

Figure S1. **(A)** Change of cumulative gene counts (removing duplicates) upon addition of pathway sources. Increase of total gene count by addition of sources approaches saturation after the first 12. The six additional sources (white) increase the total gene count by 2%. The order of source addition is based on the number of genes in each source and taking into account the popularity of the source, as reflected by the number of citations. **(B)** Switching the last 6 sources results in a very similar graph with increase of 4% in the total gene count.

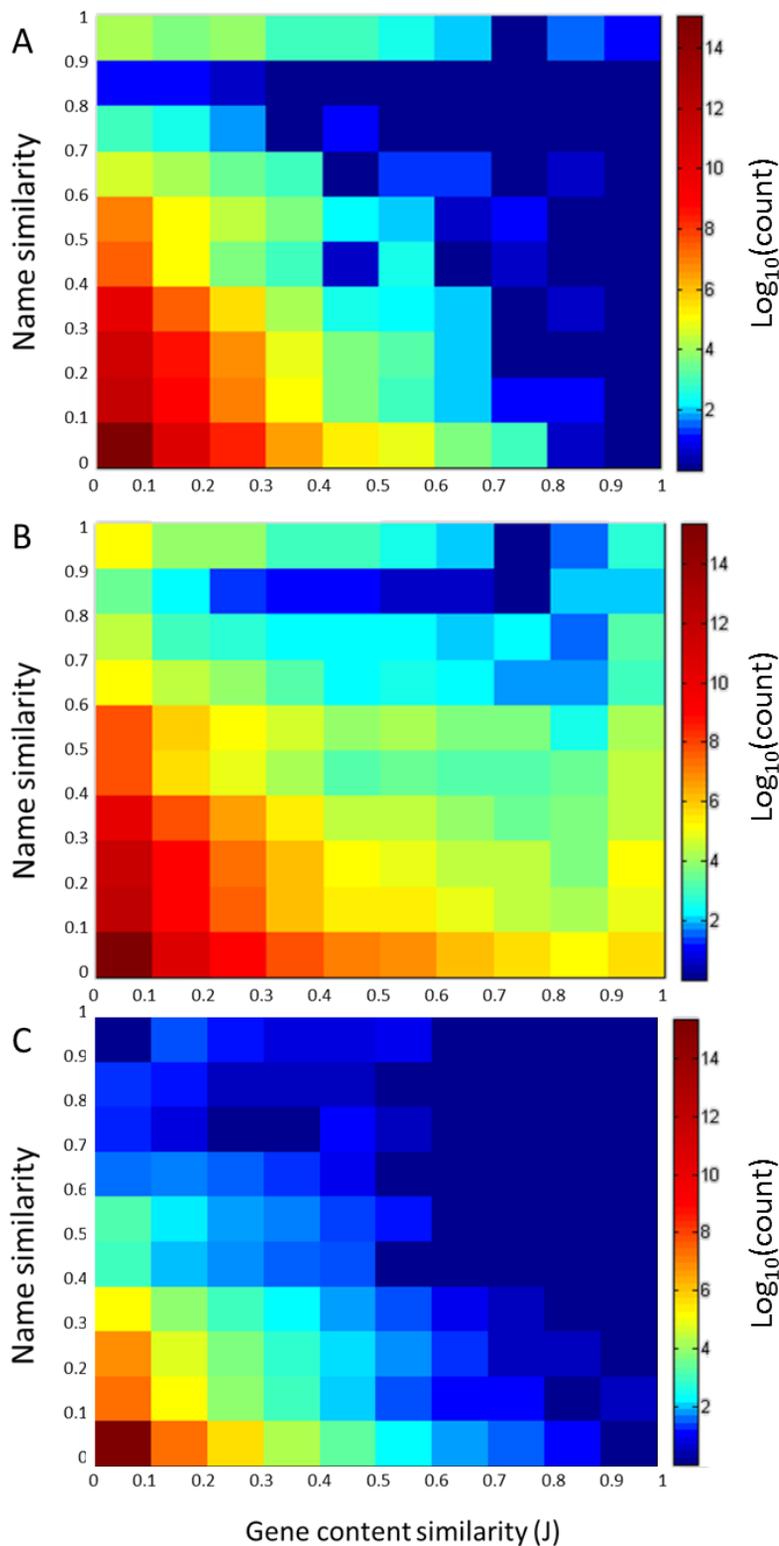


Figure S2. Name similarity versus gene-content similarity. **(A)** Name similarity vs. gene-content similarity in Pathway pairs where each pathway is from a different source. **(B)** Name similarity vs. gene-content similarity in all pathway pairs. **(C)** Name similarity vs. gene-content similarity in SuperPaths.

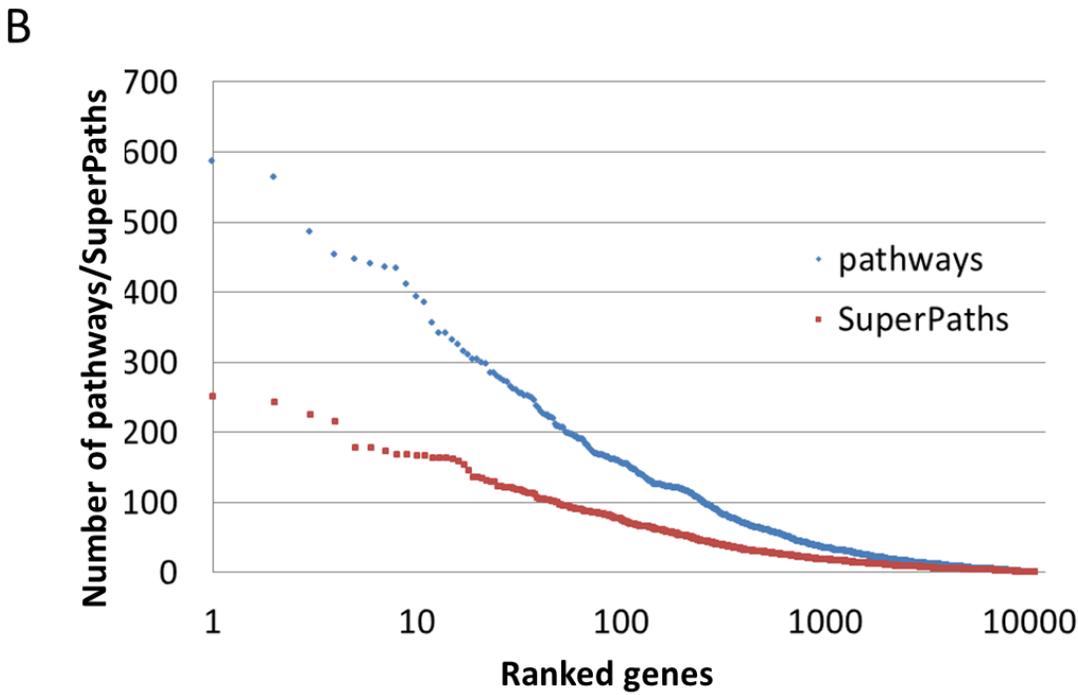
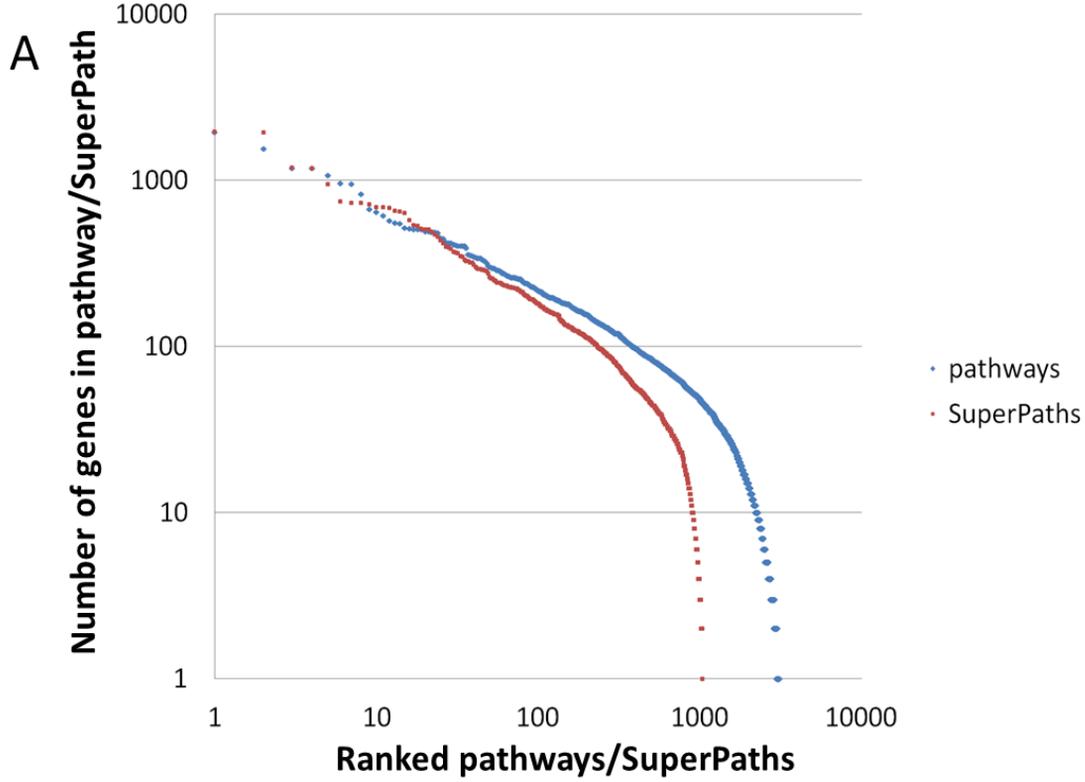


Figure S3. Genes vs. pathways and SuperPaths. **(A)** Number of genes in SuperPaths and Pathways. The pathways (blue) and SuperPaths (red) are ranked in descending order. The number of genes in pathways and SuperPaths have a similar shape indicating a similar distribution of gene count across pathways and SuperPaths. **(B)** The Number of pathways and SuperPaths across all ranked genes. Consolidation of pathways into SuperPaths reduces greatly the amount of pathway-related annotation per gene, especially for highly annotated genes.

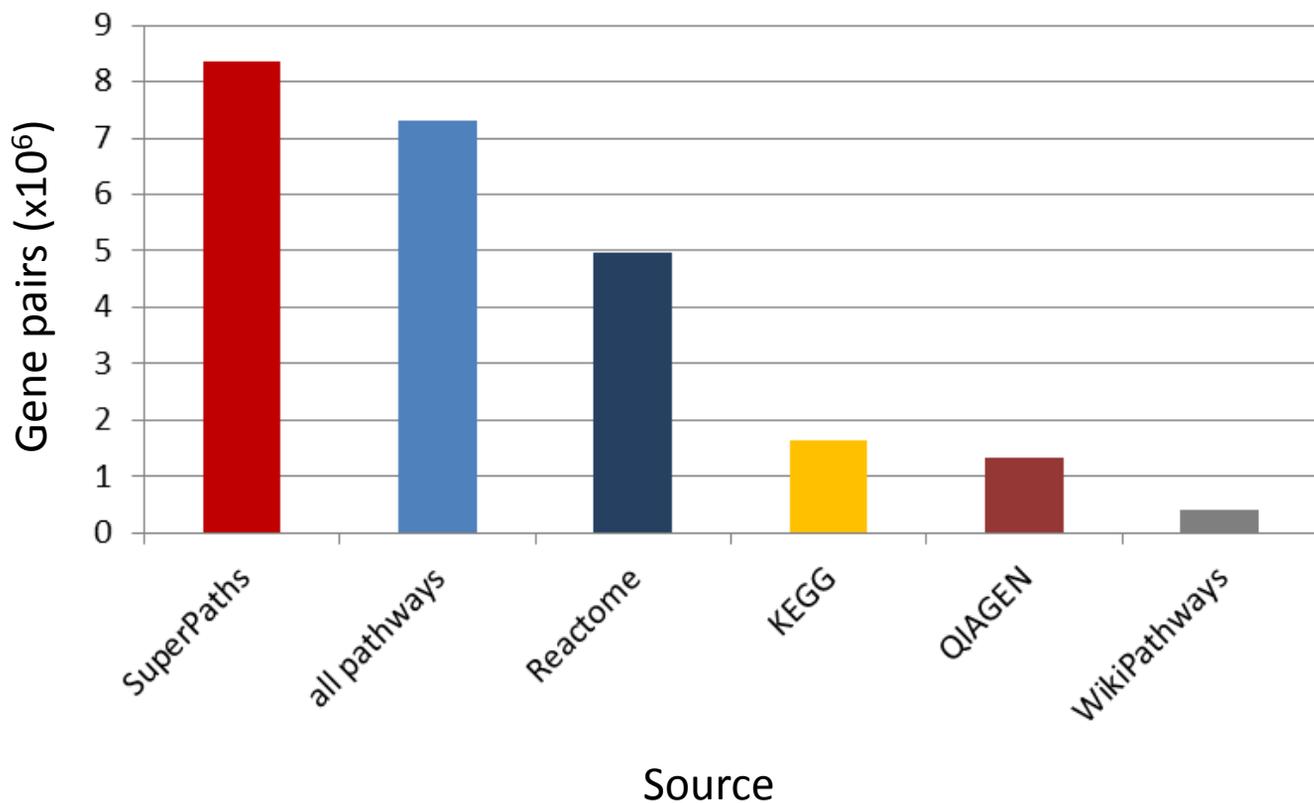


Figure S4. Enhancement of gene pair counts in SuperPaths. SuperPaths provide 14% more gene pairs than all pathway sources combined and x1.68 to x20 higher numbers than in the individual four largest pathway sources.

A

SuperPaths for SDHC [About](#) improved
 See pathways by source

SuperPath	Contained pathways About	
1 Citric acid cycle (TCA cycle)	<ul style="list-style-type: none"> Citric acid cycle (TCA cycle) 0.55 conversion of glucose to acetyl CoA and entry into the TCA cycle 0.43 Citrate cycle (TCA cycle) 0.55 TCA Cycle 0.00 Pyruvate metabolism and Citric Acid (TCA) cycle 0.49 TCA cycle 0.00 	
2 Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	<ul style="list-style-type: none"> Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. 0.81 Oxidative phosphorylation 0.64 Respiratory electron transport 0.81 Parkinson's disease 0.57 Electron Transport Chain 0.75 Huntington's disease 0.45 The citric acid (TCA) cycle and respiratory electron transport 0.71 Non-alcoholic fatty liver disease (NAFLD) 0.41 	
3 Metabolism	Metabolism 0.38 Metabolic pathways 0.38	
4 Alzheimer's disease	Alzheimer's disease 0.44	
5 Carbon metabolism	Carbon metabolism 0.38	

B

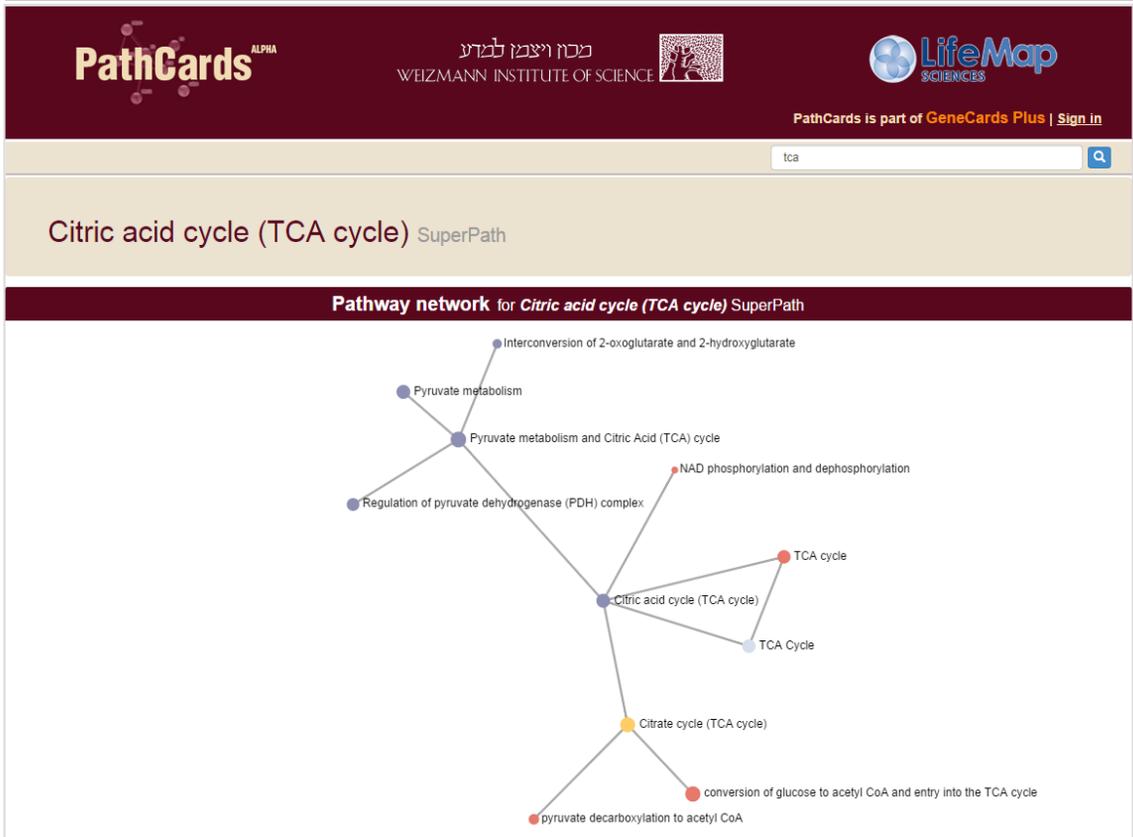


Figure S5. SuperPaths representation in GeneCards and PathCards. **(A)** SuperPath representation in GeneCards for the SDHC gene. All the gene's SuperPaths are shown (left), each with its constituent source-specific individual pathways (right), affording an effective overview. **(B)** SuperPath network representation in PathCards. The TCA cycle SuperPath is shown with 11 pathways from 4 sources, with connecting edges as defined in Fig. 3B.

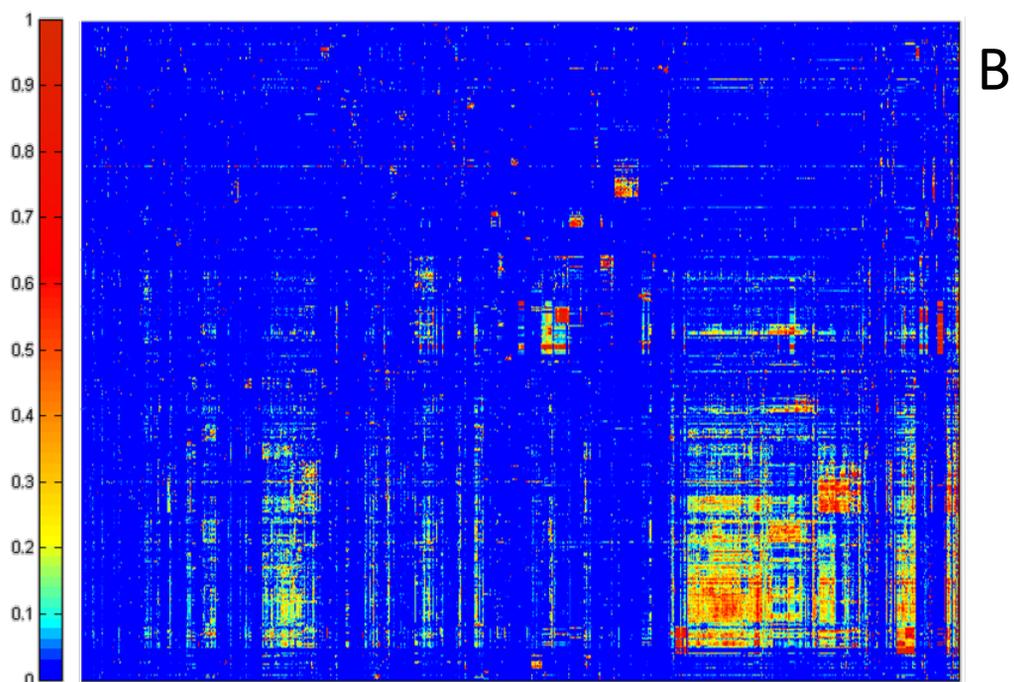
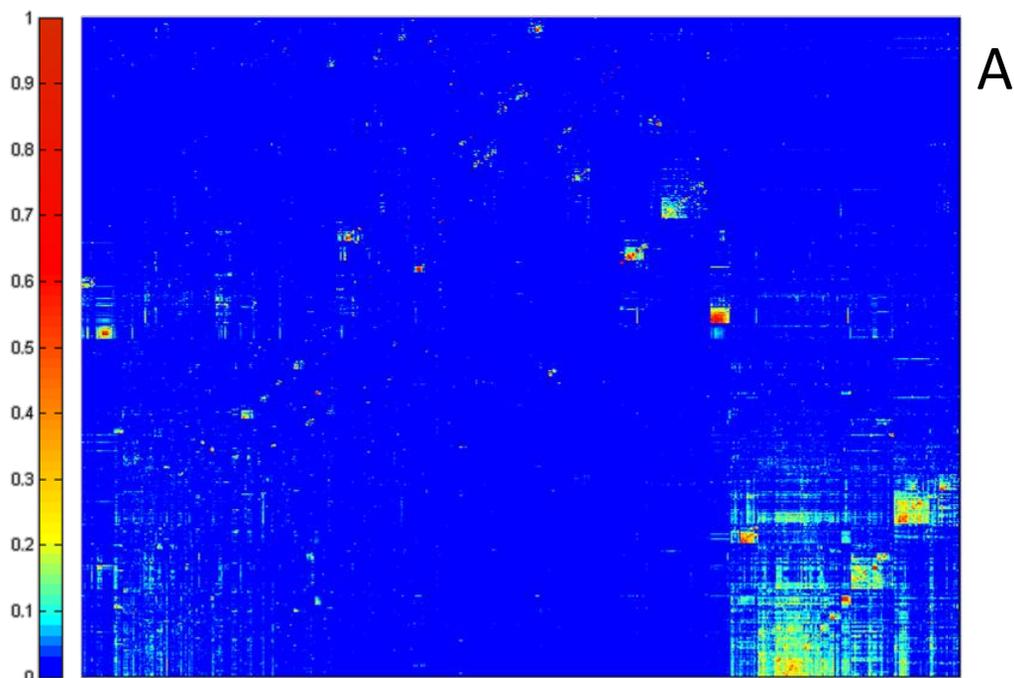


Figure S6. Pathway similarity. **(A)** All pairwise Jaccard index similarity clustered using the clustergram function **(B)** All pairwise percent similarity to the smaller pathway, clustered using the clustergram function.

Table S1. Pathway alignment significance vs. Jaccard similarity coefficient

	Pathway1 (query in MetaPathwayHunter)	Pathway2	Jaccard coefficient	ALN P	# of ALN for query where P<0.01
1	yeast_de_novo_purine_nuc_biosynth (1)	yeast_super_histidine_purine_pyrimidine_biosynth	0.486486	<0.01	1
2	yeast_phenylalanine_tyrosine_tryptophan_biosynth (2)	yeast_chorismate_pathway (5)	0.533333	<0.01	1
3	yeast_folic_acid_biosynth (3)	yeast_chorismate_pathway (5)	0.387097	<0.01	1
4	yeast_super_phenylalanine_tyrosine_tryptophane_biosynth (4)	yeast_chorismate_pathway (5)	0.3	<0.01	2
5	yeast_super_phenylalanine_tyrosine_tryptophane_biosynth (4)	yeast_phenylalanine_tyrosine_tryptophan_biosynth	0.5625	<0.01	2
6	yeast_tryptophan_biosynth (6)	yeast_phenylalanine_tyrosine_tryptophan_biosynth	0.3125	<0.01	3
7	yeast_mevalonate_pathway (7)	yeast_ergosterol_biosynth	0.466667	<0.01	1
8	yeast_glycolysis (8)	yeast_glucose_fermentation	0.5	<0.01	1
9	yeast_aerobic_glycerol_catabolism (9)	yeast_glucose_fermentation	0.333333	<0.01	1
10	yeast_phosphatidic_biosynth (10)	yeast_phosphatidic_acid_phospholipid_biosynth	0.615385	<0.01	1
11	yeast_sulfate_assimilation_pathway2 (11)	yeast_sulfur_amino_acid_biosynth	0.454545	<0.01	2
12	yeast_ubiquinone_Q_prenylation (12)	yeast_ubiquinone_biosynth	0.555556	<0.01	1
13	yeast_hexaprenyl_diphosphate_biosynth (13)	yeast_ubiquinone_biosynth	0.444444	<0.01	2
14	yeast_deoxyribose_phosphate_metabolism (14)	yeast_ribose_deoxyribose_phosphate_metabolism	0.75	<0.01	1
15	yeast_ribose_catabolism (15)	yeast_ribose_deoxyribose_phosphate_metabolism	0.375	<0.01	4
16	yeast_tryptophan_biosynth (6)	yeast_super_phenylalanine_tyrosine_tryptophane_biosynth	0.555556	<0.01	3
17	yeast_super_phenylalanine_tyrosine_biosynth (16)	yeast_super_phenylalanine_tyrosine_tryptophane_biosynth	0.444444	<0.01	3
18	yeast_tyrosine_biosynth (17)	yeast_super_phenylalanine_tyrosine_tryptophane_biosynth	0.333333	<0.01	4
19	yeast_glycolysis (8)	yeast_aerobic_glycerol_catabolism	0.5	-	1
20	yeast_glutamate_degradation8 (18)	yeast_arginine_metabolism	0.625	<0.01	1
21	yeast_fatty_acid_elongation (19)	yeast_fatty_acid_biosynth	0.375	<0.01	1
22	yeast_salvage_pyrimidine_deoxyribonucleotide_pathway (20)	yeast_salvage_pyrimidine_ribonucleotide_pathway	0.3	<0.01	1
23	yeast_super_isoleucine_valine_biosynth2 (21)	yeast_super_leucine_isoleucine_valine_biosynth1	0.571429	<0.01	5
24	yeast_leucine_biosynth (22)	yeast_super_leucine_isoleucine_valine_biosynth1	0.571429	<0.01	2
25	yeast_valine_biosynth (23)	yeast_super_leucine_isoleucine_valine_biosynth1	0.571429	<0.01	5
26	yeast_isoleucine_biosynth (24)	yeast_super_leucine_isoleucine_valine_biosynth1	0.5	<0.01	3
27	yeast_super_isoleucine_valine_biosynth1 (25)	yeast_super_leucine_isoleucine_valine_biosynth1	0.5	<0.01	3
28	yeast_super_leucine_isoleucine_valine_biosynth2 (26)	yeast_super_leucine_isoleucine_valine_biosynth1	0.333333	<0.01	3
29	yeast_methionine_biosynth (27)	yeast_threonine_methionine_biosynth	0.75	<0.01	3
30	yeast_threonine_biosynth (28)	yeast_threonine_methionine_biosynth	0.625	<0.01	2

1) yeast_de_novo_purine_nuc_biosynth

Text File Name	Match Score	P-Value
yeast_de_novo_purine_nuc_biosynth.grp	0.0	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-55.3076	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-55.3076	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-57.0441	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-58.2822	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-61.3076	0.0

Click on a column name to sort table. Click on a row to view match.

2) yeast_phenylalanine_tyrosine_tryptophan_biosynth

Text File Name	Match Score	P-Value
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	0.0	0.0
yeast_chorismate_pathway.grp	-46.851	0.0
yeast_chorismate_pathway.grp	-81.7949	0.0
yeast_chorismate_pathway.grp	-83.7949	0.0
yeast_chorismate_pathway.grp	-115.568	0.05
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-133.677	0.92
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-133.677	0.92
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-134.021	0.97
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-135.011	0.97
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-136.473	1.0

Click on a column name to sort table. Click on a row to view match.

3) yeast_folic_acid_biosynth

Text File Name	Match Score	P-Value
yeast_folic_acid_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	-29.0899	0.0
yeast_chorismate_pathway.grp	-29.9647	0.0
yeast_chorismate_pathway.grp	-31.9647	0.0
yeast_chorismate_pathway.grp	-33.9647	0.0
yeast_chorismate_pathway.grp	-35.9647	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-96.4068	0.02
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-97.2834	0.02
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-98.4068	0.03
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-99.2834	0.05
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-100.84	0.06

Click on a column name to sort table. Click on a row to view match.

4) yeast_super_phenylalalinin_tyrosine_tryptophane_biosynth

Text File Name	Match Score	P-Value
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	0.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-7.76519	0.0
yeast_chorismate_pathway.grp	-7.76519	0.0
yeast_chorismate_pathway.grp	-24.1995	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.4135	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.4135	0.0
yeast_chorismate_pathway.grp	-25.4135	0.0
yeast_chorismate_pathway.grp	-25.4135	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-27.4135	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-27.4135	0.0
yeast_chorismate_pathway.grp	-27.4135	0.0
yeast_chorismate_pathway.grp	-27.4135	0.0
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-69.4023	0.34
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-71.4023	0.55
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-71.4666	0.56
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-72.0729	0.63
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-72.3647	0.7
yeast_de_novo_purine_nuc_biosynth.grp	-75.2948	0.9
yeast_de_novo_purine_nuc_biosynth.grp	-77.2948	0.95
yeast_de_novo_purine_nuc_biosynth.grp	-79.2948	1.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-79.6956	1.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-79.6956	1.0
yeast_folic_acid_biosynth.grp	-79.7197	1.0
yeast_folic_acid_biosynth.grp	-79.7197	1.0
yeast_de_novo_purine_nuc_biosynth.grp	-80.4193	1.0
yeast_de_novo_purine_nuc_biosynth.grp	-80.4817	1.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-80.9337	1.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-80.9337	1.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-80.9337	1.0
yeast_folic_acid_biosynth.grp	-81.7197	1.0
yeast_folic_acid_biosynth.grp	-81.7197	1.0
yeast_folic_acid_biosynth.grp	-83.7197	1.0


[Click on a column name to sort table.](#)
[Click on a row to view match.](#)

5) yeast_chorismate_biosynth

Text File Name	Match Score	P-Value
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	0.0	0.0
yeast_chorismate_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	-37.6758	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-39.2454	0.0
yeast_chorismate_pathway.grp	-39.2454	0.0
yeast_chorismate_pathway.grp	-39.4951	0.01
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-40.1278	0.01
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-41.9471	0.02
yeast_chorismate_pathway.grp	-42.1304	0.04
yeast_chorismate_biosynth.grp	-44.3991	0.14
yeast_glucose_fermentation.grp	-45.438	0.24
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-45.893	0.29
yeast_heme_biosynth.grp	-46.4579	0.33
yeast_sulfur_amino_acid_biosynth.grp	-46.7048	0.36
yeast_serine_isocitrate_lyase_pathway.grp	-46.8299	0.37
yeast_glucose_fermentation.grp	-47.438	0.4
yeast_TCA_cycle_aerobic_respiration.grp	-47.4789	0.4
yeast_serine_isocitrate_lyase_pathway.grp	-47.5192	0.4
yeast_serine_isocitrate_lyase_pathway.grp	-47.7123	0.43
yeast_serine_isocitrate_lyase_pathway.grp	-48.1215	0.46
yeast_heme_biosynth.grp	-48.4579	0.47
yeast_glycolysis.grp	-48.7262	0.5
yeast_glucose_fermentation.grp	-48.7262	0.5
yeast_TCA_cycle_aerobic_respiration.grp	-48.7434	0.5
yeast_serine_isocitrate_lyase_pathway.grp	-48.8834	0.53
yeast_glucose_fermentation.grp	-49.1095	0.57
yeast_de_novo_purine_nuc_biosynth.grp	-49.2819	0.57
yeast_ergosterol_biosynth.grp	-49.3758	0.59
yeast_glucose_fermentation.grp	-49.438	0.59
yeast_ubiquinone_biosynth.grp	-49.5833	0.59
yeast_ergosterol_biosynth.grp	-49.5833	0.59
yeast_ergosterol_biosynth.grp	-49.9389	0.61
yeast_p_cymene_degradation.grp	-49.9814	0.63
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-50.1402	0.66
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-50.1642	0.67
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-50.1642	0.67
yeast_ergosterol_biosynth.grp	-50.2318	0.69
yeast_super_leucine_oleucine_valine_biosynth1.grp	-50.4795	0.7
yeast_folic_acid_biosynth.grp	-50.6838	0.72
yeast_ubiquinone_biosynth.grp	-50.7348	0.74
yeast_ergosterol_biosynth.grp	-50.7348	0.74
yeast_aerobic_glycerol_catabolism.grp	-51.1782	0.77
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-51.1852	0.77
yeast_de_novo_purine_nuc_biosynth.grp	-51.1852	0.77
yeast_de_novo_purine_nuc_biosynth.grp	-51.1852	0.77
yeast_de_novo_purine_nuc_biosynth.grp	-51.1852	0.77
yeast_phosphatidic_biosynth.grp	-51.2406	0.78
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-51.2406	0.78
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-51.2406	0.78
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-51.2406	0.78
yeast_de_novo_purine_nuc_biosynth.grp	-51.2819	0.8
yeast_super_leucine_oleucine_valine_biosynth1.grp	-51.3619	0.81
yeast_p_cymene_degradation.grp	-51.3619	0.81
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-51.3782	0.81
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-51.3782	0.81

Click on a column name to sort table. Click on a row to view match.

6) yeast_ tryptophan_biosynth

Text File Name	Match Score	P-Value
yeast_ tryptophan_biosynth.grp	0.0	0.0
yeast_super_ phenylalanine_tyrosine_ tryptophane_biosynth.grp	0.0	0.0
yeast_ phenylalanine_tyrosine_ tryptophan_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	0.0	0.0
yeast_super_ phenylalanine_tyrosine_ tryptophane_biosynth.grp	-2.0	0.0
yeast_ phenylalanine_tyrosine_ tryptophan_biosynth.grp	-2.0	0.0
yeast_chorismate_pathway.grp	-2.0	0.0
yeast_ phenylalanine_tyrosine_ tryptophan_biosynth.grp	-4.0	0.0
yeast_chorismate_pathway.grp	-4.0	0.0
yeast_ phenylalanine_tyrosine_ tryptophan_biosynth.grp	-6.0	0.0
yeast_chorismate_pathway.grp	-6.0	0.0
yeast_ phenylalanine_tyrosine_ tryptophan_biosynth.grp	-8.0	0.0
yeast_chorismate_pathway.grp	-8.0	0.0
yeast_super_ phenylalanine_tyrosine_ tryptophane_biosynth.grp	-17.9824	0.0
yeast_super_ phenylalanine_tyrosine_ tryptophane_biosynth.grp	-27.4582	0.04
yeast_super_ phenylalanine_tyrosine_ tryptophane_biosynth.grp	-27.828	0.04
yeast_ tryptophan_biosynth.grp	-27.9647	0.04
yeast_serine_isocitrate_lyase_pathway.grp	-28.1663	0.05
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-28.7184	0.07
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-28.855	0.07
yeast_hestidine_biosynth.grp	-28.855	0.07
yeast_serine_isocitrate_lyase_pathway.grp	-30.1663	0.17
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-30.8343	0.24
yeast_deoxyribose_phosphate_metabolism.grp	-30.8343	0.24
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-30.855	0.24
yeast_hestidine_biosynth.grp	-30.855	0.24
yeast_heme_biosynth.grp	-31.0411	0.28
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-31.6006	0.34
yeast_serine_isocitrate_lyase_pathway.grp	-31.7506	0.35
yeast_p_cymene_degradation.grp	-31.8726	0.35
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-31.9519	0.38
yeast_deoxyribose_phosphate_metabolism.grp	-31.9519	0.38
yeast_serine_isocitrate_lyase_pathway.grp	-31.9651	0.38
yeast_serine_isocitrate_lyase_pathway.grp	-32.1663	0.41
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.2069	0.41
yeast_hestidine_biosynth.grp	-32.2069	0.41
yeast_glucose_fermentation.grp	-32.4162	0.45
yeast_folic_acid_biosynth.grp	-32.4247	0.46
yeast_mevalonate_pathway.grp	-32.6346	0.48
yeast_ergosterol_biosynth.grp	-32.6346	0.48
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.855	0.51
yeast_glycolysis.grp	-32.8682	0.51
yeast_heme_biosynth.grp	-33.0411	0.56
yeast_de_novo_pyrimidine_ribonuc_biosynth.grp	-33.1452	0.56
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-33.2863	0.57
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-33.3071	0.57
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-33.3202	0.59
yeast_deoxyribose_phosphate_metabolism.grp	-33.3202	0.59
yeast_chorismate_biosynth.grp	-33.6895	0.6
yeast_glucose_fermentation.grp	-33.7506	0.61
yeast_p_cymene_degradation.grp	-33.8726	0.62
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-33.9519	0.62
yeast_deoxyribose_phosphate_metabolism.grp	-33.9519	0.62
yeast_threonine_methionine_biosynth.grp	-34.0229	0.63
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-34.0452	0.64
yeast_mevalonate_pathway.grp	-34.0615	0.65

Click on a column name to sort table. Click on a row to view match.

7) yeast_mevalonate_pathway

Text File Name	Match Score	P-Value
yeast_mevalonate_pathway.grp	0.0	0.0
yeast_ergosterol_biosynth.grp	0.0	0.0
yeast_ergosterol_biosynth.grp	-38.6098	0.0
yeast_ergosterol_biosynth.grp	-41.3963	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-42.2995	0.02
yeast_chorismate_pathway.grp	-42.2995	0.02
yeast_mevalonate_pathway.grp	-42.6343	0.02
yeast_glycolysis.grp	-43.4268	0.05
yeast_glucose_fermentation.grp	-43.4268	0.05
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-44.2995	0.12
yeast_chorismate_pathway.grp	-44.2995	0.12
yeast_glycolysis.grp	-45.4268	0.22
yeast_glucose_fermentation.grp	-45.4268	0.22
yeast_serine_isocitrate_lyase_pathway.grp	-46.5481	0.36
yeast_glucose_fermentation.grp	-46.5818	0.36
yeast_glycolysis.grp	-46.6058	0.36
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-46.6758	0.36
yeast_chorismate_pathway.grp	-46.6758	0.36
yeast_ergosterol_biosynth.grp	-46.827	0.41
yeast_chorismate_pathway.grp	-47.0314	0.45
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-47.1278	0.46
yeast_chorismate_pathway.grp	-47.1278	0.46
yeast_phosphatidic_biosynth.grp	-47.2166	0.49
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-47.2166	0.49
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-47.2166	0.49
yeast_ergosterol_biosynth.grp	-47.2785	0.5
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-47.3025	0.5
yeast_glucose_fermentation.grp	-47.4268	0.51
yeast_glucose_fermentation.grp	-47.8198	0.59
yeast_glycolysis.grp	-47.8438	0.59
yeast_glycolysis.grp	-47.9063	0.59
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-47.9196	0.6
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-47.9298	0.6
yeast_serine_isocitrate_lyase_pathway.grp	-47.9447	0.6
yeast_serine_isocitrate_lyase_pathway.grp	-48.2064	0.63
yeast_serine_isocitrate_lyase_pathway.grp	-48.3069	0.63
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-48.3644	0.64
yeast_de_novo_purine_nuc_biosynth.grp	-48.3644	0.64
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-48.4546	0.64
yeast_serine_isocitrate_lyase_pathway.grp	-48.5481	0.65
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-49.1202	0.67
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-49.1202	0.67
yeast_folic_acid_biosynth.grp	-49.1202	0.67
yeast_pantothenate_coenzymeA_biosynth.grp	-49.1553	0.67
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-49.2303	0.67
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-49.2642	0.67
yeast_de_novo_purine_nuc_biosynth.grp	-49.6024	0.69
yeast_pantothenate_coenzymeA_biosynth.grp	-49.7074	0.71
yeast_pantothenate_coenzymeA_biosynth.grp	-49.7074	0.71
yeast_pantothenate_coenzymeA_biosynth.grp	-49.7483	0.71
yeast_fatty_acid_biosynth.grp	-49.9471	0.72
yeast_de_novo_purine_nuc_biosynth.grp	-49.9471	0.72
yeast_folic_acid_biosynth.grp	-50.0026	0.72
yeast_TCA_cycle_aerobic_respiration.grp	-50.3103	0.74
yeast_de_novo_purine_nuc_biosynth.grp	-50.3644	0.74

Click on a column name to sort table. Click on a row to view match.

8) yeast_glycolysis

Text File Name	Match Score	P-Value
yeast_glycolysis.grp	0.0	0.0
yeast_glucose_fermentation.grp	-3.49651	0.0
yeast_glucose_fermentation.grp	-5.49651	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-57.6027	0.13
yeast_chorismate_pathway.grp	-57.6027	0.13
yeast_ergosterol_biosynth.grp	-58.6231	0.15
yeast_chorismate_pathway.grp	-59.3068	0.21
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-59.6027	0.25
yeast_chorismate_pathway.grp	-59.6027	0.25
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-60.1855	0.28
yeast_chorismate_pathway.grp	-60.1855	0.28
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-60.1879	0.28
yeast_chorismate_pathway.grp	-60.1879	0.28
yeast_ergosterol_biosynth.grp	-61.6513	0.46
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-62.1855	0.52
yeast_ergosterol_biosynth.grp	-63.0004	0.58
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-63.7403	0.63
yeast_ergosterol_biosynth.grp	-65.0004	0.66
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-65.6538	0.7
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-65.7403	0.7
yeast_pantothenate_coenzymeA_biosynth.grp	-66.3234	0.72
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-66.8865	0.75
yeast_ergosterol_biosynth.grp	-67.0004	0.76
yeast_super_phenylalanine_tyrosine_tryptophan_biosynth.grp	-67.0712	0.78
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-67.1826	0.78
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-67.6538	0.82
yeast_de_novo_purine_nuc_biosynth.grp	-68.8265	0.83
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-68.8889	0.85
yeast_de_novo_purine_nuc_biosynth.grp	-69.6125	0.9
yeast_de_novo_purine_nuc_biosynth.grp	-70.0645	0.9
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-70.1269	0.9
yeast_folic_acid_biosynth.grp	-70.2645	0.9
yeast_folic_acid_biosynth.grp	-70.2645	0.9
yeast_de_novo_purine_nuc_biosynth.grp	-70.8265	0.93
yeast_de_novo_purine_nuc_biosynth.grp	-70.913	0.93
yeast_ubiquinone_biosynth.grp	-71.4785	0.95
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-71.4785	0.95
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-71.4785	0.95
yeast_folic_acid_biosynth.grp	-72.2645	0.97
yeast_ubiquinone_biosynth.grp	-73.4785	0.99
yeast_folic_acid_biosynth.grp	-73.9545	0.99
yeast_folic_acid_biosynth.grp	-73.9545	0.99

 Click on a column name to sort table. Click on a row to view match.

9) yeast_aerobic_glycerol_catabolism

Text File Name	Match Score	P-Value
yeast_aerobic_glycerol_catabolism.grp	0.0	0.0
yeast_glucose_fermentation.grp	-32.8687	0.0
yeast_glucose_fermentation.grp	-57.6238	0.08
yeast_glucose_fermentation.grp	-57.6421	0.08
yeast_glucose_fermentation.grp	-59.6238	0.13
yeast_glucose_fermentation.grp	-60.8643	0.18
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-61.4097	0.2
yeast_chorismate_pathway.grp	-61.4097	0.2
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-61.7033	0.2
yeast_chorismate_pathway.grp	-61.7033	0.2
yeast_chorismate_pathway.grp	-63.0479	0.33
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-63.4097	0.41
yeast_chorismate_pathway.grp	-63.4097	0.41
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-63.7033	0.41
yeast_chorismate_pathway.grp	-63.7033	0.41
yeast_ergosterol_biosynth.grp	-63.8808	0.42
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-63.8822	0.42
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-63.9638	0.44
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-64.3484	0.47
yeast_serine_isocitrate_lyase_pathway.grp	-64.4969	0.49
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-64.5023	0.5
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-64.5332	0.5
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-64.8432	0.53
yeast_p_cymene_degradation.grp	-65.2262	0.63
yeast_ergosterol_biosynth.grp	-65.2299	0.63
yeast_serine_isocitrate_lyase_pathway.grp	-65.7373	0.64
yeast_serine_isocitrate_lyase_pathway.grp	-65.7373	0.64
yeast_aerobic_glycerol_catabolism.grp	-65.7373	0.64
yeast_serine_isocitrate_lyase_pathway.grp	-65.841	0.64
yeast_TCA_cycle_aerobic_respiration.grp	-66.0636	0.66
yeast_ergosterol_biosynth.grp	-66.3931	0.73
yeast_ergosterol_biosynth.grp	-66.4369	0.74
yeast_ergosterol_biosynth.grp	-66.4703	0.75
yeast_serine_isocitrate_lyase_pathway.grp	-66.4993	0.76
yeast_TCA_cycle_aerobic_respiration.grp	-66.5266	0.76
yeast_pantothenate_coenzymeA_biosynth.grp	-66.7686	0.76
yeast_de_novo_purine_nuc_biosynth.grp	-66.83	0.77
yeast_de_novo_purine_nuc_biosynth.grp	-66.9675	0.78
yeast_hestidine_biosynth.grp	-67.1021	0.8
yeast_p_cymene_degradation.grp	-67.2262	0.8
yeast_TCA_cycle_aerobic_respiration.grp	-67.2928	0.81
yeast_de_novo_purine_nuc_biosynth.grp	-67.475	0.82
yeast_phosphatidic_biosynth.grp	-67.5374	0.82
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-67.5374	0.82
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-67.5374	0.82
yeast_TCA_cycle_aerobic_respiration.grp	-67.6032	0.82
yeast_de_novo_purine_nuc_biosynth.grp	-67.6125	0.82
yeast_ubiquinone_biosynth.grp	-67.6395	0.82
yeast_hestidine_biosynth.grp	-67.8641	0.84
yeast_hestidine_biosynth.grp	-68.7819	0.88
yeast_de_novo_purine_nuc_biosynth.grp	-68.8265	0.89
yeast_p_cymene_degradation.grp	-68.9016	0.91
yeast_folic_acid_biosynth.grp	-68.9641	0.91
yeast_folic_acid_biosynth.grp	-68.9641	0.91

Click on a column name to sort table. Click on a row to view match.

10) yeast_phosphatidic_biosynth

Text File Name	Match Score	P-Value
yeast_phosphatidic_biosynth.grp	0.0	0.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	0.0	0.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-2.0	0.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-4.0	0.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-18.3744	0.0
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-20.3744	0.0
yeast_ergosterol_biosynth.grp	-59.9369	0.09
yeast_phosphatidic_biosynth.grp	-60.7853	0.15
yeast_ubiquinone_biosynth.grp	-62.4656	0.27
yeast_glucose_fermentation.grp	-62.965	0.29
yeast_ergosterol_biosynth.grp	-63.878	0.42
yeast_chorismate_pathway.grp	-64.0073	0.45
yeast_chorismate_pathway.grp	-64.2669	0.5
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-64.3954	0.51
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-64.3954	0.51
yeast_de_novo_purine_nuc_biosynth.grp	-64.4004	0.51
yeast_de_novo_purine_nuc_biosynth.grp	-64.45	0.53
yeast_ubiquinone_biosynth.grp	-64.4656	0.53
yeast_glucose_fermentation.grp	-65.0854	0.57
yeast_chorismate_pathway.grp	-65.1493	0.58
yeast_lipid_linked_oligosaccharide_biosynth.grp	-65.2884	0.6
yeast_chorismate_pathway.grp	-65.5049	0.6
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-65.5546	0.6
yeast_folic_acid_biosynth.grp	-65.5546	0.6
yeast_chorismate_pathway.grp	-65.5546	0.6
yeast_de_novo_purine_nuc_biosynth.grp	-65.6334	0.63
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-65.7469	0.65
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-65.7469	0.65
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-65.8108	0.68
yeast_ergosterol_biosynth.grp	-65.878	0.68
yeast_serine_isocitrate_lyase_pathway.grp	-66.2405	0.72
yeast_histidine_biosynth.grp	-66.2574	0.73
yeast_ergosterol_biosynth.grp	-66.2994	0.75
yeast_ergosterol_biosynth.grp	-66.3825	0.75
yeast_de_novo_purine_nuc_biosynth.grp	-66.4004	0.75
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-66.4369	0.78
yeast_de_novo_purine_nuc_biosynth.grp	-66.4369	0.78
yeast_glucose_fermentation.grp	-66.4959	0.79
yeast_histidine_biosynth.grp	-66.5008	0.79
yeast_ubiquinone_biosynth.grp	-66.5264	0.79
yeast_folic_acid_biosynth.grp	-66.9353	0.8
yeast_glucose_fermentation.grp	-67.0854	0.82
yeast_ubiquinone_biosynth.grp	-67.2884	0.82
yeast_aerobic_glycerol_catabolism.grp	-67.5374	0.84
yeast_serine_isocitrate_lyase_pathway.grp	-67.675	0.86
yeast_glucose_fermentation.grp	-67.675	0.86
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-67.7885	0.86
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-68.4369	0.91
yeast_pantothenate_coenzymeA_biosynth.grp	-68.7754	0.92
yeast_serine_isocitrate_lyase_pathway.grp	-68.8301	0.92
yeast_folic_acid_biosynth.grp	-68.8393	0.92
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-68.8889	0.92

Click on a column name to sort table. Click on a row to view match.

11) yeast_sulfate_assimilation_pathway2

Text File Name	Match Score	P-Value
yeast_sulfur_amino_acid_biosynth.grp	0.0	0.0
yeast_sulfate_assimilation_pathway2.grp	0.0	0.0
yeast_sulfur_degradation.grp	-19.9897	0.0
yeast_threonine_methionine_biosynth.grp	-28.3278	0.08
yeast_sulfur_amino_acid_biosynth.grp	-28.6916	0.1
yeast_threonine_methionine_biosynth.grp	-28.9787	0.13
yeast_methionine_biosynth.grp	-28.9787	0.13
yeast_sulfur_amino_acid_biosynth.grp	-29.5452	0.16
yeast_threonine_biosynth.grp	-30.0773	0.18
yeast_sulfur_amino_acid_biosynth.grp	-30.3926	0.22
yeast_sulfur_amino_acid_biosynth.grp	-30.3926	0.22
yeast_sulfur_degradation.grp	-31.7622	0.33
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.855	0.44
yeast_chorismate_pathway.grp	-32.855	0.44
yeast_chorismate_biosynth.grp	-32.855	0.44
yeast_sulfate_assimilation_pathway2.grp	-32.8687	0.44
yeast_de_novo_NAD_biosynth.grp	-33.0728	0.46
yeast_threonine_methionine_biosynth.grp	-33.4288	0.51
yeast_TCA_cycle_aerobic_respiration.grp	-33.8739	0.56
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-33.8853	0.56
yeast_chorismate_pathway.grp	-33.8853	0.56
yeast_mevalonate_pathway.grp	-33.9554	0.57
yeast_ergosterol_biosynth.grp	-33.9554	0.57
yeast_phosphatidic_biosynth.grp	-34.3222	0.59
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.3222	0.59
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-34.6063	0.62
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-34.6063	0.62
yeast_de_novo_purine_nuc_biosynth.grp	-34.6063	0.62
yeast_de_novo_purine_nuc_biosynth.grp	-34.6063	0.62
yeast_mevalonate_pathway.grp	-34.7439	0.64
yeast_ergosterol_biosynth.grp	-34.7439	0.64
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.8039	0.68
yeast_threonine_catabolism.grp	-34.8063	0.68
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.8063	0.68
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-34.855	0.69
yeast_chorismate_pathway.grp	-34.855	0.69
yeast_chorismate_biosynth.grp	-34.855	0.69
yeast_de_novo_NAD_biosynth.grp	-35.0728	0.71
yeast_TCA_cycle_aerobic_respiration.grp	-35.1744	0.71
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-35.1744	0.71
yeast_glutamate_degradation7.grp	-35.1744	0.71
yeast_fatty_acid_biosynth.grp	-35.1744	0.71
yeast_chorismate_pathway.grp	-35.1744	0.71
yeast_chorismate_biosynth.grp	-35.1744	0.71
yeast_threonine_methionine_biosynth.grp	-35.2445	0.71
yeast_threonine_biosynth.grp	-35.2445	0.71
yeast_salvage_pyrimidine_ribonuc_pathway.grp	-35.2559	0.72
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-35.2559	0.72
yeast_serine_isocitrate_lyase_pathway.grp	-35.3934	0.73
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-35.3934	0.73
yeast_chorismate_pathway.grp	-35.3934	0.73
yeast_phosphatidic_biosynth.grp	-35.4548	0.73
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-35.4548	0.73
yeast_glycolysis.grp	-35.8229	0.77
yeast_glucose_fermentation.grp	-35.8229	0.77
yeast_TCA_cycle_aerobic_respiration.grp	-35.8739	0.77

Click on a column name to sort table. Click on a row to view match.

12) yeast_ubiquinone_Q_prenylation

Text File Name	Match Score	P-Value
yeast_ubiquinone_Q_prenylation.grp	0.0	0.0
yeast_ubiquinone_biosynth.grp	0.0	0.0
yeast_ubiquinone_biosynth.grp	-2.0	0.0
yeast_ubiquinone_biosynth.grp	-4.0	0.0
yeast_ubiquinone_biosynth.grp	-6.0	0.0
yeast_ubiquinone_biosynth.grp	-8.0	0.0
yeast_ergosterol_biosynth.grp	-38.1796	0.31
yeast_carbon_monoxide_dehydrogenase.grp	-38.5474	0.32
yeast_sulfur_amino_acid_biosynth.grp	-39.2492	0.41
yeast_ergosterol_biosynth.grp	-40.1796	0.46
yeast_phosphatidic_biosynth.grp	-40.2901	0.46
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-40.2901	0.46
yeast_carbon_monoxide_dehydrogenase.grp	-40.5474	0.47
yeast_arginine_metabolism.grp	-41.1465	0.5
yeast_sulfur_amino_acid_biosynth.grp	-41.2492	0.5
yeast_ergosterol_biosynth.grp	-41.6788	0.53
yeast_methionine_degradation.grp	-41.7877	0.53
yeast_ergosterol_biosynth.grp	-42.1796	0.56
yeast_threonine_methionine_biosynth.grp	-42.2581	0.57
yeast_threonine_methionine_biosynth.grp	-42.2581	0.57
yeast_sulfur_amino_acid_biosynth.grp	-42.2581	0.57
yeast_methionine_biosynth.grp	-42.2581	0.57
yeast_phosphatidic_biosynth.grp	-42.2901	0.58
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-42.2901	0.58
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-42.2901	0.58
yeast_phosphatidic_biosynth.grp	-42.3205	0.58
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-42.3205	0.58
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-42.3205	0.58
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.3845	0.58
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.3845	0.58
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.3845	0.58
yeast_arginine_metabolism.grp	-42.3845	0.58
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.4805	0.59
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.4805	0.59
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-42.5177	0.59
yeast_ergosterol_biosynth.grp	-42.5177	0.59
yeast_chorismate_pathway.grp	-42.5177	0.59
yeast_chorismate_biosynth.grp	-42.5177	0.59
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-43.0201	0.68
yeast_chorismate_pathway.grp	-43.3757	0.7
yeast_carbon_monoxide_dehydrogenase.grp	-43.4961	0.7
yeast_phosphatidic_biosynth.grp	-43.5586	0.72
yeast_phosphatidic_biosynth.grp	-43.5586	0.72
yeast_folic_acid_biosynth.grp	-43.6225	0.72
yeast_folic_acid_biosynth.grp	-43.6225	0.72
yeast_chorismate_pathway.grp	-43.6225	0.72
yeast_de_novo_purine_nuc_biosynth.grp	-43.685	0.73
yeast_folic_acid_biosynth.grp	-43.7557	0.73
yeast_chorismate_pathway.grp	-43.7557	0.73
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-43.8181	0.74
yeast_folic_acid_biosynth.grp	-43.8181	0.74
yeast_chorismate_pathway.grp	-43.8181	0.74
yeast_p_cymene_degradation.grp	-43.8797	0.74
yeast_p_cymene_degradation.grp	-43.8797	0.74
yeast_de_novo_NAD_biosynth.grp	-44.2173	0.75
yeast_cerebis_phoscol_metabolism.grp	-44.2281	0.75

Click on a column name to sort table. Click on a row to view match.

13) yeast_hexaprenyl_diphosphate_biosynth

Text File Name	Match Score	P-Value
yeast_ubiquinone_biosynth.grp	0.0	0.0
yeast_hexaprenyl_diphosphate_biosynth.grp	0.0	0.0
yeast_ubiquinone_biosynth.grp	-11.9109	0.0
yeast_ubiquinone_biosynth.grp	-11.9109	0.0
yeast_ubiquinone_biosynth.grp	-13.9109	0.0
yeast_ergosterol_biosynth.grp	-15.1963	0.0
yeast_hexaprenyl_diphosphate_biosynth.grp	-15.8812	0.0
yeast_ergosterol_biosynth.grp	-17.1963	0.0
yeast_ubiquinone_biosynth.grp	-18.89	0.0
yeast_ergosterol_biosynth.grp	-19.1666	0.0
yeast_ergosterol_biosynth.grp	-19.1963	0.01
yeast_ergosterol_biosynth.grp	-19.9286	0.01
yeast_ubiquinone_Q_prenylation.grp	-22.1755	0.04
yeast_thiamine_biosynth.grp	-24.9077	0.21
yeast_ubiquinone_Q_prenylation.grp	-26.1458	0.26
yeast_riboflavin_FMN_FAD_biosynth.grp	-26.1458	0.26
yeast_riboflavin_FMN_FAD_biosynth.grp	-26.1458	0.26
yeast_chorismate_pathway.grp	-26.3749	0.39
yeast_chorismate_pathway.grp	-26.3749	0.39
yeast_chorismate_pathway.grp	-27.1369	0.4
yeast_chorismate_pathway.grp	-27.1369	0.4
yeast_sulfur_amino_acid_biosynth.grp	-27.3838	0.4
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-27.3838	0.4
yeast_methionine_degradation.grp	-27.3838	0.4
yeast_methionine_degradation.grp	-27.3838	0.4
yeast_folic_acid_biosynth.grp	-27.3838	0.4
yeast_chorismate_pathway.grp	-27.3838	0.4
yeast_chorismate_biosynth.grp	-27.3838	0.4
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-27.9166	0.49
yeast_lipid_linked_oligosaccharide_biosynth.grp	-27.9166	0.49

Click on a column name to sort table. Click on a row to view match.

14) yeast_deoxyribose_phosphate_metabolism

Text File Name	Match Score	P-Value
yeast_ribose_deoxyribose_phosphate_metabolism.grp	0.0	0.0
yeast_deoxyribose_phosphate_metabolism.grp	0.0	0.0
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-49.303	0.07
yeast_deoxyribose_phosphate_metabolism.grp	-49.303	0.07
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-50.4466	0.11
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-52.0718	0.14
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-52.6914	0.18
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-53.3628	0.2
yeast_hestidine_biosynth.grp	-53.3628	0.2
yeast_aerobic_glycerol_catabolism.grp	-54.1534	0.26
yeast_glucose_fermentation.grp	-54.6261	0.3
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-54.6914	0.31
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-54.9542	0.38
yeast_chorismate_pathway.grp	-54.9542	0.38
yeast_de_novo_purine_nuc_biosynth.grp	-55.042	0.41
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-55.0528	0.43
yeast_serine_isocitrate_lyase_pathway.grp	-55.2504	0.43
yeast_aerobic_glycerol_catabolism.grp	-55.3915	0.43
yeast_de_novo_purine_nuc_biosynth.grp	-55.6737	0.46
yeast_chorismate_pathway.grp	-55.6737	0.46
yeast_hestidine_biosynth.grp	-55.9691	0.47
yeast_chorismate_pathway.grp	-56.015	0.48
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-56.1475	0.48
yeast_chorismate_pathway.grp	-56.1475	0.48
yeast_aerobic_glycerol_catabolism.grp	-56.1534	0.48
yeast_hestidine_biosynth.grp	-56.2788	0.5
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-56.5479	0.55
yeast_chorismate_pathway.grp	-56.5479	0.55
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-56.7336	0.56
yeast_de_novo_purine_nuc_biosynth.grp	-57.042	0.58
yeast_serine_isocitrate_lyase_pathway.grp	-57.2504	0.6
yeast_glycolysis.grp	-57.3467	0.62
yeast_glucose_fermentation.grp	-57.3467	0.62
yeast_serine_isocitrate_lyase_pathway.grp	-57.3708	0.62
yeast_aerobic_glycerol_catabolism.grp	-57.3915	0.62
yeast_phosphatidic_biosynth.grp	-57.4013	0.62
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-57.4013	0.62
yeast_folic_acid_biosynth.grp	-57.606	0.63
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-57.8822	0.63
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-57.9717	0.64
yeast_serine_isocitrate_lyase_pathway.grp	-58.1328	0.64
yeast_hestidine_biosynth.grp	-58.2788	0.65
yeast_de_novo_purine_nuc_biosynth.grp	-58.4004	0.65
yeast_glycolysis.grp	-58.5847	0.66
yeast_glucose_fermentation.grp	-58.5847	0.66
yeast_ergosterol_biosynth.grp	-58.5995	0.66
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-58.6889	0.67
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-58.6889	0.67
yeast_lipid_linked_oligosaccharide_biosynth.grp	-59.1786	0.73
yeast_serine_isocitrate_lyase_pathway.grp	-59.2504	0.73
yeast_glucose_fermentation.grp	-59.3467	0.73
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-59.4013	0.73

Click on a column name to sort table. Click on a row to view match.

15) yeast_ribose_catabolism

Text File Name	Match Score	P-Value
yeast_ribose_catabolism.grp	0.0	0.0
yeast_pentose_phosphate_pathway.grp	-10.2172	0.0
yeast_non_oxidative_branch_pentose_phosphate_pathw...	-10.2172	0.0
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-13.241	0.0
yeast_deoxyribose_phosphate_metabolism.grp	-13.241	0.0
yeast_pentose_phosphate_pathway.grp	-13.9489	0.01
yeast_non_oxidative_branch_pentose_phosphate_pathw...	-13.9489	0.01
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-13.9583	0.01
yeast_xylulose_monophosphate_cycle.grp	-15.1398	0.01
yeast_super_gluconate_utilization.grp	-15.1963	0.02
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-15.1963	0.02
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-15.241	0.06
yeast_deoxyribose_phosphate_metabolism.grp	-15.241	0.06
yeast_pentose_phosphate_pathway.grp	-15.9489	0.07
yeast_non_oxidative_branch_pentose_phosphate_pathw...	-15.9489	0.07
yeast_glycolysis.grp	-16.2384	0.07
yeast_glucose_fermentation.grp	-16.2384	0.07
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-16.4343	0.07
yeast_pentose_phosphate_pathway.grp	-16.4343	0.07
yeast_deoxyribose_phosphate_metabolism.grp	-16.4343	0.07
yeast_lactose_degradation.grp	-16.9798	0.09
yeast_galactose_metabolism.grp	-16.9798	0.09
yeast_galactose_metabolism.grp	-16.9798	0.09
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-17.0028	0.1
yeast_trehalose_anabolism.grp	-17.6306	0.14
yeast_sucrose_biosynth.grp	-17.6306	0.14
yeast_strach_cellulose_biosynth.grp	-17.6306	0.14
yeast_mannose_GDP_mannose_degradation.grp	-17.6306	0.14
yeast_lactose_degradation.grp	-17.6306	0.14
yeast_galactose_metabolism.grp	-17.6306	0.14
yeast_colanic_acid_building_blocks_biosynth2.grp	-17.6306	0.14
yeast_sucrose_biosynth.grp	-17.6513	0.17
yeast_mannose_GDP_mannose_degradation.grp	-17.6513	0.17
yeast_pentose_phosphate_pathway.grp	-17.9489	0.17
yeast_serine_isocitrate_lyase_pathway.grp	-18.2178	0.18
yeast_galactose_metabolism.grp	-18.2178	0.18
yeast_glycolysis.grp	-18.2384	0.18
yeast_glucose_fermentation.grp	-18.2384	0.18
yeast_glucose_fermentation.grp	-18.2384	0.18
yeast_aerobic_glycerol_catabolism.grp	-18.2384	0.18
yeast_tryptophan_biosynth.grp	-18.2408	0.18
yeast_super_phenylalanine_tyrosine_tryptophane_biosyn...	-18.2408	0.18
yeast_sucrose_biosynth.grp	-18.2408	0.18
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-18.2408	0.18
yeast_hestidine_biosynth.grp	-18.2408	0.18
yeast_glycolysis.grp	-18.2408	0.18
yeast_glucose_fermentation.grp	-18.2408	0.18
yeast_colanic_acid_building_blocks_biosynth1.grp	-18.2408	0.18
yeast_chorismate_pathway.grp	-18.2408	0.18
yeast_aerobic_glycerol_catabolism.grp	-18.2408	0.18
yeast_aerobic_glycerol_catabolism.grp	-18.2408	0.18
yeast_mevalonate_pathway.grp	-18.3444	0.21
yeast_ergosterol_biosynth.grp	-18.3444	0.21
yeast_deoxyribose_phosphate_metabolism.grp	-18.4343	0.21
yeast_UDP_N_acetylglactosamine_biosynth.grp	-18.8687	0.21
yeast_UDP_N_acetylglactosamine_biosynth.grp	-18.8687	0.21

Click on a column name to sort table. Click on a row to view match.

16) yeast_super_phenylalanine_tyrosine_biosynth

Text File Name	Match Score	P-Value
yeast_super_phenylalanine_tyrosine_ tryptophane_biosynth.grp	0.0	0.0
yeast_super_phenylalanine_tyrosine_biosynth.grp	0.0	0.0
yeast_phenylalanine_tyrosine_ tryptophan_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	0.0	0.0
yeast_phenylalanine_tyrosine_ tryptophan_biosynth.grp	-2.0	0.0
yeast_chorismate_pathway.grp	-2.0	0.0
yeast_phenylalanine_tyrosine_ tryptophan_biosynth.grp	-12.7443	0.0
yeast_chorismate_pathway.grp	-12.7443	0.0
yeast_phenylalanine_tyrosine_ tryptophan_biosynth.grp	-13.9824	0.0
yeast_chorismate_pathway.grp	-13.9824	0.0
yeast_phenylalanine_tyrosine_ tryptophan_biosynth.grp	-14.7443	0.0
yeast_chorismate_pathway.grp	-14.7443	0.0
yeast_serine_isocitrate_lyase_pathway.grp	-29.4768	0.14
yeast_super_leucine_ isoleucine_valine_biosynth1.grp	-30.1981	0.19
yeast_ergosterol_biosynth.grp	-31.2247	0.25
yeast_serine_isocitrate_lyase_pathway.grp	-31.4768	0.25
yeast_glycolysis.grp	-31.4797	0.25
yeast_glucose_fermentation.grp	-31.4797	0.25
yeast_aerobic_glycerol_catabolism.grp	-31.4797	0.25
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-31.496	0.26
yeast_deoxyribose_phosphate_metabolism.grp	-31.496	0.26
yeast_super_leucine_ isoleucine_valine_biosynth1.grp	-31.4985	0.26
yeast_glycolysis.grp	-32.1792	0.34
yeast_glucose_fermentation.grp	-32.1792	0.34
yeast_aerobic_glycerol_catabolism.grp	-32.1792	0.34
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.2457	0.35
yeast_hestidine_biosynth.grp	-32.2457	0.35
yeast_UDP_N_acetylglactosamine_biosynth.grp	-32.4835	0.37
yeast_UDP_N_acetylglactosamine_biosynth.grp	-32.4835	0.37
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.6135	0.37
yeast_serine_isocitrate_lyase_pathway.grp	-32.7177	0.38
yeast_glycolysis.grp	-32.9412	0.41
yeast_glucose_fermentation.grp	-32.9412	0.41
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.0077	0.41
yeast_hestidine_biosynth.grp	-33.0077	0.41
yeast_ergosterol_biosynth.grp	-33.1028	0.41
yeast_super_phenylalanine_tyrosine_ tryptophane_biosynth.grp	-33.2234	0.42
yeast_ergosterol_biosynth.grp	-33.2247	0.42
yeast_super_leucine_ isoleucine_valine_biosynth1.grp	-33.3929	0.42
yeast_super_leucine_ isoleucine_valine_biosynth2.grp	-33.439	0.43
yeast_super_ isoleucine_valine_biosynth1.grp	-33.439	0.43
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.439	0.43
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.439	0.43
yeast_ isoleucine_biosynth.grp	-33.439	0.43
yeast_hestidine_biosynth.grp	-33.439	0.43
yeast_heme_biosynth.grp	-33.8352	0.47
yeast_de_novo_pyrimidine_ribonuc_biosynth.grp	-33.8515	0.48
yeast_threonine_methionine_biosynth.grp	-33.9364	0.49
yeast_sulfur_amino_acid_biosynth.grp	-33.9364	0.49
yeast_strach_cellulose_biosynth.grp	-33.948	0.49
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-33.948	0.49
yeast_deoxyribose_phosphate_metabolism.grp	-33.948	0.49
yeast_arginine_ornithine_proline_interconversion.grp	-33.9521	0.49
yeast_arginine_ornithine_proline_interconversion.grp	-33.9521	0.49
yeast_aerobic_glycerol_catabolism.grp	-34.1161	0.49
yeast_aerobic_glycerol_catabolism.grp	-34.1161	0.49

Click on a column name to sort table. Click on a row to view match.

17) yeast_tyrosine_biosynth

Text File Name	Match Score	P-Value
yeast_tyrosine_biosynth.grp	0.0	0.0
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	0.0	0.0
yeast_super_phenylalanine_tyrosine_biosynth.grp	0.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	0.0	0.0
yeast_chorismate_pathway.grp	0.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-2.0	0.0
yeast_chorismate_pathway.grp	-2.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-4.0	0.0
yeast_chorismate_pathway.grp	-4.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-6.0	0.0
yeast_chorismate_pathway.grp	-6.0	0.0
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-8.0	0.0
yeast_chorismate_pathway.grp	-8.0	0.0
yeast_ergosterol_biosynth.grp	-16.0284	0.09
yeast_UDP_N_acetylglactosamine_biosynth.grp	-16.0492	0.09
yeast_arginine_ornithine_proline_interconversion.grp	-16.2173	0.09
yeast_tyrosine_biosynth.grp	-16.4343	0.1
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-16.4343	0.1
yeast_super_phenylalanine_tyrosine_biosynth.grp	-16.4343	0.1
yeast_phenylalanine_degradation.grp	-16.4343	0.1
yeast_ergosterol_biosynth.grp	-16.6684	0.12
yeast_serine_isocitrate_lyase_pathway.grp	-16.7487	0.13
yeast_arginine_ornithine_proline_interconversion.grp	-17.5177	0.16
yeast_fatty_acid_oxidation.grp	-17.9139	0.16
yeast_fatty_acid_oxidation.grp	-17.9139	0.16
yeast_ergosterol_biosynth.grp	-18.0284	0.18
yeast_arginine_ornithine_proline_interconversion.grp	-18.2173	0.18
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-18.4343	0.18
yeast_super_phenylalanine_tyrosine_biosynth.grp	-18.4343	0.18
yeast_ergosterol_biosynth.grp	-18.6684	0.2
yeast_serine_isocitrate_lyase_pathway.grp	-18.7487	0.2
yeast_trehalose_anabolism.grp	-18.7517	0.2
yeast_sucrose_biosynth.grp	-18.7517	0.2
yeast_strach_cellulose_biosynth.grp	-18.7517	0.2
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-18.7517	0.2
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-18.7517	0.2
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-18.7517	0.2
yeast_mannose_GDP_mannose_degradation.grp	-18.7517	0.2
yeast_glycolysis.grp	-18.7517	0.2
yeast_glycogen_catabolism.grp	-18.7517	0.2
yeast_glucose_fermentation.grp	-18.7517	0.2
yeast_galactose_metabolism.grp	-18.7517	0.2
yeast_deoxyribose_phosphate_metabolism.grp	-18.7517	0.2
yeast_deoxyribose_phosphate_metabolism.grp	-18.7517	0.2
yeast_aerobic_glycerol_catabolism.grp	-18.7517	0.2
yeast_super_gluconate_utilization.grp	-18.9197	0.22
yeast_aerobic_glycerol_catabolism.grp	-18.9197	0.22
yeast_aerobic_glycerol_catabolism.grp	-18.9197	0.22
yeast_methionine_degradation.grp	-19.2069	0.23
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-19.4105	0.24
yeast_lysinine_biosynth.grp	-19.4105	0.24
yeast_lysinine_biosynth.grp	-19.4105	0.24
yeast_leucine_biosynth.grp	-19.4105	0.24
yeast_glutamate_degradation8.grp	-19.4105	0.24
yeast_glutamate_degradation7.grp	-19.4105	0.24
yeast_ectoine_synth.grp	-19.4105	0.24

Click on a column name to sort table. Click on a row to view match.

18) yeast_glutamate_degradation8

Text File Name	Match Score	P-Value
yeast_glutamate_degradation8.grp	0.0	0.0
yeast_arginine_metabolism.grp	0.0	0.0
yeast_glutamate_degradation8.grp	-24.158	0.0
yeast_arginine_metabolism.grp	-24.158	0.0
yeast_glycolysis.grp	-30.0415	0.13
yeast_glucose_fermentation.grp	-30.0415	0.13
yeast_glycolysis.grp	-31.2795	0.17
yeast_glucose_fermentation.grp	-31.2795	0.17
yeast_aerobic_glycerol_catabolism.grp	-31.2795	0.17
yeast_arginine_metabolism.grp	-31.6307	0.19
yeast_serine_isocitrate_lyase_pathway.grp	-32.0173	0.22
yeast_glycolysis.grp	-32.0415	0.23
yeast_glucose_fermentation.grp	-32.0415	0.23
yeast_aerobic_glycerol_catabolism.grp	-32.0415	0.23
yeast_arginine_metabolism.grp	-32.3926	0.25
yeast_glucose_fermentation.grp	-32.8035	0.28
yeast_sulfur_amino_acid_biosynth.grp	-32.8405	0.29
yeast_mevalonate_pathway.grp	-32.8405	0.29
yeast_ergosterol_biosynth.grp	-32.8405	0.29
yeast_triglyceride_biosynth.grp	-33.0237	0.34
yeast_threonine_catabolism.grp	-33.6132	0.38
yeast_fatty_acid_biosynth.grp	-33.6132	0.38
yeast_fatty_acid_biosynth.grp	-33.6132	0.38
yeast_aerobic_glycerol_catabolism.grp	-34.0415	0.41
yeast_glycolysis.grp	-34.1156	0.43
yeast_glucose_fermentation.grp	-34.1156	0.43
yeast_aerobic_glycerol_catabolism.grp	-34.1156	0.43
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.141	0.43
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.141	0.43
yeast_sulfur_amino_acid_biosynth.grp	-34.192	0.45
yeast_mevalonate_pathway.grp	-34.192	0.45
yeast_ergosterol_biosynth.grp	-34.192	0.45
yeast_triglyceride_biosynth.grp	-34.3752	0.46
yeast_glycolysis.grp	-34.5358	0.48
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-34.6693	0.5
yeast_strach_cellulose_biosynth.grp	-34.7822	0.53
yeast_phosphatidic_biosynth.grp	-34.7822	0.53
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.7822	0.53
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.7822	0.53
yeast_ergosterol_biosynth.grp	-34.7822	0.53
yeast_triglyceride_biosynth.grp	-34.8512	0.55
yeast_triglyceride_biosynth.grp	-34.8512	0.55
yeast_fatty_acid_biosynth.grp	-35.4301	0.59
yeast_fatty_acid_biosynth.grp	-35.4301	0.59
yeast_carbon_monoxide_dehydrogenase.grp	-35.4301	0.59
yeast_carbon_monoxide_dehydrogenase.grp	-35.4301	0.59
yeast_sulfur_amino_acid_biosynth.grp	-35.4925	0.6
yeast_sulfur_amino_acid_biosynth.grp	-35.4925	0.6
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-35.4925	0.6
yeast_aerobic_glycerol_catabolism.grp	-35.7738	0.64
yeast_lysine_biosynth.grp	-35.8449	0.66
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-35.9073	0.66
yeast_hestidine_biosynth.grp	-35.9073	0.66
yeast_threonine_methionine_biosynth.grp	-35.9578	0.68
yeast_threonine_methionine_biosynth.grp	-35.9578	0.68
yeast_threonine_biosynth.grp	-35.9578	0.68

Click on a column name to sort table. Click on a row to view match.

19) yeast_fatty_acid_elongation

Text File Name	Match Score	P-Value
yeast_fatty_acid_elongation.grp	0.0	0.0
yeast_fatty_acid_biosynth.grp	-2.0	0.0
yeast_fatty_acid_biosynth.grp	-4.0	0.0
yeast_fatty_acid_biosynth.grp	-6.0	0.0
yeast_fatty_acid_biosynth.grp	-8.0	0.0
yeast_fatty_acid_elongation.grp	-16.4343	0.06
yeast_fatty_acid_biosynth.grp	-16.4343	0.06
yeast_fatty_acid_oxidation.grp	-17.3448	0.11
yeast_threonine_methionine_biosynth.grp	-17.5887	0.11
yeast_threonine_catabolism.grp	-17.5887	0.11
yeast_methionine_biosynth.grp	-17.5887	0.11
yeast_TCA_cycle_aerobic_respiration.grp	-17.9899	0.12
yeast_glutamate_degradation7.grp	-17.9899	0.12
yeast_threonine_methionine_biosynth.grp	-18.8892	0.16
yeast_threonine_catabolism.grp	-18.8892	0.16
yeast_fatty_acid_oxidation.grp	-18.8892	0.16
yeast_TCA_cycle_aerobic_respiration.grp	-18.9333	0.18
yeast_sulfur_amino_acid_biosynth.grp	-18.9333	0.18
yeast_glutamate_degradation3.grp	-18.9333	0.18
yeast_fatty_acid_oxidation.grp	-19.3448	0.2
yeast_toluene_via_catechol_degradation.grp	-19.4105	0.2
yeast_p_cymene_degradation.grp	-19.4105	0.2
yeast_p_cymene_degradation.grp	-19.4105	0.2
yeast_ergosterol_biosynth.grp	-19.4105	0.2
yeast_threonine_biosynth.grp	-19.468	0.2
yeast_super_hexitol_degradation.grp	-19.468	0.2
yeast_pantothenate_coenzymeA_biosynth.grp	-19.468	0.2
yeast_glucuronate_degradation.grp	-19.468	0.2
yeast_threonine_methionine_biosynth.grp	-19.5887	0.22
yeast_threonine_catabolism.grp	-19.5887	0.22
yeast_methionine_biosynth.grp	-19.5887	0.22
yeast_heme_biosynth.grp	-19.8067	0.23
yeast_heme_biosynth.grp	-19.8067	0.23
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-19.8691	0.23
yeast_de_novo_pyrimidine_ribonuc_biosynth.grp	-19.8691	0.23
yeast_TCA_cycle_aerobic_respiration.grp	-19.9899	0.27
yeast_glutamate_degradation7.grp	-19.9899	0.27
yeast_sulfur_amino_acid_biosynth.grp	-20.2338	0.28
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-20.2338	0.28
yeast_phosphatidic_acid_biosynth.grp	-20.2338	0.28
yeast_mevalonate_pathway.grp	-20.2338	0.28
yeast_glutamate_degradation8.grp	-20.2338	0.28
yeast_glutamate_degradation8.grp	-20.2338	0.28
yeast_glutamate_degradation7.grp	-20.2338	0.28
yeast_ergosterol_biosynth.grp	-20.2338	0.28
yeast_ectoine_synth.grp	-20.2338	0.28
yeast_carbon_monoxide_dehydrogenase.grp	-20.2338	0.28
yeast_carbon_monoxide_dehydrogenase.grp	-20.2338	0.28
yeast_arginine_metabolism.grp	-20.2338	0.28
yeast_arginine_metabolism.grp	-20.2338	0.28
yeast_ureide_biosynth.grp	-20.706	0.33
yeast_ureide_biosynth.grp	-20.706	0.33
yeast_toluene_via_catechol_degradation.grp	-20.706	0.33
yeast_toluene_via_catechol_degradation.grp	-20.706	0.33

Click on a column name to sort table. Click on a row to view match.

20) yeast_salvage_pyrimidine_deoxyribonuc_pathway

Text File Name	Match Score	P-Value
yeast_salvage_pyrimidine_deoxyribonuc_pathway.grp	0.0	0.0
yeast_salvage_pyrimidine_ribonuc_pathway.grp	-19.9403	0.0
yeast_salvage_pyrimidine_ribonuc_pathway.grp	-21.9403	0.0
yeast_salvage_pyrimidine_ribonuc_pathway.grp	-25.3061	0.02
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-31.0857	0.23
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-31.7341	0.29
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-31.7838	0.29
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-31.7838	0.29
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-31.7838	0.29
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.0128	0.32
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.3005	0.43
yeast_thiamine_biosynth.grp	-33.3669	0.43
yeast_NAD_salvage_pathway.grp	-33.4785	0.45
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.5946	0.45
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.5946	0.45
yeast_purine_fermentation.grp	-33.6752	0.46
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.7248	0.46
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.0178	0.5
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.0178	0.5
yeast_NAD_salvage_pathway.grp	-34.127	0.52
yeast_de_novo_purine_nuc_biosynth.grp	-34.3733	0.52
yeast_de_novo_purine_nuc_biosynth.grp	-34.9629	0.58
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-35.2392	0.61
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-35.2392	0.61
yeast_threonine_methionine_biosynth.grp	-35.2559	0.61
yeast_glycolysis.grp	-35.2559	0.61
yeast_glucose_fermentation.grp	-35.2559	0.61
yeast_ergosterol_biosynth.grp	-35.3694	0.67
yeast_de_novo_purine_nuc_biosynth.grp	-35.6113	0.69
yeast_de_novo_purine_nuc_biosynth.grp	-35.9067	0.69
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-36.0178	0.74
yeast_strach_cellulose_biosynth.grp	-36.0202	0.75
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-36.0202	0.75
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-36.0202	0.75
yeast_ergosterol_biosynth.grp	-36.0202	0.75
yeast_de_novo_purine_nuc_biosynth.grp	-36.3733	0.77
yeast_threonine_methionine_biosynth.grp	-36.6074	0.77
yeast_sulfur_amino_acid_biosynth.grp	-36.6074	0.77
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-36.6074	0.77
yeast_pantothenate_coenzymeA_biosynth.grp	-36.6074	0.77
yeast_chorismate_pathway.grp	-36.6074	0.77
yeast_ureide_degradation.grp	-36.6748	0.79
yeast_ureide_degradation.grp	-36.6748	0.79
yeast_ureide_degradation.grp	-36.6748	0.79
yeast_sucrose_biosynth.grp	-37.1875	0.79
yeast_ribose_deoxyribose_phosphate_metabolism.grp	-37.2392	0.8
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-37.2392	0.8
yeast_chorismate_pathway.grp	-37.2392	0.8
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-37.2416	0.8
yeast_chorismate_pathway.grp	-37.2416	0.8
yeast_glycolysis.grp	-37.2559	0.82
yeast_glucose_fermentation.grp	-37.2559	0.82
yeast_chorismate_pathway.grp	-37.2583	0.82

Click on a column name to sort table. Click on a row to view match.

21) yeast_super_isoleucine_valine_biosynth2

Text File Name	Match Score	P-Value
yeast_valine_biosynth.grp	0.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	0.0	0.0
yeast_super_isoleucine_valine_biosynth2.grp	0.0	0.0
yeast_super_isoleucine_valine_biosynth1.grp	0.0	0.0
yeast_isoleucine_biosynth.grp	0.0	0.0
yeast_super_isoleucine_valine_biosynth1.grp	-2.0	0.0
yeast_isoleucine_biosynth.grp	-2.0	0.0
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-4.89037	0.0
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-5.76519	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-13.9824	0.0
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-19.3247	0.02
yeast_leucine_biosynth.grp	-19.3247	0.02
yeast_super_leucine_isoleucine_valine_biosynth2.grp	-19.7476	0.03
yeast_super_isoleucine_valine_biosynth1.grp	-19.7476	0.03
yeast_isoleucine_biosynth.grp	-19.7476	0.03
yeast_super_phenylalanine_tyrosine_tryptophan_biosynth1.grp	-19.8951	0.03
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-20.4932	0.03
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-21.8951	0.11
yeast_chorismate_pathway.grp	-21.8951	0.11
yeast_super_leucine_isoleucine_valine_biosynth1.grp	-22.1995	0.11
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-22.7699	0.13
yeast_chorismate_pathway.grp	-22.7699	0.13
yeast_lysinase_biosynth.grp	-23.6014	0.23
yeast_mevalonate_pathway.grp	-23.6588	0.24
yeast_ergosterol_biosynth.grp	-23.6588	0.24
yeast_serine_isocitrate_lyase_pathway.grp	-23.8356	0.25
yeast_serine_isocitrate_lyase_pathway.grp	-24.4449	0.31
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-24.7699	0.34
yeast_chorismate_pathway.grp	-24.7699	0.34
yeast_serine_isocitrate_lyase_pathway.grp	-25.0899	0.35
yeast_serine_isocitrate_lyase_pathway.grp	-25.1906	0.36
yeast_super_phenylalanine_tyrosine_biosynth.grp	-25.2219	0.37
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-25.2219	0.37
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-25.2219	0.37
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.2219	0.37
yeast_histidine_biosynth.grp	-25.2219	0.37
yeast_chorismate_pathway.grp	-25.2219	0.37
yeast_heme_biosynth.grp	-25.4724	0.4
yeast_glucuronate_degradation.grp	-25.6513	0.4
yeast_TCA_cycle_aerobic_respiration.grp	-25.6588	0.41
yeast_mevalonate_pathway.grp	-25.6588	0.41
yeast_ergosterol_biosynth.grp	-25.6588	0.41
yeast_sulfur_amino_acid_biosynth.grp	-25.8057	0.43
yeast_p_cymene_degradation.grp	-25.828	0.43
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.828	0.43
yeast_glucose_fermentation.grp	-25.828	0.43
yeast_chorismate_pathway.grp	-25.828	0.43
yeast_chorismate_biosynth.grp	-25.828	0.43
yeast_serine_isocitrate_lyase_pathway.grp	-25.8356	0.46
yeast_de_novo_purine_nuc_biosynth.grp	-25.8443	0.47
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-26.2832	0.5
yeast_histidine_biosynth.grp	-26.2832	0.5
yeast_folic_acid_biosynth.grp	-26.3039	0.5
yeast_TCA_cycle_aerobic_respiration.grp	-26.5174	0.52
yeast_lysinase_biosynth.grp	-26.5174	0.52

Click on a column name to sort table. Click on a row to view match.

22) yeast_leucine_biosynth

Text File Name	Match Score	P-Value
yeast_super_leucine_ isoleucine_valine_biosynth1.grp	0.0	0.0
yeast_leucine_biosynth.grp	0.0	0.0
yeast_super_leucine_ isoleucine_valine_biosynth1.grp	-2.0	0.0
yeast_super_leucine_ isoleucine_valine_biosynth1.grp	-4.0	0.0
yeast_super_leucine_ isoleucine_valine_biosynth1.grp	-6.0	0.0
yeast_super_leucine_ isoleucine_valine_biosynth2.grp	-16.2277	0.0
yeast_super_leucine_ isoleucine_valine_biosynth1.grp	-16.728	0.0
yeast_lysine_biosynth.grp	-17.2501	0.01
yeast_super_ isoleucine_valine_biosynth1.grp	-19.1025	0.01
yeast_ isoleucine_biosynth.grp	-19.1025	0.01
yeast_valine_biosynth.grp	-19.3247	0.02
yeast_super_ isoleucine_valine_biosynth2.grp	-19.3247	0.02
yeast_super_ isoleucine_valine_biosynth1.grp	-19.3247	0.02
yeast_ isoleucine_biosynth.grp	-19.3247	0.02
yeast_TCA_cycle_aerobic_respiration.grp	-21.1906	0.06
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-21.8489	0.1
yeast_chorismate_pathway.grp	-21.8489	0.1
yeast_super_leucine_ isoleucine_valine_biosynth2.grp	-22.1995	0.1
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-22.3009	0.11
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-22.8273	0.14
yeast_chorismate_pathway.grp	-22.8273	0.14
yeast_chorismate_biosynth.grp	-22.8273	0.14
yeast_TCA_cycle_aerobic_respiration.grp	-23.1906	0.15
yeast_serine_isocitrate_lyase_pathway.grp	-23.2425	0.16
yeast_serine_isocitrate_lyase_pathway.grp	-23.8356	0.22
yeast_p_cymene_degradation.grp	-23.8356	0.22
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-23.8519	0.23
yeast_folic_acid_biosynth.grp	-23.8519	0.23
yeast_chorismate_pathway.grp	-23.8519	0.23
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-23.945	0.23
yeast_chorismate_pathway.grp	-23.945	0.23
yeast_chorismate_biosynth.grp	-23.945	0.23
yeast_threonine_catabolism.grp	-24.0817	0.25
yeast_serine_isocitrate_lyase_pathway.grp	-24.4449	0.26
yeast_sulfur_amino_acid_biosynth.grp	-24.5052	0.28
yeast_serine_isocitrate_lyase_pathway.grp	-24.59	0.29
yeast_serine_isocitrate_lyase_pathway.grp	-25.0899	0.33
yeast_folic_acid_biosynth.grp	-25.0899	0.33
yeast_chorismate_pathway.grp	-25.0899	0.33
yeast_super_phenylalanine_tyrosine_biosynth.grp	-25.1757	0.33
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.1757	0.33
yeast_fatty_acid_oxidation.grp	-25.2793	0.36
yeast_fatty_acid_biosynth.grp	-25.2793	0.36
yeast_sulfur_amino_acid_biosynth.grp	-25.4724	0.37
yeast_methionine_degradation.grp	-25.4724	0.37
yeast_glucuronate_degradation.grp	-25.6513	0.39
yeast_sulfur_degradation.grp	-25.7433	0.39
yeast_sulfur_amino_acid_biosynth.grp	-25.7433	0.39
yeast_sulfur_degradation.grp	-25.8057	0.39
yeast_sulfur_amino_acid_biosynth.grp	-25.8057	0.39
yeast_heme_biosynth.grp	-25.828	0.39
yeast_p_cymene_degradation.grp	-25.8356	0.4
yeast_4_hydroxyproline_degradation.grp	-26.2414	0.42
yeast_mevalonate_pathway.grp	-26.3039	0.43
yeast_ergosterol_biosynth.grp	-26.3039	0.43
yeast_sulfur_degradation.grp	-26.5052	0.47

Click on a column name to sort table. Click on a row to view match.

23) yeast_valine_biosynth

Text File Name	Match Score	P-Value
yeast_valine_biosynth.grp	0.0	0.0
yeast_super_leucine_ileucine_valine_biosynth1.grp	0.0	0.0
yeast_super_ileucine_valine_biosynth2.grp	0.0	0.0
yeast_super_ileucine_valine_biosynth1.grp	0.0	0.0
yeast_ileucine_biosynth.grp	0.0	0.0
yeast_super_ileucine_valine_biosynth1.grp	-2.0	0.0
yeast_ileucine_biosynth.grp	-2.0	0.0
yeast_super_leucine_ileucine_valine_biosynth2.grp	-4.89037	0.0
yeast_super_leucine_ileucine_valine_biosynth2.grp	-5.76519	0.0
yeast_super_leucine_ileucine_valine_biosynth1.grp	-13.9824	0.0
yeast_super_leucine_ileucine_valine_biosynth1.grp	-19.3247	0.02
yeast_leucine_biosynth.grp	-19.3247	0.02
yeast_super_leucine_ileucine_valine_biosynth2.grp	-19.7476	0.03
yeast_super_ileucine_valine_biosynth1.grp	-19.7476	0.03
yeast_ileucine_biosynth.grp	-19.7476	0.03
yeast_super_phenylalanine_tyrosine_tryptophan_bio...	-19.8951	0.03
yeast_super_leucine_ileucine_valine_biosynth1.grp	-20.4932	0.03
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-21.8951	0.11
yeast_chorismate_pathway.grp	-21.8951	0.11
yeast_super_leucine_ileucine_valine_biosynth1.grp	-22.1995	0.11
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-22.7699	0.13
yeast_chorismate_pathway.grp	-22.7699	0.13
yeast_lysine_biosynth.grp	-23.6014	0.23
yeast_mevalonate_pathway.grp	-23.6588	0.24
yeast_ergosterol_biosynth.grp	-23.6588	0.24
yeast_serine_isocitrate_lyase_pathway.grp	-23.8356	0.25
yeast_serine_isocitrate_lyase_pathway.grp	-24.4449	0.31
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-24.7699	0.34
yeast_chorismate_pathway.grp	-24.7699	0.34
yeast_serine_isocitrate_lyase_pathway.grp	-25.0899	0.35
yeast_serine_isocitrate_lyase_pathway.grp	-25.1906	0.36
yeast_super_phenylalanine_tyrosine_biosynth.grp	-25.2219	0.37
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-25.2219	0.37
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-25.2219	0.37
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.2219	0.37
yeast_histidine_biosynth.grp	-25.2219	0.37
yeast_chorismate_pathway.grp	-25.2219	0.37
yeast_heme_biosynth.grp	-25.4724	0.4
yeast_glucuronate_degradation.grp	-25.6513	0.4
yeast_TCA_cycle_aerobic_respiration.grp	-25.6588	0.41
yeast_mevalonate_pathway.grp	-25.6588	0.41
yeast_ergosterol_biosynth.grp	-25.6588	0.41
yeast_sulfur_amino_acid_biosynth.grp	-25.8057	0.43
yeast_p_cymene_degradation.grp	-25.828	0.43
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-25.828	0.43
yeast_glucose_fermentation.grp	-25.828	0.43
yeast_chorismate_pathway.grp	-25.828	0.43
yeast_chorismate_biosynth.grp	-25.828	0.43
yeast_serine_isocitrate_lyase_pathway.grp	-25.8356	0.46
yeast_de_novo_purine_nuc_biosynth.grp	-25.8443	0.47
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-26.2832	0.5
yeast_histidine_biosynth.grp	-26.2832	0.5
yeast_folic_acid_biosynth.grp	-26.3039	0.5
yeast_TCA_cycle_aerobic_respiration.grp	-26.5174	0.52
yeast_lysine_biosynth.grp	-26.5174	0.52

Click on a column name to sort table. Click on a row to view match.

24) yeast_ileucine_biosynth

Text File Name	Match Score	P-Value
yeast_super_ileucine_valine_biosynth1.grp	0.0	0.0
yeast_ileucine_biosynth.grp	0.0	0.0
yeast_super_leucine_ileucine_valine_biosynth2.grp	-11.5304	0.0
yeast_super_leucine_ileucine_valine_biosynth1.grp	-22.1995	0.0
yeast_super_leucine_ileucine_valine_biosynth1.grp	-25.0899	0.02
yeast_super_leucine_ileucine_valine_biosynth1.grp	-27.0899	0.06
yeast_chorismate_pathway.grp	-27.6603	0.07
yeast_super_leucine_ileucine_valine_biosynth2.grp	-27.9647	0.08
yeast_super_ileucine_valine_biosynth1.grp	-27.9647	0.08
yeast_ileucine_biosynth.grp	-27.9647	0.08
yeast_super_phenylalanine_tyrosine_tryptophan_biosynth.grp	-28.1122	0.08
yeast_super_leucine_ileucine_valine_biosynth1.grp	-28.2584	0.08
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-28.5351	0.08
yeast_chorismate_pathway.grp	-28.5351	0.08
yeast_super_leucine_ileucine_valine_biosynth1.grp	-28.7104	0.11
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-30.1122	0.23
yeast_serine_isocitrate_lyase_pathway.grp	-30.2101	0.23
yeast_serine_isocitrate_lyase_pathway.grp	-30.9557	0.28
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-30.9871	0.29
yeast_chorismate_pathway.grp	-30.9871	0.29
yeast_heme_biosynth.grp	-31.2376	0.29
yeast_serine_isocitrate_lyase_pathway.grp	-31.7177	0.36
yeast_mevalonate_pathway.grp	-31.876	0.38
yeast_ergosterol_biosynth.grp	-31.876	0.38
yeast_serine_isocitrate_lyase_pathway.grp	-32.0527	0.4
yeast_chorismate_pathway.grp	-32.069	0.4
yeast_serine_isocitrate_lyase_pathway.grp	-32.2025	0.4
yeast_TCA_cycle_aerobic_respiration.grp	-32.2989	0.43
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.2989	0.43
yeast_chorismate_pathway.grp	-32.2989	0.43
yeast_chorismate_biosynth.grp	-32.2989	0.43
yeast_arginine_metabolism.grp	-32.3294	0.44
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.6231	0.46
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.8551	0.47
yeast_heme_biosynth.grp	-33.2784	0.49
yeast_threonine_methionine_biosynth.grp	-33.3778	0.51
yeast_super_phenylalanine_tyrosine_biosynth.grp	-33.439	0.51
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.439	0.51
yeast_histidine_biosynth.grp	-33.439	0.51
yeast_lysine_biosynth.grp	-33.5369	0.52
yeast_sulfur_degradation.grp	-33.6434	0.57
yeast_sulfur_amino_acid_biosynth.grp	-33.6434	0.57
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.6975	0.58
yeast_de_novo_purine_nuc_biosynth.grp	-33.6975	0.58
yeast_p_cymene_degradation.grp	-33.7299	0.58
yeast_heme_biosynth.grp	-33.7299	0.58
yeast_folic_acid_biosynth.grp	-33.7299	0.58
yeast_glucuronate_degradation.grp	-33.8684	0.59
yeast_TCA_cycle_aerobic_respiration.grp	-33.876	0.59
yeast_heme_biosynth.grp	-33.999	0.59
yeast_p_cymene_degradation.grp	-34.0452	0.59
yeast_glucose_fermentation.grp	-34.0452	0.59
yeast_de_novo_purine_nuc_biosynth.grp	-34.0615	0.59
yeast_chorismate_biosynth.grp	-34.2825	0.6
yeast_mevalonate_pathway.grp	-34.2989	0.6
yeast_ergosterol_biosynth.grp	-34.2989	0.6

Click on a column name to sort table. Click on a row to view match.

25) yeast_ileucine_biosynth

Text File Name	Match Score	P-Value
yeast_super_ileucine_valine_biosynth1.grp	0.0	0.0
yeast_ileucine_biosynth.grp	0.0	0.0
yeast_super_leucine_ileucine_valine_biosynth2.grp	-11.5304	0.0
yeast_super_leucine_ileucine_valine_biosynth1.grp	-22.1995	0.0
yeast_super_leucine_ileucine_valine_biosynth1.grp	-25.0899	0.02
yeast_super_leucine_ileucine_valine_biosynth1.grp	-27.0899	0.06
yeast_chorismate_pathway.grp	-27.6603	0.07
yeast_super_leucine_ileucine_valine_biosynth2.grp	-27.9647	0.08
yeast_super_ileucine_valine_biosynth1.grp	-27.9647	0.08
yeast_ileucine_biosynth.grp	-27.9647	0.08
yeast_super_phenylalanine_tyrosine_tryptophan_biosynth.grp	-28.1122	0.08
yeast_super_leucine_ileucine_valine_biosynth1.grp	-28.2584	0.08
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-28.5351	0.08
yeast_chorismate_pathway.grp	-28.5351	0.08
yeast_super_leucine_ileucine_valine_biosynth1.grp	-28.7104	0.11
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-30.1122	0.23
yeast_serine_isocitrate_lyase_pathway.grp	-30.2101	0.23
yeast_serine_isocitrate_lyase_pathway.grp	-30.9557	0.28
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-30.9871	0.29
yeast_chorismate_pathway.grp	-30.9871	0.29
yeast_heme_biosynth.grp	-31.2376	0.29
yeast_serine_isocitrate_lyase_pathway.grp	-31.7177	0.36
yeast_mevalonate_pathway.grp	-31.876	0.38
yeast_ergosterol_biosynth.grp	-31.876	0.38
yeast_serine_isocitrate_lyase_pathway.grp	-32.0527	0.4
yeast_chorismate_pathway.grp	-32.069	0.4
yeast_serine_isocitrate_lyase_pathway.grp	-32.2025	0.4
yeast_TCA_cycle_aerobic_respiration.grp	-32.2989	0.43
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.2989	0.43
yeast_chorismate_pathway.grp	-32.2989	0.43
yeast_chorismate_biosynth.grp	-32.2989	0.43
yeast_arginine_metabolism.grp	-32.3294	0.44
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.6231	0.46
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.8551	0.47
yeast_heme_biosynth.grp	-33.2784	0.49
yeast_threonine_methionine_biosynth.grp	-33.3778	0.51
yeast_super_phenylalanine_tyrosine_biosynth.grp	-33.439	0.51
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.439	0.51
yeast_histidine_biosynth.grp	-33.439	0.51
yeast_lysine_biosynth.grp	-33.5369	0.52
yeast_sulfur_degradation.grp	-33.6434	0.57
yeast_sulfur_amino_acid_biosynth.grp	-33.6434	0.57
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.6975	0.58
yeast_de_novo_purine_nuc_biosynth.grp	-33.6975	0.58
yeast_p_cymene_degradation.grp	-33.7299	0.58
yeast_heme_biosynth.grp	-33.7299	0.58
yeast_folic_acid_biosynth.grp	-33.7299	0.58
yeast_glucuronate_degradation.grp	-33.8684	0.59
yeast_TCA_cycle_aerobic_respiration.grp	-33.876	0.59
yeast_heme_biosynth.grp	-33.999	0.59
yeast_p_cymene_degradation.grp	-34.0452	0.59
yeast_glucose_fermentation.grp	-34.0452	0.59
yeast_de_novo_purine_nuc_biosynth.grp	-34.0615	0.59
yeast_chorismate_biosynth.grp	-34.2825	0.6
yeast_mevalonate_pathway.grp	-34.2989	0.6

Click on a column name to sort table. Click on a row to view match.

26) yeast_super_ileucine_valine_biosynth1

Text File Name	Match Score	P-Value
yeast_super_ileucine_valine_biosynth1.grp	0.0	0.0
yeast_ileucine_biosynth.grp	0.0	0.0
yeast_super_leucine_ileucine_valine_biosynth2.grp	-11.5304	0.0
yeast_super_leucine_ileucine_valine_biosynth1.grp	-22.1995	0.0
yeast_super_leucine_ileucine_valine_biosynth1.grp	-25.0899	0.02
yeast_super_leucine_ileucine_valine_biosynth1.grp	-27.0899	0.06
yeast_chorismate_pathway.grp	-27.6603	0.07
yeast_super_leucine_ileucine_valine_biosynth2.grp	-27.9647	0.08
yeast_super_ileucine_valine_biosynth1.grp	-27.9647	0.08
yeast_ileucine_biosynth.grp	-27.9647	0.08
yeast_super_phenylalanine_tyrosine_tryptophane_biosynth.grp	-28.1122	0.08
yeast_super_leucine_ileucine_valine_biosynth1.grp	-28.2584	0.08
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-28.5351	0.08
yeast_chorismate_pathway.grp	-28.5351	0.08
yeast_super_leucine_ileucine_valine_biosynth1.grp	-28.7104	0.11
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-30.1122	0.23
yeast_serine_isocitrate_lyase_pathway.grp	-30.2101	0.23
yeast_serine_isocitrate_lyase_pathway.grp	-30.9557	0.28
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-30.9871	0.29
yeast_chorismate_pathway.grp	-30.9871	0.29
yeast_heme_biosynth.grp	-31.2376	0.29
yeast_serine_isocitrate_lyase_pathway.grp	-31.7177	0.36
yeast_mevalonate_pathway.grp	-31.876	0.38
yeast_ergosterol_biosynth.grp	-31.876	0.38
yeast_serine_isocitrate_lyase_pathway.grp	-32.0527	0.4
yeast_chorismate_pathway.grp	-32.069	0.4
yeast_serine_isocitrate_lyase_pathway.grp	-32.2025	0.4
yeast_TCA_cycle_aerobic_respiration.grp	-32.2989	0.43
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.2989	0.43
yeast_chorismate_pathway.grp	-32.2989	0.43
yeast_chorismate_biosynth.grp	-32.2989	0.43
yeast_arginine_metabolism.grp	-32.3294	0.44
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-32.6231	0.46
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-32.8551	0.47
yeast_heme_biosynth.grp	-33.2784	0.49
yeast_threonine_methionine_biosynth.grp	-33.3778	0.51
yeast_super_phenylalanine_tyrosine_biosynth.grp	-33.439	0.51
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.439	0.51
yeast_histidine_biosynth.grp	-33.439	0.51
yeast_lysin_biosynth.grp	-33.5369	0.52
yeast_sulfur_degradation.grp	-33.6434	0.57
yeast_sulfur_amino_acid_biosynth.grp	-33.6434	0.57
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-33.6975	0.58
yeast_de_novo_purine_nuc_biosynth.grp	-33.6975	0.58
yeast_p_cymene_degradation.grp	-33.7299	0.58
yeast_heme_biosynth.grp	-33.7299	0.58
yeast_folic_acid_biosynth.grp	-33.7299	0.58
yeast_glucuronate_degradation.grp	-33.8684	0.59
yeast_TCA_cycle_aerobic_respiration.grp	-33.876	0.59
yeast_heme_biosynth.grp	-33.999	0.59
yeast_p_cymene_degradation.grp	-34.0452	0.59
yeast_glucose_fermentation.grp	-34.0452	0.59
yeast_de_novo_purine_nuc_biosynth.grp	-34.0615	0.59
yeast_chorismate_biosynth.grp	-34.2825	0.6
yeast_mevalonate_pathway.grp	-34.2989	0.6
yeast_ergosterol_biosynth.grp	-34.2989	0.6

Click on a column name to sort table. Click on a row to view match.

27) yeast_methionine_biosynth

Text File Name	Match Score	P-Value
yeast_threonine_methionine_biosynth.grp	0.0	0.0
yeast_methionine_biosynth.grp	0.0	0.0
yeast_threonine_methionine_biosynth.grp	-16.4343	0.0
yeast_sulfur_amino_acid_biosynth.grp	-28.9787	0.0
yeast_sulfur_degradation.grp	-29.6782	0.0
yeast_arginine_metabolism.grp	-36.3794	0.09
yeast_glucose_fermentation.grp	-37.0207	0.13
yeast_sulfur_degradation.grp	-37.3334	0.16
yeast_arginine_metabolism.grp	-38.3794	0.22
yeast_TCA_cycle_aerobic_respiration.grp	-39.2506	0.34
yeast_aerobic_glycerol_catabolism.grp	-39.4967	0.37
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-39.7551	0.41
yeast_glucose_fermentation.grp	-39.8807	0.44
yeast_glycolysis.grp	-40.0284	0.44
yeast_glucose_fermentation.grp	-40.0284	0.44
yeast_glycolysis.grp	-40.618	0.55
yeast_glucose_fermentation.grp	-40.618	0.55
yeast_aerobic_glycerol_catabolism.grp	-40.618	0.55
yeast_sulfur_amino_acid_biosynth.grp	-40.7396	0.58
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-41.1066	0.65
yeast_pantothenate_coenzymeA_biosynth.grp	-41.6559	0.69
yeast_phosphatidic_biosynth.grp	-41.7551	0.7
yeast_phosphatidic_biosynth.grp	-41.7551	0.7
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-41.7551	0.7
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-41.7551	0.7
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-41.7551	0.7
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-41.8365	0.73
yeast_de_novo_pyrimidine_ribonuc_biosynth.grp	-41.8365	0.73
yeast_chorismate_pathway.grp	-41.8365	0.73
yeast_lysine_biosynth.grp	-41.856	0.73
yeast_glucose_fermentation.grp	-41.8807	0.74
yeast_glycolysis.grp	-42.0284	0.74
yeast_aerobic_glycerol_catabolism.grp	-42.0284	0.74
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-42.1025	0.74
yeast_chorismate_pathway.grp	-42.1025	0.74
yeast_de_novo_pyrimidine_deoxynuc_biosynth.grp	-42.1446	0.77
yeast_super_leucine_ileucine_valine_biosynth1.grp	-42.1535	0.77
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.1535	0.77
yeast_histidine_biosynth.grp	-42.1535	0.77
yeast_phosphatidic_biosynth.grp	-42.207	0.77
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.2194	0.77
yeast_ubiquinone_Q_prenylation.grp	-42.2581	0.77
yeast_ubiquinone_biosynth.grp	-42.2581	0.77
yeast_threonine_catabolism.grp	-42.3327	0.78
yeast_super_histidine_purine_pyrimidine_biosynth.grp	-42.3784	0.78
yeast_de_novo_purine_nuc_biosynth.grp	-42.3784	0.78
yeast_de_novo_purine_nuc_biosynth.grp	-42.3784	0.78
yeast_threonine_catabolism.grp	-42.4092	0.78
yeast_ergosterol_biosynth.grp	-42.4919	0.78
yeast_aerobic_glycerol_catabolism.grp	-42.618	0.79
yeast_glucuronate_degradation.grp	-42.768	0.79
yeast_serine_isocitrate_lyase_pathway.grp	-42.809	0.79
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-42.968	0.81
yeast_chorismate_pathway.grp	-42.968	0.81
yeast_chorismate_biosynth.grp	-42.968	0.81
yeast_alutamate_denradation7.grp	-42.9746	0.81

Click on a column name to sort table. Click on a row to view match.

28) yeast_threonine_biosynth

Text File Name	Match Score	P-Value
yeast_threonine_methionine_biosynth.grp	0.0	0.0
yeast_threonine_biosynth.grp	0.0	0.0
yeast_methionine_biosynth.grp	-8.07776	0.0
yeast_threonine_methionine_biosynth.grp	-16.4343	0.0
yeast_aerobic_glycerol_catabolism.grp	-27.3941	0.04
yeast_glycolysis.grp	-28.0391	0.05
yeast_glucose_fermentation.grp	-28.0391	0.05
yeast_sulfur_degradation.grp	-28.7768	0.06
yeast_glucose_fermentation.grp	-29.6612	0.1
yeast_glucose_fermentation.grp	-30.0391	0.12
yeast_arginine_metabolism.grp	-30.0415	0.12
yeast_sulfur_amino_acid_biosynth.grp	-30.0773	0.12
yeast_sulfate_assimilation_pathway2.grp	-30.0773	0.12
yeast_TCA_cycle_aerobic_respiration.grp	-31.0335	0.25
yeast_aerobic_glycerol_catabolism.grp	-31.2795	0.26
yeast_glucose_fermentation.grp	-31.6612	0.35
yeast_arginine_metabolism.grp	-32.0415	0.39
yeast_sulfur_amino_acid_biosynth.grp	-32.5224	0.46
yeast_serine_isocitrate_lyase_pathway.grp	-32.5894	0.47
yeast_pantothenate_coenzymeA_biosynth.grp	-32.6744	0.47
yeast_threonine_methionine_biosynth.grp	-32.8687	0.52
yeast_threonine_biosynth.grp	-32.8687	0.52
yeast_methionine_biosynth.grp	-32.8687	0.52
yeast_threonine_catabolism.grp	-32.9016	0.52
yeast_TCA_cycle_aerobic_respiration.grp	-33.0335	0.53
yeast_glycolysis.grp	-33.0493	0.53
yeast_glucose_fermentation.grp	-33.0493	0.53
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-33.4548	0.61
yeast_mevalonate_pathway.grp	-33.5104	0.64
yeast_ergosterol_biosynth.grp	-33.5104	0.64
yeast_threonine_methionine_biosynth.grp	-33.6307	0.66
yeast_lysinine_biosynth.grp	-33.6388	0.66
yeast_glycolysis.grp	-33.6388	0.66
yeast_aerobic_glycerol_catabolism.grp	-33.6388	0.66
yeast_lysinine_biosynth.grp	-33.9148	0.68
yeast_aerobic_glycerol_catabolism.grp	-33.9329	0.68
yeast_sulfur_amino_acid_biosynth.grp	-34.0065	0.68
yeast_de_novo_purine_nuc_biosynth.grp	-34.1613	0.7
yeast_glucuronate_degradation.grp	-34.5508	0.71
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-34.7439	0.71
yeast_mevalonate_pathway.grp	-34.7439	0.71
yeast_ergosterol_biosynth.grp	-34.7439	0.71
yeast_chorismate_pathway.grp	-34.7439	0.71
yeast_chorismate_biosynth.grp	-34.7439	0.71
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-34.7484	0.72
yeast_chorismate_pathway.grp	-34.7484	0.72
yeast_chorismate_biosynth.grp	-34.7484	0.72
yeast_super_leucine_ileucine_valine_biosynth2.grp	-34.7508	0.72
yeast_super_ileucine_valine_biosynth1.grp	-34.7508	0.72
yeast_phenylalanine_tyrosine_tryptophan_biosynth.grp	-34.7508	0.72
yeast_ileucine_biosynth.grp	-34.7508	0.72
yeast_chorismate_pathway.grp	-34.7508	0.72
yeast_chorismate_biosynth.grp	-34.7508	0.72
yeast_glutamate_degradation7.grp	-34.7575	0.74
yeast_phosphatidic_acid_phospholipid_biosynth.grp	-34.8063	0.74

Click on a column name to sort table. Click on a row to view match.