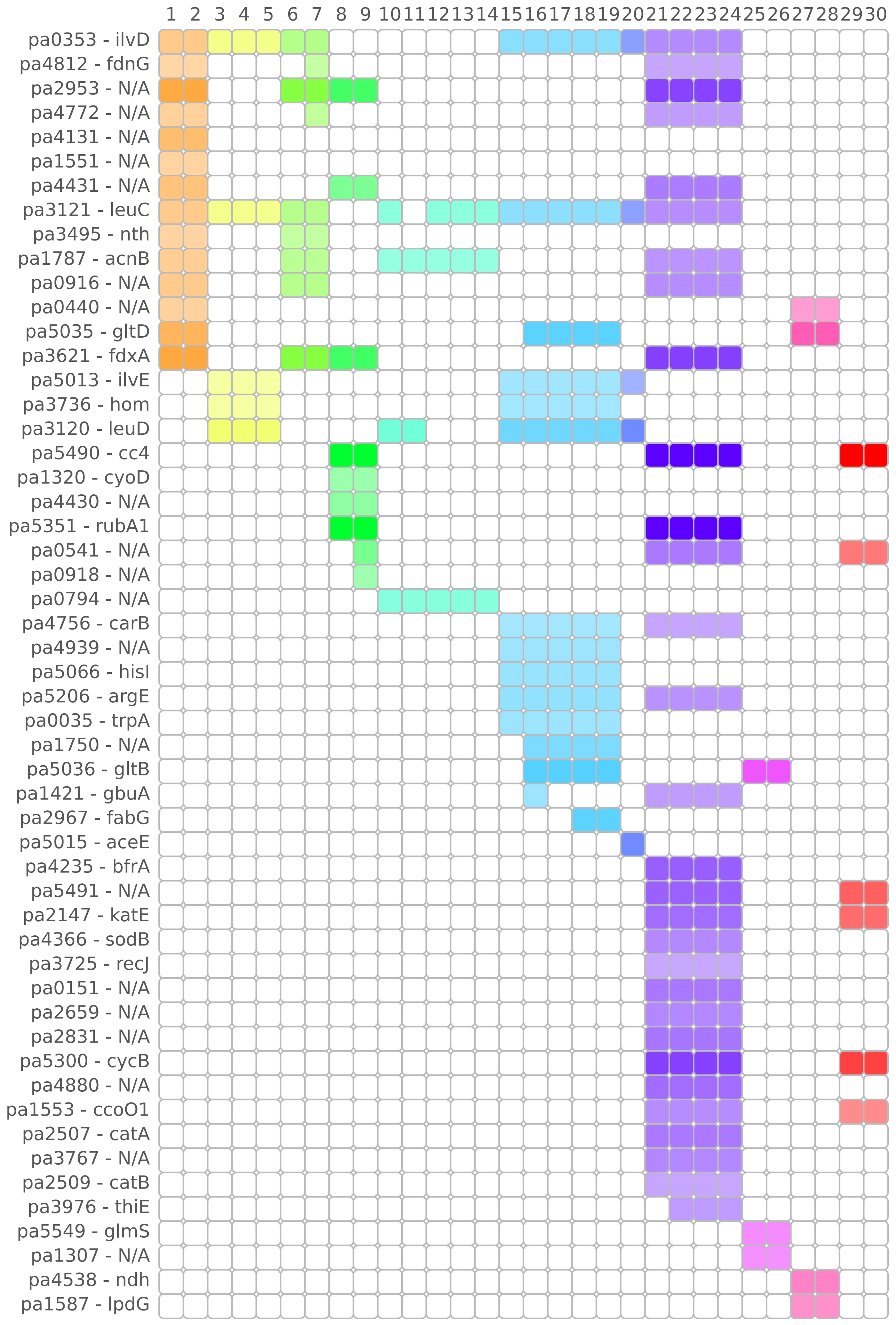

1: 3.34 GO:0051536~iron-sulfur cluster binding
2: 3.34 GO:0051540~metal cluster binding
3: 16.67 branched-chain amino acid biosynthesis
4: 9.25 GO:0009082~branched chain family amino acid biosynthetic process
5: 6.53 GO:0009081~branched chain family amino acid metabolic process
6: 5.66 4fe-4s
7: 3.91 GO:0051539~4 iron,4 sulfur cluster binding
8: 5.19 electron transport
9: 3.57 GO:0022900~electron transport chain
10: 19.92 IPR015937:Aconitase-like core
11: 18.68 IPR015928:Aconitase/3-isopropylmalate dehydratase,swivel
12: 18.68 IPR001030:Aconitase/3-isopropylmalate dehydratase large subunit,alpha/beta/alpha
13: 18.68 IPR015931:Aconitase/3-isopropylmalate dehydratase large subunit,alpha/beta/alpha,subdomain 1/3
14: 18.68 IPR015932:Aconitase/3-isopropylmalate dehydratase large subunit,alpha/beta/alpha,subdomain 2
15: 3.46 amino-acid biosynthesis
16: 2.51 GO:0009309~amine biosynthetic process
17: 2.58 GO:0008652~cellular amino acid biosynthetic process
18: 2.02 GO:0046394~carboxylic acid biosynthetic process
19: 2 GO:0016053~organic acid biosynthetic process
20: 5.91 pap00290:Valine,leucine and isoleucine biosynthesis
21: 1.79 GO:0046914~transition metal ion binding
22: 1.45 GO:0046872~metal ion binding
23: 1.42 GO:0043169~cation binding
24: 1.42 GO:0043167~ion binding
25: 9.34 IPR000583:Glutamine amidotransferase,class-II
26: 9.34 IPR017932:Glutamine amidotransferase,type II
27: 5.86 IPR001327:Pyridine nucleotide-disulphide oxidoreductase,NAD-binding region
28: 3.44 IPR013027:FAD-dependent pyridine nucleotide-disulphide oxidoreductase
29: 2.51 GO:0020037~heme binding
30: 2.37 GO:0046906~tetrapyrrole binding

group 1: 3.75
group 2: 3.01
group 3: 2.86
group 4: 2.63
group 5: 2.28
group 6: 2.24
group 7: 1.82
group 8: 1.82
group 9: 1.42
group 10: 1.26
group 11: 1.03