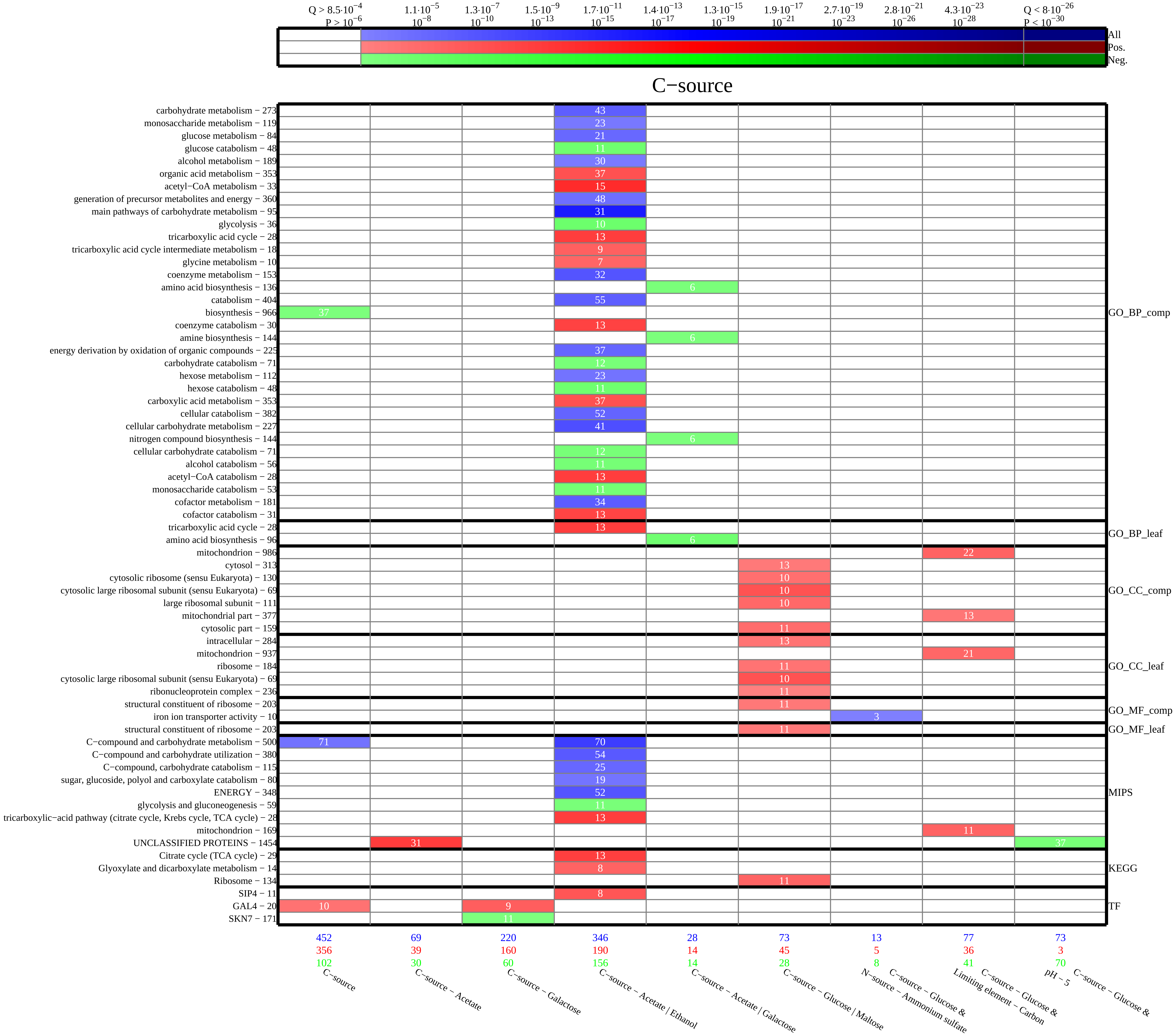
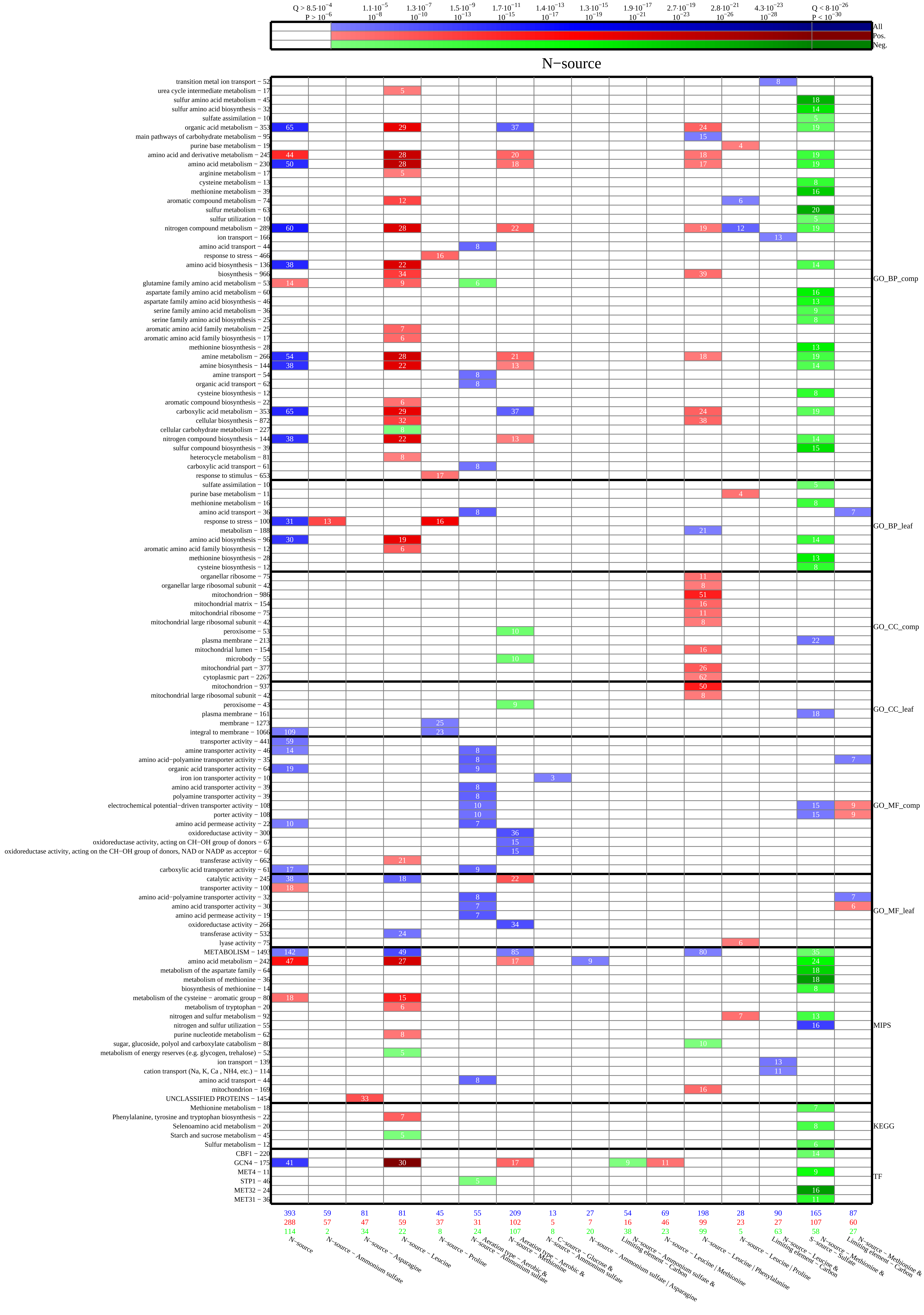
Aeration type

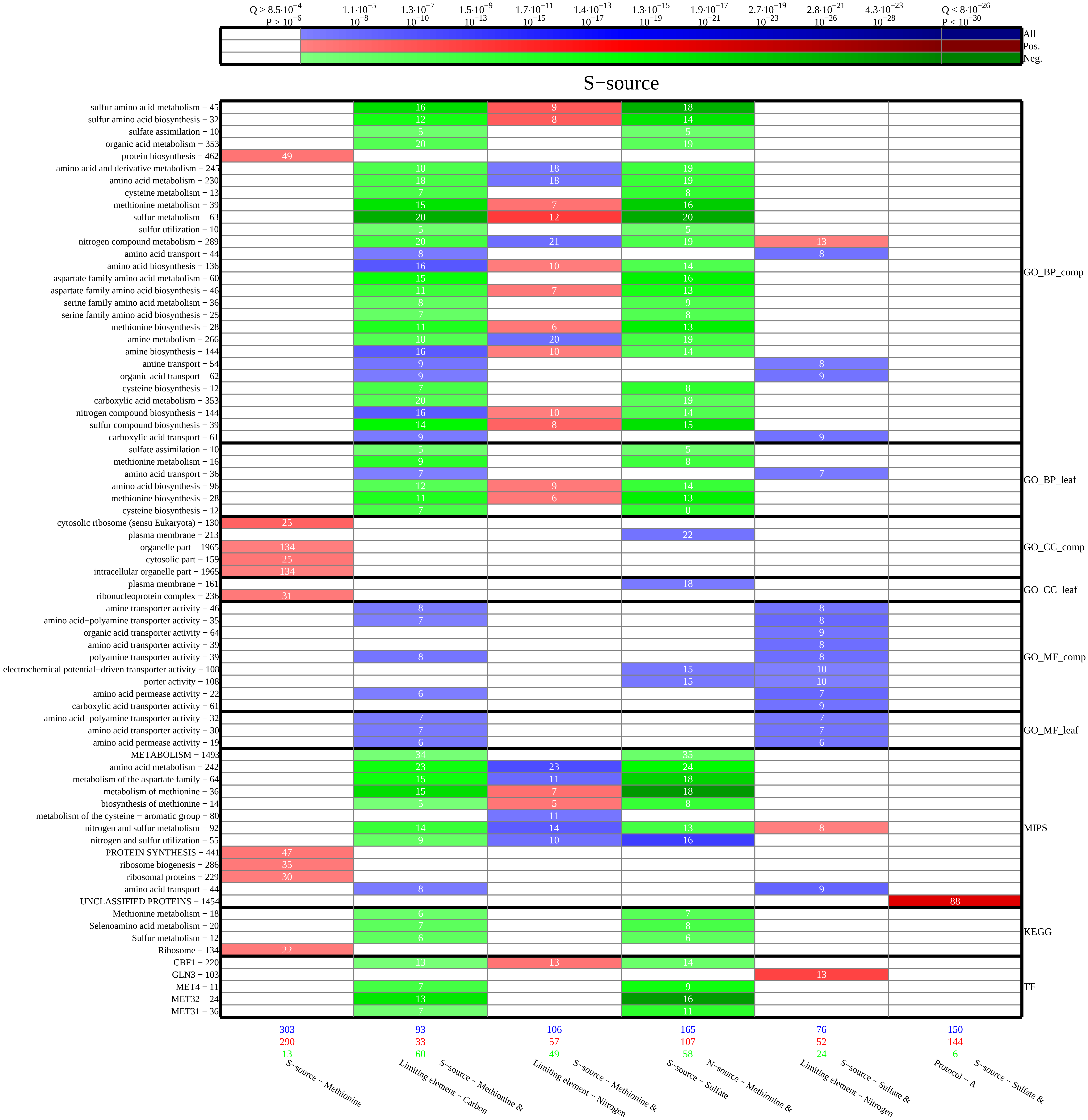
	Aeration type − Aerobic	Aeration type − Aerobic & N−source − Ammonium sulfate	Aeration type − Aerobic & N−source − Methionine	Aeration type − Aerobic & Limiting element − Carbon	Aeration type − Aerobic & Limiting element − Nitrogen	Aeration type − Aerobic & Limiting element − Zinc	Aeration type − Aerobic & pH − 5	Aeration type − Aerobic & Extra compound − CO_2	Aeration type − Aerobic & Extra compound − none	Aeration type − Aerobic & Protocol − A	Aeration type − Anaerobic & Limiting element − Carbon	Aeration type − Anaerobic & Limiting element − Nitrogen	Aeration type − Anaerobic & Limiting element − Phosphorus	Aeration type − Anaerobic & Limiting element − Zinc	Aeration type − Anaerobic & Extra compound − none	
sulfur amino acid biosynthesis − 32													🟩 6			GO_BP_comp
telomere maintenance via recombination − 26									🟩 6							
carbohydrate metabolism − 273				🟥 44												
alcohol metabolism − 189				🟦 51												
organic acid metabolism − 353			🟦 37	🟥 49												
acetyl−CoA metabolism − 33	🟥 19			🟥 12												
generation of precursor metabolites and energy − 360	🟦 116										🟥 35					
main pathways of carbohydrate metabolism − 95				🟥 20												
tricarboxylic acid cycle − 28	🟥 16			🟥 11												
electron transport − 135	🟥 51										🟥 24					
oxidative phosphorylation − 66	🟥 36										🟥 23					
mitochondrial electron transport, ubiquinol to cytochrome c − 15											🟥 8					
mitotic recombination − 37									🟩 6							
amino acid and derivative metabolism − 245			🟥 20													
amino acid metabolism − 230			🟥 18													
cysteine metabolism − 13													🟩 5			
fatty acid metabolism − 54				🟥 20												
coenzyme metabolism − 153	🟥 50			🟦 44												
vitamin metabolism − 75				🟥 21												
water−soluble vitamin metabolism − 75				🟥 21												
phosphorus metabolism − 263											🟥 26					
phosphate metabolism − 263											🟥 26					
nitrogen compound metabolism − 289			🟥 22													
amino acid transport − 44		🟦 8														
aerobic respiration − 103	🟥 45										🟥 18					
glutamine family amino acid metabolism − 53		🟩 6														
coenzyme catabolism − 30	🟥 18			🟥 11												
purine nucleoside triphosphate metabolism − 41											🟥 9					
purine nucleoside triphosphate biosynthesis − 41											🟥 9					
ribonucleoside triphosphate metabolism − 42											🟥 9					
ribonucleoside triphosphate biosynthesis − 42											🟥 9					
purine ribonucleoside triphosphate metabolism − 41											🟥 9					
purine ribonucleoside triphosphate biosynthesis − 41											🟥 9					
amine metabolism − 266			🟥 21													
amine biosynthesis − 144			🟥 13													
amine transport − 54		🟦 8														
organic acid transport − 62		🟦 8														
energy derivation by oxidation of organic compounds − 225	🟦 69										🟥 22					
phosphorylation − 215	🟥 58										🟥 25					
cysteine biosynthesis − 12													🟩 5			
carboxylic acid metabolism − 353			🟦 37	🟥 49												
ATP synthesis coupled electron transport − 30	🟥 21										🟥 17					
ATP synthesis coupled electron transport (sensu Eukaryota) − 30	🟥 21										🟥 17					
cellular lipid metabolism − 223				🟦 57												
cellular carbohydrate metabolism − 227				🟥 38												
nitrogen compound biosynthesis − 144			🟥 13													
sulfur compound biosynthesis − 39													🟩 7			
cellular respiration − 107	🟥 45										🟥 19					
acetyl−CoA catabolism − 28	🟥 16			🟥 11												
carboxylic acid transport − 61		🟦 8														
regulation of biological process − 894					🟥 77											
regulation of physiological process − 864					🟥 73											
regulation of cellular process − 858					🟥 72											
cofactor metabolism − 181	🟥 59			🟦 49												
cofactor catabolism − 31	🟥 19															
regulation of cellular physiological process − 852					🟥 72											
telomere maintenance via recombination − 26									🟩 6							GO_BP_leaf
tricarboxylic acid cycle − 28	🟥 16			🟥 11												
electron transport − 132	🟥 48										🟥 22					
mitochondrial electron transport, ubiquinol to cytochrome c − 15											🟥 8					
transport − 664											🟥 39					
amino acid transport − 36		🟦 8														
response to stress − 100	🟩 19			🟥 24									🟥 12	🟥 19		
metabolism − 188				🟥 30												
aerobic respiration − 75	🟥 29										🟥 16					
cysteine biosynthesis − 12													🟩 5			
organellar ribosome − 75						🟥 18						🟦 11				GO_CC_comp
organellar small ribosomal subunit − 31						🟥 9										
organellar large ribosomal subunit − 42												🟦 8				
cell wall − 128	🟩 15															
cytoplasm − 3266	🟥 557															
mitochondrion − 986	🟥 262										🟥 66					
mitochondrial envelope − 235	🟥 81										🟥 37					
mitochondrial inner membrane − 170	🟥 67										🟥 35					
mitochondrial electron transport chain − 34	🟥 24										🟥 20					
respiratory chain complex III (sensu Eukaryota) − 16											🟥 9					
respiratory chain complex IV (sensu Eukaryota) − 11											🟥 9					
proton−transporting ATP synthase complex (sensu Eukaryota) − 19	🟥 14															
mitochondrial matrix − 154						🟥 20										
mitochondrial ribosome − 75						🟥 18						🟦 11				
mitochondrial large ribosomal subunit − 42												🟦 8				
mitochondrial small ribosomal subunit − 31						🟥 9										
peroxisome − 53			🟩 10	🟥 22												
membrane − 1608	🟦 348							🟥 26								
integral to membrane − 1148	🟩 62															
hydrogen−translocating V−type ATPase complex − 16				🟩 9												
organelle inner membrane − 176	🟥 67										🟥 35					
external encapsulating structure − 131	🟩 15															
organelle membrane − 558	🟥 121										🟥 38					
intrinsic to membrane − 1150	🟩 62															
mitochondrial membrane − 202	🟥 73										🟥 36					
organelle envelope − 336	🟥 87										🟥 38					
envelope − 339	🟥 88										🟥 38					
mitochondrial lumen − 154						🟥 20										
microbody − 55			🟩 10	🟥 23												
membrane−bound organelle − 3409	🟥 559															
intracellular membrane−bound organelle − 3409	🟥 559															
membrane part − 1312	🟩 65										🟦 97					
mitochondrial part − 377	🟥 122					🟥 32					🟥 46					
cytoplasmic part − 2267	🟥 400															
mitochondrial membrane part − 87	🟥 40										🟥 28					
hydrogen−translocating F−type ATPase complex − 19	🟥 14															
proton−transporting ATP synthase complex − 20	🟥 14															
respiratory chain complex III − 16											🟥 9					
respiratory chain complex IV − 11											🟥 9					
ubiquinol−cytochrome−c reductase complex − 16											🟥 9					
mitochondrion − 937	🟥 251										🟥 66					GO_CC_leaf
mitochondrial electron transport chain − 20											🟥 10					
respiratory chain complex III (sensu Eukaryota) − 16											🟥 9					
respiratory chain complex IV (sensu Eukaryota) − 11											🟥 9					
mitochondrial large ribosomal subunit − 42												🟦 8				
mitochondrial small ribosomal subunit − 31						🟥 9										
peroxisome − 43			🟩 9	🟥 19												
endoplasmic reticulum − 333	🟩 25															
membrane − 1273	🟩 70							🟦 40								
integral to membrane − 1066	🟩 62															
DNA helicase activity − 42									🟩 6							GO_MF_comp
cytochrome−c oxidase activity − 12											🟥 9					
transporter activity − 441											🟥 41					
amine transporter activity − 46		🟦 8														
amino acid−polyamine transporter activity − 35		🟦 8														
organic acid transporter activity − 64		🟦 9														
ATP−dependent helicase activity − 74									🟩 6							
ubiquinol−cytochrome−c reductase activity − 15											🟥 8					
cation transporter activity − 141	🟥 44										🟥 26					
heme−copper terminal oxidase activity − 12											🟥 9					
ion transporter activity − 166	🟥 48										🟥 27					
monovalent inorganic cation transporter activity − 70	🟥 32										🟥 23					
hydrogen ion transporter activity − 67	🟥 31										🟥 23					
amino acid transporter activity − 39		🟦 8														
polyamine transporter activity − 39		🟦 8														
electrochemical potential−driven transporter activity − 108		🟦 10														
porter activity − 108		🟦 10														
amino acid permease activity − 22		🟦 7														
oxidoreductase activity − 300	🟦 106		🟦 36								🟥 33					
oxidoreductase activity, acting on CH−OH group of donors − 67			🟦 15													
oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP as acceptor − 60			🟦 15													
oxidoreductase activity, acting on heme group of donors − 12											🟥 9					
oxidoreductase activity, acting on heme group of donors, oxygen as acceptor − 12											🟥 9					
oxidoreductase activity, acting on diphenols and related substances as donors − 15											🟥 8					
oxidoreductase activity, acting on diphenols and related substances as donors, cytochrome as acceptor − 15											🟥 8					
carboxylic acid transporter activity − 61		🟦 9														
DNA helicase activity − 30									🟩 6							GO_MF_leaf
catalytic activity − 245			🟥 22													
cytochrome−c oxidase activity − 12											🟥 9					
amino acid−polyamine transporter activity − 32		🟦 8														
ATP−dependent helicase activity − 59									🟩 6							
ubiquinol−cytochrome−c reductase activity − 15											🟥 8					
amino acid transporter activity − 30		🟦 7														
amino acid permease activity − 19		🟦 7														
oxidoreductase activity − 266	🟦 93		🟦 34								🟥 30					
METABOLISM − 1493			🟦 85	🟦 265												MIPS
amino acid metabolism − 242			🟥 17													
C−compound and carbohydrate metabolism − 500				🟦 107												
C−compound and carbohydrate utilization − 380				🟦 92												
sugar, glucoside, polyol and carboxylate anabolism − 33				🟦 16												
tetracyclic and pentacyclic triterpenes (cholesterin, steroids and hopanoids) biosynthesis − 36							🟩 5									
fatty acid degradation (alpha− and beta−oxidation) − 10				🟥 9												
ENERGY − 348	🟥 111			🟥 51							🟥 36					
tricarboxylic−acid pathway (citrate cycle, Krebs cycle, TCA cycle) − 28	🟥 18															
electron transport and membrane−associated energy conservation − 54	🟥 40										🟥 24					
respiration − 129	🟥 62										🟥 28					
aerobic respiration − 73	🟥 36										🟥 20					
energy conversion and regeneration − 40	🟥 19															
energy generation (e.g. ATP synthase) − 18	🟥 15															
transported compounds (substrates) − 570											🟥 41					
amino acid transport − 44		🟦 8														
electron / hydrogen transport − 75	🟥 38										🟥 18					
transport facilitation − 187				🟦 49												
INTERACTION WITH THE CELLULAR ENVIRONMENT − 457				🟩 60												
ionic homeostasis − 178	🟥 50															
homeostasis of cations − 158	🟥 47															
pheromone response, mating−type determination, sex−specific proteins − 188				🟩 33												
mitochondrion − 169						🟥 24				🟥 16						
peroxisome − 35	🟥 19															
Citrate cycle (TCA cycle) − 29	🟥 17															KEGG
Oxidative phosphorylation − 63	🟥 36										🟥 25					
HAP4 − 54	🟥 30										🟥 20					TF
GCN4 − 175			🟥 17													
SUM1 − 55															🟥 10	
STP1 − 46		🟩 5														
STE12 − 234				🟩 41												
MCM1 − 78				🟩 23												
HAP1 − 115	🟥 50															
	1003	55	209	788	326	296	35	86	36	212	279	113	113	234	187	
	853	31	102	366	255	177	7	39	9	133	155	36	51	147	129	
	150	24	107	422	71	119	28	47	27	79	124	77	62	87	58	



C−source

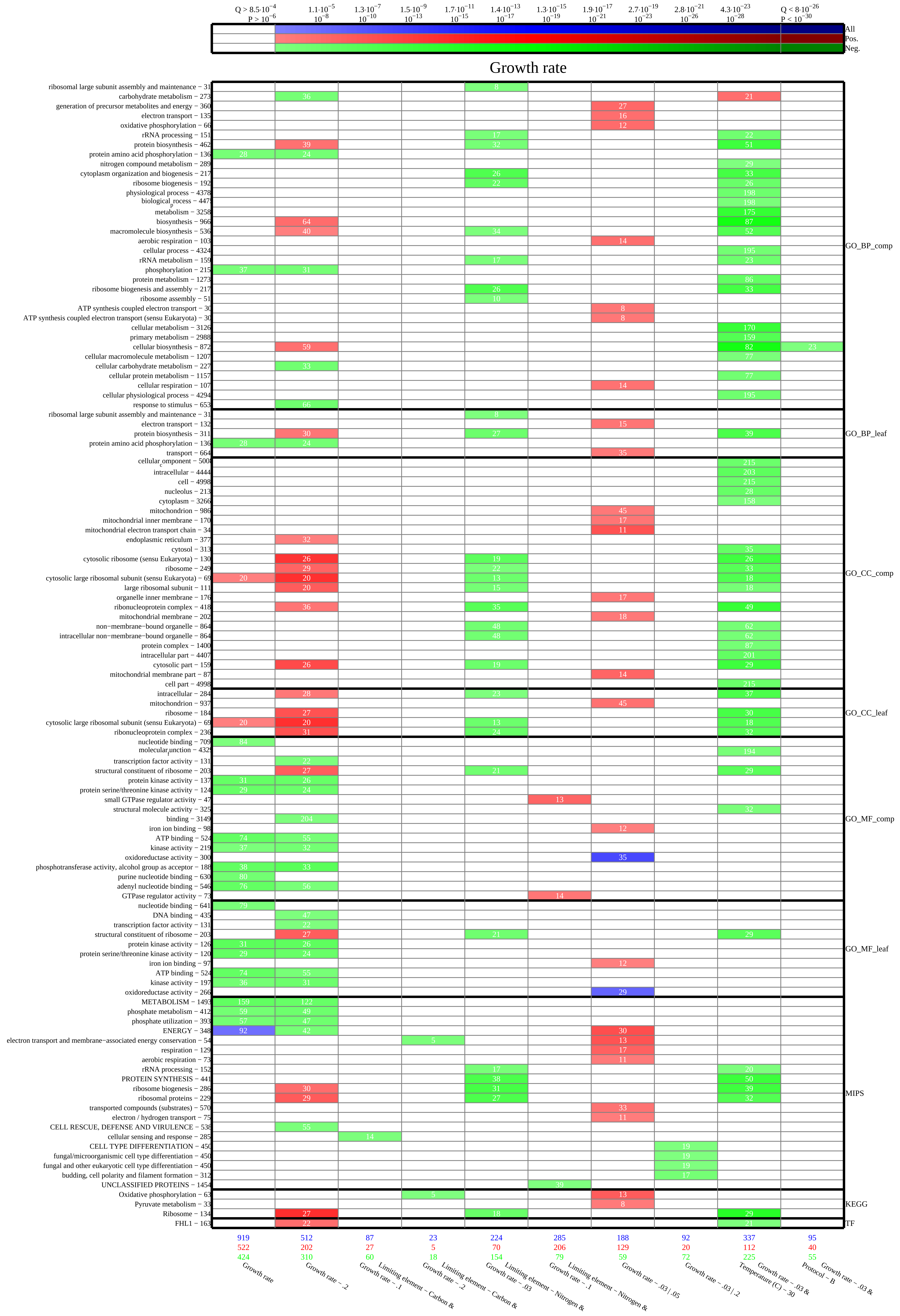
		C−source	C−source − Acetate	C−source − Galactose	C−source − Acetate | Ethanol	C−source − Acetate | Galactose	C−source − Glucose | Maltose	C−source − Glucose & N−source − Ammonium sulfate	C−source − Glucose & Limiting element − Carbon	C−source − Glucose & pH − 5
carbohydrate metabolism − 273	GO_BP_comp				🟦 43					
monosaccharide metabolism − 119	GO_BP_comp				🟦 23					
glucose metabolism − 84	GO_BP_comp				🟦 21					
glucose catabolism − 48	GO_BP_comp				🟩 11					
alcohol metabolism − 189	GO_BP_comp				🟦 30					
organic acid metabolism − 353	GO_BP_comp				🟥 37					
acetyl−CoA metabolism − 33	GO_BP_comp				🟥 15					
generation of precursor metabolites and energy − 360	GO_BP_comp				🟦 48					
main pathways of carbohydrate metabolism − 95	GO_BP_comp				🟦 31					
glycolysis − 36	GO_BP_comp				🟩 10					
tricarboxylic acid cycle − 28	GO_BP_comp				🟥 13					
tricarboxylic acid cycle intermediate metabolism − 18	GO_BP_comp				🟥 9					
glycine metabolism − 10	GO_BP_comp				🟥 7					
coenzyme metabolism − 153	GO_BP_comp				🟦 32					
amino acid biosynthesis − 136	GO_BP_comp					🟩 6				
catabolism − 404	GO_BP_comp				🟦 55					
biosynthesis − 966	GO_BP_comp	🟩 37								
coenzyme catabolism − 30	GO_BP_comp				🟥 13					
amine biosynthesis − 144	GO_BP_comp					🟩 6				
energy derivation by oxidation of organic compounds − 225	GO_BP_comp				🟦 37					
carbohydrate catabolism − 71	GO_BP_comp				🟩 12					
hexose metabolism − 112	GO_BP_comp				🟦 23					
hexose catabolism − 48	GO_BP_comp				🟩 11					
carboxylic acid metabolism − 353	GO_BP_comp				🟥 37					
cellular catabolism − 382	GO_BP_comp				🟦 52					
cellular carbohydrate metabolism − 227	GO_BP_comp				🟦 41					
nitrogen compound biosynthesis − 144	GO_BP_comp					🟩 6				
cellular carbohydrate catabolism − 71	GO_BP_comp				🟩 12					
alcohol catabolism − 56	GO_BP_comp				🟩 11					
acetyl−CoA catabolism − 28	GO_BP_comp				🟥 13					
monosaccharide catabolism − 53	GO_BP_comp				🟩 11					
cofactor metabolism − 181	GO_BP_comp				🟦 34					
cofactor catabolism − 31	GO_BP_comp				🟥 13					
tricarboxylic acid cycle − 28	GO_BP_leaf				🟥 13					
amino acid biosynthesis − 96	GO_BP_leaf					🟩 6				
mitochondrion − 986	GO_CC_comp								🟥 22	
cytosol − 313	GO_CC_comp						🟥 13			
cytosolic ribosome (sensu Eukaryota) − 130	GO_CC_comp						🟥 10			
cytosolic large ribosomal subunit (sensu Eukaryota) − 69	GO_CC_comp						🟥 10			
large ribosomal subunit − 111	GO_CC_comp						🟥 10			
mitochondrial part − 377	GO_CC_comp								🟥 13	
cytosolic part − 159	GO_CC_comp						🟥 11			
intracellular − 284	GO_CC_leaf						🟥 13			
mitochondrion − 937	GO_CC_leaf								🟥 21	
ribosome − 184	GO_CC_leaf						🟥 11			
cytosolic large ribosomal subunit (sensu Eukaryota) − 69	GO_CC_leaf						🟥 10			
ribonucleoprotein complex − 236	GO_CC_leaf						🟥 11			
structural constituent of ribosome − 203	GO_MF_comp						🟥 11			
iron ion transporter activity − 10	GO_MF_comp							🟦 3		
structural constituent of ribosome − 203	GO_MF_leaf						🟥 11			
C−compound and carbohydrate metabolism − 500	MIPS	🟦 71			🟦 70					
C−compound and carbohydrate utilization − 380	MIPS				🟦 54					
C−compound, carbohydrate catabolism − 115	MIPS				🟦 25					
sugar, glucoside, polyol and carboxylate catabolism − 80	MIPS				🟦 19					
ENERGY − 348	MIPS				🟦 52					
glycolysis and gluconeogenesis − 59	MIPS				🟩 11					
tricarboxylic−acid pathway (citrate cycle, Krebs cycle, TCA cycle) − 28	MIPS				🟥 13					
mitochondrion − 169	MIPS								🟥 11	
UNCLASSIFIED PROTEINS − 1454	MIPS		🟥 31							🟩 37
Citrate cycle (TCA cycle) − 29	KEGG				🟥 13					
Glyoxylate and dicarboxylate metabolism − 14	KEGG				🟥 8					
Ribosome − 134	KEGG						🟥 11			
SIP4 − 11	TF				🟥 8					
GAL4 − 20	TF	🟥 10		🟥 9						
SKN7 − 171	TF			🟩 11						
		452	69	220	346	28	73	13	77	73
		356	39	160	190	14	45	5	36	3
		102	30	60	156	14	28	8	41	70


Q > 8.5·10^−4 P > 10^−6
1.1·10^−5 10^−8
1.3·10^−7 10^−10
1.5·10^−9 10^−13
1.7·10^−11 10^−15
1.4·10^−13 10^−17
1.3·10^−15 10^−19
1.9·10^−17 10^−21
2.7·10^−19 10^−23
2.8·10^−21 10^−26
4.3·10^−23 10^−28
Q < 8·10^−26 P < 10^−30
All
Pos.
Neg.
N−source
transition metal ion transport − 52
urea cycle intermediate metabolism − 17
sulfur amino acid metabolism − 45
sulfur amino acid biosynthesis − 32
sulfate assimilation − 10
organic acid metabolism − 353
main pathways of carbohydrate metabolism − 95
purine base metabolism − 19
amino acid and derivative metabolism − 245
amino acid metabolism − 230
arginine metabolism − 17
cysteine metabolism − 13
methionine metabolism − 39
aromatic compound metabolism − 74
sulfur metabolism − 63
sulfur utilization − 10
nitrogen compound metabolism − 289
ion transport − 166
amino acid transport − 44
response to stress − 466
amino acid biosynthesis − 136
biosynthesis − 966
glutamine family amino acid metabolism − 53
aspartate family amino acid metabolism − 60
aspartate family amino acid biosynthesis − 46
serine family amino acid metabolism − 36
serine family amino acid biosynthesis − 25
aromatic amino acid family metabolism − 25
aromatic amino acid family biosynthesis − 17
methionine biosynthesis − 28
amine metabolism − 266
amine biosynthesis − 144
amine transport − 54
organic acid transport − 62
cysteine biosynthesis − 12
aromatic compound biosynthesis − 22
carboxylic acid metabolism − 353
cellular biosynthesis − 872
cellular carbohydrate metabolism − 227
nitrogen compound biosynthesis − 144
sulfur compound biosynthesis − 39
heterocycle metabolism − 81
carboxylic acid transport − 61
response to stimulus − 653
GO_BP_comp
sulfate assimilation − 10
purine base metabolism − 11
methionine metabolism − 16
amino acid transport − 36
response to stress − 100
metabolism − 188
amino acid biosynthesis − 96
aromatic amino acid family biosynthesis − 12
methionine biosynthesis − 28
cysteine biosynthesis − 12
GO_BP_leaf
organellar ribosome − 75
organellar large ribosomal subunit − 42
mitochondrion − 986
mitochondrial matrix − 154
mitochondrial ribosome − 75
mitochondrial large ribosomal subunit − 42
peroxisome − 53
plasma membrane − 213
mitochondrial lumen − 154
microbody − 55
mitochondrial part − 377
cytoplasmic part − 2267
GO_CC_comp
mitochondrion − 937
mitochondrial large ribosomal subunit − 42
peroxisome − 43
plasma membrane − 161
membrane − 1273
integral to membrane − 1066
GO_CC_leaf
transporter activity − 441
amine transporter activity − 46
amino acid−polyamine transporter activity − 35
organic acid transporter activity − 64
iron ion transporter activity − 10
amino acid transporter activity − 39
polyamine transporter activity − 39
electrochemical potential−driven transporter activity − 108
porter activity − 108
amino acid permease activity − 22
oxidoreductase activity − 300
oxidoreductase activity, acting on CH−OH group of donors − 67
oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP as acceptor − 60
transferase activity − 662
carboxylic acid transporter activity − 61
GO_MF_comp
catalytic activity − 245
transporter activity − 100
amino acid−polyamine transporter activity − 32
amino acid transporter activity − 30
amino acid permease activity − 19
oxidoreductase activity − 266
transferase activity − 532
lyase activity − 75
GO_MF_leaf
METABOLISM − 1493
amino acid metabolism − 242
metabolism of the aspartate family − 64
metabolism of methionine − 36
biosynthesis of methionine − 14
metabolism of the cysteine − aromatic group − 80
metabolism of tryptophan − 20
nitrogen and sulfur metabolism − 92
nitrogen and sulfur utilization − 55
purine nucleotide metabolism − 62
sugar, glucoside, polyol and carboxylate catabolism − 80
metabolism of energy reserves (e.g. glycogen, trehalose) − 52
ion transport − 139
cation transport (Na, K, Ca , NH4, etc.) − 114
amino acid transport − 44
mitochondrion − 169
UNCLASSIFIED PROTEINS − 1454
MIPS
Methionine metabolism − 18
Phenylalanine, tyrosine and tryptophan biosynthesis − 22
Selenoamino acid metabolism − 20
Starch and sucrose metabolism − 45
Sulfur metabolism − 12
KEGG
CBF1 − 220
GCN4 − 175
MET4 − 11
STP1 − 46
MET32 − 24
MET31 − 36
TF
393 288 114
59 57 2
81 47 34
81 59 22
45 37 8
55 31 24
209 102 107
13 5 8
27 7 20
54 16 38
69 46 23
198 99 99
28 23 5
90 27 63
165 107 58
87 60 27
N−source
N−source − Ammonium sulfate
N−source − Asparagine
N−source − Leucine
N−source − Proline
Aeration type − Aerobic & N−source − Ammonium sulfate
Aeration type − Aerobic & N−source − Methionine
C−source − Glucose & N−source − Ammonium sulfate
N−source − Ammonium sulfate | Asparagine
N−source − Ammonium sulfate & Limiting element − Carbon
N−source − Leucine | Methionine
N−source − Leucine | Phenylalanine
N−source − Leucine | Proline
N−source − Leucine & Limiting element − Carbon
N−source − Methionine & S−source − Sulfate
N−source − Methionine & Limiting element − Carbon



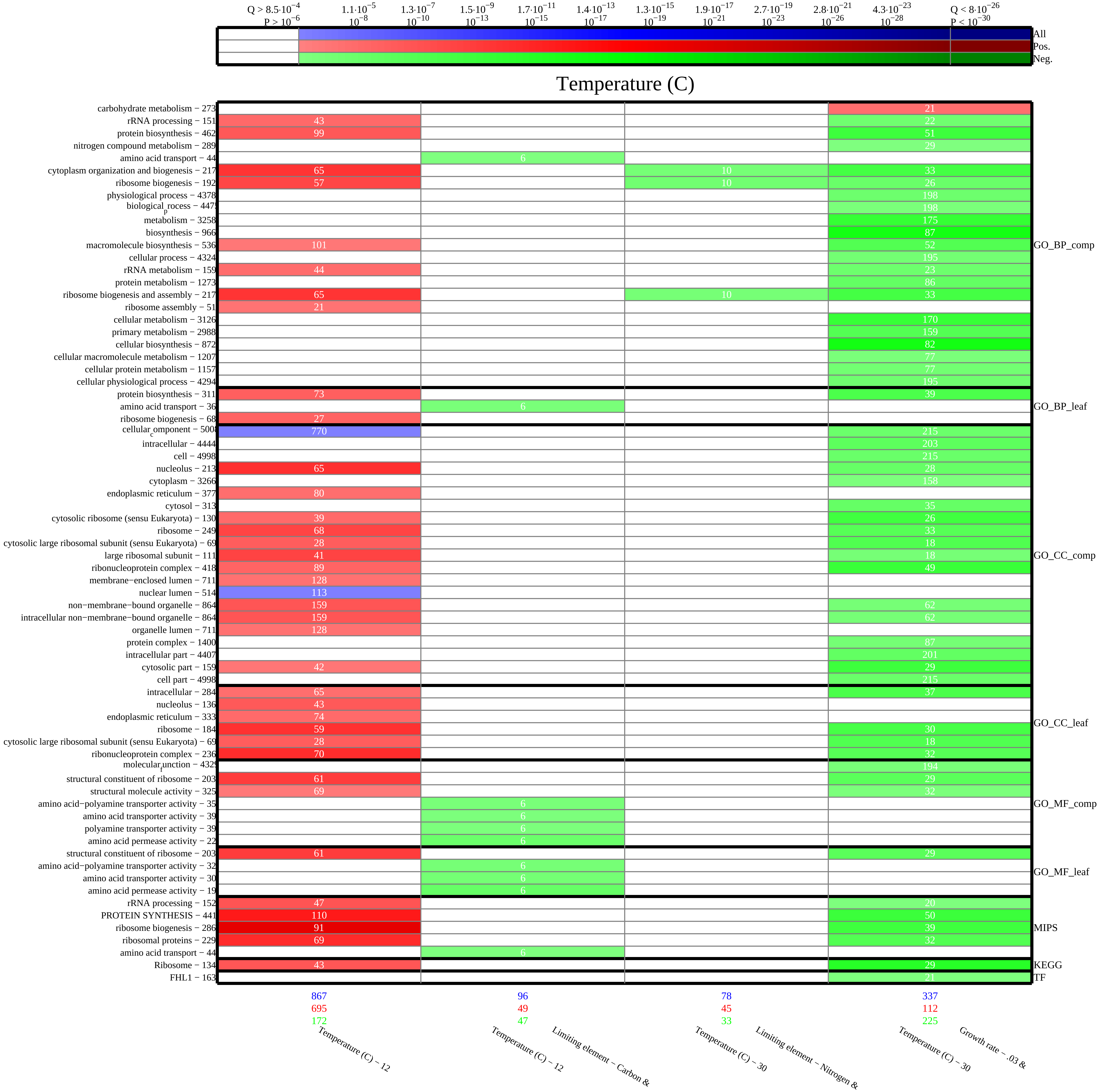
	S−source − Methionine	S−source − Methionine & Limiting element − Carbon	S−source − Methionine & Limiting element − Nitrogen	N−source − Methionine & S−source − Sulfate	S−source − Sulfate & Limiting element − Nitrogen	S−source − Sulfate & Protocol − A	
sulfur amino acid metabolism − 45		🟩 16	🟥 9	🟩 18			GO_BP_comp
sulfur amino acid biosynthesis − 32		🟩 12	🟥 8	🟩 14			
sulfate assimilation − 10		🟩 5		🟩 5			
organic acid metabolism − 353		🟩 20		🟩 19			
protein biosynthesis − 462	🟥 49						
amino acid and derivative metabolism − 245		🟩 18	🟦 18	🟩 19			
amino acid metabolism − 230		🟩 18	🟦 18	🟩 19			
cysteine metabolism − 13		🟩 7		🟩 8			
methionine metabolism − 39		🟩 15	🟥 7	🟩 16			
sulfur metabolism − 63		🟩 20	🟥 12	🟩 20			
sulfur utilization − 10		🟩 5		🟩 5			
nitrogen compound metabolism − 289		🟩 20	🟦 21	🟩 19	🟥 13		
amino acid transport − 44		🟦 8			🟦 8		
amino acid biosynthesis − 136		🟦 16	🟥 10	🟩 14			
aspartate family amino acid metabolism − 60		🟩 15		🟩 16			
aspartate family amino acid biosynthesis − 46		🟩 11	🟥 7	🟩 13			
serine family amino acid metabolism − 36		🟩 8		🟩 9			
serine family amino acid biosynthesis − 25		🟩 7		🟩 8			
methionine biosynthesis − 28		🟩 11	🟥 6	🟩 13			
amine metabolism − 266		🟩 18	🟦 20	🟩 19			
amine biosynthesis − 144		🟦 16	🟥 10	🟩 14			
amine transport − 54		🟦 9			🟦 8		
organic acid transport − 62		🟦 9			🟦 9		
cysteine biosynthesis − 12		🟩 7		🟩 8			
carboxylic acid metabolism − 353		🟩 20		🟩 19			
nitrogen compound biosynthesis − 144		🟦 16	🟥 10	🟩 14			
sulfur compound biosynthesis − 39		🟩 14	🟥 8	🟩 15			
carboxylic acid transport − 61		🟦 9			🟦 9		
sulfate assimilation − 10		🟩 5		🟩 5			GO_BP_leaf
methionine metabolism − 16		🟩 9		🟩 8			
amino acid transport − 36		🟦 7			🟦 7		
amino acid biosynthesis − 96		🟩 12	🟥 9	🟩 14			
methionine biosynthesis − 28		🟩 11	🟥 6	🟩 13			
cysteine biosynthesis − 12		🟩 7		🟩 8			
cytosolic ribosome (sensu Eukaryota) − 130	🟥 25						GO_CC_comp
plasma membrane − 213				🟦 22			
organelle part − 1965	🟥 134						
cytosolic part − 159	🟥 25						
intracellular organelle part − 1965	🟥 134						
plasma membrane − 161				🟦 18			GO_CC_leaf
ribonucleoprotein complex − 236	🟥 31						
amine transporter activity − 46		🟦 8			🟦 8		GO_MF_comp
amino acid−polyamine transporter activity − 35		🟦 7			🟦 8		
organic acid transporter activity − 64					🟦 9		
amino acid transporter activity − 39					🟦 8		
polyamine transporter activity − 39		🟦 8			🟦 8		
electrochemical potential−driven transporter activity − 108				🟦 15	🟦 10		
porter activity − 108				🟦 15	🟦 10		
amino acid permease activity − 22		🟦 6			🟦 7		
carboxylic acid transporter activity − 61					🟦 9		
amino acid−polyamine transporter activity − 32		🟦 7			🟦 7		GO_MF_leaf
amino acid transporter activity − 30		🟦 7			🟦 7		
amino acid permease activity − 19		🟦 6			🟦 6		
METABOLISM − 1493		🟩 34		🟩 35			MIPS
amino acid metabolism − 242		🟩 23	🟦 23	🟩 24			
metabolism of the aspartate family − 64		🟩 15	🟦 11	🟩 18			
metabolism of methionine − 36		🟩 15	🟥 7	🟩 18			
biosynthesis of methionine − 14		🟩 5	🟥 5	🟩 8			
metabolism of the cysteine − aromatic group − 80			🟦 11				
nitrogen and sulfur metabolism − 92		🟩 14	🟦 14	🟩 13	🟥 8		
nitrogen and sulfur utilization − 55		🟩 9	🟦 10	🟦 16			
PROTEIN SYNTHESIS − 441	🟥 47						
ribosome biogenesis − 286	🟥 35						
ribosomal proteins − 229	🟥 30						
amino acid transport − 44		🟦 8			🟦 9		
UNCLASSIFIED PROTEINS − 1454						🟥 88	
Methionine metabolism − 18		🟩 6		🟩 7			KEGG
Selenoamino acid metabolism − 20		🟩 7		🟩 8			
Sulfur metabolism − 12		🟩 6		🟩 6			
Ribosome − 134	🟥 22						
CBF1 − 220		🟩 13	🟥 13	🟩 14			TF
GLN3 − 103					🟥 13		
MET4 − 11		🟩 7		🟩 9			
MET32 − 24		🟩 13		🟩 16			
MET31 − 36		🟩 7		🟩 11			
	🟦 303	🟦 93	🟦 106	🟦 165	🟦 76	🟦 150	
	🟥 290	🟥 33	🟥 57	🟥 107	🟥 52	🟥 144	
	🟩 13	🟩 60	🟩 49	🟩 58	🟩 24	🟩 6	

Q > 8.5·10^−4 P > 10^−6
1.1·10^−5 10^−8
1.3·10^−7 10^−10
1.5·10^−9 10^−13
1.7·10^−11 10^−15
1.4·10^−13 10^−17
1.3·10^−15 10^−19
1.9·10^−17 10^−21
2.7·10^−19 10^−23
2.8·10^−21 10^−26
4.3·10^−23 10^−28
Q < 8·10^−26 P < 10^−30
All
Pos.
Neg.
Limiting element
ribosomal large subunit assembly and maintenance − 31
transition metal ion transport − 52
sulfur amino acid metabolism − 45
sulfur amino acid biosynthesis − 32
sulfate assimilation − 10
carbohydrate metabolism − 273
alcohol metabolism − 189
organic acid metabolism − 353
acetyl−CoA metabolism − 33
generation of precursor metabolites and energy − 360
main pathways of carbohydrate metabolism − 95
tricarboxylic acid cycle − 28
electron transport − 135
oxidative phosphorylation − 66
mitochondrial electron transport, ubiquinol to cytochrome c − 15
nucleobase, nucleoside, nucleotide and nucleic acid metabolism − 1505
rRNA processing − 151
protein biosynthesis − 462
ubiquitin−dependent protein catabolism − 132
ubiquitin cycle − 193
amino acid and derivative metabolism − 247
amino acid metabolism − 230
cysteine metabolism − 13
methionine metabolism − 39
fatty acid metabolism − 54
coenzyme metabolism − 153
vitamin metabolism − 75
water−soluble vitamin metabolism − 75
sulfur metabolism − 63
sulfur utilization − 10
phosphorus metabolism − 263
phosphate metabolism − 263
nitrogen compound metabolism − 289
ion transport − 166
cation transport − 139
iron ion transport − 27
amino acid transport − 44
organelle organization and biogenesis − 990
cytoplasm organization and biogenesis − 217
ribosome biogenesis − 192
amino acid biosynthesis − 136
biosynthesis − 966
macromolecule biosynthesis − 536
aerobic respiration − 103
aspartate family amino acid metabolism − 60
aspartate family amino acid biosynthesis − 46
serine family amino acid metabolism − 36
serine family amino acid biosynthesis − 25
methionine biosynthesis − 28
coenzyme catabolism − 30
nucleoside triphosphate metabolism − 44
nucleoside triphosphate biosynthesis − 43
purine nucleoside triphosphate metabolism − 41
purine nucleoside triphosphate biosynthesis − 41
ribonucleoside triphosphate metabolism − 42
ribonucleoside triphosphate biosynthesis − 42
purine ribonucleoside triphosphate metabolism − 41
purine ribonucleoside triphosphate biosynthesis − 41
amine metabolism − 266
amine biosynthesis − 144
di−, tri−valent inorganic cation transport − 62
amine transport − 54
organic acid transport − 62
energy derivation by oxidation of organic compounds − 225
rRNA metabolism − 159
phosphorylation − 215
cysteine biosynthesis − 12
carboxylic acid metabolism − 353
modification−dependent protein catabolism − 132
metal ion transport − 76
protein catabolism − 154
ribosome biogenesis and assembly − 217
ribosome assembly − 51
ATP synthesis coupled electron transport − 30
ATP synthesis coupled electron transport (sensu Eukaryota) − 30
modification−dependent macromolecule catabolism − 132
cellular biosynthesis − 872
cellular lipid metabolism − 223
cellular protein catabolism − 142
cellular carbohydrate metabolism − 227
nitrogen compound biosynthesis − 144
sulfur compound biosynthesis − 39
cellular respiration − 107
acetyl−CoA catabolism − 28
carboxylic acid transport − 61
regulation of biological process − 894
regulation of physiological process − 864
regulation of cellular process − 858
cofactor metabolism − 181
regulation of cellular physiological process − 852
proteolysis during cellular protein catabolism − 134
GO_BP_comp
ribosomal large subunit assembly and maintenance − 31
sulfate assimilation − 10
tricarboxylic acid cycle − 28
electron transport − 132
mitochondrial electron transport, ubiquinol to cytochrome c − 15
protein biosynthesis − 311
methionine metabolism − 16
transport − 664
iron ion transport − 23
amino acid transport − 36
response to stress − 100
metabolism − 188
amino acid biosynthesis − 96
aerobic respiration − 75
methionine biosynthesis − 28
cysteine biosynthesis − 12
GO_BP_leaf
organellar ribosome − 75
organellar small ribosomal subunit − 31
organellar large ribosomal subunit − 42
nucleus − 1842
nucleoplasm − 333
cytoplasm − 3266
mitochondrion − 986
mitochondrial envelope − 235
mitochondrial inner membrane − 170
mitochondrial electron transport chain − 34
respiratory chain complex III (sensu Eukaryota) − 16
respiratory chain complex IV (sensu Eukaryota) − 11
proton−transporting ATP synthase complex (sensu Eukaryota) − 19
mitochondrial matrix − 154
mitochondrial ribosome − 75
mitochondrial large ribosomal subunit − 42
mitochondrial small ribosomal subunit − 31
peroxisome − 53
endoplasmic reticulum − 377
cytosolic ribosome (sensu Eukaryota) − 130
ribosome − 249
cytosolic large ribosomal subunit (sensu Eukaryota) − 69
large ribosomal subunit − 111
integral to membrane − 1148
hydrogen−translocating V−type ATPase complex − 16
organelle inner membrane − 176
ribonucleoprotein complex − 418
organelle membrane − 558
intrinsic to membrane − 1150
mitochondrial membrane − 202
organelle envelope − 336
envelope − 339
mitochondrial lumen − 154
nuclear lumen − 514
microbody − 55
non−membrane−bound organelle − 864
intracellular non−membrane−bound organelle − 864
intracellular part − 4407
membrane part − 1312
nuclear part − 876
mitochondrial part − 377
cytoplasmic part − 2267
cytosolic part − 159
nucleoplasm part − 313
mitochondrial membrane part − 87
hydrogen−translocating F−type ATPase complex − 19
proton−transporting ATP synthase complex − 20
respiratory chain complex III − 16
respiratory chain complex IV − 11
ubiquinol−cytochrome−c reductase complex − 16
GO_CC_comp
vacuole (sensu Fungi) − 284
intracellular − 284
nucleus − 1651
mitochondrion − 937
mitochondrial electron transport chain − 20
respiratory chain complex III (sensu Eukaryota) − 16
respiratory chain complex IV (sensu Eukaryota) − 11
mitochondrial large ribosomal subunit − 42
mitochondrial small ribosomal subunit − 31
peroxisome − 43
endoplasmic reticulum − 333
cytosolic large ribosomal subunit (sensu Eukaryota) − 69
integral to membrane − 1066
ribonucleoprotein complex − 236
protein complex − 51
GO_CC_leaf
molecular_function − 432
structural constituent of ribosome − 203
cytochrome−c oxidase activity − 12
small GTPase regulator activity − 47
transporter activity − 441
amine transporter activity − 46
amino acid−polyamine transporter activity − 35
organic acid transporter activity − 64
ubiquinol−cytochrome−c reductase activity − 15
cation transporter activity − 141
heme−copper terminal oxidase activity − 12
ion transporter activity − 166
monovalent inorganic cation transporter activity − 70
hydrogen ion transporter activity − 67
amino acid transporter activity − 39
polyamine transporter activity − 39
electrochemical potential−driven transporter activity − 108
porter activity − 108
amino acid permease activity − 22
oxidoreductase activity − 300
oxidoreductase activity, acting on heme group of donors − 12
oxidoreductase activity, acting on heme group of donors, oxygen as acceptor − 12
oxidoreductase activity, acting on diphenols and related substances as donors − 15
oxidoreductase activity, acting on diphenols and related substances as donors, cytochrome as acceptor − 15
GTPase regulator activity − 73
carboxylic acid transporter activity − 61
GO_MF_comp
structural constituent of ribosome − 203
cytochrome−c oxidase activity − 12
endopeptidase activity − 29
amino acid−polyamine transporter activity − 32
ubiquinol−cytochrome−c reductase activity − 15
amino acid transporter activity − 30
amino acid permease activity − 19
oxidoreductase activity − 266
GO_MF_leaf
METABOLISM − 1493
amino acid metabolism − 242
metabolism of the aspartate family − 64
metabolism of methionine − 36
biosynthesis of methionine − 14
metabolism of the cysteine − aromatic group − 80
nitrogen and sulfur metabolism − 92
nitrogen and sulfur utilization − 55
C−compound and carbohydrate metabolism − 500
C−compound and carbohydrate utilization − 380
sugar, glucoside, polyol and carboxylate anabolism − 33
fatty acid degradation (alpha− and beta−oxidation) − 10
ENERGY − 348
electron transport and membrane−associated energy conservation − 54
respiration − 129
aerobic respiration − 73
fermentation − 45
energy generation (e.g. ATP synthase) − 18
TRANSCRIPTION − 988
RNA synthesis − 593
rRNA processing − 152
PROTEIN SYNTHESIS − 441
ribosome biogenesis − 286
ribosomal proteins − 229
protein degradation − 253
cytoplasmic and nuclear protein degradation − 188
proteasomal degradation (ubiquitin/proteasomal pathway) − 129
transported compounds (substrates) − 570
ion transport − 139
cation transport (Na, K, Ca, NH4, etc.) − 114
heavy metal ion transport (Cu, Fe, etc.) − 51
amino acid transport − 44
electron / hydrogen transport − 75
transport facilitation − 187
INTERACTION WITH THE CELLULAR ENVIRONMENT − 457
homeostasis of metal ions (Na, K, Ca etc.) − 100
cellular sensing and response − 285
pheromone response, mating−type determination, sex−specific proteins − 188
mitochondrion − 169
UNCLASSIFIED PROTEINS − 1454
MIPS
Oxidative phosphorylation − 63
Methionine metabolism − 18
Selenoamino acid metabolism − 20
Glyoxylate and dicarboxylate metabolism − 14
Sulfur metabolism − 12
Ribosome − 134
KEGG
CBF1 − 220
GLN3 − 103
HAP4 − 54
GCN4 − 175
MET4 − 11
AFT2 − 114
RCS1 − 102
STE12 − 234
UME6 − 125
MCM1 − 78
MET32 − 24
MET31 − 36
TF
1296 244 219 168 583 788 326 296 279 113 113 234 77 93 54 90 106 87 76 149 87 23 96 182 262 127 145 224 285 78 274 253
965 209 192 139 313 366 255 177 155 36 51 147 36 33 16 27 57 60 52 102 27 5 49 42 110 73 92 70 206 45 185 162
399 35 27 29 270 422 71 119 124 77 62 87 41 60 38 63 49 27 24 47 60 18 47 140 152 54 53 154 79 33 89 91
Limiting element
Limiting element − Sulfur
Limiting element − Carbon
Limiting element − Iron
Limiting element − Zinc
Aeration type − Aerobic & Limiting element − Carbon
Aeration type − Aerobic & Limiting element − Nitrogen
Aeration type − Aerobic & Limiting element − Zinc
Aeration type − Anaerobic & Limiting element − Carbon
Aeration type − Anaerobic & Limiting element − Nitrogen
Aeration type − Anaerobic & Limiting element − Phosphorus
Aeration type − Anaerobic & Limiting element − Zinc
C−source − Glucose & Limiting element − Carbon
S−source − Methionine & Limiting element − Carbon
N−source − Ammonium sulfate & Limiting element − Carbon
N−source − Leucine & Limiting element − Carbon
S−source − Methionine & Limiting element − Nitrogen
N−source − Methionine & Limiting element − Carbon
S−source − Sulfate & Limiting element − Nitrogen
Limiting element − Carbon | Iron
Growth rate − .1 & Limiting element − Carbon
Growth rate − .2 & Limiting element − Carbon
Temperature (C) − 12 & Limiting element − Carbon
Protocol − B & Limiting element − Carbon
Protocol − A & Limiting element − Carbon
Limiting element − Iron | Zinc
Limiting element − Nitrogen | Zinc
Growth rate − .03 & Limiting element − Nitrogen
Growth rate − .1 & Limiting element − Nitrogen
Temperature (C) − 30 & Limiting element − Nitrogen
Limiting element − Phosphorus | Sulfur
Limiting element − Sulfur | Zinc



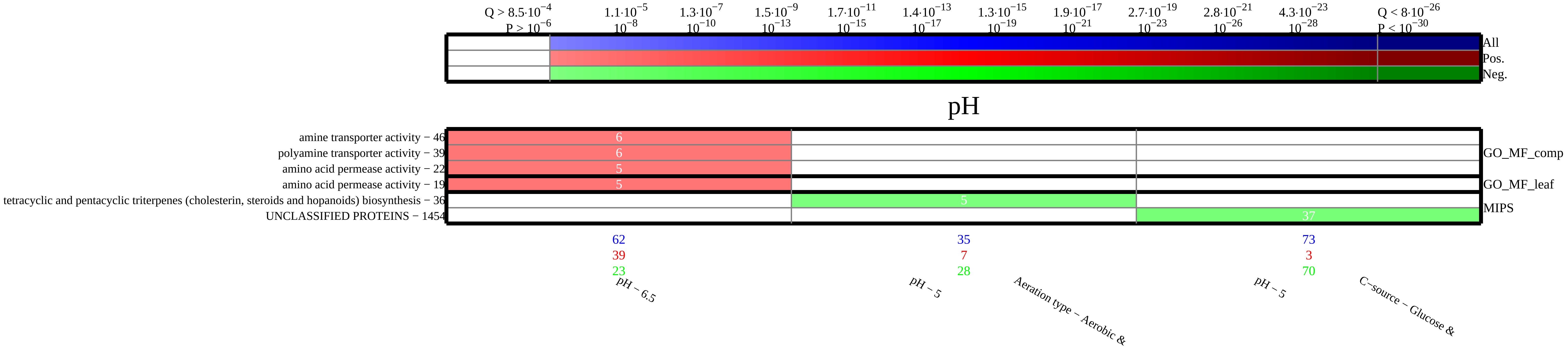
Growth rate

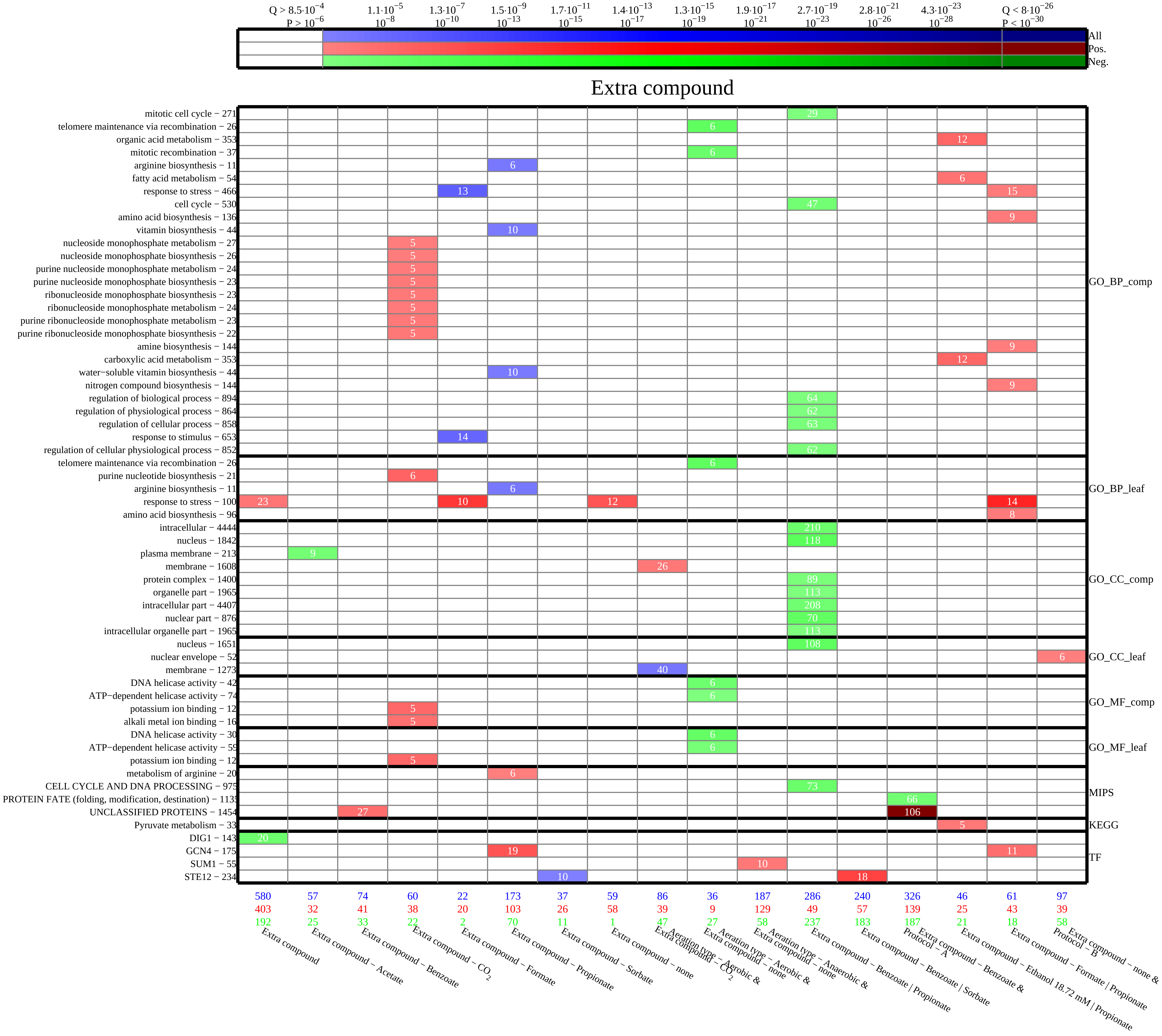
	Growth rate	Growth rate − .2	Limiting element − Carbon & Growth rate − .1	Limiting element − Carbon & Growth rate − .2	Limiting element − Nitrogen & Growth rate − .03	Limiting element − Nitrogen & Growth rate − .1	Growth rate − .03 | .05	Growth rate − .03 | .2	Growth rate − .03 & Temperature (C) − 30	Growth rate − .03 & Protocol − B	
ribosomal large subunit assembly and maintenance − 31					🟩 8						GO_BP_comp
carbohydrate metabolism − 273		🟩 36							🟥 21		
generation of precursor metabolites and energy − 360							🟥 27				
electron transport − 135							🟥 16				
oxidative phosphorylation − 66							🟥 12				
rRNA processing − 151					🟩 17				🟩 22		
protein biosynthesis − 462		🟥 39			🟩 32				🟩 51		
protein amino acid phosphorylation − 136	🟩 28	🟩 24									
nitrogen compound metabolism − 289									🟩 29		
cytoplasm organization and biogenesis − 217					🟩 26				🟩 33		
ribosome biogenesis − 192					🟩 22				🟩 26		
physiological process − 4378									🟩 198		
biological$_p$rocess − 4475									🟩 198		
metabolism − 3258									🟩 175		
biosynthesis − 966		🟥 64							🟩 87		
macromolecule biosynthesis − 536		🟥 40			🟩 34				🟩 52		
aerobic respiration − 103							🟥 14				
cellular process − 4324									🟩 195		
rRNA metabolism − 159					🟩 17				🟩 23		
phosphorylation − 215	🟩 37	🟩 31									
protein metabolism − 1273									🟩 86		
ribosome biogenesis and assembly − 217					🟩 26				🟩 33		
ribosome assembly − 51					🟩 10						
ATP synthesis coupled electron transport − 30							🟥 8				
ATP synthesis coupled electron transport (sensu Eukaryota) − 30							🟥 8				
cellular metabolism − 3126									🟩 170		
primary metabolism − 2988									🟩 159		
cellular biosynthesis − 872		🟥 59							🟩 82	🟩 23	
cellular macromolecule metabolism − 1207									🟩 77		
cellular carbohydrate metabolism − 227		🟩 33									
cellular protein metabolism − 1157									🟩 77		
cellular respiration − 107							🟥 14				
cellular physiological process − 4294									🟩 195		
response to stimulus − 653		🟩 66									
ribosomal large subunit assembly and maintenance − 31					🟩 8						GO_BP_leaf
electron transport − 132							🟥 15				
protein biosynthesis − 311		🟥 30			🟩 27				🟩 39		
protein amino acid phosphorylation − 136	🟩 28	🟩 24									
transport − 664							🟥 35				
cellular$_c$omponent − 5008									🟩 215		GO_CC_comp
intracellular − 4444									🟩 203		
cell − 4998									🟩 215		
nucleolus − 213									🟩 28		
cytoplasm − 3266									🟩 158		
mitochondrion − 986							🟥 45				
mitochondrial inner membrane − 170							🟥 17				
mitochondrial electron transport chain − 34							🟥 11				
endoplasmic reticulum − 377		🟥 32									
cytosol − 313									🟩 35		
cytosolic ribosome (sensu Eukaryota) − 130		🟥 26			🟩 19				🟩 26		
ribosome − 249		🟥 29			🟩 22				🟩 33		
cytosolic large ribosomal subunit (sensu Eukaryota) − 69	🟥 20	🟥 20			🟩 13				🟩 18		
large ribosomal subunit − 111		🟥 20			🟩 15				🟩 18		
organelle inner membrane − 176							🟥 17				
ribonucleoprotein complex − 418		🟥 36			🟩 35				🟩 49		
mitochondrial membrane − 202							🟥 18				
non−membrane−bound organelle − 864					🟩 48				🟩 62		
intracellular non−membrane−bound organelle − 864					🟩 48				🟩 62		
protein complex − 1400									🟩 87		
intracellular part − 4407									🟩 201		
cytosolic part − 159		🟥 26			🟩 19				🟩 29		
mitochondrial membrane part − 87							🟥 14				
cell part − 4998									🟩 215		
intracellular − 284		🟥 28			🟩 23				🟩 37		GO_CC_leaf
mitochondrion − 937							🟥 45				
ribosome − 184		🟥 27							🟩 30		
cytosolic large ribosomal subunit (sensu Eukaryota) − 69	🟥 20	🟥 20			🟩 13				🟩 18		
ribonucleoprotein complex − 236		🟥 31			🟩 24				🟩 32		
nucleotide binding − 709	🟩 84										GO_MF_comp
molecular$_f$unction − 4329									🟩 194		
transcription factor activity − 131		🟩 22									
structural constituent of ribosome − 203		🟥 27			🟩 21				🟩 29		
protein kinase activity − 137	🟩 31	🟩 26									
protein serine/threonine kinase activity − 124	🟩 29	🟩 24									
small GTPase regulator activity − 47						🟥 13					
structural molecule activity − 325									🟩 32		
binding − 3149		🟩 204									
iron ion binding − 98							🟥 12				
ATP binding − 524	🟩 74	🟩 55									
kinase activity − 219	🟩 37	🟩 32									
oxidoreductase activity − 300							🟦 35				
phosphotransferase activity, alcohol group as acceptor − 188	🟩 38	🟩 33									
purine nucleotide binding − 630	🟩 80										
adenyl nucleotide binding − 546	🟩 76	🟩 56									
GTPase regulator activity − 73						🟥 14					
nucleotide binding − 641	🟩 79										GO_MF_leaf
DNA binding − 435		🟩 47									
transcription factor activity − 131		🟩 22									
structural constituent of ribosome − 203		🟥 27			🟩 21				🟩 29		
protein kinase activity − 126	🟩 31	🟩 26									
protein serine/threonine kinase activity − 120	🟩 29	🟩 24									
iron ion binding − 97							🟥 12				
ATP binding − 524	🟩 74	🟩 55									
kinase activity − 197	🟩 36	🟩 31									
oxidoreductase activity − 266							🟦 29				
METABOLISM − 1493	🟩 159	🟩 122									MIPS
phosphate metabolism − 412	🟩 59	🟩 49									
phosphate utilization − 393	🟩 57	🟩 47									
ENERGY − 348	🟦 92	🟩 42					🟥 30				
electron transport and membrane−associated energy conservation − 54				🟩 5			🟥 13				
respiration − 129							🟥 17				
aerobic respiration − 73							🟥 11				
rRNA processing − 152					🟩 17				🟩 20		
PROTEIN SYNTHESIS − 441					🟩 38				🟩 50		
ribosome biogenesis − 286		🟥 30			🟩 31				🟩 39		
ribosomal proteins − 229		🟥 29			🟩 27				🟩 32		
transported compounds (substrates) − 570							🟥 33				
electron / hydrogen transport − 75							🟥 11				
CELL RESCUE, DEFENSE AND VIRULENCE − 538		🟩 55									
cellular sensing and response − 285			🟩 14								
CELL TYPE DIFFERENTIATION − 450								🟩 19			
fungal/microorganismic cell type differentiation − 450								🟩 19			
fungal and other eukaryotic cell type differentiation − 450								🟩 19			
budding, cell polarity and filament formation − 312								🟩 17			
UNCLASSIFIED PROTEINS − 1454						🟩 39					
Oxidative phosphorylation − 63				🟩 5			🟥 13				KEGG
Pyruvate metabolism − 33							🟥 8				
Ribosome − 134		🟥 27			🟩 18				🟩 29		
FHL1 − 163		🟥 22							🟩 21		TF
	919	512	87	23	224	285	188	92	337	95	
	522	202	27	5	70	206	129	20	112	40	
	424	310	60	18	154	79	59	72	225	55	



Temperature (C)

		Temperature (C) − 12	Temperature (C) − 12 Limiting element − Carbon &	Temperature (C) − 30 Limiting element − Nitrogen &	Temperature (C) − 30 Growth rate − .03 &
GO_BP_comp	carbohydrate metabolism − 273				21
	rRNA processing − 151	43			22
	protein biosynthesis − 462	99			51
	nitrogen compound metabolism − 289				29
	amino acid transport − 44		6		
	cytoplasm organization and biogenesis − 217	65		10	33
	ribosome biogenesis − 192	57		10	26
	physiological process − 4378				198
	biological_process − 447				198
	metabolism − 3258				175
	biosynthesis − 966				87
	macromolecule biosynthesis − 536	101			52
	cellular process − 4324				195
	rRNA metabolism − 159	44			23
	protein metabolism − 1273				86
	ribosome biogenesis and assembly − 217	65		10	33
	ribosome assembly − 51	21			
	cellular metabolism − 3126				170
	primary metabolism − 2988				159
	cellular biosynthesis − 872				82
	cellular macromolecule metabolism − 1207				77
	cellular protein metabolism − 1157				77
	cellular physiological process − 4294				195
GO_BP_leaf	protein biosynthesis − 311	73			39
	amino acid transport − 36		6		
	ribosome biogenesis − 68	27			
GO_CC_comp	cellular_component − 500	770			215
	intracellular − 4444				203
	cell − 4998				215
	nucleolus − 213	65			28
	cytoplasm − 3266				158
	endoplasmic reticulum − 377	80			
	cytosol − 313				35
	cytosolic ribosome (sensu Eukaryota) − 130	39			26
	ribosome − 249	68			33
	cytosolic large ribosomal subunit (sensu Eukaryota) − 69	28			18
	large ribosomal subunit − 111	41			18
	ribonucleoprotein complex − 418	89			49
	membrane−enclosed lumen − 711	128			
	nuclear lumen − 514	113			
	non−membrane−bound organelle − 864	159			62
	intracellular non−membrane−bound organelle − 864	159			62
	organelle lumen − 711	128			
	protein complex − 1400				87
	intracellular part − 4407				201
	cytosolic part − 159	42			29
	cell part − 4998				215
GO_CC_leaf	intracellular − 284	65			37
	nucleolus − 136	43			
	endoplasmic reticulum − 333	74			
	ribosome − 184	59			30
	cytosolic large ribosomal subunit (sensu Eukaryota) − 69	28			18
	ribonucleoprotein complex − 236	70			32
GO_MF_comp	molecular_function − 432				194
	structural constituent of ribosome − 203	61			29
	structural molecule activity − 325	69			32
	amino acid−polyamine transporter activity − 35		6		
	amino acid transporter activity − 39		6		
	polyamine transporter activity − 39		6		
	amino acid permease activity − 22		6		
GO_MF_leaf	structural constituent of ribosome − 203	61			29
	amino acid−polyamine transporter activity − 32		6		
	amino acid transporter activity − 30		6		
	amino acid permease activity − 19		6		
MIPS	rRNA processing − 152	47			20
	PROTEIN SYNTHESIS − 441	110			50
	ribosome biogenesis − 286	91			39
	ribosomal proteins − 229	69			32
	amino acid transport − 44		6		
KEGG	Ribosome − 134	43			29
TF	FHL1 − 163				21
		867	96	78	337
		695	49	45	112
		172	47	33	225


Q > 8.5·10^−4
P > 10^−6
1.1·10^−5
10^−8
1.3·10^−7
10^−10
1.5·10^−9
10^−13
1.7·10^−11
10^−15
1.4·10^−13
10^−17
1.3·10^−15
10^−19
1.9·10^−17
10^−21
2.7·10^−19
10^−23
2.8·10^−21
10^−26
4.3·10^−23
10^−28
Q < 8·10^−26
P < 10^−30
All
Pos.
Neg.
pH
amine transporter activity − 46
polyamine transporter activity − 39
amino acid permease activity − 22
amino acid permease activity − 19
tetracyclic and pentacyclic triterpenes (cholesterin, steroids and hopanoids) biosynthesis − 36
UNCLASSIFIED PROTEINS − 1454
6
6
5
5
5
37
GO_MF_comp
GO_MF_leaf
MIPS
62
39
23
35
7
28
73
3
70
pH − 6.5
pH − 5
Aeration type − Aerobic &
pH − 5
C−source − Glucose &

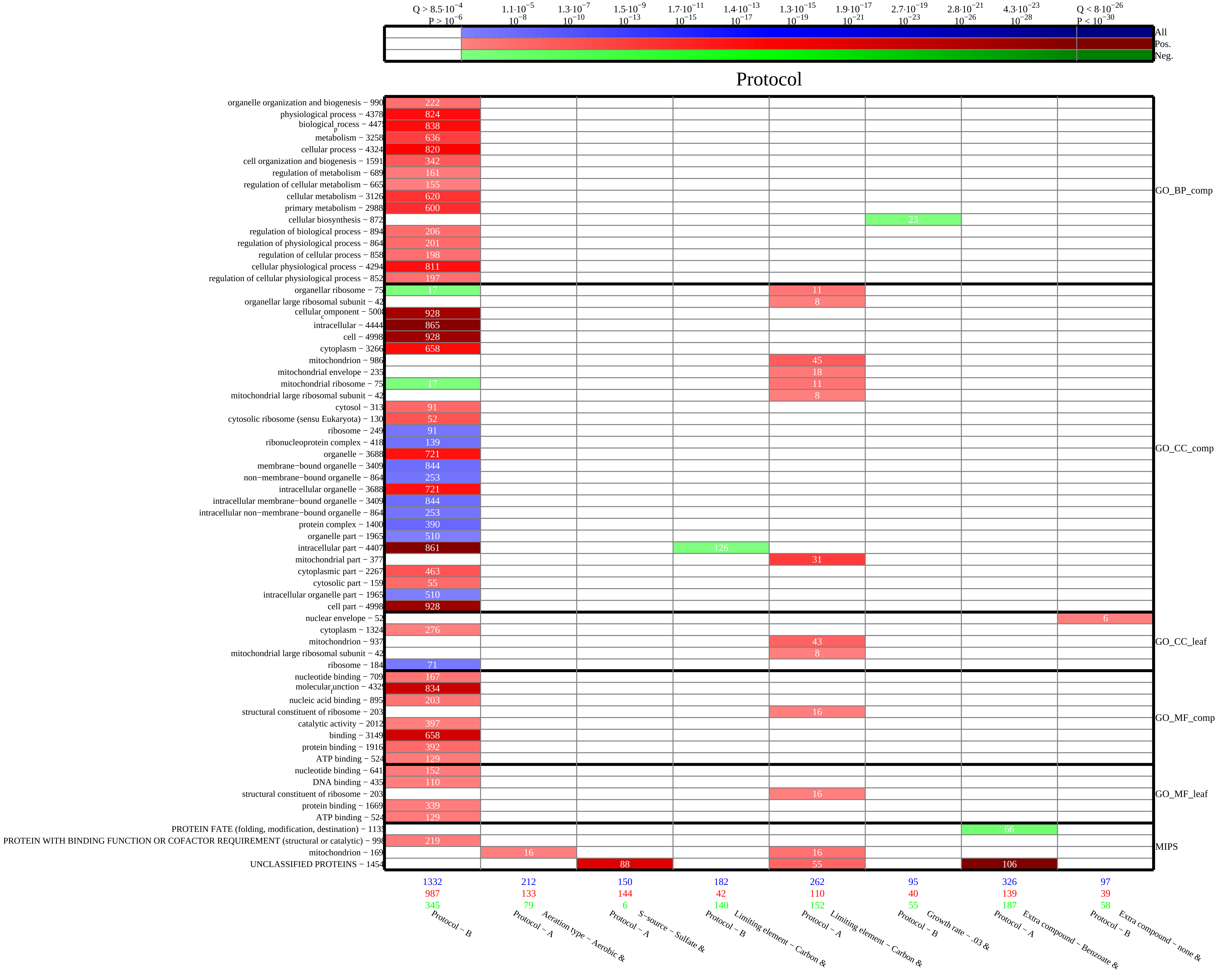


Q > $8.5\cdot10^{-4}$	$1.1\cdot10^{-5}$	$1.3\cdot10^{-7}$	$1.5\cdot10^{-9}$	$1.7\cdot10^{-11}$	$1.4\cdot10^{-13}$	$1.3\cdot10^{-15}$	$1.9\cdot10^{-17}$	$2.7\cdot10^{-19}$	$2.8\cdot10^{-21}$	$4.3\cdot10^{-23}$	Q < $8\cdot10^{-26}$
P > 10^{-6}	10^{-8}	10^{-10}	10^{-13}	10^{-15}	10^{-17}	10^{-19}	10^{-21}	10^{-23}	10^{-26}	10^{-28}	P < 10^{-30}

🟦 All
🟥 Pos.
🟩 Neg.

Extra compound

	Extra compound	Extra compound – Acetate	Extra compound – Benzoate	Extra compound – CO_2	Extra compound – Formate	Extra compound – Propionate	Extra compound – Sorbate	Extra compound – none	Aeration type – Aerobic & Extra compound – CO_2	Aeration type – Aerobic & Extra compound – none	Aeration type – Anaerobic & Extra compound – none	Extra compound – Benzoate | Propionate	Extra compound – Benzoate | Sorbate	Extra compound – Benzoate & Protocol – A	Extra compound – Ethanol 18.72 mM | Propionate	Extra compound – Formate | Propionate	Extra compound – none & Protocol – B	
mitotic cell cycle – 271												🟩 29						GO_BP_comp
telomere maintenance via recombination – 26										🟩 6								
organic acid metabolism – 353															🟥 12			
mitotic recombination – 37										🟩 6								
arginine biosynthesis – 11						🟦 6												
fatty acid metabolism – 54															🟥 6			
response to stress – 466					🟦 13											🟥 15		
cell cycle – 530												🟩 47						
amino acid biosynthesis – 136																🟥 9		
vitamin biosynthesis – 44						🟦 10												
nucleoside monophosphate metabolism – 27				🟥 5														
nucleoside monophosphate biosynthesis – 26				🟥 5														
purine nucleoside monophosphate metabolism – 24				🟥 5														
purine nucleoside monophosphate biosynthesis – 23				🟥 5														
ribonucleoside monophosphate biosynthesis – 23				🟥 5														
ribonucleoside monophosphate metabolism – 24				🟥 5														
purine ribonucleoside monophosphate metabolism – 23				🟥 5														
purine ribonucleoside monophosphate biosynthesis – 22				🟥 5														
amine biosynthesis – 144																🟥 9		
carboxylic acid metabolism – 353															🟥 12			
water−soluble vitamin biosynthesis – 44						🟦 10												
nitrogen compound biosynthesis – 144																🟥 9		
regulation of biological process – 894												🟩 64						
regulation of physiological process – 864												🟩 62						
regulation of cellular process – 858												🟩 63						
response to stimulus – 653					🟦 14													
regulation of cellular physiological process – 852												🟩 62						
telomere maintenance via recombination – 26										🟩 6								GO_BP_leaf
purine nucleotide biosynthesis – 21				🟥 6														
arginine biosynthesis – 11						🟦 6												
response to stress – 100	🟥 23				🟥 10			🟥 12								🟥 14		
amino acid biosynthesis – 96																🟥 8		
intracellular – 4444												🟩 210						GO_CC_comp
nucleus – 1842												🟩 118						
plasma membrane – 213		🟩 9																
membrane – 1608									🟥 26									
protein complex – 1400												🟩 89						
organelle part – 1965												🟩 113						
intracellular part – 4407												🟩 208						
nuclear part – 876												🟩 70						
intracellular organelle part – 1965												🟩 113						
nucleus – 1651												🟩 108						GO_CC_leaf
nuclear envelope – 52																	🟥 6	
membrane – 1273									🟦 40									
DNA helicase activity – 42										🟩 6								GO_MF_comp
ATP−dependent helicase activity – 74										🟩 6								
potassium ion binding – 12				🟥 5														
alkali metal ion binding – 16				🟥 5														
DNA helicase activity – 30										🟩 6								GO_MF_leaf
ATP−dependent helicase activity – 59										🟩 6								
potassium ion binding – 12				🟥 5														
metabolism of arginine – 20						🟥 6												MIPS
CELL CYCLE AND DNA PROCESSING – 975												🟩 73						
PROTEIN FATE (folding, modification, destination) – 1135														🟩 66				
UNCLASSIFIED PROTEINS – 1454			🟥 27											🟥 106				
Pyruvate metabolism – 33															🟥 5			KEGG
DIG1 – 143	🟩 20																	TF
GCN4 – 175						🟥 19										🟥 11		
SUM1 – 55											🟥 10							
STE12 – 234							🟦 10						🟥 18					
🟦	580	57	74	60	22	173	37	59	86	36	187	286	240	326	46	61	97	
🟥	403	32	41	38	20	103	26	58	39	9	129	49	57	139	25	43	39	
🟩	192	25	33	22	2	70	11	1	47	27	58	237	183	187	21	18	58	



Protocol

		Protocol − B	Protocol − A Aeration type − Aerobic &	Protocol − A S−source − Sulfate &	Protocol − B Limiting element − Carbon &	Protocol − A Limiting element − Carbon &	Protocol − B Growth rate − .03 &	Protocol − A Extra compound − Benzoate &	Protocol − B Extra compound − none &
GO_BP_comp	organelle organization and biogenesis − 990	222							
	physiological process − 4378	824							
	biological_process − 4475	838							
	metabolism − 3258	636							
	cellular process − 4324	820							
	cell organization and biogenesis − 1591	342							
	regulation of metabolism − 689	161							
	regulation of cellular metabolism − 665	155							
	cellular metabolism − 3126	620							
	primary metabolism − 2988	600							
	cellular biosynthesis − 872						23		
	regulation of biological process − 894	206							
	regulation of physiological process − 864	201							
	regulation of cellular process − 858	198							
	cellular physiological process − 4294	811							
	regulation of cellular physiological process − 852	197							
GO_CC_comp	organellar ribosome − 75	17				11			
	organellar large ribosomal subunit − 42					8			
	cellular_component − 5008	928							
	intracellular − 4444	865							
	cell − 4998	928							
	cytoplasm − 3266	658							
	mitochondrion − 986					45			
	mitochondrial envelope − 235					18			
	mitochondrial ribosome − 75	17				11			
	mitochondrial large ribosomal subunit − 42					8			
	cytosol − 313	91							
	cytosolic ribosome (sensu Eukaryota) − 130	52							
	ribosome − 249	91							
	ribonucleoprotein complex − 418	139							
	organelle − 3688	721							
	membrane−bound organelle − 3409	844							
	non−membrane−bound organelle − 864	253							
	intracellular organelle − 3688	721							
	intracellular membrane−bound organelle − 3409	844							
	intracellular non−membrane−bound organelle − 864	253							
	protein complex − 1400	390							
	organelle part − 1965	510							
	intracellular part − 4407	861			126				
	mitochondrial part − 377					31			
	cytoplasmic part − 2267	463							
	cytosolic part − 159	55							
	intracellular organelle part − 1965	510							
	cell part − 4998	928							
GO_CC_leaf	nuclear envelope − 52								6
	cytoplasm − 1324	276							
	mitochondrion − 937					43			
	mitochondrial large ribosomal subunit − 42					8			
	ribosome − 184	71							
GO_MF_comp	nucleotide binding − 709	167							
	molecular_function − 4329	834							
	nucleic acid binding − 895	203							
	structural constituent of ribosome − 203					16			
	catalytic activity − 2012	397							
	binding − 3149	658							
	protein binding − 1916	392							
	ATP binding − 524	129							
GO_MF_leaf	nucleotide binding − 641	152							
	DNA binding − 435	110							
	structural constituent of ribosome − 203					16			
	protein binding − 1669	339							
	ATP binding − 524	129							
MIPS	PROTEIN FATE (folding, modification, destination) − 1135							66	
	PROTEIN WITH BINDING FUNCTION OR COFACTOR REQUIREMENT (structural or catalytic) − 998	219							
	mitochondrion − 169		16			16			
	UNCLASSIFIED PROTEINS − 1454			88		55		106	
		1332	212	150	182	262	95	326	97
		987	133	144	42	110	40	139	39
		345	79	6	140	152	55	187	58