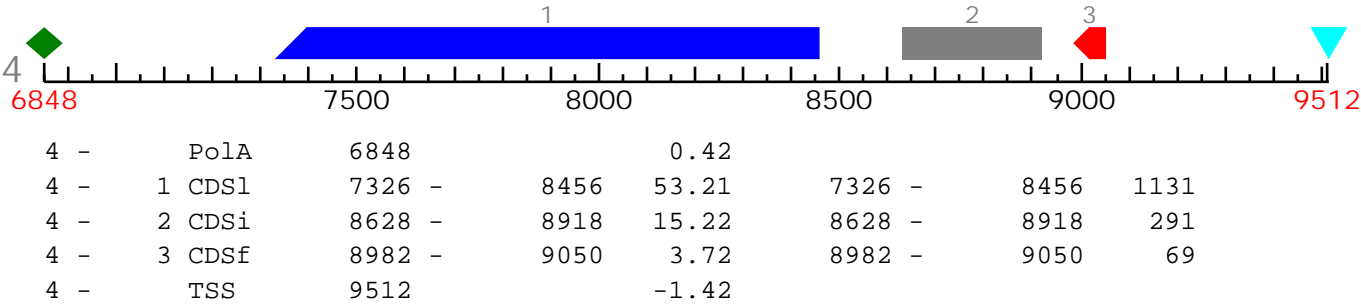
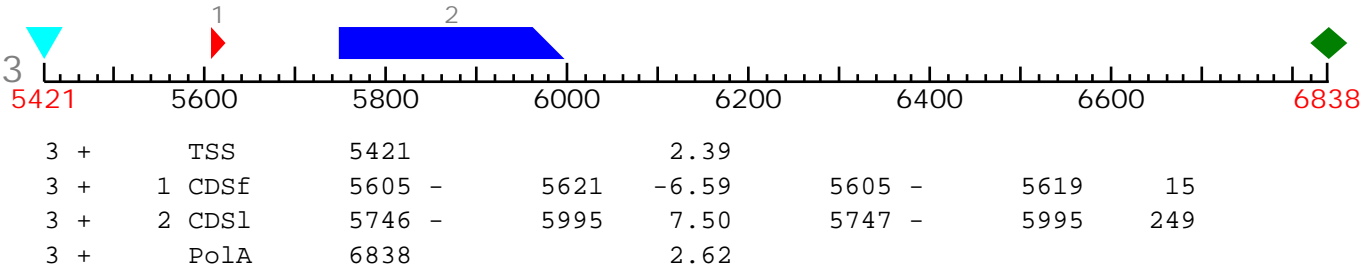
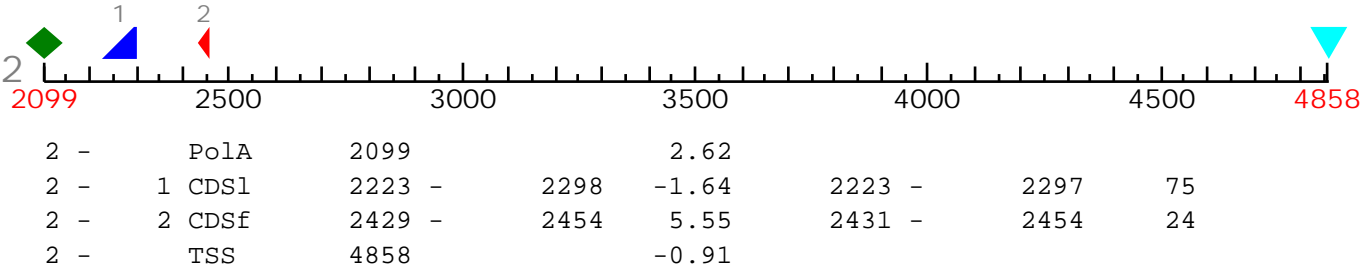
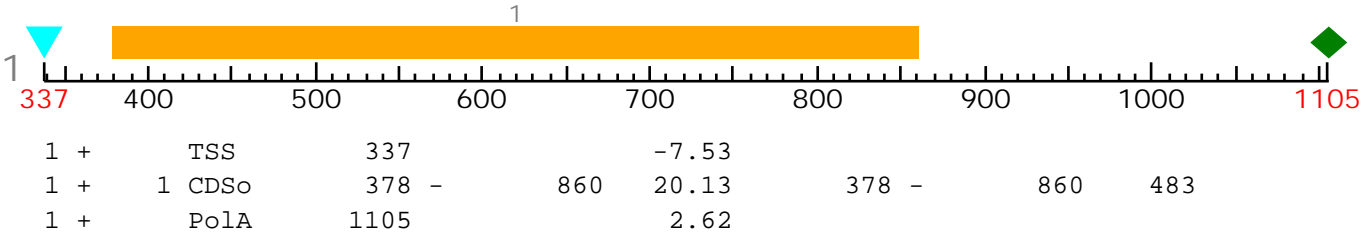
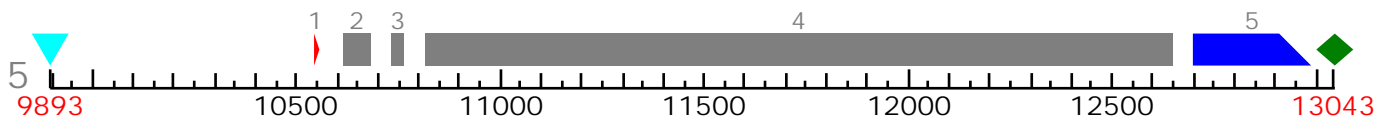


FGENESH 2.6 Prediction of potential genes in Blumeri_graminis genomic DNA
Seq name: fungal_18
Length of sequence: 13836
Number of predicted genes 5: in +chain 3, in -chain 2.
Number of predicted exons 13: in +chain 8, in -chain 5.
Positions of predicted genes and exons: Variant 1 from 1, Score:239.063477

► CDSf ■ CDSi ▽ CDSl ■ CDSo ◆ PolA ▼ TSS





5 +	TSS	9893		-4.41			
5 +	1 CDSf	10540 -	10546	-5.31	10540 -	10545	6
5 +	2 CDSi	10611 -	10678	7.11	10613 -	10678	66
5 +	3 CDSi	10730 -	10761	-4.43	10730 -	10759	30
5 +	4 CDSi	10812 -	12645	139.06	10813 -	12645	1833
5 +	5 CDSl	12695 -	12985	32.32	12695 -	12985	291
5 +	PolA	13043		-4.38			

Predicted protein(s):

```
>FGENESH:[mRNA] 1 1 exon (s) 378 - 860 483 bp, chain +
ATGCAGATTTTTGTAAAGACTCTCACCGGGAAGACTATCACCCCTTGAGGTGGAGTCTTCC
GATACCATCGACAATGTCAAGACCAAATCCAAGATAAAGAAGGAATACCTCCTGACCAA
CAACGCTTGATTTTCGCAGGAAAGCAGCTTGAAGATGGTTCGAACACTCGCCGATTACAAC
ATCCAAAAGAGTCTACCTTACATCTTGTCTACGTCTGCGAGGTGGGGCAAAGAAGCGA
AAGAAGAAGGTTTACACAACCCCTAAAAAGATCAAGCACAAGCGAAAGAAGACAAAGTTA
GCTGTGCTCAAATATTACAAAGTGGATGGCGACGGAAAAATTGAGCGTCTTCGCAGAGAA
TGTCCTTCAACAGATGTAAGTCCTTTGTCCGTTGTATCACACATTCTAATCCTTATCAGT
GCGGTGCCGGTGTTCATGGCTGCTATGCAGGACCGTCAATATTGTGGACGATGCCATC
TAA
>FGENESH: 1 1 exon (s) 378 - 860 160 aa, chain +
MQIFVKTLTGKTITLEVESSDTIDNVKTKIQDKEGIPPDQQRLLIFAGKQLEDGRTLADYN
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CPSTDVSPSLSVSHILILISAVPVFSWLLCRTVNIVDDAI
>FGENESH:[mRNA] 2 2 exon (s) 2223 - 2454 102 bp, chain -
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GAGCATATTGGGCTCCTCTCTAACCCAGACCACGTATTTTAA
>FGENESH: 2 2 exon (s) 2223 - 2454 33 aa, chain -
MSFAHVAFRLYIVPPESLIVEHIGLLSNPDHVF
>FGENESH:[mRNA] 3 2 exon (s) 5605 - 5995 267 bp, chain +
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AGCCAAGAAGAATCGCATCCGAATCGAAGTCGAAAGCAACCTCAAGCATGTCTCCATTTG
ACAACCTTCTCGACAATGCCTTTCTTACCATCCTCATCTCAGTCATCAACCTTCTTTTGAC
CACGCCTCATCTCGCCTCAACAATAA
>FGENESH: 3 2 exon (s) 5605 - 5995 88 aa, chain +
MGQLVRKSRTGYLLGLPAKTNSSPSSGAGVIAQYALHIWDSQEESHPNRSRKQPQACLHL
TTSRQCLSYHPLSHQPSFDHASSRLNN
>FGENESH:[mRNA] 4 3 exon (s) 7326 - 9050 1491 bp, chain -
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TCATTCTTATTGACTCCAGATCTTCGAAGATTTCACTCAGCTAACAGTATCGCAGCCGAT
TATCTCTTTCATACAGAGTCAACCAGGTCTGAAGTCTGGGATCTAGCTGAACTTACCATA
CAGTGTGGCCGGCGTGCTGATAGTCTCAAACCTCGCGCTGAGCTGGATCTATTATGGCACG
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>FGENESH: 4 3 exon (s) 7326 - 9050 496 aa, chain -
MESNHYASGEPQGPDPHASELEDLLHAVQALIIIPFVRSADSVACKSMTGSVPVAPGASV
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VHVFKVSPALSVIEKLTAKALAVQFGFDGPDSSGISTQSGSASNATSIVIARNCLYPSTK
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QCRRADSLKLALS WIYYGTEGFEQQIEYAFSVAAYMAAQIESNPHFHLVSENPPCLQV
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>FGENESH: [mRNA] 5 5 exon (s) 10540 - 12985 2232 bp, chain +
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>FGENESH: 5 5 exon (s) 10540 - 12985 743 aa, chain +
MSVIGVDFGTAGTVIAVARNRGVDVITNEVSNRSTPSLVGFGPKSRYLGESAKTQEISNL
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REGLEKLVEPLLNRVHVPLEQALADAKLKVEDIDVIELVGGCTRVPAKLERIQKFFNKT
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VF NQGNLMPSTKILTFYRKEPFNLEAKYATPEKLPKTKPWIGNFSVKGVKADAKDDFMICK
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