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MEME - Motif discovery tool  
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MEME version 3.0 (Release date: 2001/03/05 14:24:28)

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

This file may be used as input to the MAST algorithm for searching sequence databases for matches to groups of motifs. MAST is available for interactive use and downloading at <http://meme.sdsc.edu>.

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\*\*\*\*\*  
REFERENCE  
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If you use this program in your research, please cite:

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.

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TRAINING SET  
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DATAFILE= Node61b\_usr.txt  
ALPHABET= ACGT

Sequence name	Weight	Length	Sequence name	Weight	Length
YMR304c-a	1.0000	800	SIM1	1.0000	800
SVS1	1.0000	800	YKR012c	1.0000	800
PRY2	1.0000	800	TOS11	1.0000	800
UTH1	1.0000	800	SCW10	1.0000	800
SRL1	1.0000	800	YNL046w	1.0000	800
CRH1	1.0000	800	GOG5	1.0000	800
LCB2	1.0000	800	AXL2	1.0000	800
TOS6	1.0000	800	YOR199w	1.0000	800
YKL046c	1.0000	800	CIS3	1.0000	800
WSC2	1.0000	800			

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COMMAND LINE SUMMARY  
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This information can also be useful in the event you wish to report a problem with the MEME software.

command: meme Node61b\_usr.txt -dna -mod zoops -nmotifs 3 -minw 6 -maxw 12 -bfile /home/tools/meme/meme.3.0.3/tests/yeast.nc.3.freq -revcomp -cons CGCGAA

model: mod= zoops nmotifs= 3 evt= inf  
object function= E-value of product of p-values

```

width:  minw=          6    maxw=          12    minic=          0.00
width:  wg=           11    ws=           1    endgaps=         yes
nsites: minsites=     2    maxsites=      19    wnsites=         0.8
theta:  prob=         1    spmap=         uni    spfuzz=          0.5
em:     prior=  dirichlet  b=           0.01    maxiter=         50
        distance= 1e-05
data:   n=           15200    N=           19
strands: + -
sample: seed=         0    seqfrac=         1

```

Letter frequencies in dataset:

A 0.301 C 0.199 G 0.199 T 0.301

Background letter frequencies (from

/home/tools/meme/meme.3.0.3/tests/yeast.nc.3.freq):

A 0.324 C 0.176 G 0.176 T 0.324

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MOTIF 1 width = 11 sites = 16 llr = 168 E-value = 1.0e+001

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Motif 1 Description  
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```

Simplified      A  :11:a9524::
pos.-specific   C  6:9:::14:96
probability     G  481a:113614
matrix          T  :2:::32:::

```

```

        bits  2.5  *
              2.3  *  *
              2.0  *  *
              1.8  ** *
Information   1.5 * *** **
content      1.3 ***** ***
(15.1 bits)  1.0 ***** ***
              0.8 ***** ***
              0.5 ***** ***
              0.3 ***** ****
              0.0 -----

```

```

Multilevel      CGCGAAACGCC
consensus      G      TGA G
sequence

```

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Motif 1 sites sorted by position p-value  
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Sequence name	Strand	Start	P-value	Site
SIM1	-	571	3.08e-08	TATTGACTGA CGCGAAACGCC AAAAAAAGGC
SRL1	+	215	7.55e-07	GCTTAGAAGA CGCGAAAGACC TGTGGCTCAA
SCW10	+	299	7.55e-07	GTCTAGATTT CGCGAAAGACC GTTTGCAGTA
PRY2	+	439	7.55e-07	CGGCGACATT CGCGAAATGCC AAATGAAATC
CRH1	+	333	8.36e-07	GGACAAATAT CGCGAACCGCG TGAAGTGGCT
LCB2	+	297	1.27e-06	TTTAGGCAGA GGCGAAGCGCG GTGATTGGGT

AXL2	-	454	2.05e-06	TTATTTGTGA	CGCGAATTGCC	AAAAGTTCTA
WSC2	-	651	6.38e-06	GTTTTCTTTT	GGCGAAAAACG	AAGGTAGAAA
UTH1	-	194	9.16e-06	CGCCAATACT	GTCGAACGGCC	CGCGCGTAGC
TOS11	-	272	1.01e-05	GAGAGAAATA	CGCGAGAAACC	TCTTGGTTGG
YKL046c	-	78	1.69e-05	TACGCGTCGC	GGGGAATCGCG	TAAAACTCGA
SVS1	-	568	1.97e-05	TACTTAAGAA	CACGAAATGCC	AATTATTAGC
YKR012c	-	48	2.24e-05	ATCTTGCGGT	GGCGAATGGGG	CGATTACATC
TOS6	-	573	3.00e-05	TTATTTTCCT	CGAGAATCACC	ACCGTTCATT
CIS3	+	517	3.36e-05	TTTTGCTACG	GTCGAGACACG	GTCGCCCAAA
YMR304c-a	-	14	3.83e-05	TGAGGATGAA	GTCGAAGAACC	AACCGTAGAT

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 Motif 1 block diagrams  
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SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
SIM1		3.1e-08	570_ <sup>[-1]</sup> _219
SRL1		7.5e-07	214_ <sup>[+1]</sup> _575
SCW10		7.5e-07	298_ <sup>[+1]</sup> _491
PRY2		7.5e-07	438_ <sup>[+1]</sup> _351
CRH1		8.4e-07	332_ <sup>[+1]</sup> _457
LCB2		1.3e-06	296_ <sup>[+1]</sup> _493
AXL2		2e-06	453_ <sup>[-1]</sup> _336
WSC2		6.4e-06	650_ <sup>[-1]</sup> _139
UTH1		9.2e-06	193_ <sup>[-1]</sup> _596
TOS11		1e-05	271_ <sup>[-1]</sup> _518
YKL046c		1.7e-05	77_ <sup>[-1]</sup> _712
SVS1		2e-05	567_ <sup>[-1]</sup> _222
YKR012c		2.2e-05	47_ <sup>[-1]</sup> _742
TOS6		3e-05	572_ <sup>[-1]</sup> _217
CIS3		3.4e-05	516_ <sup>[+1]</sup> _273
YMR304c-a		3.8e-05	13_ <sup>[-1]</sup> _776

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 Motif 1 in BLOCKS format  
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```

BL  MOTIF 1 width=11 seqs=19
SIM1      ( 571) CGCGAAACGCC  1
SRL1      ( 215) CGCGAAAGACC  1
SCW10     ( 299) CGCGAAAGACC  1
PRY2      ( 439) CGCGAAATGCC  1
CRH1      ( 333) CGCGAACCGCG  1
LCB2      ( 297) GGCGAAGCGCG  1
AXL2      ( 454) CGCGAATTGCC  1
WSC2      ( 651) GGCGAAAAACG  1
UTH1      ( 194) GTCGAACGGCC  1
TOS11     ( 272) CGCGAGAAACC  1
YKL046c   (  78) GGGGAATCGCG  1
SVS1      ( 568) CACGAAATGCC  1
YKR012c   (  48) GGCGAATGGGG  1
TOS6      ( 573) CGAGAATCACC  1
CIS3      ( 517) GTCGAGACACG  1
YMR304c-a (  14) GTCGAAGAACC  1
//

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Motif 1 position-specific scoring matrix  
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log-odds matrix: alength= 4 w= 11 n= 15010 bayes= 10.6097 E= 1.0e+001

```
-1064   168   132  -1064
 -237  -1064   209   -79
 -237   232  -149  -1064
-1064  -1064   251  -1064
  162  -1064 -1064  -1064
  143  -1064   -49  -1064
   62   -49   -49   -38
  -79   109    51   -79
   43  -1064   168  -1064
-1064   242  -149  -1064
-1064   183   109  -1064
```

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Motif 1 position-specific probability matrix  
-----

letter-probability matrix: alength= 4 w= 11 n= 15010 E= 1.0e+001

```
0.000203  0.562258  0.437336  0.000203
0.062664  0.000110  0.749641  0.187586
0.062664  0.874563  0.062571  0.000203
0.000203  0.000110  0.999485  0.000203
0.999578  0.000110  0.000110  0.000203
0.874656  0.000110  0.125032  0.000203
0.499890  0.125032  0.125032  0.250046
0.187586  0.374875  0.249954  0.187586
0.437429  0.000110  0.562258  0.000203
0.000203  0.937024  0.062571  0.000203
0.000203  0.624719  0.374875  0.000203
```

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Time 39.56 secs.

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MOTIF 2 width = 12 sites = 14 llr = 155 E-value = 1.0e+003

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Motif 2 Description  
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```
Simplified      A  7::33::4:1::
pos.-specific   C  32257:921::2
probability     G  :381:a143:a7
matrix          T  :5:1::::69:1
```

bits 2.5 \* \*

```

                2.3      **   *
                2.0      **   *
                1.8      *   **  *
Information     1.5      *  ***  *
content        1.3      *  ***  **
(16.0 bits)   1.0      *  *  ***  ***
                0.8      *  *  ***  ***
                0.5      *****
                0.3      *****
                0.0      -----

```

```

Multilevel      ATGCCGCATTGG
consensus      CGCAA  GG  C
sequence       C      C

```

-----  
Motif 2 sites sorted by position p-value  
-----

Sequence name	Strand	Start	P-value	Site
TOS11	-	684	5.50e-08	AAGGAGGAGG AGGCCGCATTGG TAATGGTGGC
SVS1	+	530	1.91e-07	TTTGATTTTC CCGCCGCATTGG ATATTCAATT
SIM1	-	417	5.24e-07	TAACGTTTTG AGGACGCATTGG CGGTATTGGA
TOS6	+	164	1.67e-06	AAAGCCATAT CGGGCGCGCTGG TTTGTGAGCC
SRL1	-	178	2.15e-06	GATAAAGAAA ATGCCGCCCTGC TTAATCACTG
WSC2	+	94	2.85e-06	ATGAACCCTG CTGTCGCGTTGG CCAGAACAGC
CRH1	+	176	2.85e-06	ATATTTCAAG ATGAAGCGGTGG CTCAATGGTA
PRY2	-	391	3.67e-06	GATCGAGATG ATGGCGCAGTGC AGTGCAGTCT
YNL046w	-	697	4.62e-06	TTCTTGTTTCG AGCCAGCATTGG CGAAAAAAT
GOG5	+	589	6.69e-06	GAATCCTCTT ACCCAGCCTTGG ATAATAGTTT
YKR012c	+	237	6.69e-06	ACCGTATGGA CCGCCGAGTGG ACTAGGTTGC
AXL2	-	433	9.62e-06	CAAAAGTTCT ATGACGCGTTGT TCTTTTTTTT
YMR304c-a	-	72	1.43e-05	GAGATACTAG ATGAAGCGGAGG ATGAAGCTGA
CIS3	+	472	1.65e-05	CACGGGCCAG ATCCCGCCTAGC CCTTCCAGCT

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Motif 2 block diagrams  
-----

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
TOS11		5.5e-08	683_-[-2]_105
SVS1		1.9e-07	529_[+2]_259
SIM1		5.2e-07	416_-[-2]_372
TOS6		1.7e-06	163_[+2]_625
SRL1		2.1e-06	177_-[-2]_611
WSC2		2.9e-06	93_[+2]_695
CRH1		2.9e-06	175_[+2]_613
PRY2		3.7e-06	390_-[-2]_398
YNL046w		4.6e-06	696_-[-2]_92
GOG5		6.7e-06	588_[+2]_200
YKR012c		6.7e-06	236_[+2]_552
AXL2		9.6e-06	432_-[-2]_356
YMR304c-a		1.4e-05	71_-[-2]_717
CIS3		1.7e-05	471_[+2]_317

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Motif 2 in BLOCKS format  
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```
BL  MOTIF 2 width=12 seqs=19
TOS11          ( 684) AGGCCGCATTGG  1
SVS1           ( 530) CCGCCGCATTGG  1
SIM1           ( 417) AGGACGCATTGG  1
TOS6           ( 164) CGGGCGCGCTGG  1
SRL1           ( 178) ATGCCGCCCTGC  1
WSC2           (  94) CTGTCGCGTTGG  1
CRH1           ( 176) ATGAAGCGGTGG  1
PRY2           ( 391) ATGGCGCAGTGC  1
YNL046w       ( 697) AGCCAGCATTGG  1
GOG5           ( 589) ACCCAGCCTTGG  1
YKR012c       ( 237) CCGCCGGAGTGG  1
AXL2           ( 433) ATGACGCGTTGT  1
YMR304c-a     (  72) ATGAAGCGGAGG  1
CIS3           ( 472) ATCCCGCCTAGC  1
//
```

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Motif 2 position-specific scoring matrix  
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```
log-odds matrix:  length= 4 w= 12 n= 14991 bayes= 11.2863 E= 1.0e+003
  114    70  -1045  -1045
-1045    29    70    62
-1045    29   216  -1045
  -18   151   -30  -218
  -18   202 -1045 -1045
-1045 -1045   251 -1045
-1045   240  -130 -1045
   40    29   102 -1045
-1045   -30    70    82
 -118 -1045 -1045   140
-1045 -1045   251 -1045
-1045    29   202  -218
```

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-----  
Motif 2 position-specific probability matrix  
-----

```
letter-probability matrix:  length= 4 w= 12 n= 14991 E= 1.0e+003
0.714007 0.285636 0.000125 0.000232
0.000232 0.214258 0.285636 0.499875
0.000232 0.214258 0.785279 0.000232
0.285742 0.499768 0.142880 0.071609
0.285742 0.713901 0.000125 0.000232
0.000232 0.000125 0.999412 0.000232
0.000232 0.928034 0.071503 0.000232
0.428497 0.214258 0.357013 0.000232
0.000232 0.142880 0.285636 0.571252
0.142987 0.000125 0.000125 0.856763
0.000232 0.000125 0.999412 0.000232
```

0.000232 0.214258 0.713901 0.071609

Time 192.17 secs.

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MOTIF 3 width = 11 sites = 10 llr = 119 E-value = 3.0e+003

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Motif 3 Description

Simplified A :::::42::::  
pos.-specific C 41:::6:4::3  
probability G 6:1aa::61:7  
matrix T :99:::8:9a:

bits 2.5 \*\*  
2.3 \*\*  
2.0 \*\*  
1.8 \*\*  
Information 1.5 \* \*\* \* \*\*  
content 1.3 \*\*\*\*\* \*\*  
(17.2 bits) 1.0 \*\*\*\*\*  
0.8 \*\*\*\*\*  
0.5 \*\*\*\*\*  
0.3 \*\*\*\*\*  
0.0 -----

Multilevel GTTGGCTGTTG  
consensus C AAC C  
sequence

Motif 3 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
PRY2	+	725	3.16e-07	TGATGGATCT GTTGGCTCTTG GTATCATCGT
SRL1	-	593	7.21e-07	AAACCTCTTG GTTGGATGTTG TGCTAAACTA
TOS11	-	256	7.21e-07	AAACCTCTTG GTTGGATGTTG TGCTAAACTA
AXL2	-	51	1.04e-06	TGCCAAAATG GTTGGCAGTTG TCTCAGAGCA
YOR199w	+	481	2.30e-06	TTCAAGTCAG CTTGGATCTTG ATGATCTCCT
SCW10	-	705	2.30e-06	AGACGTGACA GTTGGATGTTG AGCTCAATAT
YKR012c	-	211	2.85e-06	ACGGTGAAAA CTTGGCACTTG GTTACGGTAC
WSC2	-	109	3.78e-06	CATTGGTCTA GCTGGCTGTTG TGGCCAACGC
YKL046c	+	268	3.78e-06	CGCCGTGCTT CTGGGCTCTTG ATGATGTAAG
SVS1	+	41	5.23e-06	CGATCTTATC CTTGGCTGGTC AGATTTCATGG

---

Motif 3 block diagrams

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SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
PRY2		3.2e-07	724_[+3]_65
SRL1		7.2e-07	592_-[-3]_197
TOS11		7.2e-07	255_-[-3]_534
AXL2		1e-06	50_-[-3]_739
YOR199w		2.3e-06	480_[+3]_309
SCW10		2.3e-06	704_-[-3]_85
YKR012c		2.9e-06	210_-[-3]_579
WSC2		3.8e-06	108_-[-3]_681
YKL046c		3.8e-06	267_[+3]_522
SVS1		5.2e-06	40_[+3]_749

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Motif 3 in BLOCKS format

---

```
BL MOTIF 3 width=11 seqs=19
PRY2 ( 725) GTTGGCTCTTG 1
SRL1 ( 593) GTTGGATGTTG 1
TOS11 ( 256) GTTGGATGTTG 1
AXL2 ( 51) GTTGGCAGTTG 1
YOR199w ( 481) CTTGGATCTTG 1
SCW10 ( 705) GTTGGATGTTC 1
YKR012c ( 211) CTTGGCACTTG 1
WSC2 ( 109) GCTGGCTGTTC 1
YKL046c ( 268) CTGGGCTCTTG 1
SVS1 ( 41) CTTGGCTGGTC 1
//
```

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Motif 3 position-specific scoring matrix

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```
log-odds matrix: alength= 4 w= 11 n= 15010 bayes= 10.8024 E= 3.0e+003
-997 119 177 -997
-997 -81 -997 147
-997 -997 -81 147
-997 -997 251 -997
-997 -997 251 -997
30 177 -997 -997
-70 -997 -997 130
-997 119 177 -997
-997 -997 -81 147
-997 -997 -997 162
-997 77 199 -997
```

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Motif 3 position-specific probability matrix

---

```
letter-probability matrix: alength= 4 w= 11 n= 15010 E= 3.0e+003
```



0.000324	0.399776	0.599576	0.000324
0.000324	0.100075	0.000175	0.899425
0.000324	0.000175	0.100075	0.899425
0.000324	0.000175	0.999176	0.000324
0.000324	0.000175	0.999176	0.000324
0.399925	0.599576	0.000175	0.000324
0.200124	0.000175	0.000175	0.799525
0.000324	0.399776	0.599576	0.000324
0.000324	0.000175	0.100075	0.899425
0.000324	0.000175	0.000175	0.999325
0.000324	0.299876	0.699476	0.000324

Time 343.67 secs.

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 SUMMARY OF MOTIFS  
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 Combined block diagrams: non-overlapping sites with p-value < 0.0001  
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SEQUENCE NAME	COMBINED P-VALUE	MOTIF DIAGRAM
YMR304c-a	4.39e-03	13_ <sup>-1</sup> (3.83e-05)]_47_ <sup>-2</sup> (1.43e-05)]_717
SIM1	5.11e-06	369_ <sup>-2</sup> (1.31e-05)]_35_ <sup>-2</sup> (5.24e-
07)]_142_ <sup>-1</sup> (3.08e-08)]_219		
SVS1	1.15e-05	40_ <sup>+3</sup> (5.23e-06)]_478_ <sup>+2</sup> (1.91e-
07)]_26_ <sup>-1</sup> (1.97e-05)]_222		
YKR012c	1.69e-04	47_ <sup>-1</sup> (2.24e-05)]_152_ <sup>-3</sup> (2.85e-
06)]_15_ <sup>+2</sup> (6.69e-06)]_552		
PRY2	7.23e-07	14_ <sup>-1</sup> (2.24e-05)]_365_ <sup>-2</sup> (3.67e-
06)]_36_ <sup>+1</sup> (7.55e-07)]_275_ <sup>+3</sup> (3.16e-07)]_12_ <sup>+1</sup> (4.60e-05)]_42		
TOS11	3.56e-07	255_ <sup>-3</sup> (7.21e-07)]_5_ <sup>-1</sup> (1.01e-
05)]_401_ <sup>-2</sup> (5.50e-08)]_105		
UTH1	7.84e-03	12_ <sup>-1</sup> (1.25e-05)]_170_ <sup>-1</sup> (9.16e-
06)]_379_ <sup>+1</sup> (5.61e-05)]_206		
SCW10	1.28e-04	298_ <sup>+1</sup> (7.55e-07)]_89_ <sup>+1</sup> (1.01e-
05)]_295_ <sup>-3</sup> (2.30e-06)]_85		
SRL1	9.38e-07	177_ <sup>-2</sup> (2.15e-06)]_25_ <sup>+1</sup> (7.55e-
07)]_35_ <sup>+1</sup> (6.64e-06)]_321_ <sup>-3</sup> (7.21e-07)]_5_ <sup>-1</sup> (1.01e-05)]_181		
YNL046w	5.57e-02	696_ <sup>-2</sup> (4.62e-06)]_92
CRH1	1.63e-04	175_ <sup>+2</sup> (2.85e-06)]_145_ <sup>+1</sup> (8.36e-
07)]_457		
GOG5	5.08e-02	588_ <sup>+2</sup> (6.69e-06)]_200
LCB2	2.11e-02	296_ <sup>+1</sup> (1.27e-06)]_493
AXL2	1.20e-05	50_ <sup>-3</sup> (1.04e-06)]_371_ <sup>-2</sup> (9.62e-
06)]_9_ <sup>-1</sup> (2.05e-06)]_44_ <sup>+2</sup> (8.48e-05)]_71_ <sup>+1</sup> (4.04e-05)]_84_ <sup>-3</sup> (1.80e-05)]_103		
TOS6	3.73e-03	163_ <sup>+2</sup> (1.67e-06)]_287_ <sup>+2</sup> (9.91e-
05)]_98_ <sup>-1</sup> (3.00e-05)]_217		

YOR199w	6.15e-02	480_	[+3(2.30e-06)]	_160_	[+3(7.85e-
05)]_138					
YKL046c	3.20e-03	77_	[-1(1.69e-05)]	_179_	[+3(3.78e-
06)]_522					
CIS3	1.78e-02	471_	[+2(1.65e-05)]	_33_	[+1(3.36e-
05)]_273					
WSC2	3.50e-05	50_	[-1(2.58e-05)]	_32_	[+2(2.85e-
06)]_3_					
[-3(3.78e-06)]_345_					
[-2(8.27e-05)]_174_					
[-1(6.38e-06)]_139					

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Stopped because nmotifs = 3 reached.

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CPU: rana7.lbl.gov

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