



SIXTH FRAMEWORK PROGRAMME

Specific Targeted Research Projects

PRIORITY 1

LIFE SCIENCES, GENOMICS AND BIOTECHNOLOGY FOR HEALTH

Contract no: LSHG-CT-2004-512143

DIAMONDS

Dedicated Integration And Modelling Of Novel Data and prior knowledge to enable Systems biology

EU Deliverable

D2.6

Partial functional annotation for cell cycle regulators gene families

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(Public)

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D2.6: Partial functional annotation for cell cycle regulators gene families

D.2.6.1 Cell cycle Regulators – Multiple resources for different granularity

We combined resources to ensure that the coverage for CC genes and proteins will be maximal. All these resources are fully supported by EVEREST, ProtoNet and PANDORA DB. Note that the GO annotation (for Biological process) is the most extensive one with over 16K sequences but also a very specific annotation with a single sequence is recorded. The different levels of annotation provide a powerful mode for statistical evaluation for any set of experimental data (as implemented through PANDORA resource).

Keyword Type	Keyword	# Proteins
GO biological process	cell cycle	16287
GO biological process	mitotic cell cycle	11779
GO biological process	S phase of mitotic cell cycle	10150
GO biological process	M phase of mitotic cell cycle	1030
GO biological process	G2/M transition of mitotic cell cycle	434
GO biological process	cell cycle checkpoint	270
GO biological process	cell cycle arrest	255
GO biological process	G1/S transition of mitotic cell cycle	218
GO biological process	G1 phase of mitotic cell cycle	51
GO biological process	mitotic cell cycle, embryonic	24
GO biological process	regulation of S phase of mitotic cell cycle	22
GO biological process	G1-specific transcription in mitotic cell cycle	15
GO biological process	negative regulation of S phase of mitotic cell cycle	14
GO biological process	G1/S-specific transcription in mitotic cell cycle	14
GO biological process	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	13
GO biological process	cell cycle arrest in response to pheromone	13
GO biological process	G2 phase of mitotic cell cycle	9
GO biological process	re-entry into mitotic cell cycle	8
GO biological process	endomitotic cell cycle	5
GO biological process	M/G1 transition of mitotic cell cycle	5
GO biological process	re-entry into mitotic cell cycle after pheromone arrest	3
GO biological process	positive regulation of S phase of mitotic cell cycle	1
GO biological process	G2/M-specific transcription in mitotic cell cycle	1
GO biological process	G2-specific transcription in mitotic cell cycle	1
PFAM domain	Cell cycle protein	864
PFAM domain	Cwf15/Cwc15 cell cycle control protein	52
PFAM domain	GcrA cell cycle regulator	45
PROSITE domain	Cell cycle protein	490
PIRSF domain	Cell cycle control PP-loop ATPase MesJ/YaeO	392
InterPro Family	Cell cycle protein	864
InterPro Family	Cell cycle control PP-loop ATPase MesJ/YaeO	392
InterPro Family	Cwf15/Cwc15 cell cycle control protein	52
InterPro Family	GcrA cell cycle regulator	45
UniProt keyword	Cell cycle	7409

Table 2: All cell cycle resources supported in HUJI database (currently covers 2.5 millions proteins from UniProtKB).

Furthermore, for improved level of resolution for the enrichment and statistical evaluation of experimental data, a detailed resolution is further supported. As seen in Table 3, we support 18 different types of resources for domain and families in addition to 3D structural based annotations that are based on CATH, SCOP (7 types)

CATH class	CATH architecture	CATH topology	CATH homologous superfamily	EC - x	EC - xx
EC - xxx	EC - xxx	GO cellular component	GO molecular function	GO biological process	SMART domain
PRINTS domain	PFAM domain	PROSITE domain	PRODOM domain	TIGRFAMs domain	PIRSF domain
SSF domain	InterPro Domain	InterPro Family	InterPro Repeat	InterPro PTM	InterPro Active_site
InterPro Binding_site	PANTHER domain	PROFILE domain	GENE3D domain	PFAM CLANS domain	SCOP superfamily
SCOP fold	SCOP class	Taxonomy species	Taxonomy genus	Taxonomy family	Taxonomy order
Taxonomy class	Taxonomy phylum	Taxonomy kingdom	Taxonomy superkingdom	Other Taxonomy	UniProt keyword

Table 3: The 42 resources that are fully integrated in PANDORA visualization tool. The different resources are colored according to their topics (i.e., structural, domain and family, taxonomy)

To illustrate the power of this detailed annotation resource, we show the set of proteins from Human and Mouse that are included in CC checkpoint (marked in Table 2).

Protein ID	Protein Name HUMAN	Length	PIRSF ID
KNTC1_HUMAN	Kinetochores-associated protein 1	2209	
FANCG_HUMAN	Fanconi anemia group G protein	622	PIRSF015159
ERCC3_HUMAN	TFIIH basal transcription factor complex helicase XPB subunit	782	PIRSF003332
DDB1_HUMAN	DNA damage-binding protein 1	1140	PIRSF002088
CHFR_HUMAN	E3 ubiquitin-protein ligase CHFR	664	A3471984 (103 p)
CD2A1_HUMAN	Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3	156	PIRSF036346
CCNG2_HUMAN	Cyclin-G2	344	
CCNE2_HUMAN	G1/S-specific cyclin-E2	404	PIRSF001771 PIRSF001769;
BUB3_HUMAN	Mitotic checkpoint protein BUB3	328	PIRSF500904
BUB1_HUMAN	Mitotic checkpoint serine/threonine-protein kinase BUB1	1085	A3512888 (58pr)
BUB1B_HUMAN	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	1050	A3512888 (58 pr)
SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A	1233	PIRSF005719
RBBP8_HUMAN	Retinoblastoma-binding protein 8	897	
RAD9A_HUMAN	Cell cycle checkpoint control protein RAD9A	391	PIRSF009303
RAD1_HUMAN	Cell cycle checkpoint protein RAD1	282	PIRSF007657
RAD17_HUMAN	Cell cycle checkpoint protein RAD17	681	
MLTK_HUMAN	Mitogen-activated protein kinase kinase kinase MLT	800	
MD2L1_HUMAN	Mitotic spindle assembly checkpoint protein MAD2A	205	PIRSF005984
MD1L1_HUMAN	Mitotic spindle assembly checkpoint protein MAD1	718	
ZWINT_HUMAN	ZW10 interactor	277	PIRSF038330
ZWILC_HUMAN	Protein zwilch homolog	591	
ZW10_HUMAN	Centromere/kinetochores protein zw10 homolog	779	
XPC_HUMAN	DNA-repair protein complementing XP-C cells	940	
Protein ID	Protein Name MOUSE	Length	PIRSF ID
KNTC1_MOUSE	Kinetochores-associated protein 1	2207	
ERCC3_MOUSE	TFIIH basal transcription factor complex helicase XPB subunit	783	PIRSF003332
DDB1_MOUSE	DNA damage-binding protein 1	1140	PIRSF002088
SMC1A_MOUSE	Structural maintenance of chromosomes protein 1A	1233	PIRSF005719
RAD9A_MOUSE	Cell cycle checkpoint control protein RAD9A	389	PIRSF009303
MLTK_MOUSE	Mitogen-activated protein kinase kinase kinase MLT	802	

ZWILC_MOUSE	Protein zwilch homolog	589
ZW10_MOUSE	Centromere/kinetochore protein zw10 homolog	779
XPC_MOUSE	DNA-repair protein complementing XP-C cells homolog	930
TRRAP_MOUSE	Transformation/transcription domain-associated protein	2565
Q91VV5_MOUSE	Trrap protein	124
Q8BW25_MOUSE	2 days pregnant adult female ovary cDNA...	267
Q3TIP5_MOUSE	CRL-1722 L5178Y-R cDNA...	374

Table 4: A human and Mouse proteins that are annotated as “Cell Cycle Checkpoint“ (based on GO). Color coded by the shared PIRSF family annotation. Text in blue is for the two human proteins that were identified in a coherent cluster by ProtoNet 5.1.

There are 23 instances that meet this annotation in Human and only 13 in mouse. As seen in Table 4. Only 15/36 of the proteins are associated with any PIRSF annotation. For information extraction on the others see section 4.2.1.

2.6.2.. Expanding family view of ‘Cell Cycle Checkpoint’ proteins

Searching the cluster that best capture the ‘Cell Cycle Checkpoint’ is an additional mode by which the biologist can navigate through the CC annotation list.

We included an advanced mode in ProtoNet 5.1 that allow search the tree by any annotation. The results of such search suggested few clusters that are substantially enriched for this annotation. The top one in cluster A3512888 (58 proteins, Cluster Name: Mad3/BUB1 homology region 1). The statistics for all other enriched keywords are shown (only for P-value <0.0001).

The taxonomical view of this cluster was unable to detect homologues in mouse however homologues in other vertebrates (not mammals) showed the homologues in Xenopus (2), Chicken (2) and Tetraodon nigroviridis (Green puffer) (3). In addition there are 7 insect homologues.

The summary of the taxonomical view for model organisms are Arabidopsis thaliana (3 proteins), Oryza sativa (3 proteins), Schizosaccharomyces pombe (2 proteins), Saccharomyces cerevisiae (2 proteins), Neurospora crassa (1 protein), Plasmodium falciparum (1 protein), Caenorhabditis elegans (2 proteins), Anopheles gambiae (3 proteins), Drosophila melanogaster (2 proteins), Xenopus laevis (2 proteins), Homo sapiens (2 proteins).

Keyword type	Keyword	Amount	Sensitivity	Specificity	P-value	Corrected P-value
SSF domain	Protein kinase-like	39	0.001	0.672	2.77e-66	1.36e-64
InterPro Domain	Mad3/BUB1 homology region 1	47	0.723	0.810	2.04e-220	9.98e-219
InterPro Domain	Protein kinase-like	39	0.001	0.672	2.77e-66	1.36e-64
InterPro Domain	Tyrosine protein kinase	4	9.04e-4	0.069	5.55e-7	2.72e-5
InterPro Domain	Protein kinase	40	0.002	0.690	3.75e-70	1.84e-68
InterPro Domain	Mad3-like	8	1.000	0.138	7.23e-39	3.54e-37

Table 5: Annotation and statistical evaluation of cluster A3512888 (58 proteins, Cluster Name: Mad3/BUB1 homology region 1).

Similar analysis was performed for all other proteins that lack a family annotation assignment. The result of such expansion is essential for the task of organism based modeling of CC.

The protein CHFR_HUMAN is best associated with cluster A3471984 combined 103 proteins 93 of which are marked as 'Zn finger –Ring finger'. The cluster include all 13 protein that are Rad18 proteins (see statistical table)

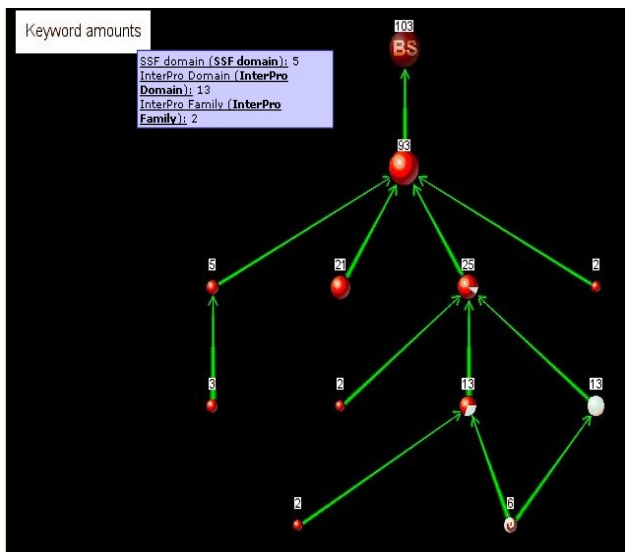


Table 6: PANDORA representation of the ProtoNet cluster (A3471984) of 103 proteins that are best match CHFR_HUMAN.

The expansion of cluster A3471984 (103 proteins) that are best match CHFR_HUMAN indicated clear homologues in *Arabidopsis thaliana* (2 proteins), *Oryza sativa* (3 proteins), *Schizosaccharomyces pombe* (1 protein), *Saccharomyces cerevisiae* (1 protein), *Neurospora crassa* (2 proteins), *Caenorhabditis elegans* (1 protein), *Anopheles gambiae* (2 proteins), *Drosophila melanogaster* (3 proteins), *Danio rerio* (5 proteins), *Xenopus laevis* (3 proteins), *Homo sapiens* (11 proteins).

Keyword type	Keyword	Amount	Sensitivity	Specificity	P-value	Corrected P-value
SSF domain	Src homology-3	5	0.001	0.049	4.19e-8	8.38e-7
SSF domain	SMAD/FHA	21	0.011	0.204	3.43e-47	6.86e-46
InterPro Domain	Src homology-3	5	0.001	0.049	7.41e-8	1.48e-6
InterPro Domain	Zinc finger, ZZ-type	3	0.006	0.029	2.09e-7	4.18e-6
InterPro Domain	Zinc finger, RING-type	93	0.011	0.903	1.72e-226	3.44e-225
InterPro Domain	DNA-binding SAP	25	0.052	0.243	3.00e-73	6.01e-72
InterPro Domain	Zinc finger, Rad18-type putative	13	0.283	0.126	7.06e-49	1.41e-47
InterPro Domain	Proteinase inhibitor I1, Kazal	2	0.002	0.019	1.26e-4	0.003
InterPro Domain	SMAD/FHA	21	0.011	0.204	3.43e-47	6.86e-46
InterPro Domain	Forkhead-associated	20	0.015	0.194	1.63e-47	3.26e-46
InterPro Family	DNA repair protein, Rad18	13	1.000	0.126	1.89e-59	3.78e-58

Conclusions:

1. Cell cycle proteins are under-annotated.
2. Phylogenetic perspective allows a safe expansion of the class of CC proteins.
3. Automatic classification is a valuable procedure to support experimental results. However statistical evaluation if the functional inference is essential.
4. Integration of annotations doubles the biological information on genes and proteins relative to sequence based alone.

- The annotation levels for regulators of CC are rather poor. While the high level of CC is extensive, the definition for CC regulators is limited. Extensive automatic classification will be essential to include the regulation level in future modeling effort.

SANGER has performed a comprehensive functional annotation of all fission yeast genes with respect to cell cycle and other Gene Ontology (GO) terms. There are 544 *S. pombe* protein coding gene products annotated to the GO term cell cycle (GO:0007049) or to one of its children. These genes represent over 10% of the manually curated (total) annotations to this term from any organism (4503). Of these gene products, 396 have at least one experimentally derived annotation from *S. pombe*, supported by the appropriate evidence code and citation.

The remaining 148 gene products represent inferences made from sequence similarity to experimentally characterised *S. cerevisiae* orthologs. The majority of the annotations are more granular than 'cell cycle'. For example, 132 gene products are annotated specifically to 'regulation of mitotic cell cycle'.

All the functional annotations have been incorporated in the public *S. pombe* model organism database (GeneDB), where they can be searched and analyzed:

<http://www.genedb.org/genedb/pombe/>

Below, the numbers of gene products annotated to the 168 different cell cycle-related GO terms are indicated:

***** 1. row ***** acc: GO:0007049 name: cell cycle gp_count: 548	gp_count: 122 ***** 13. row ***** acc: GO:0000075 name: cell cycle checkpoint gp_count: 92
***** 2. row ***** acc: GO:0022402 name: cell cycle process gp_count: 379	***** 14. row ***** acc: GO:0007127 name: meiosis I gp_count: 77
***** 3. row ***** acc: GO:0022403 name: cell cycle phase gp_count: 327	***** 15. row ***** acc: GO:0051325 name: interphase gp_count: 66
***** 4. row ***** acc: GO:0000279 name: M phase gp_count: 282	***** 16. row ***** acc: GO:0000819 name: sister chromatid segregation gp_count: 63
***** 5. row ***** acc: GO:0051726 name: regulation of cell cycle gp_count: 260	***** 17. row ***** acc: GO:0010564 name: regulation of cell cycle process gp_count: 62
***** 6. row ***** acc: GO:0000278 name: mitotic cell cycle gp_count: 233	***** 18. row ***** acc: GO:0051329 name: interphase of mitotic cell cycle gp_count: 60
***** 7. row ***** acc: GO:0051321 name: meiotic cell cycle gp_count: 176	***** 19. row ***** acc: GO:0045132 name: meiotic chromosome segregation gp_count: 57
***** 8. row ***** acc: GO:0007126 name: meiosis gp_count: 172	***** 20. row ***** acc: GO:0000070 name: mitotic sister chromatid segregation gp_count: 55
***** 9. row ***** acc: GO:0051327 name: M phase of meiotic cell cycle gp_count: 172	***** 21. row ***** acc: GO:0007131 name: meiotic recombination gp_count: 55
***** 10. row ***** acc: GO:0007346 name: regulation of mitotic cell cycle gp_count: 132	***** 22. row ***** acc: GO:0031570 name: DNA integrity checkpoint gp_count: 53
***** 11. row ***** acc: GO:0000087 name: M phase of mitotic cell cycle gp_count: 129	***** 23. row ***** acc: GO:0033205 name: cytokinesis during cell cycle gp_count: 48
***** 12. row ***** acc: GO:0007067 name: mitosis	***** 24. row ***** acc: GO:0007093

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name: mitotic cell cycle checkpoint
gp_count: 41
***** 25. row *****
acc: GO:0007088
name: regulation of mitosis
gp_count: 39
***** 26. row *****
acc: GO:0000076
name: DNA replication checkpoint
gp_count: 36
***** 27. row *****
acc: GO:0000077
name: DNA damage checkpoint
gp_count: 34
***** 28. row *****
acc: GO:0031577
name: spindle checkpoint
gp_count: 30
***** 29. row *****
acc: GO:0007094
name: mitotic cell cycle spindle assembly checkpoint
gp_count: 30
***** 30. row *****
acc: GO:0000916
name: contractile ring contraction involved in cytokinesis
gp_count: 27
***** 31. row *****
acc: GO:0007091
name: mitotic metaphase/anaphase transition
gp_count: 27
***** 32. row *****
acc: GO:0007062
name: sister chromatid cohesion
gp_count: 26
***** 33. row *****
acc: GO:0000912
name: formation of actomyosin apparatus in cytokinesis
gp_count: 25
***** 34. row *****
acc: GO:0000915
name: cytokinesis, contractile ring formation
gp_count: 25
***** 35. row *****
acc: GO:0007096
name: regulation of exit from mitosis
gp_count: 24
***** 36. row *****
acc: GO:0010458
name: exit from mitosis
gp_count: 24
***** 37. row *****
acc: GO:0045143
name: homologous chromosome segregation
gp_count: 22
***** 38. row *****
acc: GO:0000079
name: regulation of cyclin-dependent protein kinase activity
gp_count: 22
***** 39. row *****
acc: GO:0031028
name: septation initiation signaling
gp_count: 22
***** 40. row *****
acc: GO:0031991
name: regulation of contractile ring contraction in cytokinesis
gp_count: 22
***** 41. row *****
acc: GO:0000082
name: G1/S transition of mitotic cell cycle
gp_count: 20
***** 42. row *****
acc: GO:0006311
name: meiotic gene conversion
gp_count: 20
***** 43. row *****
acc: GO:0000086
name: G2/M transition of mitotic cell cycle
gp_count: 19
***** 44. row *****
acc: GO:0051445
name: regulation of meiotic cell cycle
gp_count: 19
***** 45. row *****
acc: GO:0007052
name: mitotic spindle organization and biogenesis
gp_count: 17
***** 46. row *****
acc: GO:0051320
name: S phase
gp_count: 16
***** 47. row *****
acc: GO:0007080
name: mitotic metaphase plate congression
gp_count: 15
***** 48. row *****
acc: GO:0000084
name: S phase of mitotic cell cycle
gp_count: 15
***** 49. row *****
acc: GO:0040020
name: regulation of meiosis
gp_count: 15
***** 50. row *****
acc: GO:0031134
name: sister chromatid biorientation
gp_count: 15
***** 51. row *****
acc: GO:0045896
name: regulation of transcription, mitotic
gp_count: 15
***** 52. row *****
acc: GO:0045786
name: negative regulation of cell cycle
gp_count: 14
***** 53. row *****
acc: GO:0008054
name: cyclin catabolic process
gp_count: 13
***** 54. row *****
acc: GO:0031029
name: regulation of septation initiation signaling
gp_count: 13
***** 55. row *****
acc: GO:0051316
name: attachment of spindle microtubules to kinetochore
during meiotic chromosome segregation
gp_count: 13
***** 56. row *****
acc: GO:0007135
name: meiosis II
gp_count: 12
***** 57. row *****
acc: GO:0000080
name: G1 phase of mitotic cell cycle
gp_count: 12
***** 58. row *****
acc: GO:0051318
name: G1 phase
gp_count: 12
***** 59. row *****
acc: GO:0045141
name: meiotic telomere clustering
gp_count: 12
***** 60. row *****
acc: GO:0051455
name: attachment of spindle microtubules to kinetochore
during meiosis I
gp_count: 11
***** 61. row *****
acc: GO:0030071
name: regulation of mitotic metaphase/anaphase transition
gp_count: 11
***** 62. row *****
acc: GO:0007129
name: synapsis
gp_count: 10
***** 63. row *****
acc: GO:0031573

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name: intra-S DNA damage checkpoint
gp_count: 10
***** 64. row *****
acc: GO:0007050
name: cell cycle arrest
gp_count: 10
***** 65. row *****
acc: GO:0051177
name: meiotic sister chromatid cohesion
gp_count: 9
***** 66. row *****
acc: GO:0007076
name: mitotic chromosome condensation
gp_count: 9
***** 67. row *****
acc: GO:0030989
name: horsetail nuclear movement
gp_count: 9
***** 68. row *****
acc: GO:0051300
name: spindle pole body organization and biogenesis
gp_count: 9
***** 69. row *****
acc: GO:0042138
name: meiotic DNA double-strand break formation
gp_count: 9
***** 70. row *****
acc: GO:0007064
name: mitotic sister chromatid cohesion
gp_count: 8
***** 71. row *****
acc: GO:0007089
name: traversing start control point of mitotic cell cycle
gp_count: 8
***** 72. row *****
acc: GO:0045144
name: meiotic sister chromatid segregation
gp_count: 7
***** 73. row *****
acc: GO:0045930
name: negative regulation of mitotic cell cycle
gp_count: 6
***** 74. row *****
acc: GO:0000216
name: M/G1 transition of mitotic cell cycle
gp_count: 6
***** 75. row *****
acc: GO:0046021
name: regulation of transcription from RNA pol II promoter
gp_count: 6
***** 76. row *****
acc: GO:0000709
name: meiotic joint molecule formation
gp_count: 6
***** 77. row *****
acc: GO:0030996
name: cell cycle arrest in response to nitrogen starvation
gp_count: 6
***** 78. row *****
acc: GO:0051304
name: chromosome separation
gp_count: 6
***** 79. row *****
acc: GO:0031030
name: negative regulation of septation initiation signaling
gp_count: 6
***** 80. row *****
acc: GO:0000022
name: mitotic spindle elongation
gp_count: 5
***** 81. row *****
acc: GO:0031572
name: G2/M transition DNA damage checkpoint
gp_count: 5
***** 82. row *****
acc: GO:0051231
name: spindle elongation
gp_count: 5
***** 83. row *****
acc: GO:0000711
name: meiotic DNA repair synthesis
gp_count: 5
***** 84. row *****
acc: GO:0045787
name: positive regulation of cell cycle
gp_count: 5
***** 85. row *****
acc: GO:0051754
name: meiotic sister chromatid cohesion, centromeric
gp_count: 5
***** 86. row *****
acc: GO:0000751
name: cell cycle arrest in response to pheromone
gp_count: 5
***** 87. row *****
acc: GO:0031576
name: G2/M transition checkpoint
gp_count: 5
***** 88. row *****
acc: GO:0051415
name: interphase microtubule nucleation by interphase
microtubule organizing center
gp_count: 5
***** 89. row *****
acc: GO:0051315
name: attachment of spindle microtubules to kinetochore
during mitosis
gp_count: 5
***** 90. row *****
acc: GO:0031031
name: positive regulation of septation initiation signaling
gp_count: 5
***** 91. row *****
acc: GO:0031322
name: ascospore-type prospore-specific SPB modification
gp_count: 5
***** 92. row *****
acc: GO:0051322
name: anaphase
gp_count: 4
***** 93. row *****
acc: GO:0007063
name: regulation of sister chromatid cohesion
gp_count: 4
***** 94. row *****
acc: GO:0034086
name: maintenance of sister chromatid cohesion
gp_count: 4
***** 95. row *****
acc: GO:0045736
name: negative regulation of cyclin-dependent protein
kinase activity
gp_count: 4
***** 96. row *****
acc: GO:0007068
name: negative regulation of transcription, mitotic
gp_count: 4
***** 97. row *****
acc: GO:0034088
name: maintenance of mitotic sister chromatid cohesion
gp_count: 4
***** 98. row *****
acc: GO:0034091
name: regulation of sister chromatid cohesion maintenance
gp_count: 4
***** 99. row *****
acc: GO:0031574
name: S-M checkpoint
gp_count: 4
***** 100. row *****
acc: GO:0045835
name: negative regulation of meiosis
gp_count: 4
***** 101. row *****
acc: GO:0030999
name: linear element formation
gp_count: 4
***** 102. row *****

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acc: GO:0034182
name: regulation of mitotic sister chromatid cohesion
gp_count: 4
***** 103. row *****

acc: GO:0051307
name: meiotic chromosome separation
gp_count: 4
***** 104. row *****

acc: GO:0007095
name: cell cycle G2/M transition DNA damage checkpoint
gp_count: 4
***** 105. row *****

acc: GO:0031565
name: cytokinesis checkpoint
gp_count: 3
***** 106. row *****

acc: GO:0045931
name: positive regulation of mitotic cell cycle
gp_count: 3
***** 107. row *****

acc: GO:0030037
name: actin filament reorganization during cell cycle
gp_count: 3
***** 108. row *****

acc: GO:0000706
name: meiotic DNA double-strand break processing
gp_count: 3
***** 109. row *****

acc: GO:0007070
name: negative regulation of transcription from RNA
pol II promoter
gp_count: 3
***** 110. row *****

acc: GO:0030474
name: spindle pole body duplication
gp_count: 3
***** 111. row *****

acc: GO:0000712
name: resolution of meiotic joint molecules as recombinants
gp_count: 3
***** 112. row *****

acc: GO:0000078
name: cell morphogenesis checkpoint
gp_count: 3
***** 113. row *****

acc: GO:0045836
name: positive regulation of meiosis
gp_count: 3
***** 114. row *****

acc: GO:0051437
name: positive regulation of ubiquitin-protein ligase activity
during mitotic cell cycle
gp_count: 3
***** 115. row *****

acc: GO:0000083
name: G1/S-specific transcription in mitotic cell cycle
gp_count: 3
***** 116. row *****

acc: GO:0051439
name: regulation of ubiquitin-protein ligase activity
during mitotic cell cycle
gp_count: 3
***** 117. row *****

acc: GO:0040001
name: establishment of mitotic spindle localization
gp_count: 3
***** 118. row *****

acc: GO:0007092
name: activation of anaphase-promoting complex
during mitotic cell cycle
gp_count: 3
***** 119. row *****

acc: GO:0033261
name: regulation of S phase
gp_count: 3
***** 120. row *****

acc: GO:0000132
name: establishment of mitotic spindle orientation
gp_count: 3
***** 121. row *****

acc: GO:0031566
name: contractile ring maintenance involved in cytokinesis
gp_count: 2
***** 122. row *****

acc: GO:0051456
name: attachment of spindle microtubules to kinetochore
during meiosis II
gp_count: 2
***** 123. row *****

acc: GO:0031567
name: cell size control checkpoint
gp_count: 2
***** 124. row *****

acc: GO:0007138
name: meiotic anaphase II
gp_count: 2
***** 125. row *****

acc: GO:0034093
name: positive regulation of maintenance of sister
chromatid cohesion
gp_count: 2
***** 126. row *****

acc: GO:0045839
name: negative regulation of mitosis
gp_count: 2
***** 127. row *****

acc: GO:0051306
name: mitotic sister chromatid separation
gp_count: 2
***** 128. row *****

acc: GO:0045840
name: positive regulation of mitosis
gp_count: 2
***** 129. row *****

acc: GO:0007090
name: regulation of S phase of mitotic cell cycle
gp_count: 2
***** 130. row *****

acc: GO:0032121
name: attachment of telomeres to spindle pole body
gp_count: 2
***** 131. row *****

acc: GO:0034184
name: positive regulation of maintenance of mitotic sister
chromatid cohesion
gp_count: 2
***** 132. row *****

acc: GO:0051440
name: regulation of ubiquitin-protein ligase activity
during meiotic cell cycle
gp_count: 2
***** 133. row *****

acc: GO:0045876
name: positive regulation of sister chromatid cohesion
gp_count: 2
***** 134. row *****

acc: GO:0000090
name: mitotic anaphase
gp_count: 2
***** 135. row *****

acc: GO:0051447
name: negative regulation of meiotic cell cycle
gp_count: 1
***** 136. row *****

acc: GO:0033313
name: meiotic cell cycle checkpoint
gp_count: 1
***** 137. row *****

acc: GO:0034085
name: establishment of sister chromatid cohesion
gp_count: 1
***** 138. row *****

acc: GO:0051324
name: prophase
gp_count: 1
***** 139. row *****

acc: GO:0051487
name: activation of anaphase-promoting complex

during meiotic cell cycle
gp_count: 1
***** 140. row *****
acc: GO:0007128
name: meiotic prophase I
gp_count: 1
***** 141. row *****
acc: GO:0034087
name: establishment of mitotic sister chromatid cohesion
gp_count: 1
***** 142. row *****
acc: GO:0045749
name: negative regulation of S phase of mitotic cell cycle
gp_count: 1
***** 143. row *****
acc: GO:0051598
name: meiotic recombination checkpoint
gp_count: 1
***** 144. row *****
acc: GO:0030472
name: mitotic spindle organization and biogenesis in nucleus
gp_count: 1
***** 145. row *****
acc: GO:0051328
name: interphase of meiotic cell cycle
gp_count: 1
***** 146. row *****
acc: GO:0051255
name: spindle midzone assembly
gp_count: 1
***** 147. row *****
acc: GO:0034092
name: negative regulation of maintenance of sister chromatid cohesion
gp_count: 1
***** 148. row *****
acc: GO:0051331
name: G2 phase of meiotic cell cycle
gp_count: 1
***** 149. row *****
acc: GO:0051756
name: meiotic sister chromatid centromere separation
gp_count: 1
***** 150. row *****
acc: GO:0051757
name: meiotic sister chromatid separation
gp_count: 1
***** 151. row *****
acc: GO:0051426
name: spindle pole body maturation
gp_count: 1
***** 152. row *****
acc: GO:0034183
name: negative regulation of maintenance of mitotic sister chromatid cohesion
gp_count: 1
***** 153. row *****
acc: GO:0010389
name: regulation of G2/M transition of mitotic cell cycle
gp_count: 1
***** 154. row *****
acc: GO:0045841
name: negative regulation of mitotic metaphase/anaphase transition

gp_count: 1
***** 155. row *****
acc: GO:0051314
name: attachment of spindle microtubules to mitotic chromosome
gp_count: 1
***** 156. row *****
acc: GO:0032189
name: maintenance of contractile ring localization
gp_count: 1
***** 157. row *****
acc: GO:0045842
name: positive regulation of mitotic metaphase/anaphase transition
gp_count: 1
***** 158. row *****
acc: GO:0010503
name: negative regulation of cell cycle arrest in response to nitrogen starvation
gp_count: 1
***** 159. row *****
acc: GO:0032887
name: regulation of spindle elongation
gp_count: 1
***** 160. row *****
acc: GO:0045875
name: negative regulation of sister chromatid cohesion
gp_count: 1
***** 161. row *****
acc: GO:0051441
name: positive regulation of ubiquitin-protein ligase activity during meiotic cell cycle
gp_count: 1
***** 162. row *****
acc: GO:0010504
name: regulation of cell cycle arrest in response to nitrogen starvation
gp_count: 1
***** 163. row *****
acc: GO:0032888
name: regulation of mitotic spindle elongation
gp_count: 1
***** 164. row *****
acc: GO:0051319
name: G2 phase
gp_count: 1
***** 165. row *****
acc: GO:0051442
name: negative regulation of ubiquitin-protein ligase activity during meiotic cell cycle
gp_count: 1
***** 166. row *****
acc: GO:0010520
name: regulation of meiotic recombination
gp_count: 1
***** 167. row *****
acc: GO:0031536
name: positive regulation of exit from mitosis
gp_count: 1
***** 168. row *****
acc: GO:0045897
name: positive regulation of transcription, mitotic
gp_count: 1