


## Supplementary File 2

A. MultiGeneBlast search with the *Leptosphaeria maculans* sirodesmin biosynthesis gene cluster as query. The results match those of Fox & Howlett (2008), who found similarity between this sirodesmin biosynthesis gene cluster and the gene cluster for the biosynthesis of gliotoxin from *Aspergillus fumigatus* (shown in the results as hit nr 5). Two gene clusters with still different architectures from *Aspergillus flavus* and *Penicillium marneffei* show up as hits nrs 3 and 4, and may encode different and yet unknown molecules from the same structural family.



# Search Results

Results pages: 1, 2, 3, 4, 5

### MultiGeneBlast hits


Select gene cluster alignment  Display all

Query: *Leptosphaeria maculans* HDX1 (HDX1), PKS1 (PKS1), and UVI-1h

1. : AY553235 *Leptosphaeria maculans* HDX1 (HDX1), PKS1 (PKS1), and UVI-1h (UVI-1h) genes Total score: 25.0 Cumulative Blast bit score: 213740
2. : FP929134 *Leptosphaeria maculans* JN3 Im\_SuperContig\_13\_v2 genomic supercontig Total score: 23.5 Cumulative Blast bit score: 204140
3. : [EQ963479](#) *Aspergillus flavus* NRRL3357 scf\_1106286418500 genomic scaffold Total score: 9.5 Cumulative Blast bit score: 32050
4. : D5995899 *Penicillium marneffei* ATCC 18224 scf\_1105668340764 genomic scaffold Total score: 8.5 Cumulative Blast bit score: 29460
5. : D5499599 *Aspergillus fumigatus* A1163 scf\_000006 genomic scaffold Total score: 8.5 Cumulative Blast bit score: 25230
6. : D5027698 *Neosartorya fischeri* NRRL 181 1099437636266 genomic scaffold Total score: 8.5 Cumulative Blast bit score: 25070
7. : ABDf02000065 *Trichoderma virens* Gv29-8 Total score: 7.5 Cumulative Blast bit score: 26340
8. : D5995735 *Trichophyton equinum* CBS 127.97 supercont1.18 genomic scaffold Total score: 7.5 Cumulative Blast bit score: 25390
9. : D5989823 *Arthroderma gypseum* CBS 118893 supercont1.2 genomic scaffold Total score: 7.5 Cumulative Blast bit score: 25160
10. : GG700652 *Trichophyton rubrum* CBS 118892 genomic scaffold supercont2.5 Total score: 7.5 Cumulative Blast bit score: 25070
11. : GG698503 *Trichophyton tonsurans* CBS 112818 genomic scaffold supercont1.27 Total score: 7.5 Cumulative Blast bit score: 25050
12. : GL698711 *Metarhizium anisopliae* ARSEF 23 unplaced genomic scaffold Scf\_001 Total score: 7.5 Cumulative Blast bit score: 22940

B. MultiGeneBlast search with the *Aspergillus nidulans* aflatoxin/sterigmatocystin biosynthesis gene cluster as query. The results match those of Slot & Rokas (2011), who showed that *Podospora anserina* possesses a gene cluster highly similar to those in *Aspergillus nidulans* and *Aspergillus flavus*. The *P. anserina* gene cluster is hit nr 3. Additionally, a number of other homologous gene clusters from *Aspergillus* and one from *Emericella* are identified by MultiGeneBlast.

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## Search Results

Results pages: [1](#), [2](#), [3](#), [4](#), [5](#)

**MultiGeneBlast hits** ?

Select gene cluster alignment Display all

Query: *Aspergillus nidulans* FGSC A4 chromosome IV ANcontig1.132, whole



1. : AACD01000132 *Aspergillus nidulans* FGSC A4 Total score: 31.5 Cumulative Blast bit score: 276040
2. : AY092402 *Aspergillus ochraceoroseus* strain SRRC 1492 aflatoxin/sterigmatocystin gene cluster Total score: 29.0 Cumulative Blast bit score: 196760
3. : CU640366 *Podospora anserina* S mat+ genomic DNA chromosome Z, supercontig Z. Total score: 29.0 Cumulative Blast bit score: 160040
4. : EQ963478 *Aspergillus flavus* NRRL3357 scf\_1106286417182 genomic scaffold Total score: 22.5 Cumulative Blast bit score: 144450
5. : U94740 *Emericella nidulans* sterigmatocystin biosynthetic gene cluster: (stcA), (stcB), (stcC),... Total score: 22.0 Cumulative Blast bit score: 221930
6. : AKHY01000106 *Aspergillus oryzae* 3.042 Total score: 22.0 Cumulative Blast bit score: 141170
7. : AY510451 *Aspergillus flavus* isolate AF13 aflatoxin biosynthesis gene cluster Total score: 21.5 Cumulative Blast bit score: 143430
8. : AY510453 *Aspergillus flavus* isolate AF70 aflatoxin biosynthesis gene cluster Total score: 21.5 Cumulative Blast bit score: 142320
9. : AB196490 *Aspergillus oryzae* DNA, aflatoxin biosynthesis gene cluster Total score: 21.5 Cumulative Blast bit score: 140870
10. : AY510454 *Aspergillus nomius* isolate AN13137 aflatoxin biosynthesis gene cluster Total score: 21.0 Cumulative Blast bit score: 146400
11. : AY510452 *Aspergillus flavus* isolate BN008 aflatoxin biosynthesis gene cluster Total score: 21.0 Cumulative Blast bit score: 145520
12. : AY371490 *Aspergillus parasiticus* aflatoxin pathway gene cluster Total score: 21.0 Cumulative Blast bit score: 145460

C. MultiGeneBlast search with the clorobiocin biosynthesis gene cluster as query, matching the results of Pojer (2011), who compared the gene clusters encoding the biosynthesis of clorobiocin, coumermycin (hit nr 2) and novobiocin (hit nr 3), which have different combinations of subclusters encoding different combinations of chemical moieties in the final compound. Besides these gene clusters, evolutionary similarities with the gene clusters encoding phenalinolactone (hit nr 4) and simocyclinone (hits nr 8-10) are also detected, matching subclusters encoding the shared pyrrole and coumarin chemical moieties, respectively.

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## Search Results

Results pages: [1](#), [2](#), [3](#), [4](#), [5](#)

MultiGeneBlast hits ?


Select gene cluster alignment ▼

Display all

Query: *Streptomyces roseochromogenes* subsp. *oscitans* clorobiocin

1. : AF329398 *Streptomyces roseochromogenes* subsp. *oscitans* clorobiocin biosynthetic gene cluster Total score: 41.5 Cumulative Blast bit score: 190660
2. : AF235050 *Streptomyces nishiniensis* strain DSM 40489 hypothetical protein gene Total score: 32.0 Cumulative Blast bit score: 138770
3. : AF170880 *Streptomyces caeruleus* strain NCIB 11891 novobiocin biosynthetic gene cluster Total score: 25.0 Cumulative Blast bit score: 109370
4. : DQ230532 *Streptomyces* sp. Tu6071 phenalinolactone biosynthetic gene cluster Total score: 9.0 Cumulative Blast bit score: 30790
5. : CM001165 *Streptomyces* sp. Tu6071 chromosome Total score: 7.5 Cumulative Blast bit score: 29850
6. : CP002040 *Nocardopsis dassonvillei* subsp. *dassonvillei* DSM 43111 chromosome 1 Total score: 7.5 Cumulative Blast bit score: 17920
7. : CP001700 *Catenulospira acidiphila* DSM 44928 Total score: 6.0 Cumulative Blast bit score: 23440
8. : AF324838 *Streptomyces antibioticus* simocyclinone biosynthetic gene cluster Total score: 6.0 Cumulative Blast bit score: 18640
9. : AF322256 *Streptomyces antibioticus* simocyclinone biosynthetic gene cluster Total score: 6.0 Cumulative Blast bit score: 18580
10. : AF321122 *Streptomyces antibioticus* simocyclinone biosynthetic gene cluster Total score: 6.0 Cumulative Blast bit score: 18580
11. : CP002047 *Streptomyces bingchenggensis* BCW-1 Total score: 5.5 Cumulative Blast bit score: 10410
12. : AM889123 *Streptomyces olivaceus* NDP-L-rhamnose biosynthesis gene cluster, *galE3* and *proB* genes, ... Total score: 5.0 Cumulative Blast bit score: 14580

D. MultiGeneBlast search with the cladoniamide biosynthesis gene cluster as query, matching the results of Ryan (2011), who compared the gene clusters encoding the biosynthesis of cladoniamide, BE-54017, rebeccamycin, AT2433, K252a and staurosporine.



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## Search Results

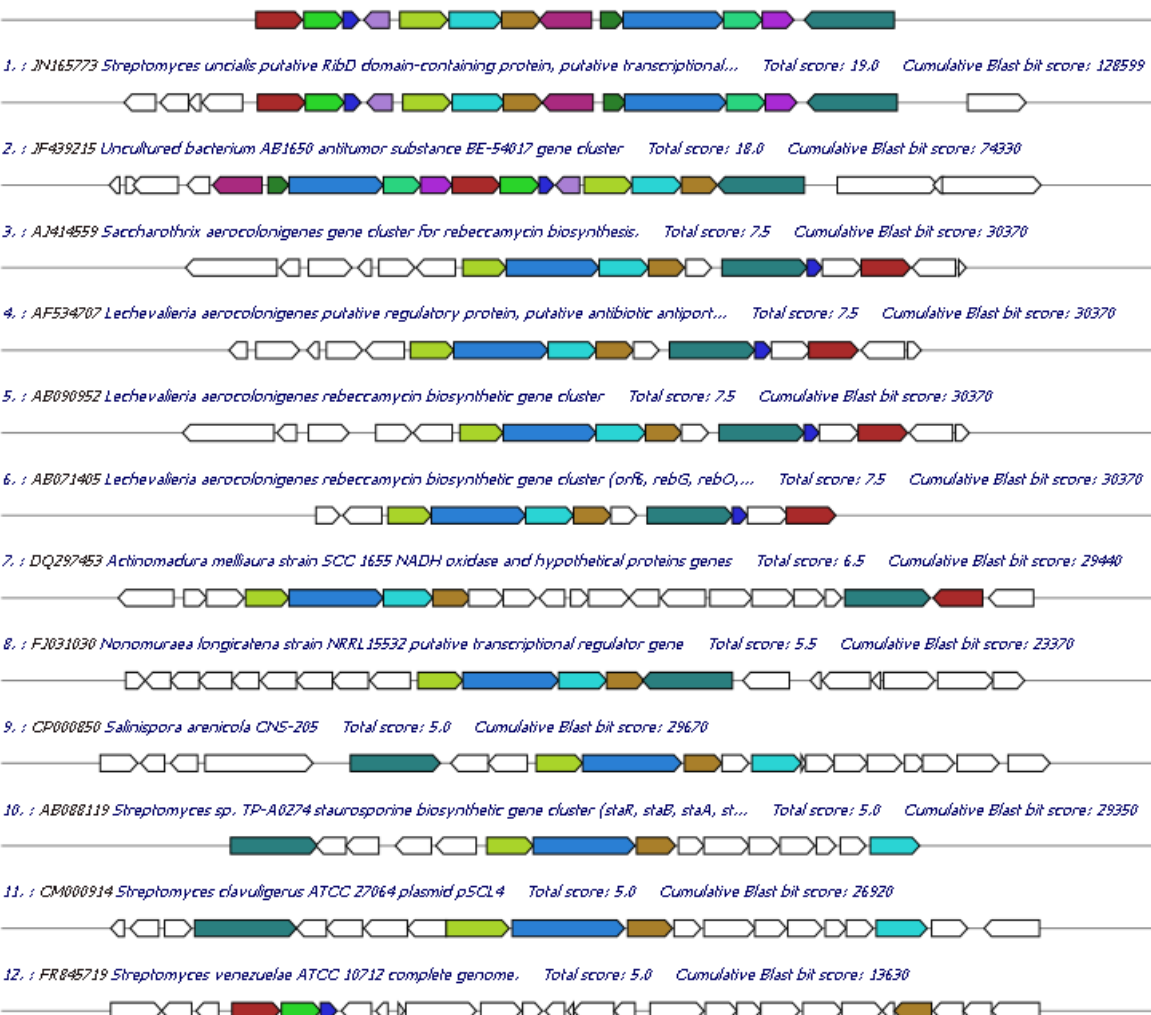
Results pages: 1, 2, 3, 4, 5

**MultiGeneBlast hits** ?

Select gene cluster alignment


Display all

Query: *Streptomyces uncialis* putative RibD domain-containing protein,



1. : JN165773 *Streptomyces uncialis* putative RibD domain-containing protein, putative transcriptional... Total score: 19.0 Cumulative Blast bit score: 128599
2. : JF439215 Uncultured bacterium AB1650 antitumor substance BE-54017 gene cluster Total score: 18.0 Cumulative Blast bit score: 74330
3. : AJ414559 *Saccharothrix aerocolonigenes* gene cluster for rebeccamycin biosynthesis. Total score: 7.5 Cumulative Blast bit score: 30370
4. : AF534707 *Lechevaleria aerocolonigenes* putative regulatory protein, putative antibiotic antiport... Total score: 7.5 Cumulative Blast bit score: 30370
5. : AB090952 *Lechevaleria aerocolonigenes* rebeccamycin biosynthetic gene cluster Total score: 7.5 Cumulative Blast bit score: 30370
6. : AB071405 *Lechevaleria aerocolonigenes* rebeccamycin biosynthetic gene cluster (orf6, rebG, rebO,... Total score: 7.5 Cumulative Blast bit score: 30370
7. : DQ297453 *Actinomadura melliura* strain SCC 1655 NADH oxidase and hypothetical proteins genes Total score: 6.5 Cumulative Blast bit score: 29440
8. : FJ031030 *Nonomuraea longicatena* strain NRRL15532 putative transcriptional regulator gene Total score: 5.5 Cumulative Blast bit score: 23370
9. : CP000850 *Salinispora arenicola* CNS-205 Total score: 5.0 Cumulative Blast bit score: 29670
10. : AB088119 *Streptomyces* sp. TP-A0274 staurosporine biosynthetic gene cluster (staR, staB, staA, st... Total score: 5.0 Cumulative Blast bit score: 29350
11. : CM000914 *Streptomyces clavuligerus* ATCC 27064 plasmid pSCL4 Total score: 5.0 Cumulative Blast bit score: 26920
12. : FR845719 *Streptomyces venezuelae* ATCC 10712 complete genome. Total score: 5.0 Cumulative Blast bit score: 13630

E. MultiGeneBlast search with the *Xanthomonas gardneri* lipopolysaccharide biosynthesis gene cluster as query. The results match those of Potnis et al. (2011), who compared the gene clusters of *Xanthomonas gardneri*, *Xanthomonas vesicatoria*, and *Xanthomonas campestris pv. vesicatoria*. Additionally, a number of additional gene cluster variants from other species can be observed.



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## Search Results

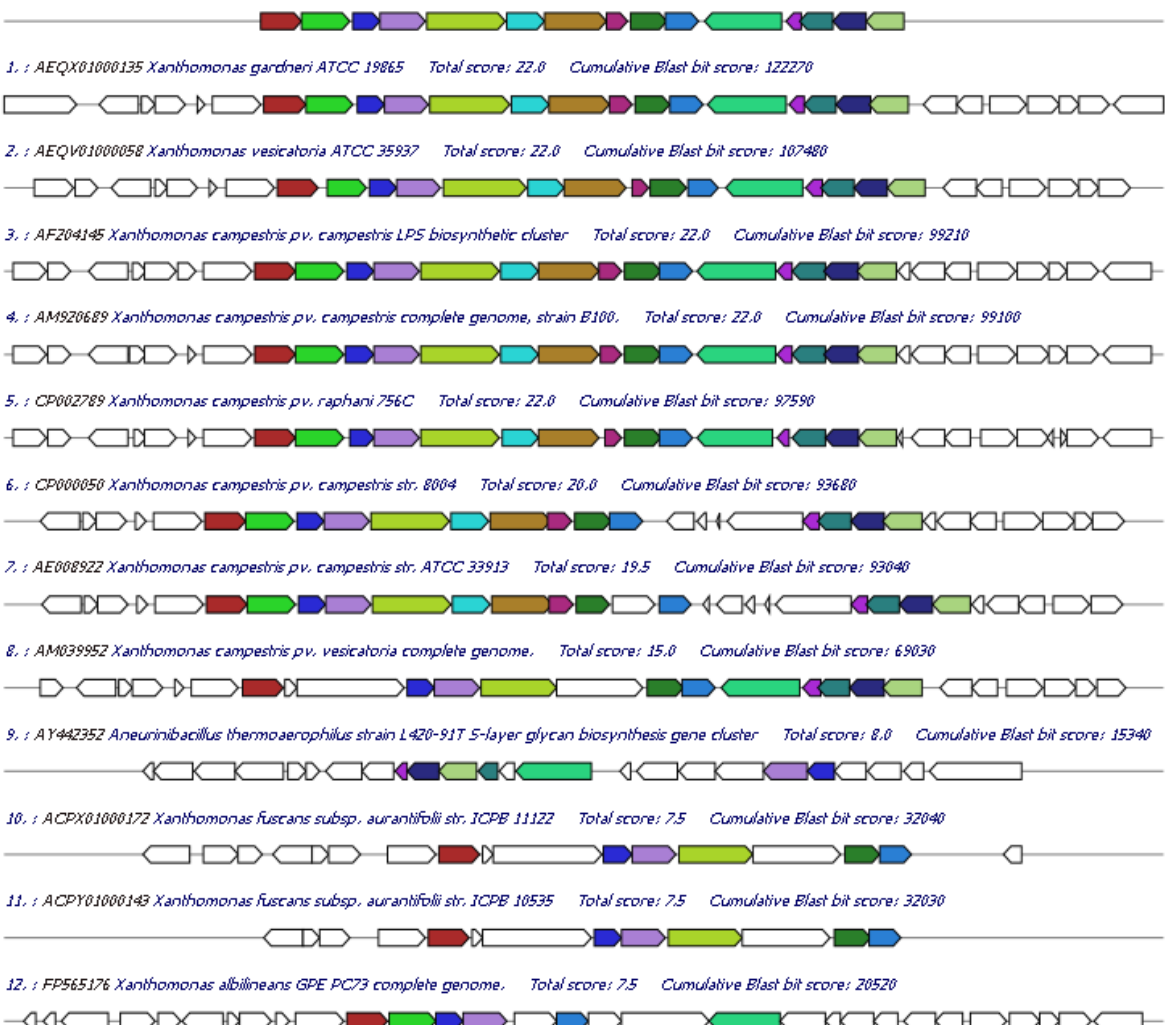
Results pages: [1](#), [2](#), [3](#), [4](#), [5](#)

MultiGeneBlast hits
?

Select gene cluster alignment

Display all

Query: *Xanthomonas gardneri* ATCC 19865 XANTHO7DRAF\_Contig3, whole genome



1. : AEQX01000135 *Xanthomonas gardneri* ATCC 19865 Total score: 22.0 Cumulative Blast bit score: 122270
2. : AEQV01000050 *Xanthomonas vesicatoria* ATCC 35937 Total score: 22.0 Cumulative Blast bit score: 107480
3. : AF204145 *Xanthomonas campestris pv. campestris* LPS biosynthetic cluster Total score: 22.0 Cumulative Blast bit score: 99210
4. : AM920689 *Xanthomonas campestris pv. campestris* complete genome, strain B100. Total score: 22.0 Cumulative Blast bit score: 99100
5. : CP002789 *Xanthomonas campestris pv. raphani* 756C Total score: 22.0 Cumulative Blast bit score: 97590
6. : CP000050 *Xanthomonas campestris pv. campestris* str. 8004 Total score: 20.0 Cumulative Blast bit score: 93680
7. : AE008922 *Xanthomonas campestris pv. campestris* str. ATCC 33913 Total score: 19.5 Cumulative Blast bit score: 93040
8. : AM039952 *Xanthomonas campestris pv. vesicatoria* complete genome. Total score: 15.0 Cumulative Blast bit score: 69030
9. : AY442352 *Aneurinibacillus thermoaerophilus* strain L420-917 5-layer glycan biosynthesis gene cluster Total score: 8.0 Cumulative Blast bit score: 15340
10. : ACPX01000172 *Xanthomonas fuscans* subsp. *aurantifolii* str. ICPB 11122 Total score: 7.5 Cumulative Blast bit score: 32040
11. : ACPY01000143 *Xanthomonas fuscans* subsp. *aurantifolii* str. ICPB 10535 Total score: 7.5 Cumulative Blast bit score: 32030
12. : FP565176 *Xanthomonas albilineans* GPE PC73 complete genome. Total score: 7.5 Cumulative Blast bit score: 20520

## References

1. Fox E.M., Howlett B.J. (2008) Biosynthetic gene clusters for epipolythiodioxopiperazines in filamentous fungi. *Mycological Research* 112: 162-169.
2. Slot J.C., Rokas A. (2011) Horizontal transfer of large and highly toxic secondary metabolic gene cluster between fungi. *Current Biology* 21: 134-139.
3. F. Pojer, S.M. Li, L. Heide (2002) Molecular cloning and sequence analysis of the clorobiocin biosynthetic gene cluster: new insights into the biosynthesis of aminocoumarin antibiotics. *Microbiology* 148: 3901-3911.
4. Ryan K.S. (2011) Biosynthetic gene cluster for the cladoniamides, bis-indoles with a rearranged scaffold. *PLoS ONE* 6(8): e23694.
5. Potnis N., Krasileva K., Chow V., Almeida N.F., Patil P.B., Ryan R.P., Sharlach M., Behlau F., Dow J.M., Momol M.T., White F.F., Preston J.F., Vinatzer B.A., Koebnik R., Setubal J.C., Norman D.J., Staskawicz B.J., Jones J.B. (2011) Comparative genomics reveals diversity among xanthomonads infecting tomato and pepper. *BMC Genomics* 12: 146.