

# Package ‘yeastCC’

October 14, 2025

**Version** 1.49.0

**Title** Spellman et al. (1998) and Pramila/Breeden (2006) yeast cell cycle microarray data

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**Description** ExpressionSet for Spellman et al. (1998) yeast cell cycle microarray experiment

**License** Artistic-2.0

**LazyData** yes

**Depends** Biobase (>= 2.5.5)

**biocViews** ExperimentData, CellCulture, Saccharomyces\_cerevisiae\_Data, CancerData, MicroarrayData, OneChannelData, GEO

**git\_url** <https://git.bioconductor.org/packages/yeastCC>

**git\_branch** devel

**git\_last\_commit** bf718eb

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-10-14

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breeden

*Breeden et al. yeast cell cycle experiment***Description**

ExpressionSet instance; 50 samples from a 25-sample dye-swap of alpha-synchronized yeast cultures

**Usage**

```
data(breeden)
```

**Format**

The format is:

Formal class 'ExpressionSet' [package "Biobase"] with 7 slots

```
..@ assayData :<environment: 0x10221ebc8>
```

```
..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
```

```
.. ..@ varMetadata : 'data.frame': 37 obs. of 1 variable:
```

```
.. .. ..$ labelDescription: chr [1:37] NA NA NA NA ...
```

```
.. ..@ data : 'data.frame': 50 obs. of 37 variables:
```

```
.. .. ..$ title : Factor w/ 50 levels "Yeast cell cycle-time point 0 min 2001-08-17_0000.rfm Yeast W303 cells",...: 1 29 3 15 17 19 21 23 25 27 ...
```

```
.. .. ..$ geo_accession : Factor w/ 50 levels "GSM112133","GSM112134",...: 1 2 3 4 5 6 7 8 9 10
```

```
...
```

```
.. .. ..$ status : Factor w/ 1 level "Public on Aug 05 2006": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ submission_date : Factor w/ 1 level "Jun 01 2006": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ last_update_date : Factor w/ 1 level "Jun 23 2006": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ type : Factor w/ 1 level "RNA": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ channel_count : Factor w/ 1 level "2": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ source_name_ch1 : Factor w/ 25 levels "Yeast cell cycle-time point 0 min",...: 1 15 2 8 9 10 11 12 13 14 ...
```

```
.. .. ..$ organism_ch1 : Factor w/ 1 level "Saccharomyces cerevisiae": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ characteristics_ch1 : Factor w/ 25 levels "Yeast cell cycle-time point 0 min",...: 1 15 2 8 9 10 11 12 13 14 ...
```

```
.. .. ..$ treatment_protocol_ch1 : Factor w/ 1 level "Cells were arrested with alpha factor,and released into YEPD to get a synchronized population. Cells were sampled every 5 min a"l __truncated__": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ molecule_ch1 : Factor w/ 1 level "total RNA": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ label_ch1 : Factor w/ 2 levels "Cy3","Cy5": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ source_name_ch2 : Factor w/ 1 level "Yeast asynchronous culture": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ organism_ch2 : Factor w/ 1 level "Saccharomyces cerevisiae": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ characteristics_ch2 : Factor w/ 1 level "Yeast asynchronous culture": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ treatment_protocol_ch2 : Factor w/ 1 level "Cells were grown overnight to an OD of 0.6 in YEPD": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ molecule_ch2 : Factor w/ 1 level "total RNA": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ label_ch2 : Factor w/ 2 levels "Cy3","Cy5": 2 2 2 2 2 2 2 2 2 2 ...
```

```
.. .. ..$ description : Factor w/ 1 level "Yeast cell cycle": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ data_processing : Factor w/ 1 level "normalized log ratio using Rosetta Resolver": 1 1 1 1 1 1 1 1 1 1 ...
```

```
.. .. ..$ platform_id : Factor w/ 1 level "GPL1914": 1 1 1 1 1 1 1 1 1 1 ...
```

```

.. .. ..$ contact_name : Factor w/ 1 level "Tata,,Pramila": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_email : Factor w/ 1 level "tpramila@fhcrc.org": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_phone : Factor w/ 1 level "(206)6674483": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_laboratory : Factor w/ 1 level "Breedden Lab": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_department : Factor w/ 1 level "Basic Sciences": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_institute : Factor w/ 1 level "FHCRC": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_address : Factor w/ 1 level "1100, Fairview Avenue N": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_city : Factor w/ 1 level "Seattle": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_state : Factor w/ 1 level "WA": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_zip/postal_code: Factor w/ 1 level "98109": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_country : Factor w/ 1 level "USA": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ supplementary_file : Factor w/ 50 levels "ftp://ftp.ncbi.nih.gov/pub/geo/DATA/supplementary/samples/GSM112
1 2 3 4 5 6 7 8 9 10 ...
.. .. ..$ data_row_count : Factor w/ 1 level "6228": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ mins : num [1:50] 0 5 10 15 20 25 30 35 40 45 ...
.. .. ..$ sign : num [1:50] 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"
.. .. ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. .. ..@ varMetadata : 'data.frame': 10 obs. of 3 variables:
.. .. ..$ Column : chr [1:10] "ID" "ORF" "SPOT_ID" "Gene" ...
.. .. ..$ Description : Factor w/ 2 levels "", "LINK_PRE:" "http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?CMD=search&LINK_SUF:\\"[gene name]\"": 1 2 1 1 1 1 1 1 1 1
.. .. ..$ labelDescription: chr [1:10] NA NA NA NA NA ...
.. .. ..@ data : 'data.frame': 6228 obs. of 10 variables:
.. .. ..$ ID : Factor w/ 6337 levels "YPR105C","YPR106W",...: 116 6322 119 6327 124 133 6328
6329 6330 6331 ...
.. .. ..$ ORF : Factor w/ 6222 levels "YPR105C","YPR106W",...: 6221 6221 6221 6221 6221
6221 6221 6221 6221 6221 ...
.. .. ..$ SPOT_ID : chr [1:6228] "<blank>" "blank" "E. coli control" "empty" ...
.. .. ..$ Gene : Factor w/ 3347 levels "", "AOS1", "APG13",...: 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ SGDID : Factor w/ 6205 levels "S0006309","S0006310",...: 1001 1001 1001 1001 1001
1001 1001 1001 1001 1001 ...
.. .. ..$ CHR : Factor w/ 17 levels "XVI","XV","XIV",...: 13 13 13 13 13 13 13 13 13 13 ...
.. .. ..$ ORF.Length: chr [1:6228] "" "" "" "" "" "" "" "" "" "" ...
.. .. ..$ Process : Factor w/ 488 levels "DNA repair*",...: 194 194 194 194 194 194 194 194 194
194 ...
.. .. ..$ Function : Factor w/ 760 levels "CDP-diacylglycerol-inositol 3-phosphatidyltransferase",...:
215 215 215 215 215 215 215 215 215 ...
.. .. ..$ Component : Factor w/ 211 levels "19S proteasome regulatory particle",...: 90 90 90 90 90
90 90 90 90 90 ...
.. .. ..@ dimLabels : chr [1:2] "featureNames" "featureColumns"
.. .. ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. .. ..@ .Data:List of 1
.. .. .. ..$ : int [1:3] 1 1 0
..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots
.. .. ..@ name : chr [1:2] "Pramila T" "Breedden LL"
.. .. ..@ lab : chr "Fred Hutchinson Cancer Research Center, Seattle, Washington 98109, USA."
.. .. ..@ contact : chr ""
.. .. ..@ title : chr "The Forkhead transcription factor Hcm1 regulates chromosome segregation
genes and fills the S-phase gap in the transcriptional "l__truncated__
.. .. ..@ abstract : chr "Transcription patterns shift dramatically as cells transit from one phase of

```

```

the cell cycle to another. To better define this t"! __truncated__
.. .. @ url : chr "http://labs.fhcrc.org/breeden/cellcycle/index.html"
.. .. @ pubMedIds : chr "16912276"
.. .. @ samples : list()
.. .. @ hybridizations : list()
.. .. @ normControls : list()
.. .. @ preprocessing : list()
.. .. @ other : list()
.. .. @ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. @ .Data:List of 1
.. .. @ ..$ : int [1:3] 1 0 0
.. @ annotation : chr(0)
.. @ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. .. @ varMetadata : 'data.frame': 0 obs. of 1 variable:
.. .. @ ..$ labelDescription: chr(0)
.. .. @ data : 'data.frame': 50 obs. of 0 variables
.. .. @ dimLabels : chr [1:2] "sampleNames" "sampleColumns"
.. .. @ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. @ .Data:List of 1
.. .. @ ..$ : int [1:3] 1 1 0
.. @ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. @ .Data:List of 4
.. .. @ ..$ : int [1:3] 2 10 0
.. .. @ ..$ : int [1:3] 2 5 5
.. .. @ ..$ : int [1:3] 1 3 0
.. .. @ ..$ : int [1:3] 1 0 0

```

## Details

Retrieved from GEO using `getGEO` in package `GEOquery`, August 27 2009. Variables `mins` and `sign` added to `pData` manually.

## Source

PMID 16912276; see `url` slot of `experimentData` slot.

## Examples

```

data(breeden)
#
# show how to use the dye-swap 'sign' variable
#
plot(exprs(breeden)["YBL002W",]~breeden$mins)
plot(I(exprs(breeden)["YBL002W",]*breeden$sign)~breeden$mins)

```

**Description**

Vector of ORF names for the 800 cell cycle regulated genes identified by the analysis of Spellman et al. (1998). The expression measures and sample descriptions are stored in the [ExpressionSet](#) instance [yeastCC](#).

**Usage**

```
data(orf800)
```

**Format**

The format is: chr [1:800] "YAL022C" "YAL040C" "YAL053W" "YAL067C" "YAR003W" "YAR007C"  
...

**Source**

The 800 ORF names were obtained from the file "CellCycle98.xls" on the Yeast Cell Cycle Analysis Project website (<http://genome-www.stanford.edu/cellcycle/>). The raw data (images, TIFF) and processed data "combine.txt" used to create the [ExpressionSet](#) instance [yeastCC](#) are also available on the website. Gene annotation information is available from the Saccharomyces Genome Database (SGD, [http://genome-www.stanford.edu/Saccharomyces/gene\\_list.shtml](http://genome-www.stanford.edu/Saccharomyces/gene_list.shtml)). The script "createYeastCC.R" for generating the yeastCC package is available in [../doc](#).

**References**

Spellman et al. (1998). Comprehensive Identification of Cell Cycle-regulated Genes of the Yeast *Saccharomyces cerevisiae* by Microarray Hybridization. *Molecular Biology of the Cell*, 9: 3273-3297 ([../doc](#)).

**Examples**

```
data(orf800)
```

---

spYCCmeta

*metadata on yeast cell cycle microarray experiment*


---

**Description**

data.frame instance with metadata on 800 genes

**Usage**

```
data(spYCCmeta)
```

**Format**

A data frame with 800 observations on the following 75 variables.

Process a factor with levels 4-nitroquinoline-N-oxide resistance ATP synthesis ...

Function a factor with levels (1->6)-beta-glucan synthase subunit (putative) Glc7p regulatory subunit ...

X a logical vector

Peak a factor with levels G1 G2/M M/G1 S S/G2  
 Phase.Order a numeric vector  
 Cluster.Order a numeric vector  
 ORF a factor with levels YAL022C YAL040C YAL053W YAL067C YAR003W YAR007C ...  
 YPD a factor with levels AAD10 ACE2 ADA2 ADK2 AFR1 AGA1 AGA2 AGP1 ...  
 SGD a factor with levels AAD10 ACE2 ADA2 ADK2 AFR1 AGA1 AGA2 ...  
 YPD.1 a factor with levels YPD  
 SGD.1 a factor with levels SGD  
 MIPS a factor with levels MIPS  
 n1 a numeric vector  
 n2 a numeric vector  
 Geomean a numeric vector  
 Absolute a numeric vector  
 g1 a numeric vector  
 g2 a numeric vector  
 Geomean.1 a numeric vector  
 Absolute.1 a numeric vector  
 Deletion a factor with levels irrelevant lethal undocumented viable  
 Known. a factor with levels Known New New  
 Description a factor with levels Inhibitor of Cdc28p/Cln1p and Cdc28p/Cln2p complexes  
 involved in cell cycle arrest for mating 1,3-beta-D-glucan synthase 3\'-Phosphoadenylylsulfate  
 reductase; part of the sulfate assimilation pathway ...  
 Aggregate.Score a numeric vector  
 Phase a numeric vector  
 No..Elements a numeric vector  
 Most.Relevant.Promoter.Elements a factor with levels AATAGATGACCCGATTTGGAAAAAGGTAAACAACAATG  
 ATTTGATTGCCGAAAGAGGCAAAAC GTAAATAGGTTGT C 156 TCTGCCAGCCAA C 253 AAAGCCAGCCAT C  
 256 TATGCCAGCCAA C 276 AAGGCCAGCCTC C 293 TTGACCAGCTAA ...  
 X.1 a factor with levels ATATAGCGACCGAATCAGGAAAAG GTCAACAACGAAG C 102 CGAGCCAGCATT C  
 252 AAGACCAGCATG C 301 AGTGCCAGCAAA C 496 GAAGCCAGCAC A 550 GCGGCCAGCAAC c 106 attACGCGaaaat  
 c 112 aaaACGCGagaaa c 121 ggaACGCGacgc ...  
 X.2 a factor with levels C 125 GCAACCAGCTCT C 146 CAAGCCAGCCAT C 195 CGCACCAGCAAC C 212  
 TATACCAGCGTT C 245 TAAACCAGCGCA C 402 TATGCCAGCAAA c 112 ttaACGCGatcga c 115 agtACGCGaaagg  
 c 123 acaACGCGaacac c 127 gtgACGCGaaaaa ...  
 X.3 a factor with levels C 307 AAGACCAGCATT c 163 ctgACGCGcgaac c 190 aatACGCGagaaa c 220  
 tagACGCGcctta c 241 cgaACGCGaaact c 275 aaaACGCGaccgt c 282 aagACGCGatttt c 289  
 attACGCGcatta c 290 aggACGCGaaact ...  
 X.4 a factor with levels C 200 CAAACCAGCATC c 117 gtcACGCGaaaaa c 314 cctACGCGaaagt c 338  
 caaACGCGaaaaa c 359 acgACGCGccttc c 382 gttACGCGaagtc c 384 tcaACGCGaattt c 397  
 aaaACGCGaaaac c 440 gtgACGCGcggtt ...  
 X.5 a factor with levels C 306 GGAGCCAGCGCG c 467 accACGCGaaaag c 588 gaaACGCGccaaa w 266  
 ATAACCAGCAAA w 383 cagACGCGagaac w 478 GGAGCCAGCGCG w401 tatCGCGAAAatt  
 X.6 a factor with levels C 337 AGAGCCAGCAAG C 417 TCGGCCAGCAAT c 501 acaACGCGaaaaa w 370  
 gcgACGCGaaaaa w 447 AGAGCCAGCAAG

X.7 a factor with levels C 388 GGAACCAGCAGA w 396 GGAACCAGCAGA

Number a numeric vector

SCB a factor with levels c 103 gacCACGAAAttt c 105 atgCACGAAAaag c 106 ctaCACGAAAcac c 108 tacCACGAAAgta c 110 ccaCACGAAAaga c 123 agaCACGAAAtgt c 127 acaCACGAAAacg c 181 cagCACGAAAtgg ...

SCB.1 a factor with levels c178 tgaCACGAAAaac c232 gaaCACGAAAtgc c539 gtaCACGAAAttc w269 agcCACGAAAtgc w347 tgaCACGAAAtgt w541 agtCACGAAAacg w601 tgtCACGAAAggt

SCB.2 a factor with levels c330 aacCACGAAAaaa c582 agtCACGAAAacg w467 attCACGAAAtaa

SCB.3 a factor with levels w435 atcCACGAAAatc

X.8 a factor with levels w252 aacCACGAAAagt

Number.1 a numeric vector

SCB\_d a factor with levels c 156 gatCGCGAAAttt c 184 cgaCGCGAAAtg c 218 cagCGCGAAAggt c 222 tatCGCGAAAaaa c 229 tgaCGCGAAAacg c 237 tatCGCGAAAaga c 238 atcCGCGAAAagg a 283 aagCGCGAAAcaa ....

SCB\_d.1 a factor with levels c 126 tttCGCGAAActg c 415 tttCGCGAAAtct c 566 ttcCGCGAAAaaa c 592 aggCGCGAAAtac c 633 aaaCGCGAAAtgt c242 gaaCGCGAAActt c297 ctcCGCGAAAaat c306 tcgCGCGAAAaga ...

SCB\_d.2 a factor with levels c468 ccaCGCGAAAaga c508 tttCGCGAAAtct

SCB\_d.3 a factor with levels c502 caaCGCGAAAaat

Number.2 a numeric vector

MCB a factor with levels w 126 gcaACGCGTcgc w 187 caaACGCGTaca w 207 ctcACGCGTcgg w 209 attACGCGTtta w 226 cagACGCGTtgc w 228 acaACGCGTctt w 23 acaACGCGTgct w 267 cccACGCGTagg ...

MCB.1 a factor with levels w111 gaaACGCGTtct w124 ttgACGCGTttc w128 gtgACGCGTtat w130 agaACGCGTtct w131 gcgACGCGTaac w138 aagACGCGTgaa w139 attACGCGTtta w153 ctaACGCGTttt ...

MCB.2 a factor with levels w374 taaACGCGTcat

MCB.3 a factor with levels w309 aggACGCGTaaa

Number.3 a numeric vector

MCB\_d a factor with levels c 106 attACGCGaaaat c 109 acaACGCGactgg c 112 aaaACGCGagaaa c 115 agtACGCGaaagg c 117 gtcACGCGaaaaa c 121 ggaACGCGacgc c 127 gtgACGCGaaaaa c 129 acaACGCGcccg ...

MCB\_d.1 a factor with levels c 123 acaACGCGaacac c 136 aatACGCGattgg c 147 gcaACGCGagaga c 158 tctACGCGgaag c 163 ctgACGCGgaaa c 176 gcgACGCGgttgt c 187 agtACGCGatttg c 189 gaaACGCGggcac ...

MCB\_d.2 a factor with levels c 112 ttaACGCGatcga c 220 tagACGCGcctta c 294 ttcACGCGcttaa c 382 gttACGCGaagtc c 477 gcaACGCGcctgg c 501 acaACGCGaaaaa c 549 attACGCGcacg c 557 tgtACGCGgaac ...

MCB\_d.3 a factor with levels c 617 gaaACGCGcagta w 50 gtaACGCGctttt

X.9 a factor with levels c 359 acgACGCGccttc

Number.4 a numeric vector

SFF a factor with levels AATAGATGACCCGATTTGGAAAAAGGTAAACAACAATG ATTTGATTGCCGAAAGAGGCAAAAC GTAAATAGTTGT CAAAACAAACCAATAAAGAAAATCCAAAATATAGAAC GTACTTTAACCTGTTTAGGAAAAAG GTAAACAATAACA TCGAACAATTCTAAAAAGGTAAT AAAACAATGGTA ...

Number.5 a factor with levels 1 2 3 4 ATATAGCGACCGAATCAGGAAAAGGTCAACAACGAAG

Swi5 a factor with levels C 102 CGAGCCAGCATT C 156 TCTGCCAGCCAA C 200 CAAACCAGCATC C 252  
AAGACCAGCATG C 253 AAAGCCAGCCAT C 256 TATGCCAGCCAA C 276 AAGGCCAGCCTC C 293 TTGACCAGCTAA  
...

Swi5.1 a factor with levels C 125 GCAACCAGCTCT C 146 CAAGCCAGCCAT C 195 CGCACCAGCAAC C  
245 TAAACCAGCGCA C 301 AGTGCCAGCAAA C 306 GGAGCCAGCGCG C 307 AAGACCAGCATT C 402 TATGCCAGCAAA  
...

Swi5.2 a factor with levels C 212 TATACCAGCGTT C 337 AGAGCCAGCAAG c 19 AGAACCAGCTGA c 320  
ACCACCAGCTTA c 545 ACCACCAGCGTA c 569 TTCACCAGCGGC c 642 GAGACCAGCGGA c 651 ATCACCAGCAAA  
...

Swi5.3 a factor with levels C 388 GGAACCAGCAGA C 417 TCGGCCAGCAAT c 336 TTTACCAGCTCA c  
363 TGCACCAGCATT c 494 CTGGCCAGCAAG w 396 GGAACCAGCAGA

Number.6 a numeric vector

Swi5e a factor with levels c 102 CGAGCCAGCATT c 137 TAGGCCAGCAAA c 155 ACAACCAGCAGT c 156  
CTAACCAGCAAG c 16 AGAGCCAGCAGA c 174 TAAACCAGCATT c 184 ATGGCCAGCATA c 200 CAAACCAGCATC  
...

Swi5e.1 a factor with levels c 222 TTGACCAGCGCC c 256 TAAACCAGCAAA c 306 GGAGCCAGCGCG c  
307 AAGACCAGCATT c 637 GGAGCCAGCGAT w 265 TAAACCAGCAAT w 266 ATAACCAGCAAA w 467 TGAGCCAGCAAT  
w 478 GGAGCCAGCGCG w 536 GAAACCAGCAAC w 554 ATGGCCAGCACC

Swi5e.2 a factor with levels c 337 AGAGCCAGCAAG c 417 TCGGCCAGCAAT c 642 GAGACCAGCGGA w  
447 AGAGCCAGCAAG

Swi5e.3 a factor with levels c 388 GGAACCAGCAGA w 396 GGAACCAGCAGA

Number.7 a numeric vector

ECB a factor with levels c 185 TTACCCATTTAGGAAA c 221 TTACCCAATTAGGAAA c 251 TTTCCCTTTAAGGAAA  
c 258 TTTCCCAAAAAGGAAA c 387 TTTCCCTTTTAGGAAA c 394 TTACCCACTTAGGAAA w 154 TTTCCCTTTTAGGAAA  
w 177 TTACCCACTTAGGAAA w 229 TTACCCAGAAAAGGAAA w 378 TTTCCCTAATAGGAAA w 453 TTTCCCGTTTAGGAAA  
w 595 TTTCCCACTAAGGAAA

Number.8 a numeric vector

STE12 a factor with levels c 243 CCTTTTTTCAGTTTCTATTTTTTAACACTGAAACT w 112 CCCTATTTGGTTGCAATTCAATTCCGTGAAA  
w 119 CCCAATGTAGAAAAGTACATCATATGAAACA w 218 CCTAATTGGGTAAGTACATGATGAAACA w 224  
CCCCAAAAGGAAATTTACATGTAAATGAAACC ...

MIG1.sites a factor with levels c 114 AATAGACTGGGG c 137 TCTATCCTGGGG c 147 TGAATGCTGGGG  
c 165 AATAAAGTGGGG c 215 TATAATGCGGGG c 304 AAATCGCCGGGG c 332 AAATATCTGGGG c 368  
AATTGCGCGGGG ...

X.10 a factor with levels c 161 AGTTTGGTGGGG c 262 AAGATGGTGGGG c 498 AAAAAACCGGGG c 499  
AAAAATGCGGGG w 296 TATTCGGCGGGG w 578 CTTTTGCCGGGG

X.11 a logical vector

## Details

taken from the Spellman support web site.

## Source

[cellcycle-www.stanford.edu](http://cellcycle-www.stanford.edu)

## References

PMID 9843569

## Examples

```
data(spYCCmeta)
spYCCmeta[1:5,1:6]
```

---

|         |                                                                                    |
|---------|------------------------------------------------------------------------------------|
| yeastCC | <i>Data from the Spellman et al. (1998) yeast cell cycle microarray experiment</i> |
|---------|------------------------------------------------------------------------------------|

---

## Description

This data package contains an [ExpressionSet](#) instance for the yeast cell cycle microarray experiment. The dataset contains gene expression measures (log-ratios, with Cy3-labeled common reference) for 6,178 yeast genes in 77 conditions.

## Usage

```
data(yeastCC)
```

## Details

There are four main timecourses: alpha (alpha factor arrest), cdc15, cdc28, and elu (elutriation), corresponding to different synchronization methods. For details on experimental procedures and analysis, refer to Spellman et al. (1998) (in [../doc](#)) and the Yeast Cell Cycle Analysis Project website (<http://genome-www.stanford.edu/cellcycle/>). The [ExpressionSet](#) instance yeastCC was derived from the file "combined.txt" on the website. The ORF names for the 800 cell cycle regulated genes are stored in [orf800](#).

## Source

The raw data (images, TIFF) and processed data "combine.txt" used to create the [ExpressionSet](#) instance yeastCC are available from the Yeast Cell Cycle Analysis Project website (<http://genome-www.stanford.edu/cellcycle/>). Gene annotation information is available from the Saccharomyces Genome Database (SGD, [http://genome-www.stanford.edu/Saccharomyces/gene\\_list.shtml](http://genome-www.stanford.edu/Saccharomyces/gene_list.shtml)). The script "createYeastCC.R" for generating the yeastCC package is available in [../doc](#).

Note that spYCCES is an [ExpressionSet](#) instance with the same data and slightly different phenodata annotation.

## References

Spellman et al. (1998). Comprehensive Identification of Cell Cycle-regulated Genes of the Yeast *Saccharomyces cerevisiae* by Microarray Hybridization. *Molecular Biology of the Cell*, 9: 3273-3297.

## Examples

```
data(yeastCC)
yeastCC
varLabels(yeastCC)
pData(yeastCC)
description(yeastCC)
abstract(yeastCC)
featureNames(yeastCC)[1:10]
dim(exprs(yeastCC))
```

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