

bählerlab

Genome Regulation



AnGeLi: Analysis of Gene Lists

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GO Biological Process	List frequency / Value	Background frequency / Value	Details	p- value
biosynthetic process	52.32% (79/151)	27.46% (827/3012)	Explain!	1.93399e-07
cellular biosynthetic process	51.66% (78/151)	26.83% (808/3012)	Explain!	1.93399e-07
organic substance biosynthetic process	51.66% (78/151)	27.03% (814/3012)	Explain!	1.93399e-07
gene expression	43.05% (65/151)	21.51% (648/3012)	Explain!	3.85943e-06
cytoplasmic translation	14.57% (22/151)	3.92% (118/3012)	Explain!	4.52177e-05
cellular metabolic process	74.17% (112/151)	54.81% (1651/3012)	Explain!	0.000311727
cellular macromolecule biosynthetic process	35.76% (54/151)	19.16% (577/3012)	Explain!	0.000374479
translation	15.89% (24/151)	5.38% (162/3012)	Explain!	0.000393392
macromolecule biosynthetic process	35.76% (54/151)	19.19% (578/3012)	Explain!	0.000488568
primary metabolic process	69.54% (105/151)	51.59% (1554/3012)	Explain!	0.00157793
organic substance metabolic process	72.19% (109/151)	54.81% (1651/3012)	Explain!	0.00288129
metabolic process	74.17% (112/151)	57.40% (1729/3012)	Explain!	0.00350104
positive regulation of macromolecule biosynthetic process	11.26% (17/151)	3.59% (108/3012)	Explain!	0.00414487
nitrogen compound metabolic process	47.68% (72/151)	31.47% (948/3012)	Explain!	0.00465528
positive regulation of biosynthetic process	11.26% (17/151)	3.65% (110/3012)	Explain!	0.00474125
positive regulation of cellular	14.57% (22/151)	5.61% (169/3012)	Explain!	0.00474125

metabolic process				
positive regulation of cellular biosynthetic process	11.26% (17/151)	3.65% (110/3012)	Explain!	0.00474125
cellular process	89.40% (135/151)	75.76% (2282/3012)	Explain!	0.00475789
positive regulation of nucleobase-containing compound metabolic process	11.26% (17/151)	3.69% (111/3012)	Explain!	0.00508184
positive regulation of nitrogen compound metabolic process	11.26% (17/151)	3.69% (111/3012)	Explain!	0.00508184
positive regulation of macromolecule metabolic process	13.91% (21/151)	5.41% (163/3012)	Explain!	0.00785298
positive regulation of transcription from RNA polymerase II promoter	9.27% (14/151)	2.76% (83/3012)	Explain!	0.00862492
positive regulation of gene expression	10.60% (16/151)	3.55% (107/3012)	Explain!	0.0109697
positive regulation of RNA metabolic process	9.93% (15/151)	3.19% (96/3012)	Explain!	0.011044
cellular nitrogen compound metabolic process	43.71% (66/151)	28.88% (870/3012)	Explain!	0.0120305
aromatic compound biosynthetic process	23.84% (36/151)	12.58% (379/3012)	Explain!	0.0137472
organic cyclic compound biosynthetic process	24.50% (37/151)	13.31% (401/3012)	Explain!	0.0174561
heterocycle biosynthetic process	23.84% (36/151)	12.62% (380/3012)	Explain!	0.0180025
cellular aromatic compound metabolic process	41.06% (62/151)	26.99% (813/3012)	Explain!	0.0203696
positive regulation of transcription, DNA-templated	9.27% (14/151)	3.05% (92/3012)	Explain!	0.0203696

<u>positive regulation of RNA biosynthetic process</u>	9.27% (14/151)	3.05% (92/3012)	Explain!	0.0203696
<u>positive regulation of nucleic acid-templated transcription</u>	9.27% (14/151)	3.05% (92/3012)	Explain!	0.0203696
<u>heterocycle metabolic process</u>	41.06% (62/151)	27.29% (822/3012)	Explain!	0.0226773
<u>positive regulation of metabolic process</u>	14.57% (22/151)	6.27% (189/3012)	Explain!	0.0230273
<u>one-carbon metabolic process</u>	2.65% (4/151)	0.23% (7/3012)	Explain!	0.0249744
<u>cellular macromolecule metabolic process</u>	54.97% (83/151)	40.24% (1212/3012)	Explain!	0.0292466
<u>organic cyclic compound metabolic process</u>	41.72% (63/151)	28.15% (848/3012)	Explain!	0.0320673
<u>cellular nitrogen compound biosynthetic process</u>	23.84% (36/151)	13.15% (396/3012)	Explain!	0.0323305
<u>organophosphate biosynthetic process</u>	7.95% (12/151)	2.59% (78/3012)	Explain!	0.0448616
<u>cellular component biogenesis</u>	25.83% (39/151)	15.17% (457/3012)	Explain!	0.0475675
<u>macromolecular complex assembly</u>	15.89% (24/151)	7.70% (232/3012)	Explain!	0.0487476
<u>sulfite transport</u>	1.99% (3/151)	0.13% (4/3012)	Explain!	0.0504981
<u>2-oxoglutarate metabolic process</u>	1.99% (3/151)	0.13% (4/3012)	Explain!	0.0504981
<u>nucleobase-containing compound biosynthetic process</u>	21.19% (32/151)	11.55% (348/3012)	Explain!	0.0579171
<u>organonitrogen compound biosynthetic process</u>	12.58% (19/151)	5.44% (164/3012)	Explain!	0.0595185
<u>macromolecule metabolic process</u>	54.97% (83/151)	41.27% (1243/3012)	Explain!	0.0624844
<u>small molecule biosynthetic process</u>	10.60% (16/151)	4.35% (131/3012)	Explain!	0.0631356
<u>cellular protein metabolic</u>	33.77% (51/151)	22.28% (671/3012)	Explain!	0.0796029

process				
macromolecular complex subunit organization	23.18% (35/151)	13.55% (408/3012)	Explain!	0.080945
mitochondrial RNA processing	2.65% (4/151)	0.33% (10/3012)	Explain!	0.0903884
nucleobase biosynthetic process	2.65% (4/151)	0.33% (10/3012)	Explain!	0.0903884
positive regulation of cellular process	15.89% (24/151)	8.10% (244/3012)	Explain!	0.094156

GO Cellular Component	List frequency / Value	Background frequency / Value	Details	p- value
cytosolic ribosome	12.58% (19/151)	2.76% (83/3012)	Explain!	2.3027e-05
cytosolic part	13.25% (20/151)	3.15% (95/3012)	Explain!	2.85156e-05
ribosome	12.58% (19/151)	3.22% (97/3012)	Explain!	0.000132257
ribosomal subunit	11.92% (18/151)	2.95% (89/3012)	Explain!	0.000151413
cytosolic large ribosomal subunit	7.95% (12/151)	1.36% (41/3012)	Explain!	0.000221975
organelle part	62.91% (95/151)	43.39% (1307/3012)	Explain!	0.000393392
intracellular organelle part	62.25% (94/151)	42.90% (1292/3012)	Explain!	0.000488568
large ribosomal subunit	7.95% (12/151)	1.63% (49/3012)	Explain!	0.00110061
ribonucleoprotein complex	16.56% (25/151)	6.31% (190/3012)	Explain!	0.00146361
macromolecular complex	47.68% (72/151)	31.47% (948/3012)	Explain!	0.00465528
organelle lumen	31.13% (47/151)	18.29% (551/3012)	Explain!	0.0141152
intracellular organelle lumen	31.13% (47/151)	18.29% (551/3012)	Explain!	0.0141152
transcription factor complex	3.97% (6/151)	0.63% (19/3012)	Explain!	0.0292466
membrane-enclosed lumen	31.13% (47/151)	18.92% (570/3012)	Explain!	0.0313001
mitochondrial part	15.89% (24/151)	7.37% (222/3012)	Explain!	0.0340205
RNA polymerase II transcription factor complex	3.31% (5/151)	0.46% (14/3012)	Explain!	0.045613
nuclear transcription factor complex	3.31% (5/151)	0.50% (15/3012)	Explain!	0.0605355
mitochondrial matrix	7.95% (12/151)	2.72% (82/3012)	Explain!	0.0624844
non-membrane-bounded organelle	34.44% (52/151)	22.64% (682/3012)	Explain!	0.0624844
intracellular non-membrane-	34.44% (52/151)	22.64% (682/3012)	Explain!	0.0624844

<u>bounded</u> <u>organelle</u>				
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GO Molecular Function	List frequency / Value	Background frequency / Value	Details	p- value
<u>structural constituent of ribosome</u>	11.92% (18/151)	2.76% (83/3012)	Explain!	5.96301e-05
<u>structural molecule activity</u>	11.92% (18/151)	3.52% (106/3012)	Explain!	0.00110061
<u>rRNA binding</u>	4.64% (7/151)	0.60% (18/3012)	Explain!	0.0034658
<u>sulfite transmembrane transporter activity</u>	1.99% (3/151)	0.13% (4/3012)	Explain!	0.0504981
<u>RNA polymerase II transcription regulatory region sequence-specific DNA binding</u> <u>transcription factor activity involved in positive regulation of transcription</u>	3.97% (6/151)	0.73% (22/3012)	Explain!	0.0577574
<u>RNA binding</u>	13.91% (21/151)	6.71% (202/3012)	Explain!	0.0992461

Gene Expression	List frequency / Value	Background frequency / Value	Details	p- value
<u>Ribosomal protein module Homol D E</u>	14.57% (22/151)	3.69% (111/3012)	Explain!	2.3027e-05
<u>Ribosomal protein module 2</u>	15.89% (24/151)	4.45% (134/3012)	Explain!	2.85156e-05
<u>Highly expressed genes</u>	19.21% (29/151)	6.91% (208/3012)	Explain!	0.000151413
<u>Oxidative Stress Cluster 11</u>	8.61% (13/151)	1.86% (56/3012)	Explain!	0.000862108
<u>Oxidative Stress Cluster 9</u>	9.93% (15/151)	2.52% (76/3012)	Explain!	0.00110061
<u>Caffeine and Rapamycin repressed</u>	13.25% (20/151)	4.58% (138/3012)	Explain!	0.00288129
<u>Core Environmental Stress Response repressed</u>	15.89% (24/151)	6.18% (186/3012)	Explain!	0.00288129

<u>Oxidative Stress Cluster 6</u>	9.93% (15/151)	2.79% (84/3012)	Explain!	0.00298838
<u>Reproduction module</u>	1.32% (2/151)	7.77% (234/3012)	Explain!	0.075592

Phenotypes (FYPO)	List frequency / Value	Background frequency / Value	Details	p- value
<u>decreased cell population growth</u>	41.06% (62/151)	21.48% (647/3012)	Explain!	2.85156e-05
<u>slow vegetative cell population growth</u>	23.84% (36/151)	9.43% (284/3012)	Explain!	5.89229e-05
<u>decreased vegetative cell population growth</u>	40.40% (61/151)	21.25% (640/3012)	Explain!	5.89229e-05
<u>decreased cell population growth on glycerol carbon source</u>	23.84% (36/151)	10.03% (302/3012)	Explain!	0.000221975
<u>viable vegetative cell with normal cell morphology</u>	68.87% (104/151)	84.69% (2551/3012)	Explain!	0.000311727
<u>viable vegetative cell with abnormal cell shape</u>	31.13% (47/151)	16.04% (483/3012)	Explain!	0.000789108
<u>abnormal cell morphology</u>	39.07% (59/151)	22.41% (675/3012)	Explain!	0.00108862
<u>abnormal cellular physical quality phenotype during vegetative growth</u>	52.98% (80/151)	34.96% (1053/3012)	Explain!	0.001393
<u>abnormal cell shape</u>	37.09% (56/151)	21.08% (635/3012)	Explain!	0.00146361
<u>abnormal cellular physical quality phenotype</u>	60.26% (91/151)	42.43% (1278/3012)	Explain!	0.00187901
<u>abnormal vegetative cell morphology</u>	28.48% (43/151)	15.07% (454/3012)	Explain!	0.00437397
<u>abnormal cell size</u>	27.81% (42/151)	15.04% (453/3012)	Explain!	0.00649623
<u>abnormal vegetative cell shape</u>	26.49% (40/151)	14.18% (427/3012)	Explain!	0.00743953

<u>abnormal vegetative cell population growth</u>	78.81% (119/151)	64.08% (1930/3012)	Explain!	0.0138158
<u>increased RNA level</u>	16.56% (25/151)	7.40% (223/3012)	Explain!	0.0141152
<u>increased cell length</u>	25.83% (39/151)	14.08% (424/3012)	Explain!	0.0153267
<u>gene expression phenotype</u>	28.48% (43/151)	16.24% (489/3012)	Explain!	0.0156214
<u>abnormal cell population growth</u>	78.81% (119/151)	64.44% (1941/3012)	Explain!	0.0173581
<u>increased sensitivity to chemical during vegetative growth</u>	65.56% (99/151)	50.10% (1509/3012)	Explain!	0.0173581
<u>increased sensitivity to chemical</u>	65.56% (99/151)	50.17% (1511/3012)	Explain!	0.0173581
<u>normal cell morphology</u>	80.79% (122/151)	90.80% (2735/3012)	Explain!	0.0174561
<u>normal vegetative cell morphology</u>	80.79% (122/151)	90.80% (2735/3012)	Explain!	0.0174561
<u>increased RNA level during vegetative growth</u>	15.89% (24/151)	7.17% (216/3012)	Explain!	0.0200397
<u>elongated vegetative cell</u>	20.53% (31/151)	10.52% (317/3012)	Explain!	0.0242883
<u>abnormal mitochondrion</u>	3.97% (6/151)	0.63% (19/3012)	Explain!	0.0292466
<u>altered level of substance in cell</u>	27.81% (42/151)	16.37% (493/3012)	Explain!	0.0320673
<u>altered level of substance in cell during vegetative growth</u>	26.49% (40/151)	15.27% (460/3012)	Explain!	0.0320673
<u>altered RNA level during vegetative growth</u>	18.54% (28/151)	9.33% (281/3012)	Explain!	0.0320673
<u>elongated cell</u>	22.52% (34/151)	12.25% (369/3012)	Explain!	0.0340205
<u>increased level of substance in cell</u>	21.19% (32/151)	11.29% (340/3012)	Explain!	0.0340205
<u>inviable cell</u>	19.21% (29/151)	9.73% (293/3012)	Explain!	0.0367082
<u>altered RNA level</u>	19.21% (29/151)	9.99% (301/3012)	Explain!	0.0448616

<u>increased level of substance in cell during vegetative growth</u>	19.87% (30/151)	10.69% (322/3012)	Explain!	0.0606887
<u>cell population growth phenotype</u>	80.13% (121/151)	67.70% (2039/3012)	Explain!	0.0624844
<u>vegetative cell population growth phenotype</u>	80.13% (121/151)	67.63% (2037/3012)	Explain!	0.0624844
<u>abolished protein localization to chromatin during vegetative growth</u>	2.65% (4/151)	0.30% (9/3012)	Explain!	0.0624844
<u>increased cell population growth rate</u>	1.32% (2/151)	7.64% (230/3012)	Explain!	0.0744508
<u>decreased cell population growth on galactose carbon source</u>	12.58% (19/151)	5.68% (171/3012)	Explain!	0.07555
<u>normal RNA level oscillation during mitotic cell cycle</u>	1.99% (3/151)	0.17% (5/3012)	Explain!	0.0992461
<u>altered level of substance in mitochondrion</u>	1.99% (3/151)	0.17% (5/3012)	Explain!	0.0992461

Phenotypic Profiles	List frequency / Value	Background frequency / Value	Details	p- value
<u>Slowly proliferating mutants</u>	17.88% (27/151)	6.21% (187/3012)	Explain!	0.000183716

Protein Domains (Pfam)	List frequency / Value	Background frequency / Value	Details	p- value
<u>Voltage-dependent anion channel</u>	1.99% (3/151)	0.17% (5/3012)	Explain!	0.0992461

Protein Features	List frequency / Value	Background frequency / Value	Details	p- value
<u>Arginine</u>	0.0578795	0.0487965	Explain!	0.00146361
<u>Protein copies per proliferating cell</u>	31596	13684.6	Explain!	0.00147236

Isoelectric point (predicted pH)	8.10106	7.31765	<div>Explain!</div>	0.00292079
Nitrogen content	1.39043	1.35942	<div>Explain!</div>	0.0102
Charge	6.69536	2.39287	<div>Explain!</div>	0.0320673

Transcript Features	List frequency / Value	Background frequency / Value	Details	p- value
mRNA level (WT)	4020.91	2387.37	<div>Explain!</div>	0.000221101
mRNA copies per proliferating cell	18.5993	5.82368	<div>Explain!</div>	0.000412101

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 **0.10**.

Bähler Lab, University College London, 2015.