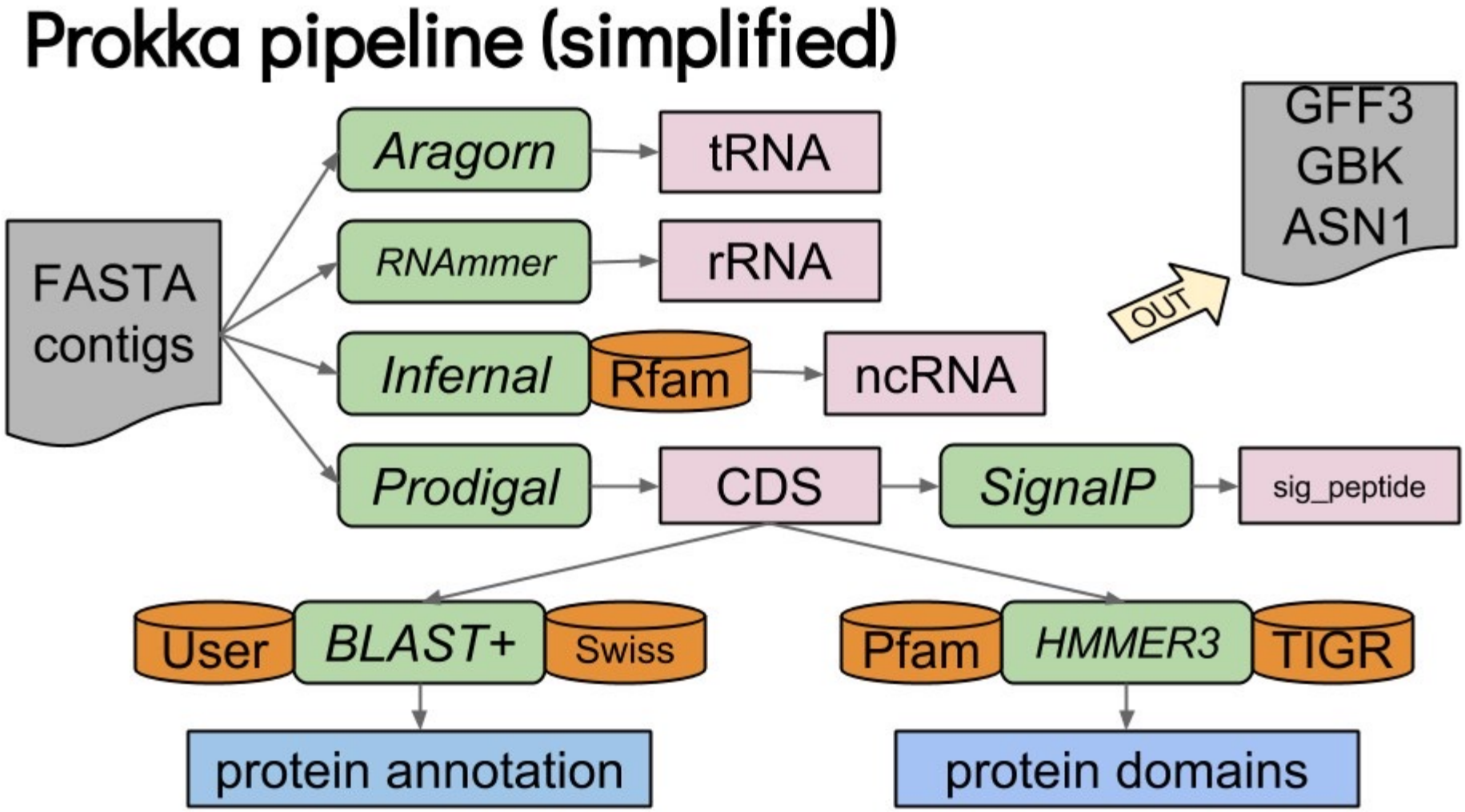
EGGNOG: ASSIGNMENT OF PFAM, COG, KEEG AND GO ANNOTATIONS





http://eggnog5.embl.de
http://eggnog-mapper.embl.de/

PROKKA: AUTOMATED PIPELINE FOR GENOMES ANNOTATION



https://github.com/tseemann/prokka

SPECIFIC FUNCTIONAL ANNOTATION TOOLS

THE CAZY DATABASE CLASSIFIES CARBOHYDRATE-ACTING ENZYMES, DBCAN PROVIDES LIBRARIES OF HMMs TO DETECT THEM

Bacteroides thetaiotaomicron DSM 2079

Taxonomy ID : 818
Lineage: cellular organisms; Bacteria; FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides

Glycoside Hydrolase Family	2	3	13	16	18	20	23	25	27	28	29	30	31	32	33	35	36
Number of sequences	31	10	7	3	12	14	3	1	5	9	9	3	6	4	2	3	4

GlycosylTransferase Family	1	2	3	4	5	8	9	14	19	25	28	30	32	35	51	101	NC
Number of sequences	1	40	1	26	1	1	1	3	1	1	1	1	3	2	4	2	5

Polysaccharide Lyase Family	1	8	9	10	11	12	13	15	26	27	29	33	40	42
Number of sequences	5	3	2	1	1	2	1	1	1	1	1	2	1	1

Carbohydrate Esterase Family	2	4	6	7	8	9	11	12	19	20	NC
Number of sequences	1	1	1	1	2	3	1	4	1	9	1

Carbohydrate-Binding Module Family	6	20	32	35	50	51	57	58	91	93	NC
Number of sequences	1	2	13	2	7	1	1	1	5	1	5

List Of Proteins

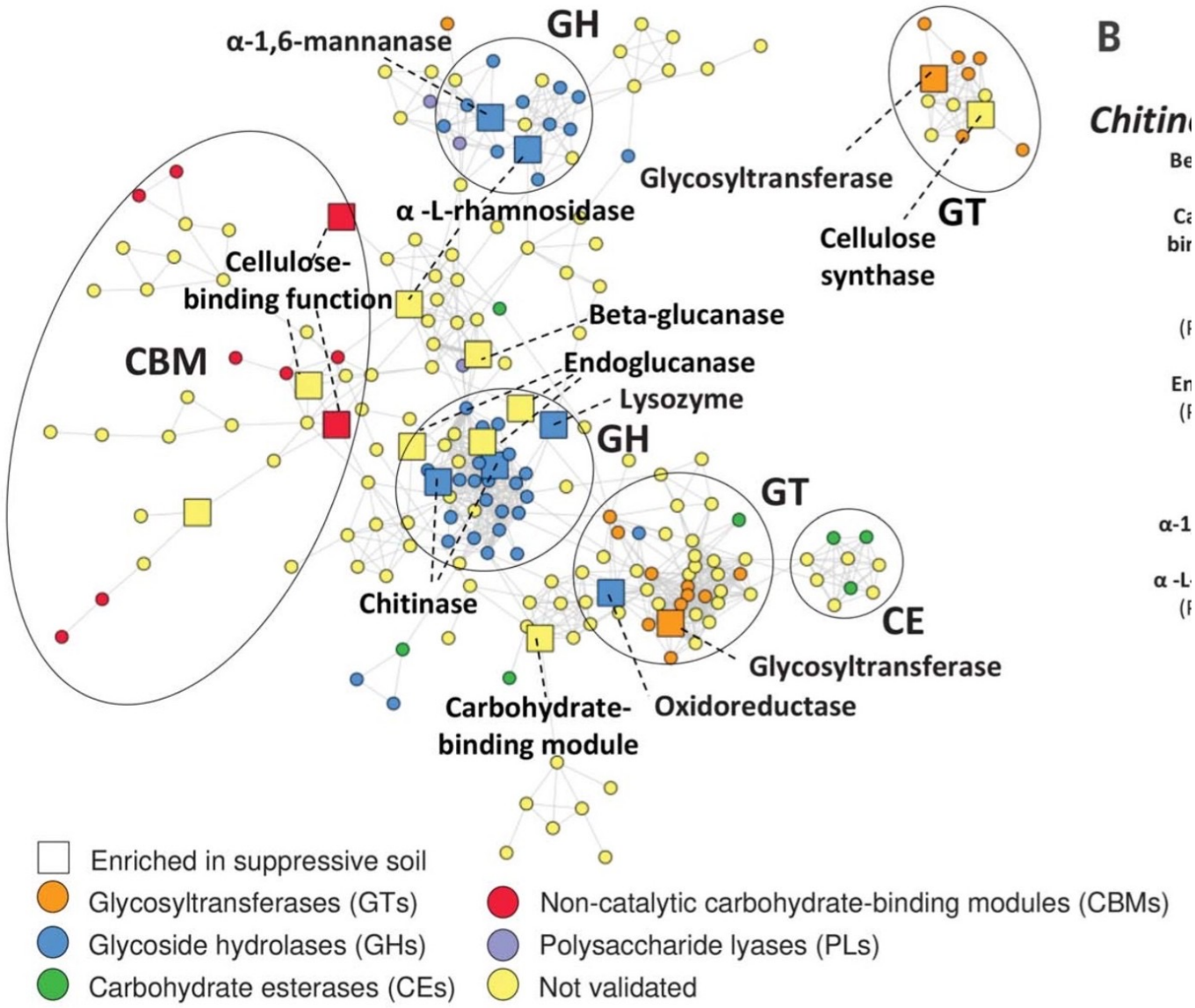
Protein Name	Family	Reference Accession
FE838_00230	CBM20,CBM20,GH77	QMW84610.1
FE838_00240	GT4	QMW84612.1
FE838_00255	GT2	QMW84615.1
FE838_00455	GH29	QMW84652.1
FE838_00465	CBM32	QMW89084.1

dbCAN

CAZY
CARBOHYDRATE-ACTIVE ENZYMES

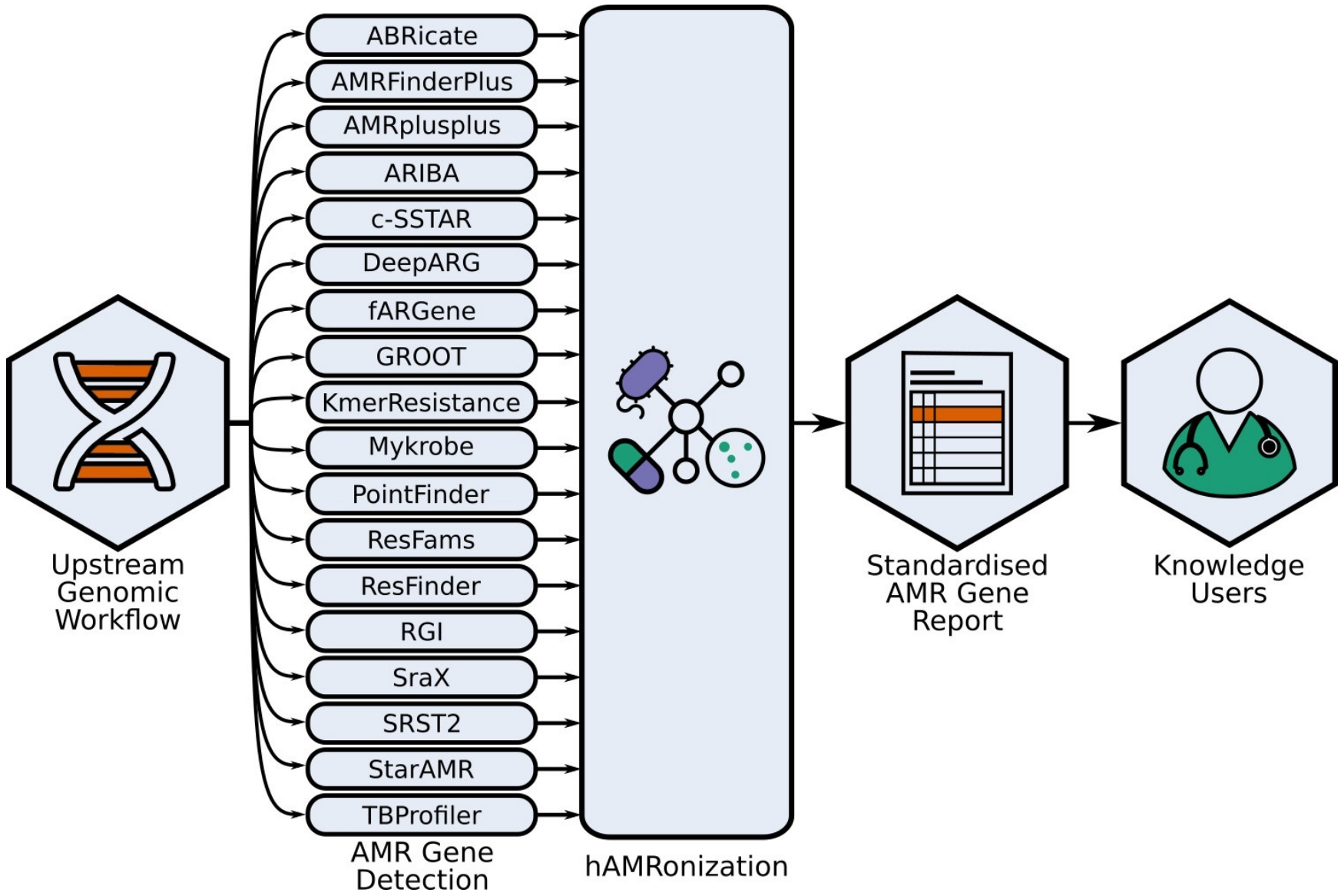
http://www.cazy.org
https://bcb.unl.edu/dbCAN2

THE dBCAN DATABASE (USING HMMs): EXAMPLE USE CASE



Carrion et al., 2019 (SCIENCE)

IDENTIFYING ANTIMICROBIAL RESISTANCE



https://github.com/pha4ge/hAMRonization

BUT … WHY … SO MANY ANNOTATIONS???????

COG

PFAM

KEGG

Gen_id	COG.descr	COG.typ	COG.ID	pfam_dom	pfam_descr	kegg	kegg_d
Gen 1	Ribosomal_protein_S18_acetylase_RimI_and_related_acety	J	COG0456	PF00583	Acetyltransferase_(GN	K03395	aac3-I;_ar
Gen 2	Ribosomal_protein_S18_acetylase_RimI_and_related_acety	J	COG0456	PF00583	Acetyltransferase_(GN	K03395	aac3-I;_ar
Gen 3	Ribosomal_protein_S18_acetylase_RimI_and_related_acety	J	COG0456	PF00583	Acetyltransferase_(GN	K03395	aac3-I;_ar
Gen 4	Protein_N-acetyltransferase,_RimJ/RimL_family	JO	COG1670	PF13523	Acetyltransferase_(GN	K00663	aacA;_ami
Gen 5	Aminoglycoside_N3'-acetyltransferase	V	COG2746	PF02522	Aminoglycoside_3-N-a	K00662	aacC;_ami
Gen 6	Aminoglycoside_N3'-acetyltransferase	V	COG2746	PF02522	Aminoglycoside_3-N-a	K00662	aacC;_ami
Gen 7	Aminoglycoside_N3'-acetyltransferase	V	COG2746	PF02522	Aminoglycoside_3-N-a	K00662	aacC;_ami
Gen 8	Acyl-coenzyme_A_synthetase/AMP-(fatty)_acid_ligase	I	COG0365	PF16177;PF00501	Acetyl-coenzyme_A_sy	K01907	AACS,_acs
Gen 9	Acyl-coenzyme_A_synthetase/AMP-(fatty)_acid_ligase	I	COG0365	PF16177;PF00501;PF13	Acetyl-coenzyme_A_sy	K01907	AACS,_acs
Gen 10	Acyl-coenzyme_A_synthetase/AMP-(fatty)_acid_ligase	I	COG0365	PF16177;PF00501;PF13	Acetyl-coenzyme_A_sy	K01907	AACS,_acs
Gen 11	Acyl-coenzyme_A_synthetase/AMP-(fatty)_acid_ligase	I	COG0365	PF16177;PF00501;PF13	Acetyl-coenzyme_A_sy	K01907	AACS,_acs
Gen 12	Acyl-coenzyme_A_synthetase/AMP-(fatty)_acid_ligase	I	COG0365	PF16177;PF00501;PF13	Acetyl-coenzyme_A_sy	K01907	AACS,_acs
Gen 13	Acyl-coenzyme_A_synthetase/AMP-(fatty)_acid_ligase	I	COG0365	PF16177;PF00501;PF13	Acetyl-coenzyme_A_sy	K01907	AACS,_acs
Gen 14	A		COG0365	PF16177;PF00501;PF13	Acetyl-coenzyme_A_sy	K01907	AACS,_acs
Gen 15	A		COG0365	PF16177;PF00501;PF13	Acetyl-coenzyme_A_sy	K01907	AACS,_acs
Gen 16	A		COG0365	PF16177;PF00501;PF13	Acetyl-coenzyme_A_sy	K01907	AACS,_acs
Gen 17	A		COG0365	PF00501;PF13193	AMP-binding_enzyme_	K01907	AACS,_acs
Gen 18	A		COG0365	PF00501;PF13193	AMP-binding_enzyme_	K01907	AACS,_acs
Gen 19	A	Q	COG3321	PF00975	Thioesterase_domain	K01907	AACS,_acs
Gen 20	P	R	COG1708	PF13427;PF01909	Domain_of_unknown_	K00984	aadA;_stre
Gen 21	P	R	COG1708	PF13427;PF01909	Domain_of_unknown_	K00984	aadA;_stre
Gen 22	P	R	COG1708	PF13427;PF01909	Domain_of_unknown_	K00984	aadA;_stre
Gen 23	P	R	COG1708	PF01909	Nucleotidyltransferase	K00984	aadA;_stre
Gen 24	A		COG0657	PF07859	alpha/beta_hydrolase_	K13616	AADAC;_a

COUNT/ABUNDANCE TABLE

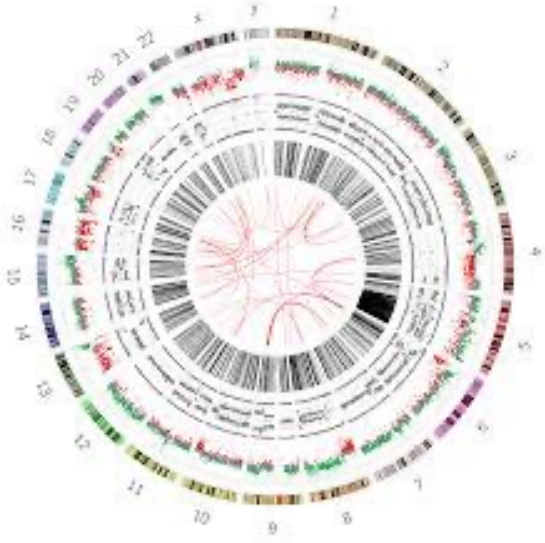
	S1	S2	S3	SR1	SR2	SR3
1	68	13	37	28	27	34
2	79	47	55	41	37	26
3	23	33	11	24	24	16
4	24	18	17	14	17	9
5	33	9	26	105	68	20
6	16	14	52	24	26	20
7	4	10	8	18	9	6
10	27	67	13	18	16	29
11	86	45	94	164	15	
12	724	527	475	635	560	372
13	154	463	507	542	508	70
16	112	58	45	37	45	44
17	161	326	221	562	470	68
18	21	235	68	41	92	35

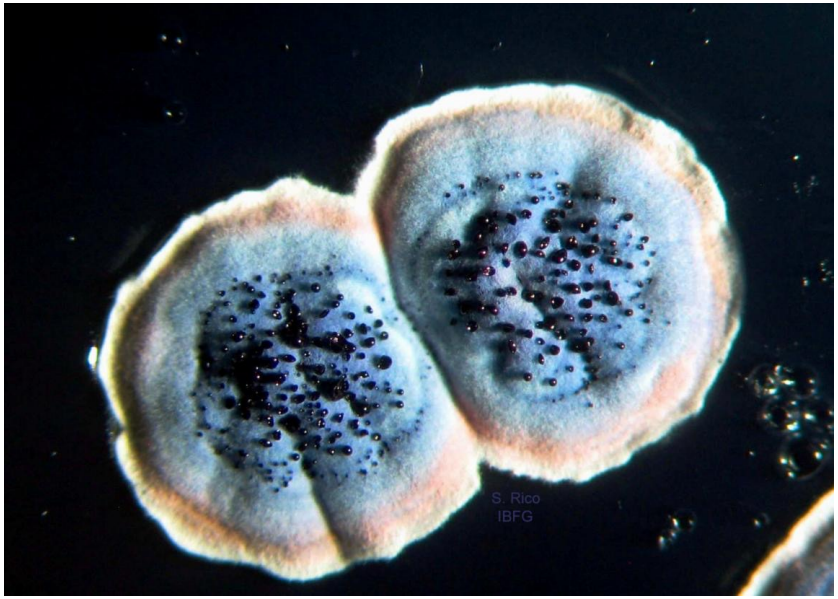
METADATA

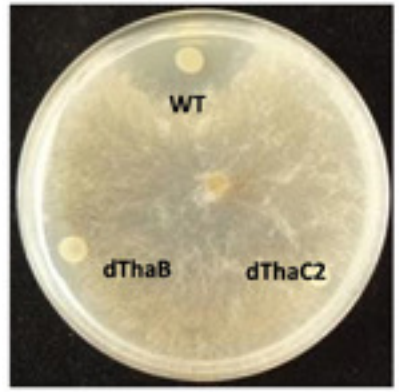
SampleID	Treatment	Description	Fungi	Status
C1	Endo_Conducive	Endosphere	No_Rhizo	Conducive
C2	Endo_Conducive	Endosphere	No_Rhizo	Conducive
C3	Endo_Conducive	Endosphere	No_Rhizo	Conducive
C4	Endo_Conducive	Endosphere	No_Rhizo	Conducive
S1	Endo_Suppressive	Endosphere	No_Rhizo	Suppressive
S2	Endo_Suppressive	Endosphere	No_Rhizo	Suppressive
S3	Endo_Suppressive	Endosphere	No_Rhizo	Suppressive
SR1	Endo_SuppressiveR	Endosphere	Rhizo	Suppressive
SR2	Endo_SuppressiveR	Endosphere	Rhizo	Suppressive
SR3	Endo_SuppressiveR	Endosphere	Rhizo	Suppressive


S. Rico
IBFG

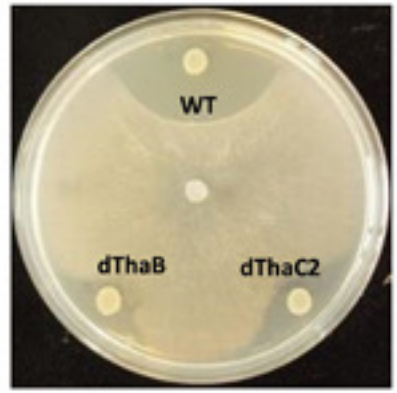
SECONDARY METABOLISM



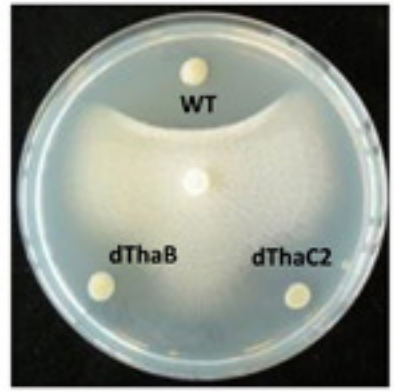




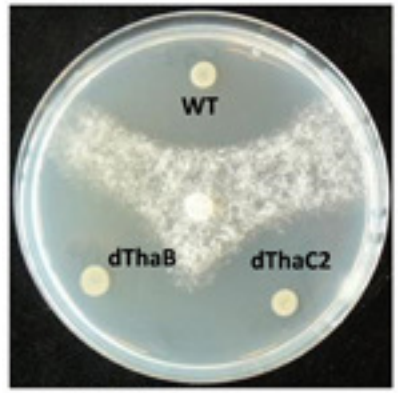
R. solani



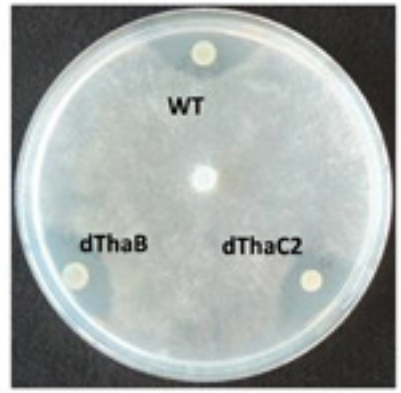
B. cinerea



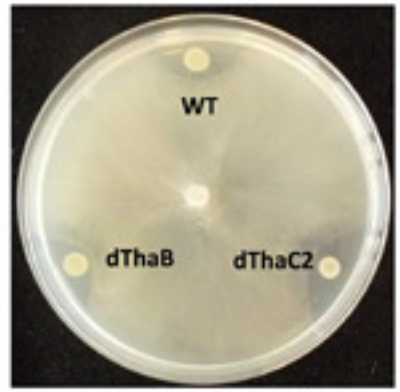
Geotrichum sp.



P. infestans



P. ultimum



P. capsici

ANTISMASH: A WEB SERVER FOR THE DETECTION AND ANALYSIS OF BIOSYNTHETIC GENE CLUSTERS

Web server and a stand-alone software to identify, annotate, and compare gene clusters that encode the biosynthesis of secondary metabolites in bacterial and fungal genomes (Medema et al. 2011)

Table 1 Examples of secondary metabolite types

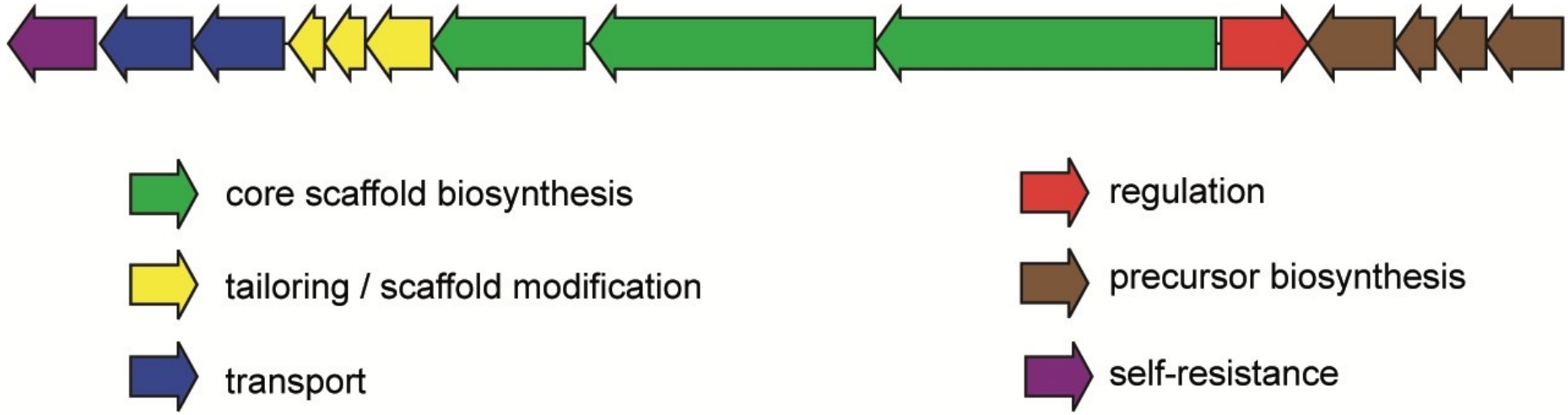
Secondary metabolite type	No. records*	Example	Reference
PK	799	Erythromycin	Rawlings (2001)
NRP	605	Penicillin	Fierro *et al.* (2006)
RiPP	258	Bottromycin	Shimamura *et al.* (2009)
Saccharide	173	Streptomycin	Ohnishi *et al.* (2008)
Terpene	130	Mycophenolic acid	Regueira *et al.* (2011)
Alkaloid	49	Violacein	Hoshino (2011)
Other	253	Clavulanic acid	Aidoo *et al.* (1994)

PK, polyketide; NRP, nonribosomal peptide; RiPPS, ribosomally synthesized and post-translationally modified peptide.

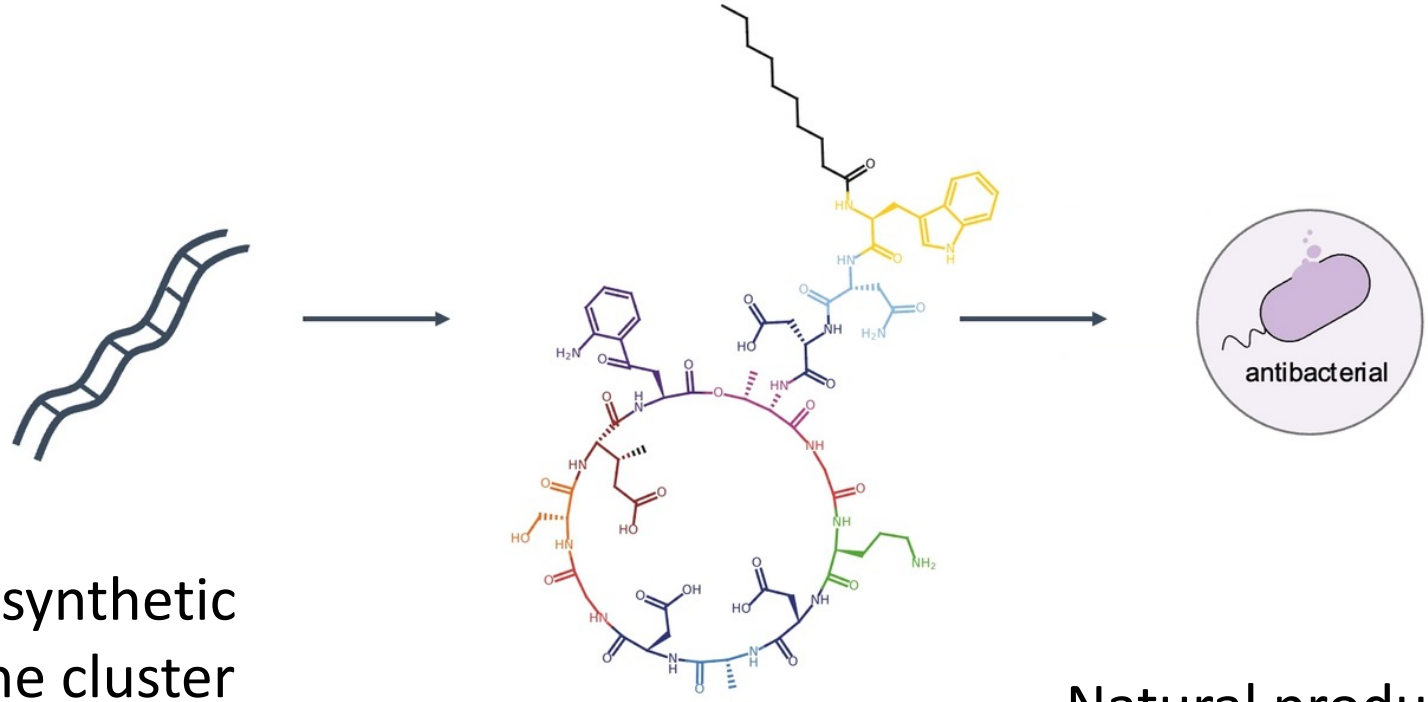
*Number of gene clusters related to each type of secondary metabolite in the MIBIG platform (https://mibig.secondarymetabolites.org/stats).

BIOSYNTHETIC GENE CLUSTERS (BGCs) COMPRISE SEVERAL TYPES OF GENE FUNCTIONS

A BGC can be defined as a physically clustered group of two or more genes in a particular genome that together encode a biosynthetic pathway for the production of a specialized metabolite (including its chemical variants).



THE “CENTRAL DOGMA”OF SPECILIZED METABOLISM

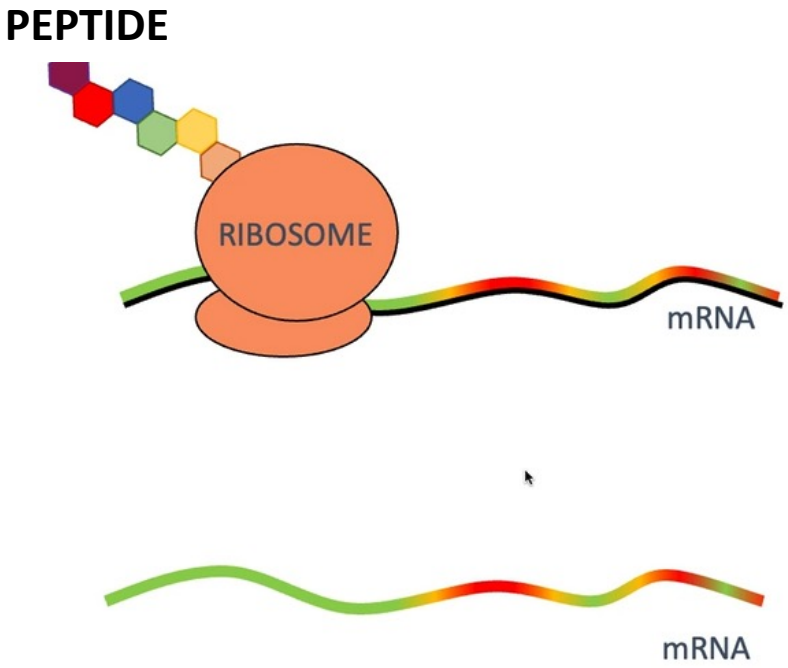


Biosynthetic gene cluster sequence

Natural product structure

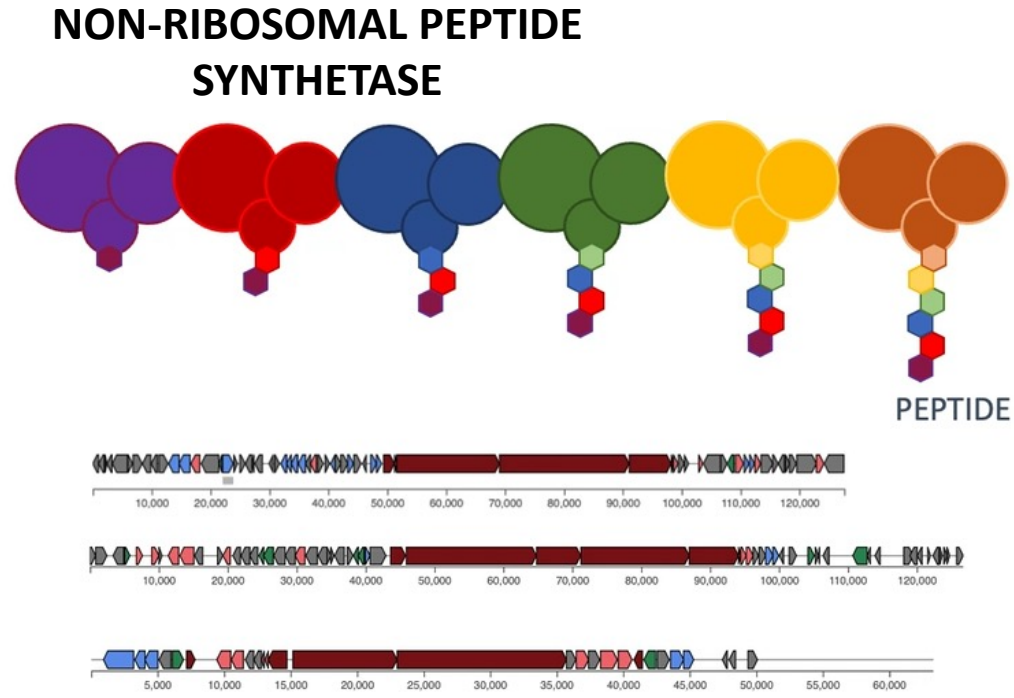
Natural product function

RIBOSOMAL PEPTIDE SYNTHESIS



Peptide sequence depends on template

NON-RIBOSOMAL PEPTIDE SYNTHESIS



Peptide sequence depends on machinery

Server status: working
Running jobs: 20
Queued jobs: 0
Jobs processed: 1429532

Nucleotide input | Results for existing job

Search a genome sequence for secondary metabolite biosynthetic gene clusters

Load sample input | Open example output

antiSMASH 7 beta is now available
Dear antiSMASH users, we have just made antiSMASH 7 available as a beta version. We're very happy with how it works, but if you still want to run the old 6.1.1 release, just uncheck the "enable antiSMASH beta" checkbox.

Notification settings

your@email.com — **Email address (optional)**

antiSMASH beta features

- [x] **Enable antiSMASH beta**

Data input

Upload file | Get from NCBI

NCBI acc # — **NCBI accession number of desired sequence**

Extra features

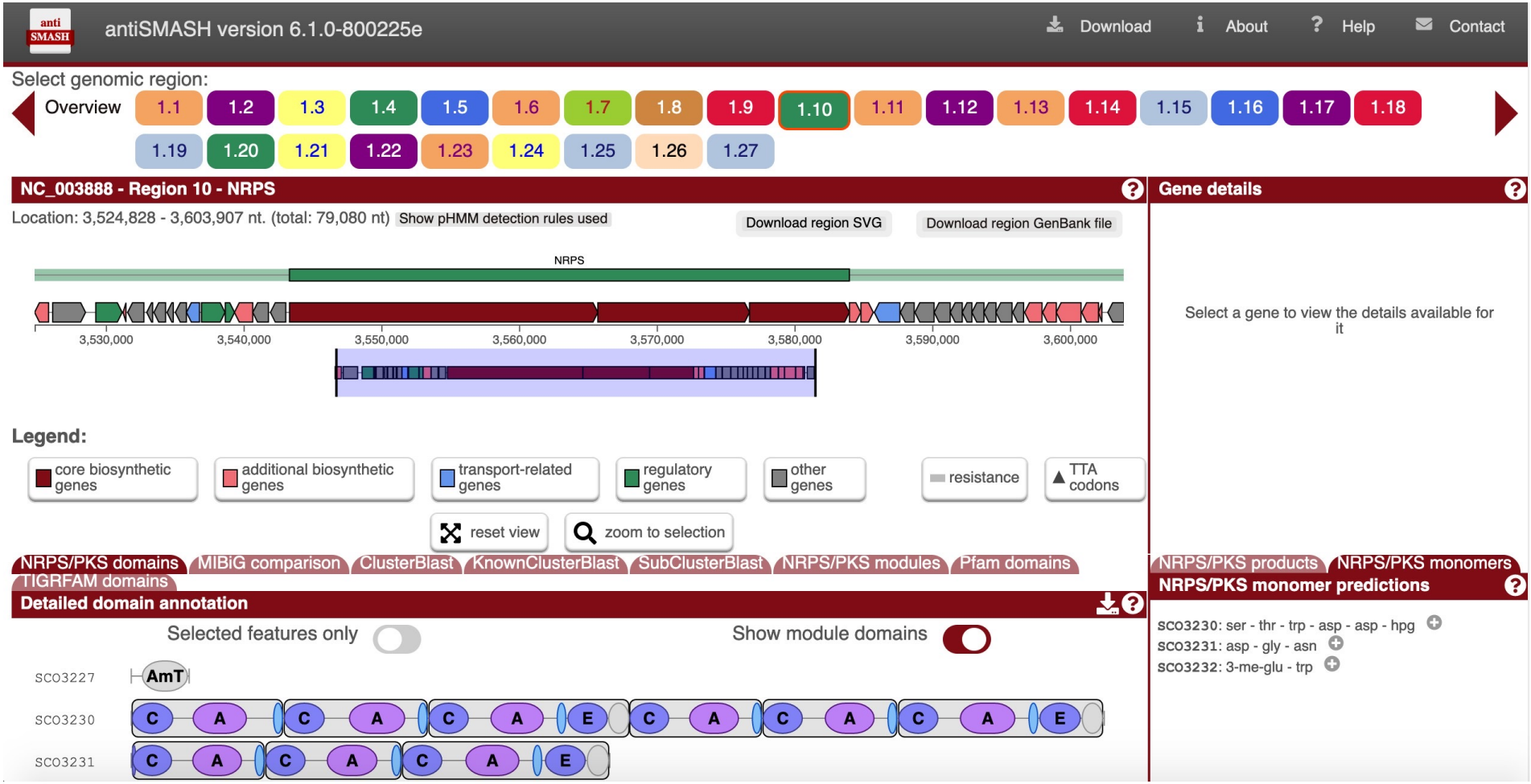
All off | All on

- [x] **KnownClusterBlast**
- [ ] **ClusterBlast**
- [x] **SubClusterBlast**
- [ ] **MIBiG cluster comparison**
- [x] **ActiveSiteFinder**
- [x] **RREFinder**
- [ ] **Cluster Pfam analysis**
- [ ] **Pfam-based GO term annotation**
- [ ] **TIGRFam analysis**
- [x] **TFBS analysis**

Submit

Please be considerate in your use of antiSMASH. Help us keep antiSMASH available for everybody by limiting yourself to 5 concurrent jobs. Need to run more? See the antiSMASH install guide for instructions for getting your own antiSMASH installation.

ANTISMASH: GENOME



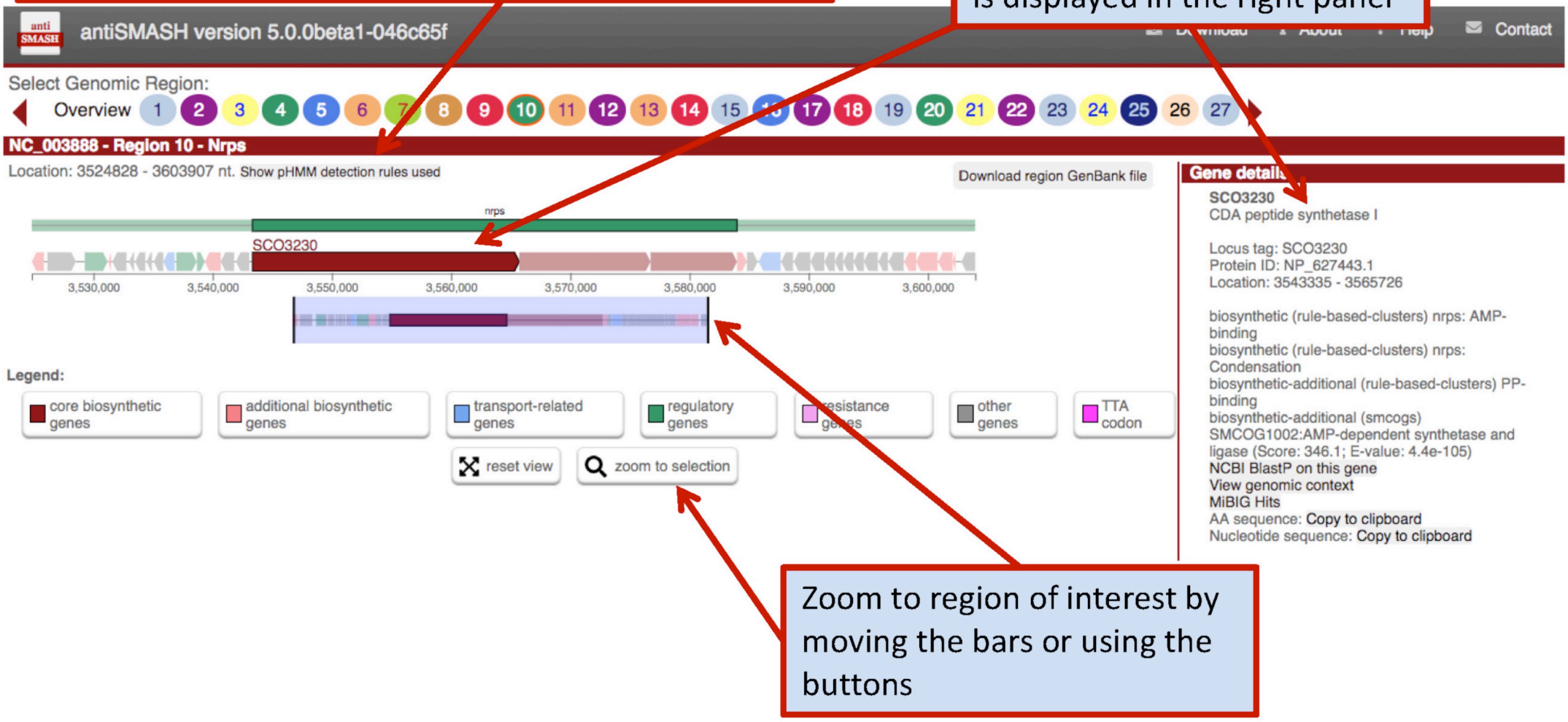
http://antismash.secondarymetabolites.org

http://antismash-db.secondarymetabolites.org

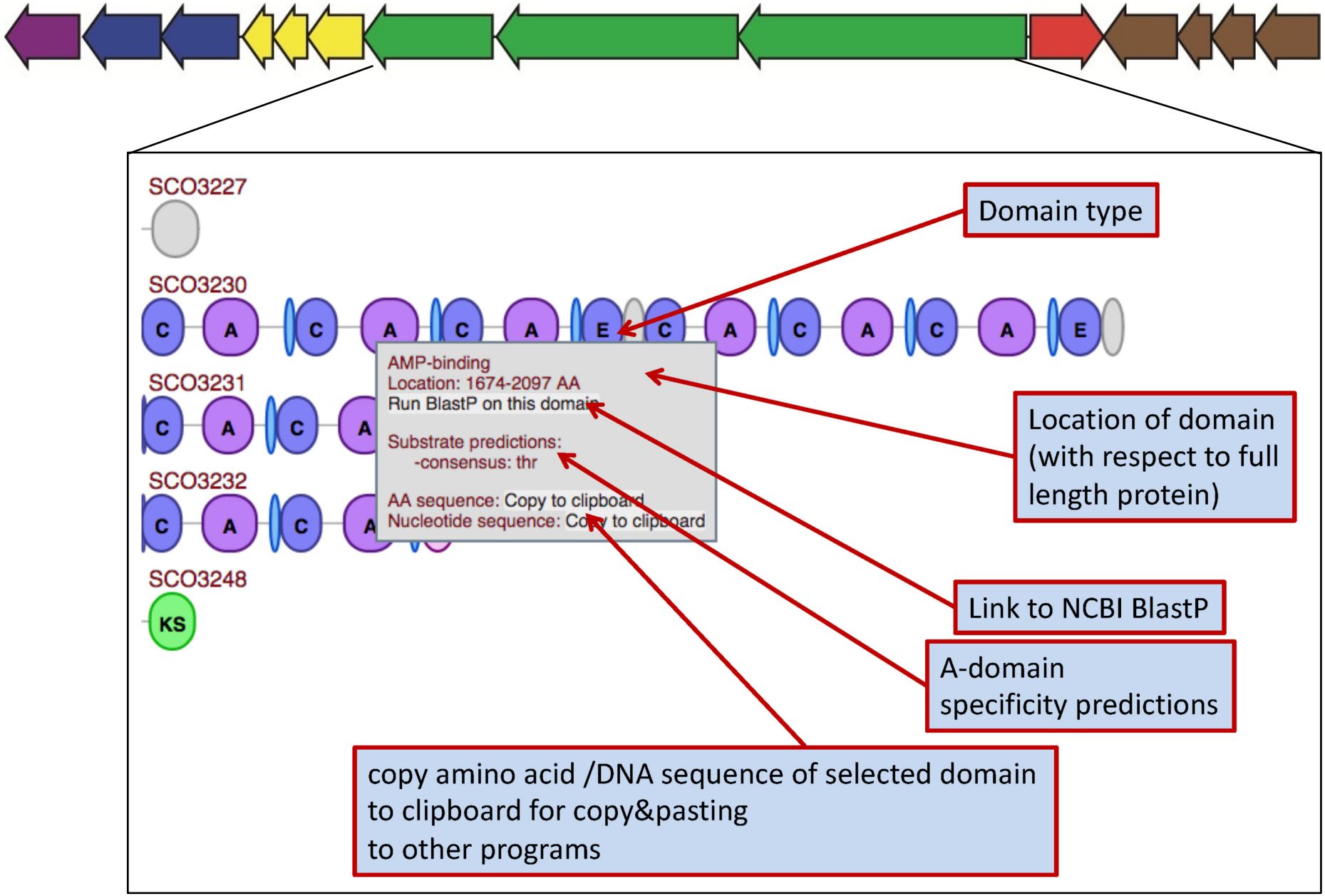
Medema et al. (2011) *Nucl. Acids Res.* 39: W339-W346.
Blin, Medema et al. (2013) *Nucl. Acids Res.* 41: W204-W212.
Weber et al. (2015) *Nucl. Acids Res.* 43: W237-W243.
Blin et al. (2017) *Nucl. Acids Res.* 45: W36-W41.
Blin et al. (2019) *Nucl. Acids Res.* 47: W81-W87.
Blin et al. (2021) *Nucl. Acids Res.* 49: W29-W35.

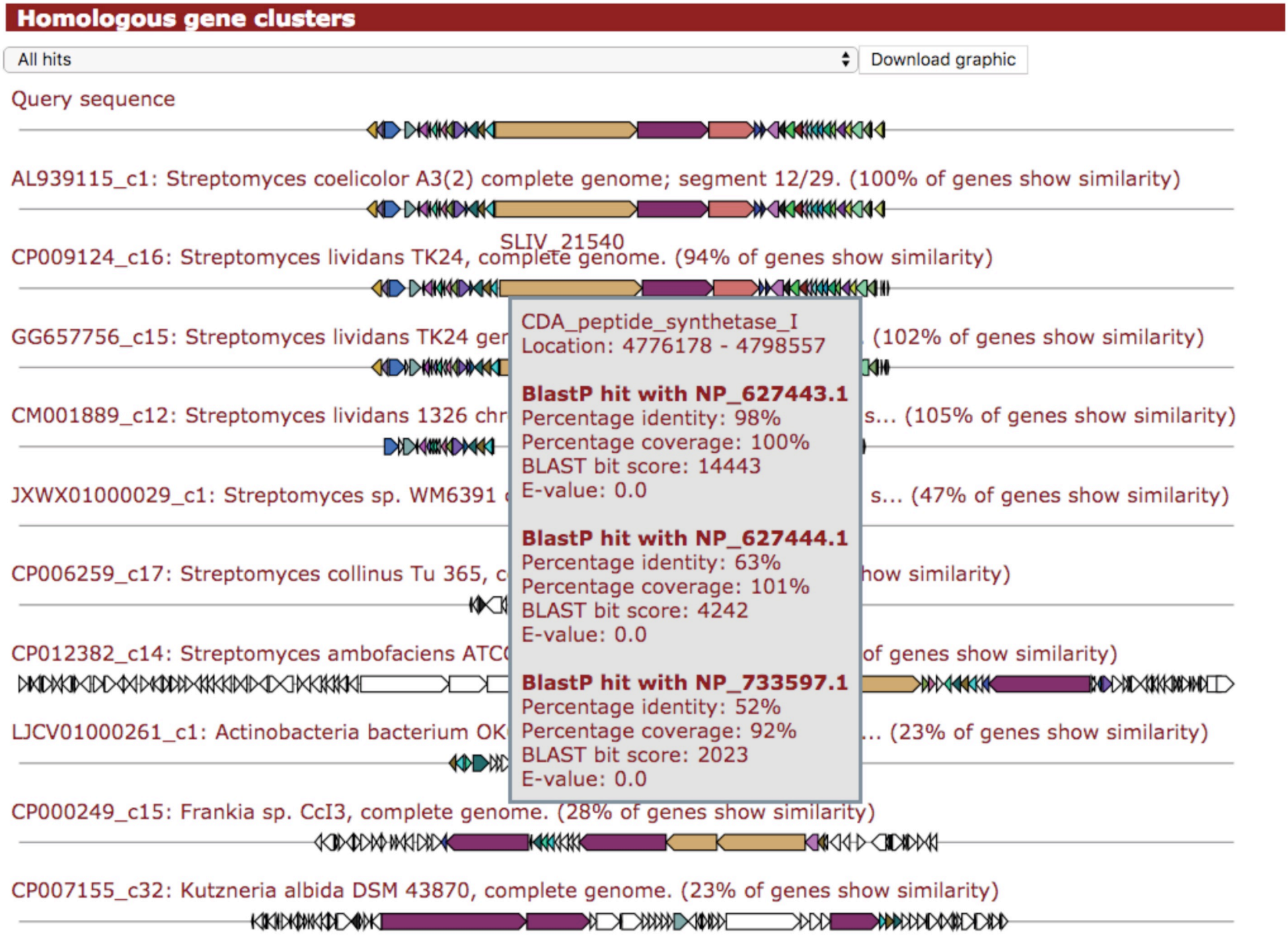
To get information on
the rule that antiSMASH used to identify the genetic region as a secondary metabolite biosynthetic gene cluster, click here

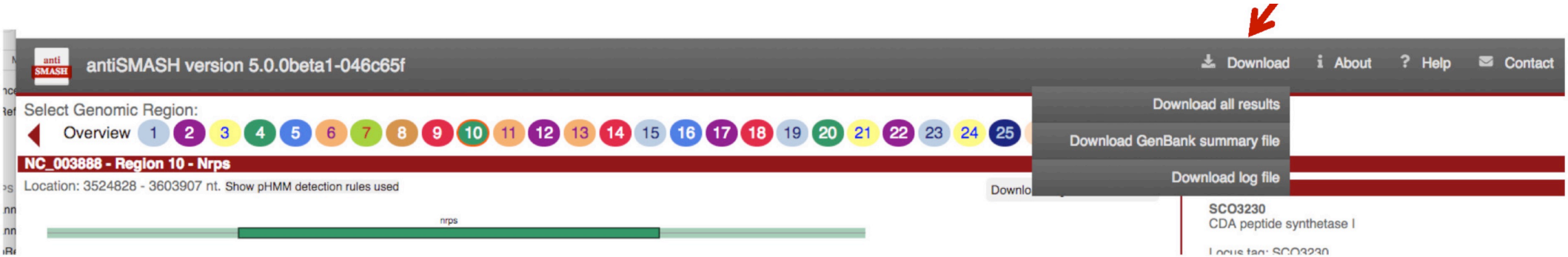
To get information on a specific gene of the cluster, click on the gene arrows; info is displayed in the right panel



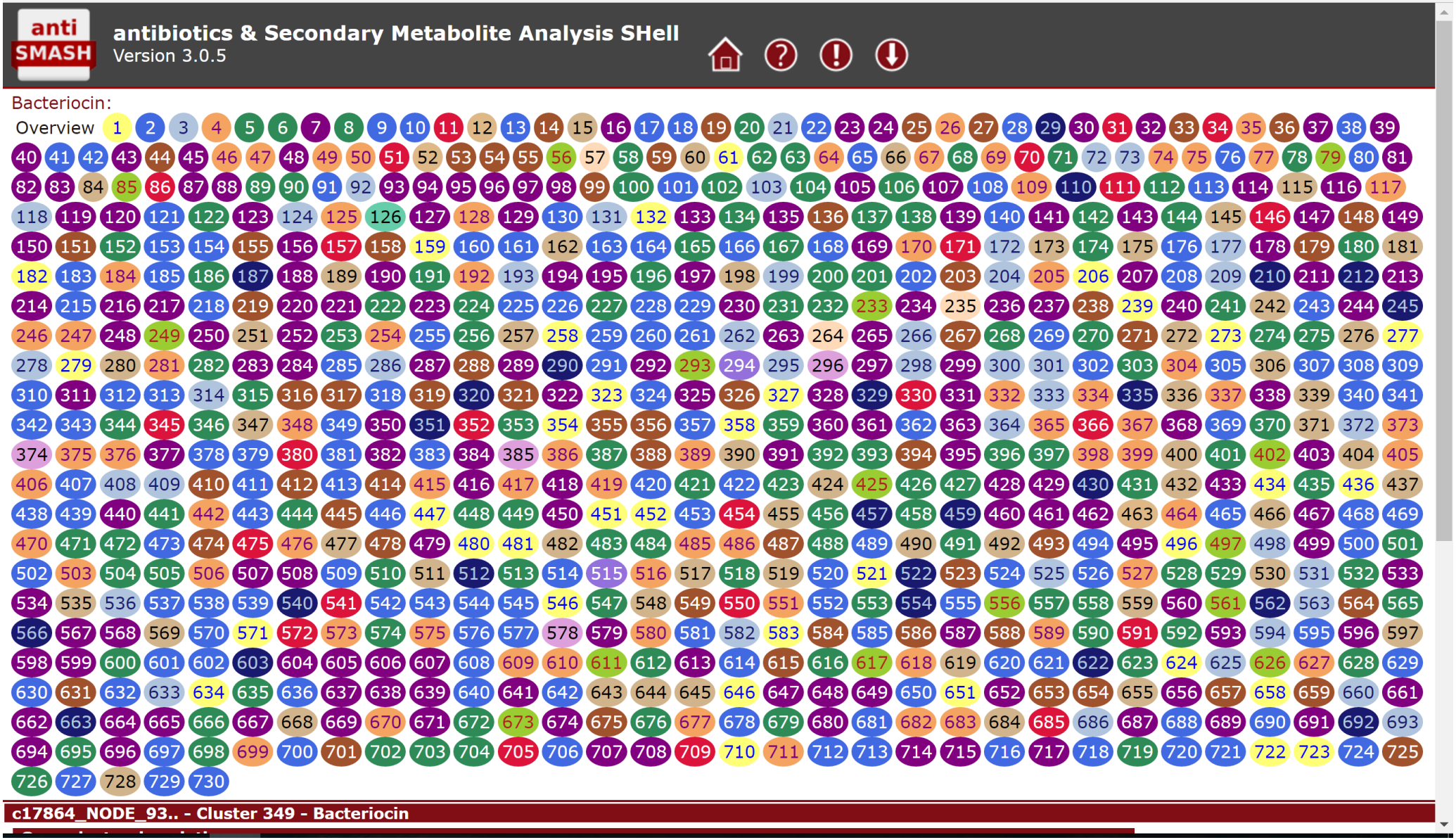
Zoom to region of interest by moving the bars or using the buttons


SCO3227
SCO3230
SCO3231
SCO3232
SCO3248
KS
AMP-binding
Location: 1674-2097 AA
Run BlastP on this domain
Substrate predictions:
-consensus: thr
AA sequence: Copy to clipboard
Nucleotide sequence: Copy to clipboard
Domain type
Location of domain (with respect to full length protein)
Link to NCBI BlastP
A-domain specificity predictions
copy amino acid /DNA sequence of selected domain to clipboard for copy&pasting to other programs


Homologous gene clusters
All hits
Download graphic
Query sequence
AL939115_c1: Streptomyces coelicolor A3(2) complete genome; segment 12/29. (100% of genes show similarity)
SLIV_21540
CP009124_c16: Streptomyces lividans TK24, complete genome. (94% of genes show similarity)
GG657756_c15: Streptomyces lividans TK24 ger
(102% of genes show similarity)
CM001889_c12: Streptomyces lividans 1326 chr
s... (105% of genes show similarity)
JXWX01000029_c1: Streptomyces sp. WM6391
s... (47% of genes show similarity)
CP006259_c17: Streptomyces collinus Tu 365, c
how similarity)
CP012382_c14: Streptomyces ambofaciens ATC
of genes show similarity)
LJCV01000261_c1: Actinobacteria bacterium OK
... (23% of genes show similarity)
CP000249_c15: Frankia sp. CcI3, complete genome. (28% of genes show similarity)
CP007155_c32: Kutzneria albida DSM 43870, complete genome. (23% of genes show similarity)
CDA_peptide_synthetase_I
Location: 4776178 - 4798557
BlastP hit with NP_627443.1
Percentage identity: 98%
Percentage coverage: 100%
BLAST bit score: 14443
E-value: 0.0
BlastP hit with NP_627444.1
Percentage identity: 63%
Percentage coverage: 101%
BLAST bit score: 4242
E-value: 0.0
BlastP hit with NP_733597.1
Percentage identity: 52%
Percentage coverage: 92%
BLAST bit score: 2023
E-value: 0.0

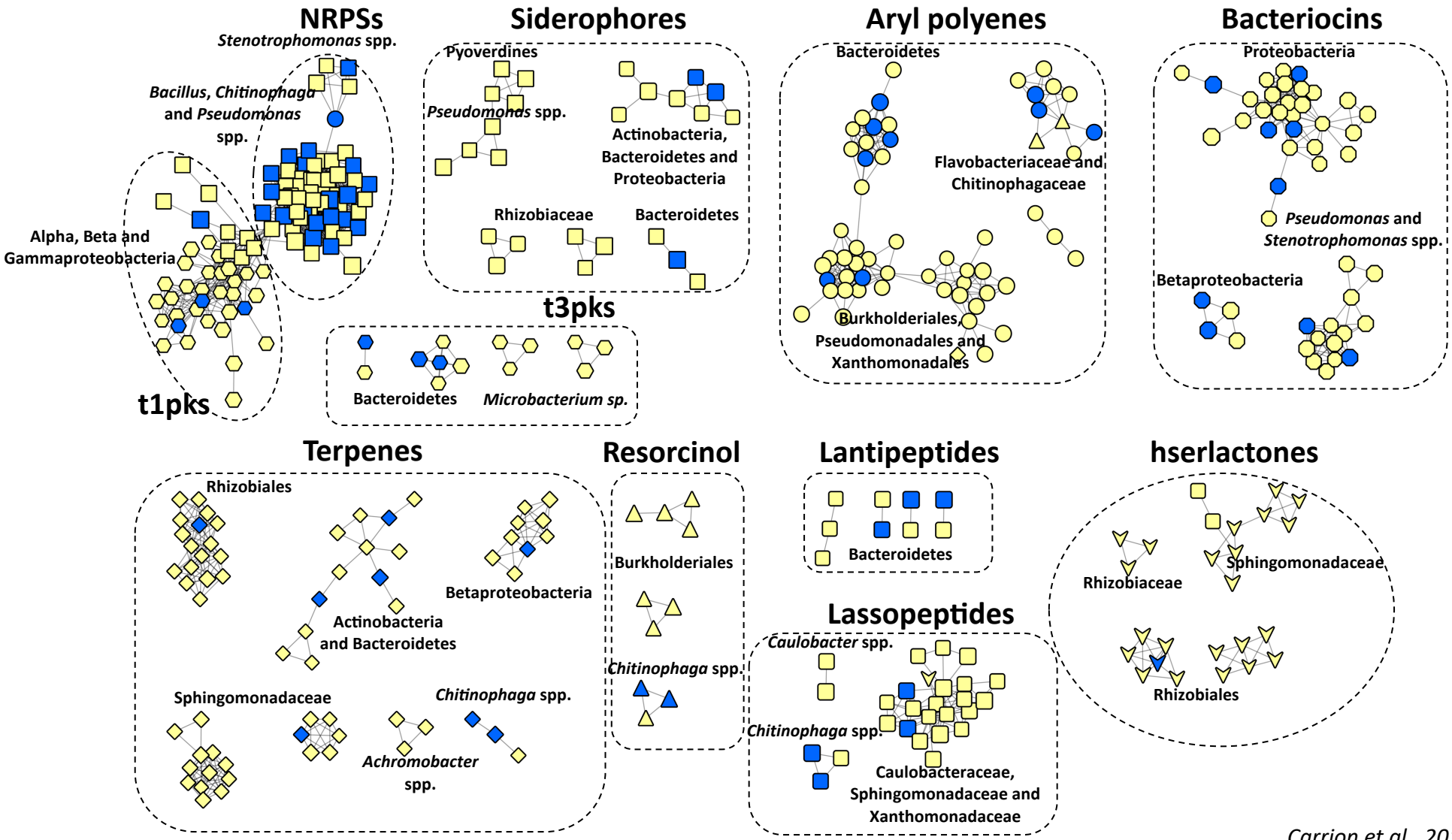

antiSMASH version 5.0.0beta1-046c65f
Download
About
Help
Contact
Download all results
Download GenBank summary file
Download log file
Select Genomic Region:
Overview 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
NC_003888 - Region 10 - Nrps
Location: 3524828 - 3603907 nt. Show pHMM detection rules used
nrps
SCO3230
CDA peptide synthetase I

ANTISMASH: METAGENOME



Enriched functions: secondary metabolism

(network based on HMM domains of BGCs)



Carrion et al., 2019 (SCIENCE)

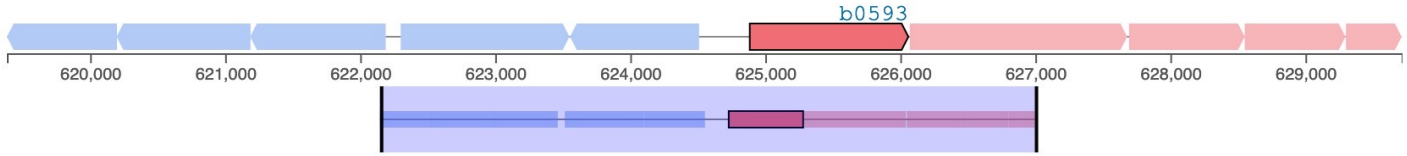
MIBiG PROVIDES AN ONLINE REPOSITORY OF BGCs WITH KNOWN FUNCTION

MIBiG Repository of Known Biosynthetic Gene Clusters — Download — Contact

BGC0002476: enterobactin biosynthetic gene cluster from *Escherichia coli str. K-12 substr. MG1655*

Location: 619,384 - 629,713 nt. (total: 10,330 nt).
This entry is originally from NCBI GenBank U00096.3.

Download region SVG | Download Cluster GenBank file | View antiSMASH-generated output



Legend:

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

reset view | zoom to selection

General | Compounds | Genes | History | NRPS/PKS domains | KnownClusterBlast

General information about the BGC

MIBiG accession	BGC0002476
Short description	enterobactin biosynthetic gene cluster from *Escherichia coli str. K-12 substr. MG1655*
Status	Minimal annotation: yes Completeness: Unknown
Biosynthetic class(es)	NRP
Loci	NCBI GenBank: U00096.3
Compounds	enterobactin
Species	*Escherichia coli str. K-12 substr. MG1655* [taxonomy]
References	Enterobactin: an archetype for microbial iron transport. Raymond KN et al., Proc Natl Acad Sci U S A (2003) PMID:12655062 Enterobactin: An archetype for microbial iron transport. Raymond, K et al., Proceedings of the National Academy of Sciences (2003) DOI:10.1073/pnas.0630018100

Gene details

b0593
isochorismate synthase EntC

Locus tag: b0593
Protein ID: AAC73694.1
Gene: entC
Location: 624,885 - 626,060, (total: 1176 nt)

Functions:
-

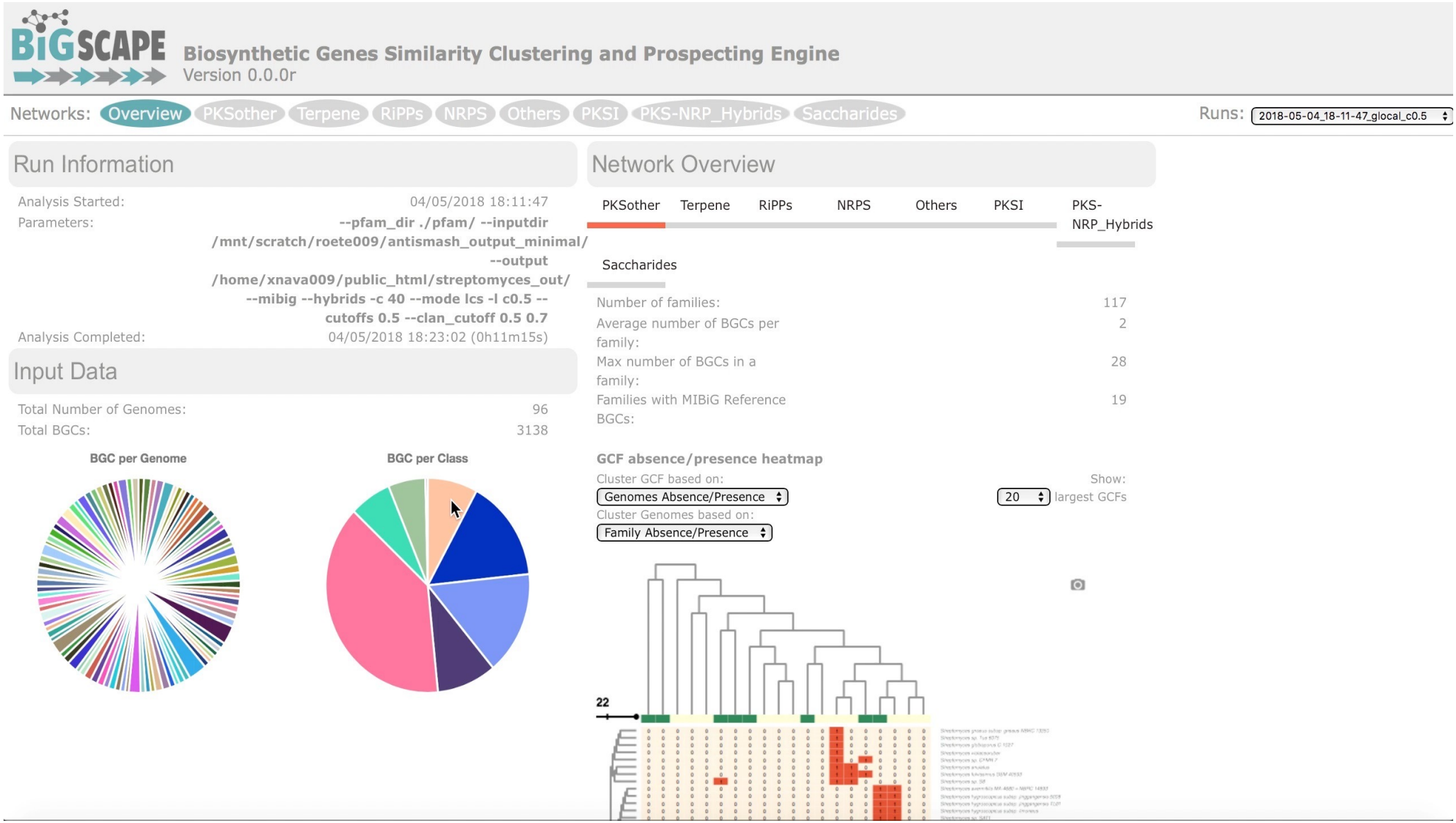
biosynthetic-additional (smcogs)
SMCOG1018:isochorismate synthase
(Score: 412.6; E-value: 4.1e-125)

NCBI BlastP on this gene
View genomic context
MiBIG Hits

AA sequence: Copy to clipboard
Nucleotide sequence: Copy to clipboard

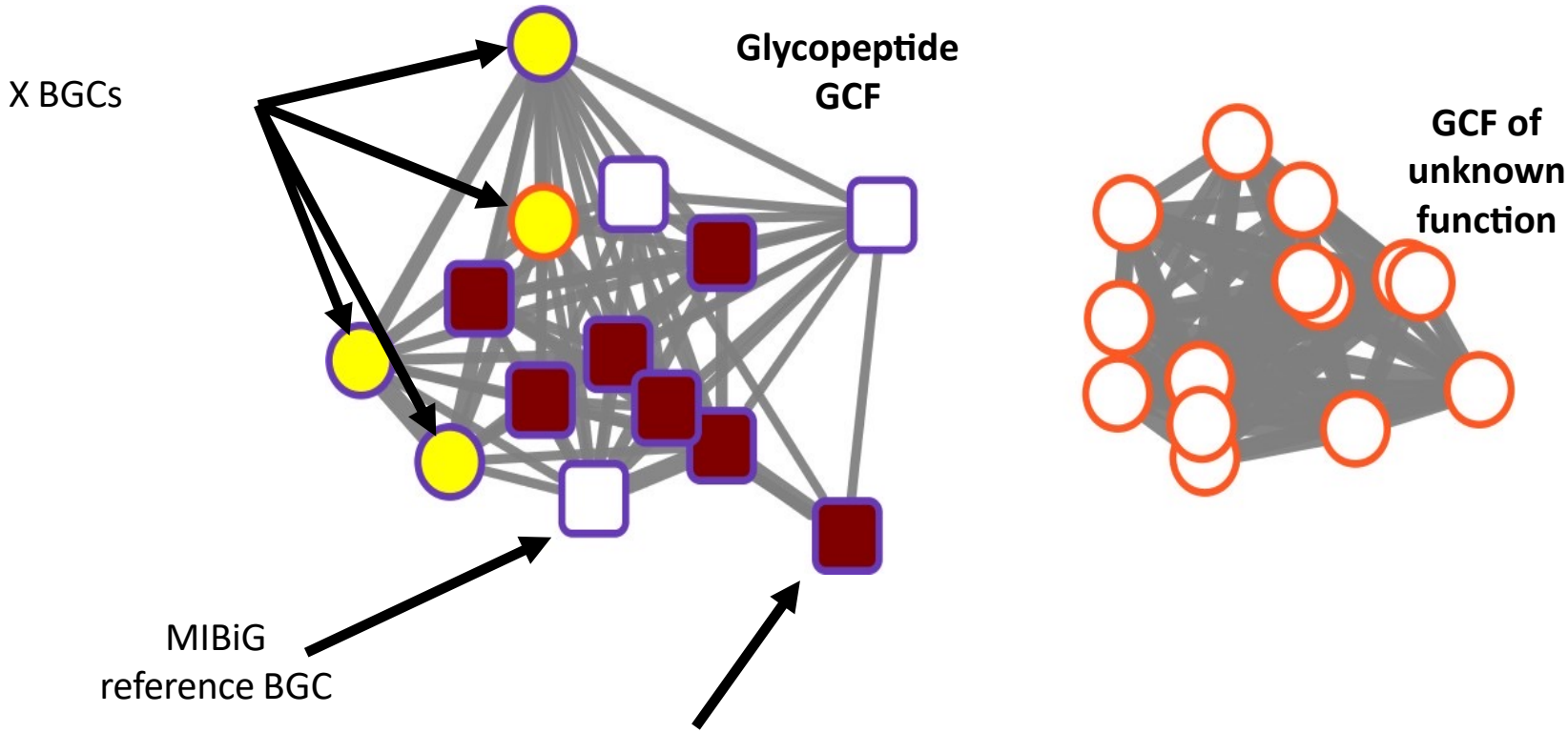
http://mibig.secondarymetabolites.org

A RICH WEB INTERFACE ALLOWS EFFECTIVELY EXPLORING BIG-SCAPE OUTPUTS



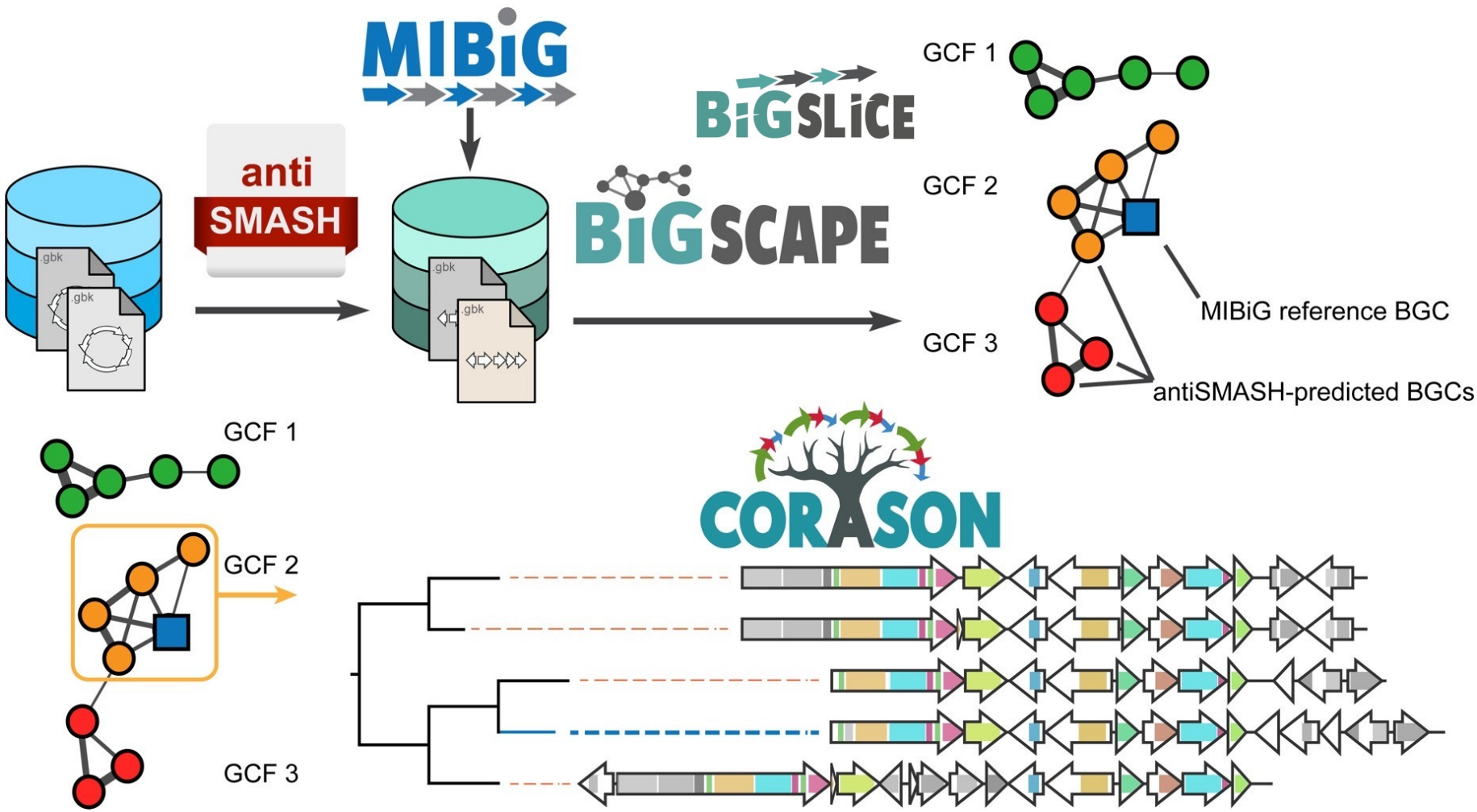
http://bigscape-corason.secondarymetabolites.org
https://git.wageningenur.nl/medema-group/BiG-SCAPE

MIBiG REFERENCE DATA ALLOWS RAPID ANNOTATION PROPAGATION AND NETWORK ANALYSIS



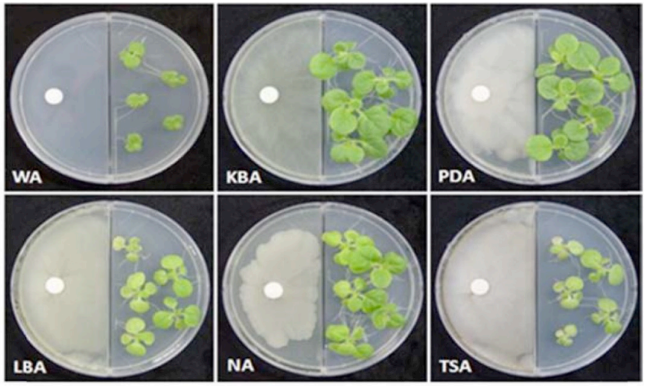
https://mibig.secondarymetabolites.org

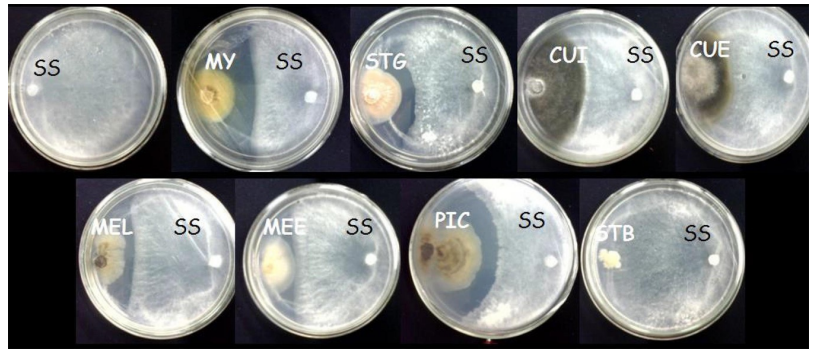
AN EXTENSIVE SOFTWARE ECOSYSTEM FACILITATES COMPUTATIONAL GENOMIC ANALYSIS OF LARGE-SCALE BIOSYNTHETIC DIVERSITY



https://antismash.secondarymetabolites.org
https://mibig.secondarymetabolites.org
http://bigscape-corason.secondarymetabolites.org

Navarro-Muñoz, Selem-Mojica, Mullowney et al. (2020) *Nature Chemical Biology* 16(1):60-68.





DNA reads

Quality control

FastQC

Filtered DNA reads

Genome assembly

Velvet

SPAdes

MEGAHIT

MEGAHIT

(meta)Genome

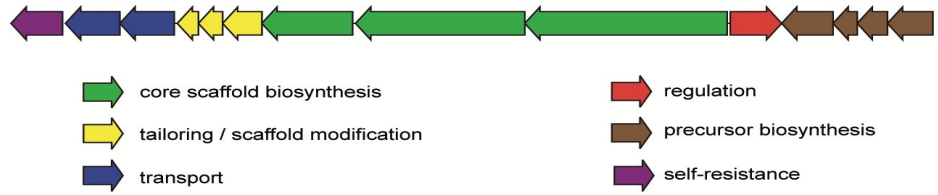
Quast

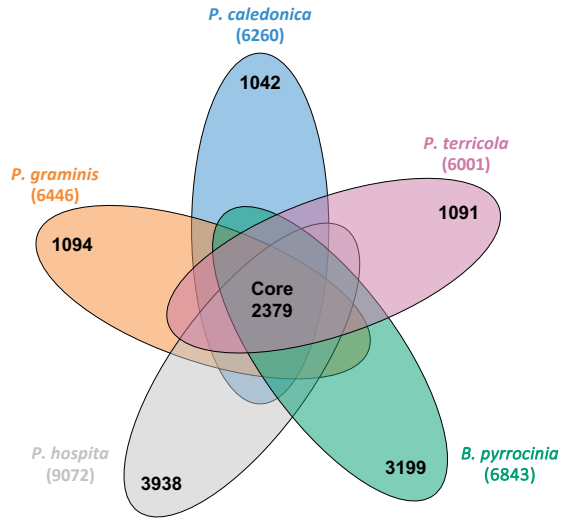
Quality Assessment Tool for Genome Assemblies

CheckM

Annotation

Comp. Genomics





WHAT HAVE WE LEARN?

1. Annotation tools (general and specific)
2. Secondary metabolism and more …