

## 7.1 Identification of specific DNA motifs.

Note: For this exercise use <http://fungidb.org>

- a. Find all BamHI restriction sites in all *Pythium ultimum* genomic sequences available in FungiDB. Note: you can use the DNA motif search to find complex motifs like transcription factor binding sites using regular expressions.

Hint: BamHI = GGATCC and the DNA motif search is under the heading “Genomic Segments”.

The screenshot shows the FungiDB website interface. The main content area is divided into three columns: "Identify Genes by:", "Identify Other Data Types:", and "Tools:". A red arrow points from the "DNA Motif Pattern" option in the "Identify Other Data Types:" column to the "Tools:" column.

### Identify Genomic Segments based on DNA Motif Pattern

Organism select all | clear all | expand all | collapse all | reset to default

- Blastocladiomycetes
- Agaricomycetes
- Schizosaccharomycetes
- Leotiomycetes
- Chytridiomycetes
- Saccharomycetes
- Tremellomycetes
- Oomycetes
  - Pythium*
  - Hyaloperonospora
  - Saprolegnia
  - Phytophthora
- Ustilaginomycetes
- Zygomycetes
- Pneumocystidomycetes
- Eurotiomycetes
- Sordariomycetes
- Pucciniomycetes

select all | clear all | expand all | collapse all | reset to default

Pattern GGATCC

Advanced Parameters

Get Answer

- b. How many times does the BamHI site occur in the genomes you searched? Take a look at your results; notice the Genomic location and the Motif columns.

My Strategies: [New](#) [Opened \(1\)](#) [All \(5\)](#) [Basket](#) [Public Strategies \(1\)](#) [Help](#)

(Segments) Strategy: DNA Motif \*

DNA Motif  
18800 Segments  
Step 1

Rename  
Duplicate  
Save As  
Share  
Delete

---

**18800 Genomic Segments from Step 1** Add 18800 Genomic Segments to Basket | Download 18800 Genomic Segments

Strategy: DNA Motif

Genomic Segment Results Genomic Locations

First 1 2 3 4 5 Next Last Advanced Paging Add Columns

Segment ID	Organism	Genomic Location	Motif
<a href="#">PuiDAOMBR144_SC1231:148-154.f</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1231: 148 - 154 (+)	...TGGGTGTCGTTTACGTGTGAGGATCCCTCAGGAGCGGCCATTCCGC...
<a href="#">PuiDAOMBR144_SC1231:148-154.r</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1231: 148 - 154 (-)	...GCGGAATGGCCGCTCTGTGAGGGATCCCTCACACGTAAACGACACCCA...
<a href="#">PuiDAOMBR144_SC1237:1395-1401.f</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1237: 1395 - 1401 (+)	...GAGAAGAGGAGTCGAGTCTGGATCCCAACGGCGTGTTCAGATCGCC...
<a href="#">PuiDAOMBR144_SC1237:1395-1401.r</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1237: 1395 - 1401 (-)	...GGCGATCTGAACACGCGCTGGATCCCAAGACTCGACTCCTCTTCC...
<a href="#">PuiDAOMBR144_SC1237:2140-2146.f</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1237: 2140 - 2146 (+)	...CAGACGGGTGCAGTGTGAGTGGATCCAGGGCACCGGCATACCCGTC...
<a href="#">PuiDAOMBR144_SC1237:2140-2146.r</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1237: 2140 - 2146 (-)	...GACGGGTATGCCGGTGCCTGGATCCCAAGTCACTGCACCCGCTCG...
<a href="#">PuiDAOMBR144_SC1237:2173-2179.f</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1237: 2173 - 2179 (+)	...CGGCATACCCGTCAGGTAAGTGGATCCAGTGTGCTTTGCGAAGATT...
<a href="#">PuiDAOMBR144_SC1237:2173-2179.r</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1237: 2173 - 2179 (-)	...AATCTTCGCAACGACCACTGGATCCAGTACCTGACGGGTATGCCG...
<a href="#">PuiDAOMBR144_SC1237:266-272.f</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1237: 266 - 272 (+)	...TAGTTGCTGGCTCGGCTCTGGATCCCTCTGTAAAGGACGACGA...
<a href="#">PuiDAOMBR144_SC1237:266-272.r</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1237: 266 - 272 (-)	...TCGTGCTTCTTACAAGAAGGGATCCAGAGCCGAGCCAGGCAACTA...
<a href="#">PuiDAOMBR144_SC1237:602-608.f</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1237: 602 - 608 (+)	...CTATCGGGATCTCCATCTCGATCCCAAGTGTCTCAGGAAGCGAA...
<a href="#">PuiDAOMBR144_SC1237:602-608.r</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1237: 602 - 608 (-)	...TTCGCTTCTGGAGCAGCTGGATCCAGAGTGGGAGATCCCGATAG...
<a href="#">PuiDAOMBR144_SC1239:100825-100831.f</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1239: 100825 - 100831 (+)	...TCTTTCGCTTTTCTTTGCGGATCCACTTGGGGTCTTCAGAGCCT...
<a href="#">PuiDAOMBR144_SC1239:100825-100831.r</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1239: 100825 - 100831 (-)	...AGGCTCTGAAGACCGCAAGTGGATCCGAAAGAAAAAGACGAAAGA...
<a href="#">PuiDAOMBR144_SC1239:102460-102466.f</a>	Pythium ultimum DAOM BR144	PuiDAOMBR144_SC1239: 102460 - 102466 (+)	...GCCAAGGTGCGCTCTGTGCGGATCCGATCGGACACACGTTTCT...

## 7.2 Find genes that have one of these BamHI sites within 250 nucleotides upstream of their start.

In the section 7.1 you found BamHI sites, but now you are looking for genes that have one of these sites located within 250 nucleotides upstream of their start.

Hint: You can achieve this by running a genomic collocation search that defines the genomic relationship between the BamHI sites and genes. Add a “Genes by Organism” step to the motif search and select the “1 relative to 2, using genomic locations” option.

My Strategies: New Opened (1)

(Segments)

DNA Motif  
18800 Segments  
Step 1

18800 Genomic Segments from Strategy: DNA Motif

Genomic Segment Results Genomic Locations

First 1 2 3 4 5 Next Last Advanced Paging Add Columns

Segment ID	Organism	Genomic Location	Motif
PuIDAOIMBR144_SC1231:148-154.f	Pythium ultimum DAOM BR144	PuIDAOIMBR144_SC1231: 148 - 154 (+)	...TGGSTGTCGTTTACGTGTGAGGATCCCTCAGGAGCGGCCATTCCGC...
PuIDAOIMBR144_SC1231:148-154.r	Pythium ultimum DAOM BR144	PuIDAOIMBR144_SC1231: 148 - 154 (-)	...TCGGGAATGGCCGCTCCTGAGGGATCCTCACACGTAAACGACACCCA...
PuIDAOIMBR144_SC1237:1395-1401.f	Pythium ultimum DAOM BR144	PuIDAOIMBR144_SC1237: 1395 - 1401 (+)	...GAGAAGAGGAGTCTGAGTCTGGGATCCCAACGGCGTGTTCAGATCGCC...
PuIDAOIMBR144_SC1237:1395-1401.r	Pythium ultimum DAOM BR144	PuIDAOIMBR144_SC1237: 1395 - 1401 (-)	...GGCGATCTGAACACGCCGTTGGATCCAGACTCGACTCCTCTCTTC...
PuIDAOIMBR144_SC1237:2140-2146.f	Pythium ultimum DAOM BR144	PuIDAOIMBR144_SC1237: 2140 - 2146 (+)	...CAGACGGGTGCACTGACTCGATCCAGGCAACGGGATACCCGCTC...

### Add Step 2 : Organism

Organism  select all | clear all | expand all | collapse all | reset to default

- Agaricomycetes
- Blastocladiomycetes
- Chytridiomycetes
- Eurotiomycetes
- Leotiomycetes
- Oomycetes
  - Hyaloperonospora
  - Phytophthora
  - Pythium
  - Saprolegnia
- Pneumocystidomycetes
- Pucciniomycetes
- Saccharomycetes
- Schizosaccharomycetes
- Sordariomycetes
- Tremellomycetes
- Ustilaginomycetes
- Zygomycetes

select all | clear all | expand all | collapse all | reset to default

Advanced Parameters

### Combine Genomic Segments in Step 1 with Genes in Step 2:

1 Intersect 2     1 Minus 2  
 1 Union 2     2 Minus 1  
 1 Relative to 2, using genomic colocation

Continue....

### 5 Genomic Colocation

Combine Step 1 and Step 2 using relative locations in the genome  
 You had 18800 Genomic Segments in your Strategy (Step 1). Your new Genes search (Step 2) returned 15986 Genes.

"Return each Gene from Step 2 whose upstream region overlaps the exact region of a Genomic Segment in Step 1 and is on either strand"

(15986 Genes in Step 2)

Region  
Gene

Exact  
 Upstream: 250 bp  
 Downstream: 1000 bp  
 Custom:  
 begin at: start - 250 bp  
 end at: start + 1 bp

(18800 Genomic Segments in Step 1)

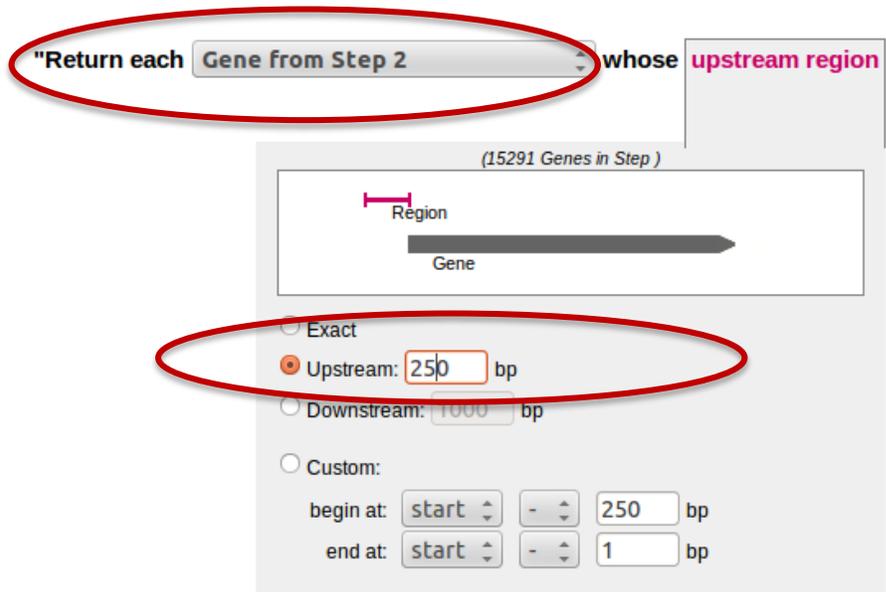
Region  
Genomic Segment

Exact  
 Upstream: 1000 bp  
 Downstream: 1000 bp  
 Custom:  
 begin at: start + 0 bp  
 end at: stop + 0 bp

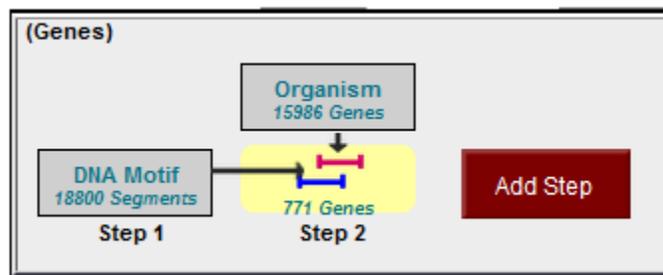
Submit

Close

How did you modify the location relative to genes?

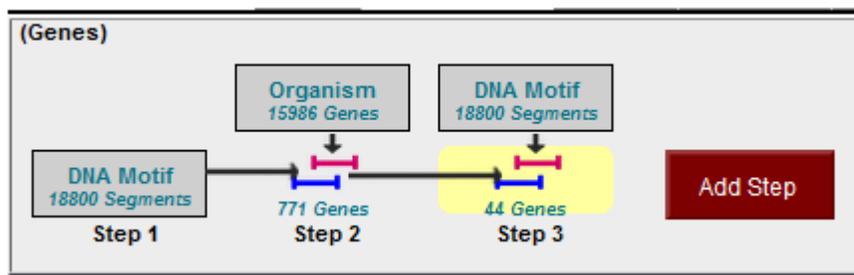


How many genes did you get?



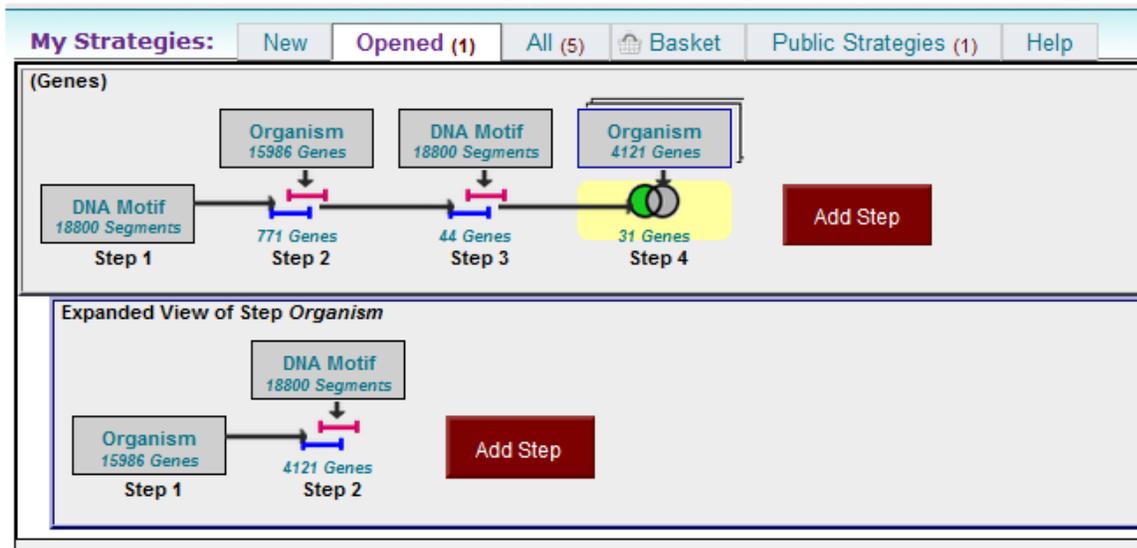
7.3 Using a similar sequence of steps as in part 7.2, define which of these genes also have a BamHI site in their 250 nucleotide downstream region.

Hint: after you click on add step you will have to select DNA motif search and select the genomic collocation option.



7.4 Taking this a step further, define which of these genes do NOT contain a BamHI site within them.

Hint: you will have to use a nested strategy.



**31 Genes from Step 4**  
Strategy: DNA Motif

Click on a number in this table to limit/filter your results

All Results	Ortholog Groups	<i>Ajellomyces</i>		<i>Allomyces</i>		<i>Aspergillus</i>					
		<i>A.capsulatus</i> (nr Genes: 0)		<i>A.macrogynus</i>		<i>A.aculeatus</i>	<i>A.carbonarius</i>	<i>A.clavatus</i>	<i>A.flavus</i>	<i>A.fumigatus</i>	<i>A.nidulans</i>
		G186AR	NAm1	ATCC 38327		ATCC 16872	ITEM 5010	NRRL 1	NRRL3357	Af293	FGSC A4
31	31	0	0	0	0	0	0	0	0	0	0

Look at your results. Do they make sense?

Confirm your results by looking at one of the genes in Gbrowse and showing BamHI restriction sites.

**Note:** you can add a column to any result table that allows you to go directly to GBrowse at the genomic coordinates of any ID in your result list. Click on the Add Columns button.

The screenshot shows a web interface for gene results. At the top, there are tabs for 'Gene Results' and 'Genome View'. Below the tabs, there are navigation links: 'First 1 2 Next Last' and 'Advanced Paging'. On the right side, there is a button labeled 'Add Columns' which is circled in red. Below the navigation is a table with three columns: 'Gene ID', 'Genomic Location', and 'Product Description'. The table contains several rows of data, including gene IDs like Pytul\_G007170 and genomic coordinates like PytulBR144\_SC1242: 96,660 - 97,169 (-). A dialog box titled 'Select Columns' is open on the right side of the table. It has a close button (X) in the top right corner. At the top of the dialog, there is an 'Update Columns' button. Below this, there are links: 'clear all | expand all | collapse all' and 'reset to current | reset to default'. The dialog contains a list of categories with expand/collapse icons and checkboxes for various columns. The categories are: 'Text, IDs, Species', 'Genomic Position' (with sub-items: 'Chromosome', 'Genomic Location' (checked), 'Gene Strand'), 'Gene Attributes', 'Protein Attributes' (with sub-items: 'Product Description' (checked), 'Molecular Weight', 'Isoelectric Point'), 'Protein Features', 'Transcript Expression', 'Putative Function', 'Evolution', 'Search PDB by the protein sequence', 'GBrowse' (highlighted with a red arrow), and 'Weight'. At the bottom of the dialog, there are links: 'clear all | expand all | collapse all' and 'reset to current | reset to default', and an 'Update Columns' button.

Gene ID	Genomic Location	Product Description
Pytul_G007170	PytulBR144_SC1242: 96,660 - 97,169 (-)	Similar to TPRXL: Putative protein TPRXL (Homo sapiens);
Pytul_G007107	PytulBR144_SC1242: 242,551 - 242,829 (-)	Similar to TIM9: Mitochondrial import inner membrane translocase subunit Tim9 (Mesembryanthemum crys...
Pytul_G005845	PytulBR144_SC1402: 231,053 - 231,591 (+)	Protein of unknown function;
Pytul_G005579	PytulBR144_SC1402: 940,179 - 940,864 (-)	Similar to Tbc1d10c: Carabin (Mus musculu...
Pytul_G012872	PytulBR144_SC1722: 11,333 - 12,344 (+)	Protein of unknown function;
Pytul_G014631	PytulBR144_SC1811: 81,730 - 83,030 (+)	Protein of unknown function;
Pytul_G014158	PytulBR144_SC1895: 66,174 - 67,031 (+)	Similar to GARP: Glutamic acid-rich protein...
Pytul_G013849	PytulBR144_SC1980: 106,849 - 108,519 (+)	Protein of unknown function;
Pytul_G012238	PytulBR144_SC1991: 33,753 - 34,190 (+)	Similar to Cd36: Platelet glycoprotein 4 (Ra...
Pytul_G003273	PytulBR144_SC2006: 695,146 - 696,223 (+)	Similar to loc1: 60S ribosomal subunit asse...
Pytul_G002517	PytulBR144_SC2008: 374,121 - 376,923 (-)	Similar to 4CLL4: 4-coumarate-CoA ligase...
Pytul_G002216	PytulBR144_SC2008: 1,284,832 - 1,285,680 (-)	Similar to xecD: 2-(R)-hydroxypropyl-CoM c...
Pytul_G011671	PytulBR144_SC2014: 139,259 - 139,786 (+)	Protein of unknown function;
Pytul_G007849	PytulBR144_SC2020: 536,762 - 537,941 (-)	Similar to WDR77: Methylosome protein 50...
Pytul_G008131	PytulBR144_SC2022: 527,213 - 527,683 (+)	Similar to Rv2228c: Uncharacterized protei...
Pytul_G000785	PytulBR144_SC2023: 1,108,433 - 1,109,577 (-)	Protein of unknown function;
Pytul_G010215	PytulBR144_SC2026: 83,496 - 83,770 (-)	Protein of unknown function;

**Note:** you can configure restriction sites by clicking on the configure button in GBrowse and selecting the restriction sites you would like to display. To view restriction sites, the “Restriction Sites” data track must be turned on. Go to the “Select Tracks” page and click “Restriction Sites” under the “Analysis” section.

**Browser** | Select Tracks | Snapshots | Custom Tracks | Preferences

Search

Landmark or Region : Pytu1BR144\_SC1980:91,849..123,519 Search

Annotate Restriction Sites **Configure...** Save Snapshot Load Snapshot

Data Source: FungiDB GBrowse v2.48

Scroll/Zoom: << < > >> Show 31.67 kbp Flip

Pytu1BR144\_SC1980

Pytu1BR144\_SC1980: 31.67 kbp

upload\_5535

Synetic Sequences and Genes (Shaded by Orthology) (Showing 11 of 103 subtracks)

Annotated Genes (with UTRs in gray when available)

Pytu1\_G013856 Pytu1\_G013854 Pytu1\_G013852 Pytu1\_G013849 Pytu1\_G013847

Pytu1\_G013855 Pytu1\_G013853 Pytu1\_G013851 Pytu1\_G013850 Pytu1\_G013848

Select Tracks Clear highlighting

The restriction site plugin generates a restriction map on the current view. This plugin was written Elizabeth Nickerson & Lincoln Stein.

Cancel Configure

Select Restriction Sites To Annotate

Restriction Site Display  off  on

<input type="checkbox"/> AatII	<input type="checkbox"/> BspDI	<input type="checkbox"/> HpaII	<input type="checkbox"/> PspGI
<input type="checkbox"/> Acc65I	<input type="checkbox"/> BspEI	<input type="checkbox"/> Hpy188I	<input type="checkbox"/> PspOMI
<input type="checkbox"/> AccI	<input type="checkbox"/> BspHI	<input type="checkbox"/> Hpy188III	<input type="checkbox"/> PstI
<input type="checkbox"/> AclI	<input type="checkbox"/> BsrFI	<input type="checkbox"/> Hpy99I	<input type="checkbox"/> PvuI
<input type="checkbox"/> AfeI	<input type="checkbox"/> BsrGI	<input type="checkbox"/> HpyCH4III	<input checked="" type="checkbox"/> PvuII
<input type="checkbox"/> AflII	<input type="checkbox"/> BssHII	<input type="checkbox"/> HpyCH4IV	<input type="checkbox"/> RsaI
<input type="checkbox"/> AflIII	<input type="checkbox"/> BssKI	<input type="checkbox"/> HpyCH4V	<input type="checkbox"/> RsrII
<input type="checkbox"/> AgeI	<input type="checkbox"/> BstAPI	<input type="checkbox"/> KasI	<input type="checkbox"/> SacI
<input type="checkbox"/> AhdI	<input type="checkbox"/> BstBI	<input type="checkbox"/> KpnI	<input type="checkbox"/> SacII
<input type="checkbox"/> AluI	<input type="checkbox"/> BstEII	<input type="checkbox"/> MboI	<input type="checkbox"/> SalI
<input type="checkbox"/> AlwNI	<input type="checkbox"/> BstNI	<input type="checkbox"/> MfeI	<input type="checkbox"/> Sau3AI
<input type="checkbox"/> ApaI	<input type="checkbox"/> BstUI	<input type="checkbox"/> MluI	<input type="checkbox"/> Sau96I
<input type="checkbox"/> ApaLI	<input type="checkbox"/> BstXI	<input type="checkbox"/> MscI	<input type="checkbox"/> SbfI
<input type="checkbox"/> ApoI	<input type="checkbox"/> BstYI	<input type="checkbox"/> MseI	<input type="checkbox"/> Scal
<input type="checkbox"/> AscI	<input type="checkbox"/> BstZ17I	<input type="checkbox"/> MslI	<input type="checkbox"/> ScrFI
<input type="checkbox"/> AseI	<input type="checkbox"/> Bsu36I	<input type="checkbox"/> MspA1I	<input type="checkbox"/> SexAI

Pytu1BR144\_SC1980

Pytu1BR144\_SC1980: 5 kbp

Frame Usage

Annotated Genes (with UTRs in gray when available)

Pytu1\_G013849 Pytu1\_G013848

Restriction Sites

BamHI restriction site

BamHI BamHI

upload\_5535

Synetic Sequences and Genes (Shaded by Orthology) (Showing 11 of 103 subtracks)