

Look up the following sequences in the Subilist website and obtain the 100 bp upstream region of the genes. Save the sequences in a document

yvgT
yvbA
ydcH
yvrD
lrpA

The sequences should look like the following:

```
>yvgT
tcttttttctcatgaaaatgttattgattttacgctggagcgattataaaatctagaggctcgtcagaaaatttaac
aaacataaaagggagtcacaga
```

```
>yvbA
tttgagggttgTTTTTAAAAAattcaagttataatgaaaataatacatttatacaaatatctaaatgtctaaatgt
TTTTTgtaaaggagaaaacgct
```

```
>ydcH
caggaaaccaagcatcttggctTTTTtatttcgcagaggacactttgaaataagcaaaaaagatttttgcacaatagc
acaagcgatgggagttaacataa
```

```
>yvrD
atgacttttccccatattgtgtatggaagcaaaatcctcgtaaactaaatttgatcttgtataacttaataaccatc
atctatcaaaaggaatgattctt
```

```
>lrpA
caatttcactttactTTTTaaagTTTTaagcaaacataAAAAAatgTTCAGTgaacaaaatATGTAAAATACATCTTA
TTTTcagaaaggatacaagaaa
```

Insert and submit the sequences in the Meme website and the resulting motifs should be obtained



For further information on how to interpret these results or to get a copy of the MEME software please access <http://meme.nbc.net>.

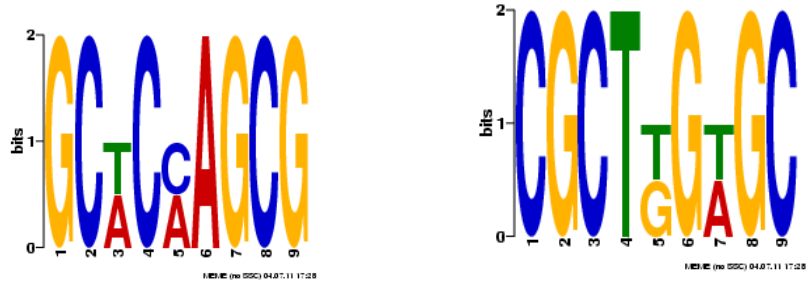
[Discovered Motifs](#) | [Block diagrams of Motifs](#) | [Program information](#) | [Explanation](#)

Discovered Motifs

Motif Overview

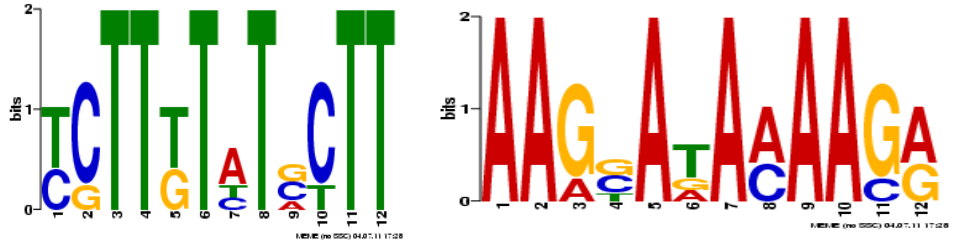
[Motif 1](#)

- 4.7e+002
- 2 sites



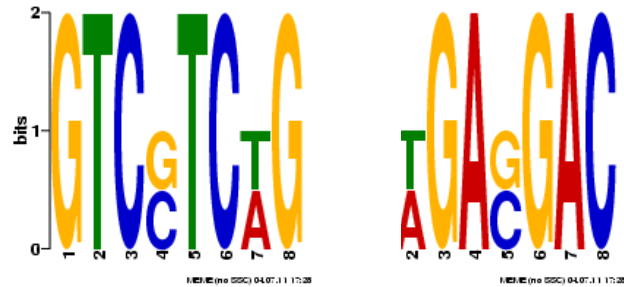
[Motif 2](#)

- 2.3e+002
- 5 sites



[Motif 3](#)

- 1.4e+003
- 2 sites



Motif 1

[Next Top](#)

Summary

E-value 4.7e+002
Width 9
Sites 2

[show more](#)

Log Likelihood Ratio

28

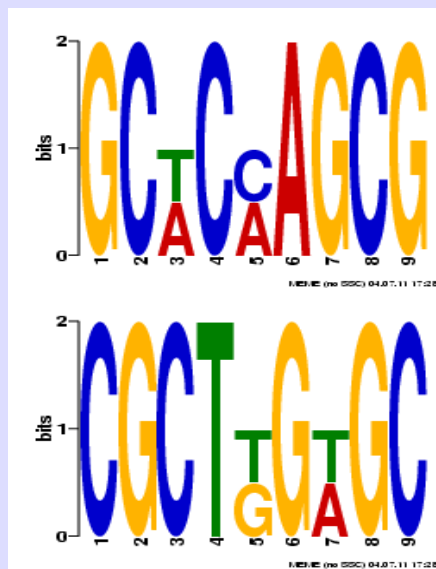
Information Content

16.0 (bits)

Relative Entropy

20.0 (bits)

Sequence Logo



[StandardReverse Complement](#)

Download LOGO

Orientation:

SSC:

Format:

Width:

cm

Height:

7.5

cm

Download

Regular expression

GC[AT]C[AC]AGCG

Name Strand Start p-value

Sites

yvgT	-	33	2.98e-07	TTTTATAATC	GCTCCAGCG	TAAAATCAAT
ydcH	+	75	1.05e-06	TTTGACAATA	GCACAAGCG	ATGGGAGTTA

Block Diagrams

The height of the motif "block" is proportional to $-\log(p\text{-value})$, truncated at the height for a motif with a p-value of $1e-10$.

Click on any row to highlight sequence in all motifs. Mouse over the center of the motif blocks to see more information.

Name	Lowest p-value	Motif Location
yvgT	2.98e-07	+ - + - 0 20 40 60 80 100
ydcH	1.05e-06	

Time 0.5 secs.

Motif 2

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Summary

Sequence Logo

E-value 2.3e+002
Width 12
Sites 5

[show more](#)

Log Likelihood Ratio

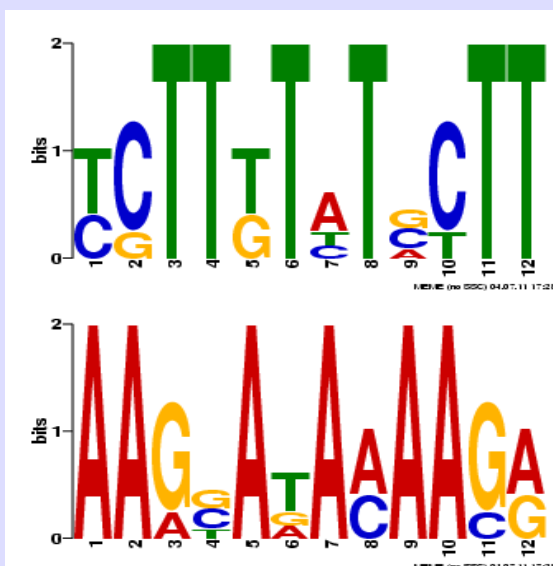
57

Information Content

17.7 (bits)

Relative Entropy

16.3 (bits)



[StandardReverse Complement](#)

Download LOGO

Orientation:

SSC:

Format:

Width: cm

Height:

cm

Regular expression

[TC][CG]TT[TG]T[ACT]T[CGA][CT]TT

Name	Strand	Start	<i>p</i> -value	Sites
lrpA	-	86	5.60e-07	TT TCTTGTATCCTT TCTGAAAAAT
yvbA	-	86	2.92e-06	AG CGTTTTCTCCTT TACAAAAAAA
yvrD	+	56	4.03e-06	CTAAATTTGA TCTTGTATACTT AATACCATCA
ydch	-	50	4.03e-06	TGTCAAAAAA TCTTTTTTGCTT ATTTCAAAGT
yvgT	-	77	7.60e-06	CTGATGACTC CCTTTTATGTT GTTAAATTTT

Block Diagrams

The height of the motif "block" is proportional to $-\log(\text{p-value})$, truncated at the height for a motif with a p-value of $1e-10$.

Click on any row to highlight sequence in all motifs. Mouse over the center of the motif blocks to see more information.

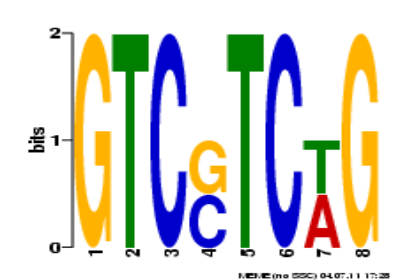
Name	Lowest <i>p</i> -value	Motif Location
yvgT	7.60e-06	+ -
yvbA	2.92e-06	+ -
ydcH	4.03e-06	+ -
yvrD	4.03e-06	+ -
lrpA	5.60e-07	+ -

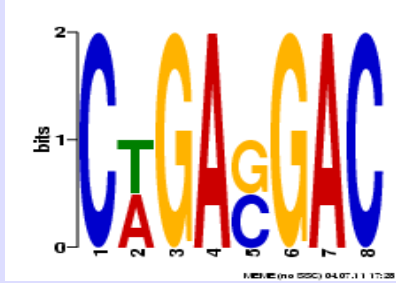
0
20
40
60
80
100

Time 0.9 secs.

Motif 3

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Summary	Sequence Logo
E-value 1.4e+003	
Width 8	
Sites 2	
show more	
Log Likelihood Ratio	
23	
Information Content	
14.0 (bits)	
Relative Entropy	
16.5 (bits)	



[StandardReverse Complement](#)

Download LOGO

Orientation:

SSC:

Format:

Width: cm

Height: cm

Regular expression

GTC[CG]TC[AT]G

Name Strand Start *p*-value

Sites

ydcH -	32	1.06e-05	ATTTCAAAGT	GTCCTCTG	CGAAATAAAA
yvgT +	59	1.06e-05	AAATCTAGAG	GTCGTCAG	AAAATTTAAC

Block Diagrams

The height of the motif "block" is proportional to $-\log(p\text{-value})$, truncated at the height for a motif with a p -value of $1e-10$.

Click on any row to highlight sequence in all motifs. Mouse over the center of the motif blocks to see more information.

Name	Lowest <i>p</i> -value	Motif Location
yvgT	1.06e-05	+ -
ydcH	1.06e-05	+ -
		0
		20
		40
		60
		80
		100

Time 1.1 secs.

All Motifs

[Top](#)

Combined Block Diagrams

Non-overlapping sites with a p -value better than 0.0001.

The height of the motif "block" is proportional to $-\log(p\text{-value})$, truncated at the height for a motif with a p -value of $1e-10$.

Click on any row to highlight sequence in all motifs. The motif blocks have tool tips with more information.

Name	Combined p -value	Motif Location
yvgT	4.09e-08	+ -
yvbA	1.82e-02	+ -
ydcH	7.24e-08	+ -
yvrD	1.69e-02	+ -
lrpA	1.66e-03	+ -
		0
		20
		40
		60
		80
		100

Motif 1

Motif 2

Motif 3

Motif 1

Motif 2

Motif 3

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4.6.1 (Release date: Mon Mar 21 13:41:45 EST 2011)

Reference

Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology, pp. 28-36, AAAI Press, Menlo Park, California, 1994.

[show training set...](#)

Sequence name	Weighting	Length	Sequence name	Weighting	Length	Sequence name	Weighting	Length
yvgT	1.000000	100	yvbA	1.000000	100	ydcH	1.000000	100
yvrD	1.000000	100	lrpA	1.000000	100			

Command line summary



Letter frequencies in dataset

A: 0.359 C: 0.141 G: 0.141 T: 0.359

Background letter frequencies (from dataset with add-one prior applied):

A: 0.358 C: 0.142 G: 0.142 T: 0.358

Stopping Reason

Stopped because nmotifs = 3 reached. Program ran on *compute-0-10.local*.

[show model parameters...](#)