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|--|----------------|
| 1: 6.17 GO:0006099--tricarboylate acid cycle | group 1: 2-49 |
| 2: 6.17 GO:0046356--acetyl-CoA catabolic process | group 2: 2-16 |
| 3: 5.94 GO:0009109--coenzyme catabolic process | group 3: 2-12 |
| 4: 5.94 GO:0051187--cofactor catabolic process | group 4: 1-94 |
| 5: 5.15 GO:0006084--acetyl-CoA metabolic process | group 5: 1-51 |
| 6: 5.95 tricarboylate acid cycle | group 6: 1-45 |
| 7: 4.2 eca00020: Citrate cycle (TCA cycle) | group 7: 1-41 |
| 8: 2.22 GO:0008643--carbohydrate transport | group 8: 1-40 |
| 9: 2.36 sugar transport | group 9: 1-28 |
| 10: 1.12 magnesium | group 10: 1-21 |
| 11: 1.85 GO:0002817--magnesium ion binding | group 11: 1-15 |
| 12: 5.91 eca00020: glycine,serine and threonine metabolism | group 12: 1-14 |
| 13: 1.95 GO:0006732--coenzyme metabolic process | group 13: 1-14 |
| 14: 1.62 GO:0051186--cofactor metabolic process | |
| 15: 3.19 GO:0009060--aerobic respiration | |
| 16: 1.49 GO:0050893--generation of precursor metabolites and energy | |
| 17: 1.49 GO:0048333--cellular respiration | |
| 18: 1.23 GO:0006093--generation of precursor metabolites and energy | |
| 19: 3.89 eca00260: glycine,serine and threonine metabolism | |
| 20: 2.34 GO:0005373--cellular amino acid derivative metabolic process | |
| 21: 2.61 GO:0042398--cellular amino acid derivative biosynthetic process | |
| 22: 1.76 GO:0046872--metal ion binding | |
| 23: 1.24 GO:0043169--cation binding | |
| 24: 1.24 GO:0043167--ion binding | |
| 25: 2.45 manganese | |
| 26: 2.03 GO:0030145--manganese ion binding | |
| 27: 1.43 GO:0030258--lipid modification | |
| 28: 1.06 GO:0019395--fatty acid oxidation | |
| 29: 3.06 GO:0034440--lipid oxidation | |
| 30: 2.02 GO:0006631--fatty acid metabolic process | |
| 31: 7.01 metal ion binding site:Calcium | |
| 32: 4.16 calcium | |
| 33: 2.71 GO:0005509--calcium ion binding | |
| 34: 2.11 GO:0034470--mRNA processing | |
| 35: 1.83 GO:0034660--mRNA metabolic process | |
| 36: 1.88 GO:0006396--RNA processing | |