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|--|----------------|
| 1: 4.93 GO:0022900--electron transport chain | group 1: 4.59 |
| 2: 5.35 electron transport | group 2: 4.38 |
| 3: 3.18 iron | group 3: 4.31 |
| 4: 2.72 GO:0005506--iron ion binding | group 4: 3.69 |
| 5: 5.25 GO:0013980--energy derivation by oxidation of organic compounds | group 5: 3.33 |
| 6: 5.32 GO:0045333--cellular respiration | group 6: 2.59 |
| 7: 3.68 GO:0051540--metal cluster binding | group 7: 2.27 |
| 8: 3.68 GO:0051536--iron-sulfur cluster binding | group 8: 2.21 |
| 9: 4.91 4Fe-4S | group 9: 1.95 |
| 10: 4.25 GO:0051539--4 iron,4 sulfur cluster binding | group 10: 1.75 |
| 11: 3.84 iron-sulfur | group 11: 1.70 |
| 12: 5.25 GO:0046906--tetrapyrrole binding | group 12: 1.55 |
| 13: 5.25 GO:0020037--heme binding | group 13: 1.47 |
| 14: 5.23 heme | group 14: 1.35 |
| 15: 2.56 GO:0050662--coenzyme binding | group 15: 1.23 |
| 16: 1.79 GO:0048037--cofactor binding | group 16: 1.13 |
| 17: 8.15 tricarboxylic acid cycle | group 17: 1.08 |
| 18: 4.23 bsu00020:Citrate cycle (TCA cycle) | group 18: 1.06 |
| 19: 5.54 GO:0009060--aerobic respiration | group 19: 1.02 |
| 20: 5.28 GO:0006084--acetyl-CoA metabolic process | |
| 21: 5.28 GO:0006099--tricarboxylic acid cycle | |
| 22: 5.28 GO:0046336--acetyl-CoA catabolic process | |
| 23: 4.93 GO:0009109--coenzyme catabolic process | |
| 24: 4.93 GO:0051187--cofactor catabolic process | |
| 25: 1.87 metal-binding | |
| 26: 1.43 GO:0046872--metal ion binding | |
| 27: 1.37 GO:0043167--ion binding | |
| 28: 1.37 GO:0043169--cation binding | |
| 29: 15.91 IPR006067:Nitrite and sulphite reductase 4Fe-4S region | |
| 30: 15.91 IPR005117:Nitrite/sulphite reductase,hemoprotein beta-component,ferredoxin-like | |
| 31: 5.68 IPR013027:FAD-dependent pyridine nucleotide-disulphide oxidoreductase | |
| 32: 5.3 IPR001327:Pyridine nucleotide-disulphide oxidoreductase,NAD-binding region | |
| 33: 13.28 binding site:Heme (covalent) | |
| 34: 11.93 IPR003088:Cytochrome c, class I | |
| 35: 11.93 IPR009056:Cytochrome c,monohaem | |
| 36: 10.63 domain:4Fe-4S ferredoxin-type 2 | |
| 37: 10.63 domain:4Fe-4S ferredoxin-type 1 | |
| 38: 10.6 lipoyl | |
| 39: 9.54 IPR003016:2-oxo acid dehydrogenase,lipoyl-binding site | |
| 40: 8.66 GO:0031405--lipic acid binding | |
| 41: 10.6 acetoin catabolism | |
| 42: 8.87 GO:0042182--ketone catabolic process | |
| 43: 8.87 GO:0045150--acetoin catabolic process | |
| 44: 5.54 GO:0045149--acetoin metabolic process | |
| 45: 7.22 GO:0016675--oxidoreductase activity,acting on heme group of donors | |
| 46: 7.22 GO:0016676--oxidoreductase activity,acting on heme group of donors,oxygen as acceptor | |
| 47: 7.22 GO:0015002--heme-copper terminal oxidase activity | |
| 48: 7.22 GO:0004129--cytochrome-c oxidase activity | |
| 49: 2.11 GO:0005996--monosaccharide metabolic process | |
| 50: 2.35 GO:0019318--hexose metabolic process | |
| 51: 2.33 GO:0006006--glucose metabolic process | |
| 52: 2.72 GO:0046164--alcohol catabolic process | |
| 53: 2.59 GO:0044275--cellular carbohydrate catabolic process | |
| 54: 1.5 GO:0016052--carbohydrate catabolic process | |
| 55: 3.14 GO:0015077--monovalent inorganic cation transmembrane transporter activity | |
| 56: 3.14 GO:0015078--hydrogen ion transmembrane transporter activity | |
| 57: 2.11 GO:0022890--inorganic cation transmembrane transporter activity | |
| 58: 5.54 GO:0046148--pigment biosynthetic process | |
| 59: 5.54 GO:0042440--pigment metabolic process | |