

bählerlab

Genome Regulation



AnGeLi: Analysis of Gene Lists

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GO Biological Process	List frequency / Value	Background frequency / Value	Details	p- value
flocculation	13.33% (6/45)	0.24% (12/4920)	Explain!	7.21494e-07
aggregation of unicellular organisms	13.33% (6/45)	0.28% (14/4920)	Explain!	1.54204e-06
cell aggregation	13.33% (6/45)	0.28% (14/4920)	Explain!	1.54204e-06
cellular macromolecule metabolic process	15.56% (7/45)	47.28% (2326/4920)	Explain!	0.00384847
multi-organism process	20.00% (9/45)	3.62% (178/4920)	Explain!	0.00667303
macromolecule metabolic process	17.78% (8/45)	48.50% (2386/4920)	Explain!	0.00782087
metabolic process	35.56% (16/45)	64.11% (3154/4920)	Explain!	0.028052
cellular metabolic process	33.33% (15/45)	61.73% (3037/4920)	Explain!	0.0336177
primary metabolic process	31.11% (14/45)	58.98% (2902/4920)	Explain!	0.0420094

GO Cellular Component	List frequency / Value	Background frequency / Value	Details	p- value
organelle part	13.33% (6/45)	52.30% (2573/4920)	Explain!	3.98678e-05
intracellular organelle part	13.33% (6/45)	51.89% (2553/4920)	Explain!	4.39767e-05
external side of cell wall	11.11% (5/45)	0.28% (14/4920)	Explain!	4.91025e-05
cell wall part	11.11% (5/45)	0.33% (16/4920)	Explain!	9.6185e-05
external encapsulating structure part	11.11% (5/45)	0.33% (16/4920)	Explain!	9.6185e-05
cell surface	17.78% (8/45)	1.54% (76/4920)	Explain!	0.000127589
cell wall	15.56% (7/45)	1.10% (54/4920)	Explain!	0.000166109
external encapsulating structure	15.56% (7/45)	1.10% (54/4920)	Explain!	0.000166109

<u>intracellular</u>	75.56% (34/45)	94.98% (4673/4920)	Explain!	0.00266858
<u>intracellular part</u>	75.56% (34/45)	94.98% (4673/4920)	Explain!	0.00266858
<u>macromolecular complex</u>	11.11% (5/45)	41.91% (2062/4920)	Explain!	0.00307654
<u>protein complex</u>	4.44% (2/45)	29.63% (1458/4920)	Explain!	0.0112065

GO Molecular Function	List frequency / Value	Background frequency / Value	Details	p- value
<u>cell adhesion molecule binding</u>	11.11% (5/45)	0.24% (12/4920)	Explain!	2.51611e-05
<u>protein binding involved in cell adhesion</u>	11.11% (5/45)	0.26% (13/4920)	Explain!	3.65486e-05

Gene Expression	List frequency / Value	Background frequency / Value	Details	p- value
<u>Induced Dbr1 deletion</u>	42.22% (19/45)	2.38% (117/4920)	Explain!	5.40843e-16
<u>Induced usp102 mutant</u>	20.00% (9/45)	0.91% (45/4920)	Explain!	3.93786e-07
<u>Stress module</u>	26.67% (12/45)	2.76% (136/4920)	Explain!	1.90046e-06
<u>Atf1 activated</u>	20.00% (9/45)	1.38% (68/4920)	Explain!	6.83289e-06
<u>Lowly expressed</u>	37.78% (17/45)	7.46% (367/4920)	Explain!	6.85031e-06
<u>Late meiotic genes</u>	24.44% (11/45)	2.72% (134/4920)	Explain!	1.46635e-05
<u>Induced erl1 mutant</u>	13.33% (6/45)	0.45% (22/4920)	Explain!	2.04057e-05
<u>Meiosis sporulation module</u>	31.11% (14/45)	5.41% (266/4920)	Explain!	2.95908e-05
<u>Core Environmental Stress Response induced</u>	40.00% (18/45)	10.65% (524/4920)	Explain!	0.000111508
<u>Induced Amo1 mutant</u>	13.33% (6/45)	0.77% (38/4920)	Explain!	0.000349336
<u>Induced zfs1 mutant</u>	15.56% (7/45)	1.40% (69/4920)	Explain!	0.000856491
<u>Sporulation module</u>	22.22% (10/45)	3.72% (183/4920)	Explain!	0.00133186
<u>Induced pan3 mutant</u>	11.11% (5/45)	0.61% (30/4920)	Explain!	0.00194864
<u>htb1 brl1 brl2 set1 mutant induced</u>	17.78% (8/45)	2.62% (129/4920)	Explain!	0.00468933
<u>Caffeine and Rapamycin</u>	24.44% (11/45)	5.71% (281/4920)	Explain!	0.00787628

<u>induced</u>				
<u>Induced SPBC56F2 08c mutant</u>	6.67% (3/45)	0.24% (12/4920)	Explain!	0.0336177

Gene Features	List frequency / Value	Background frequency / Value	Details	p- value
<u>Intron-containing genes</u>	15.56% (7/45)	49.09% (2415/4920)	Explain!	0.00110918
<u>Intron-less genes</u>	84.44% (38/45)	50.91% (2505/4920)	Explain!	0.00110918

Phenotypes (FYPO)	List frequency / Value	Background frequency / Value	Details	p- value
<u>increased flocculation</u>	15.56% (7/45)	1.00% (49/4920)	Explain!	9.6185e-05
<u>inviable cell</u>	6.67% (3/45)	33.05% (1626/4920)	Explain!	0.0103569
<u>decreased pseudohyphal growth</u>	4.44% (2/45)	0.04% (2/4920)	Explain!	0.0196502
<u>inviable cell population</u>	6.67% (3/45)	30.45% (1498/4920)	Explain!	0.0488223
<u>inviable vegetative cell population</u>	6.67% (3/45)	30.16% (1484/4920)	Explain!	0.0488223

Protein Domains (Pfam)	List frequency / Value	Background frequency / Value	Details	p- value
<u>Cell-wall adhesin ligand-binding C-terminal</u>	6.67% (3/45)	0.08% (4/4920)	Explain!	0.00101391

Protein Features	List frequency / Value	Background frequency / Value	Details	p- value
<u>Homo sapiens orthologs</u>	24.44% (11/45)	70.53% (3470/4920)	Explain!	4.36645e-07
<u>S.cerevisiae orthologs</u>	35.56% (16/45)	78.66% (3870/4920)	Explain!	7.68266e-07
<u>Threonine</u>	0.0814396	0.0536787	Explain!	9.3088e-06
<u>Leucine</u>	0.0787938	0.0965112	Explain!	0.00196102

Transcript Features	List frequency / Value	Background frequency / Value	Details	p- value
<u>mRNA level (WT)</u>	655.488	2827.23	Explain!	4.36063e-11
<u>mRNA copies per</u>	1.4344	8.2283	Explain!	3.83365e-07

	cdk8			
proliferating cell				
Relative Pol II occupancy	0.806711	1.34768	Explain!	6.85031e-06
mRNA copies per quiescent cell	1.12133	1.4789	Explain!	2.38558e-05

11769 statistical tests (49 two-sided Wilcoxon rank sum tests , 11720 two-sided Fisher's exact tests) were performed, corrected according to **FDR** and evaluated given an alpha of **0.05**. **Additionally, 4** permutation tests (with 1000 permutations) were performed and **NOT** corrected for multiple tests.

Bähler Lab, University College London, 2015.