## FungiDB: Secondary Metabolites and clusters

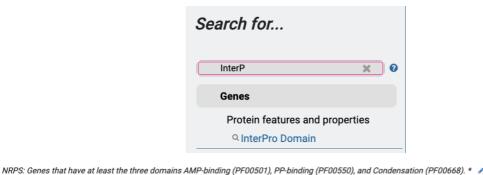
## **Learning objectives:**

- Explore InterPro search in FungiDB
- Cross-reference the results with MycoCosm data

## 1. Finding secondary metabolites and gene clusters

There are several main classes of secondary metabolites in fungi: the non-ribosomal peptides and amino acid-derived compounds, polyketides and fatty acid-derived compounds, and terpenes (Hoffmeister and Keller, 2007). The secondary metabolites can be segregated into groups based on the first step of their biosynthesis, more specifically, the "key enzymes" that are required: Non-ribosomal peptide syntheses (NRPSs), NRPS-like, Polyketide synthases (PKSs), PKS-like, Hybrid PKS – NRPS, Prenyltransferases (DMAT), Terpene cyclases/synthase (TC) (Read more: https://www.ncbi.nlm.nih.gov/pubmed/24692239)

• InterPro search to identify NRPS genes in all Aspergilli. NRPS genes have at least the three domains: AMP-binding (PF00501), PP-binding (PF00550), and Condensation (PF00668).



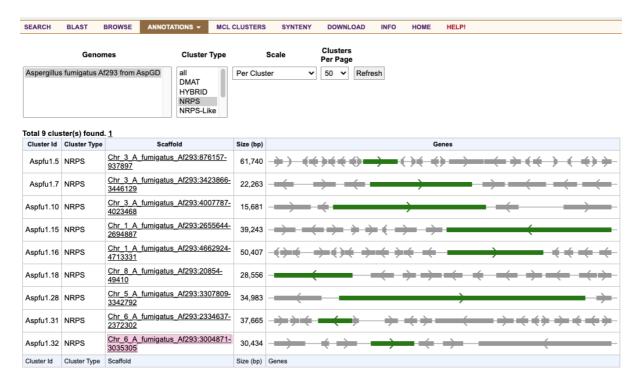


• How many genes were identified in *Aspergillus fumigatus* Af293?

Hint: use the organism filter on the left to limit your search results to Af293 genes only.



 Create a search for NRPS genes in MycoCosm. Access the A. fumigatus Af293 portal (<a href="https://mycocosm.jgi.doe.gov/Aspfu1">https://mycocosm.jgi.doe.gov/Aspfu1</a>) and navigate to the secondary metabolism clusters page (under the 'annotations' tab). How many genes did you get?



- What do you think may be causing the difference in the predicted gene number?
- This view on MycoCosm allows you to analyze backbone and auxiliary proteins across the entire predicted secondary metabolism cluster. How conserved are these secondary metabolite clusters across related Aspergilli? Click on the scaffold coordinates for Aspfu1.5 and analyze the Vista curve tracks. How many related Aspergilli show some synteny with this region? Repeat this exercise for the next cluster, Aspfu1.7.
  - Answer: Synteny is observed across most Aspergilli for Aspfu1.5, raising the possibility that this SM cluster is widespread across the genus. However, Aspfu1.7 shows no synteny except for at a couple auxiliary genes in *Aspergillus wentii*, suggesting that it is possibly lineage specific.

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