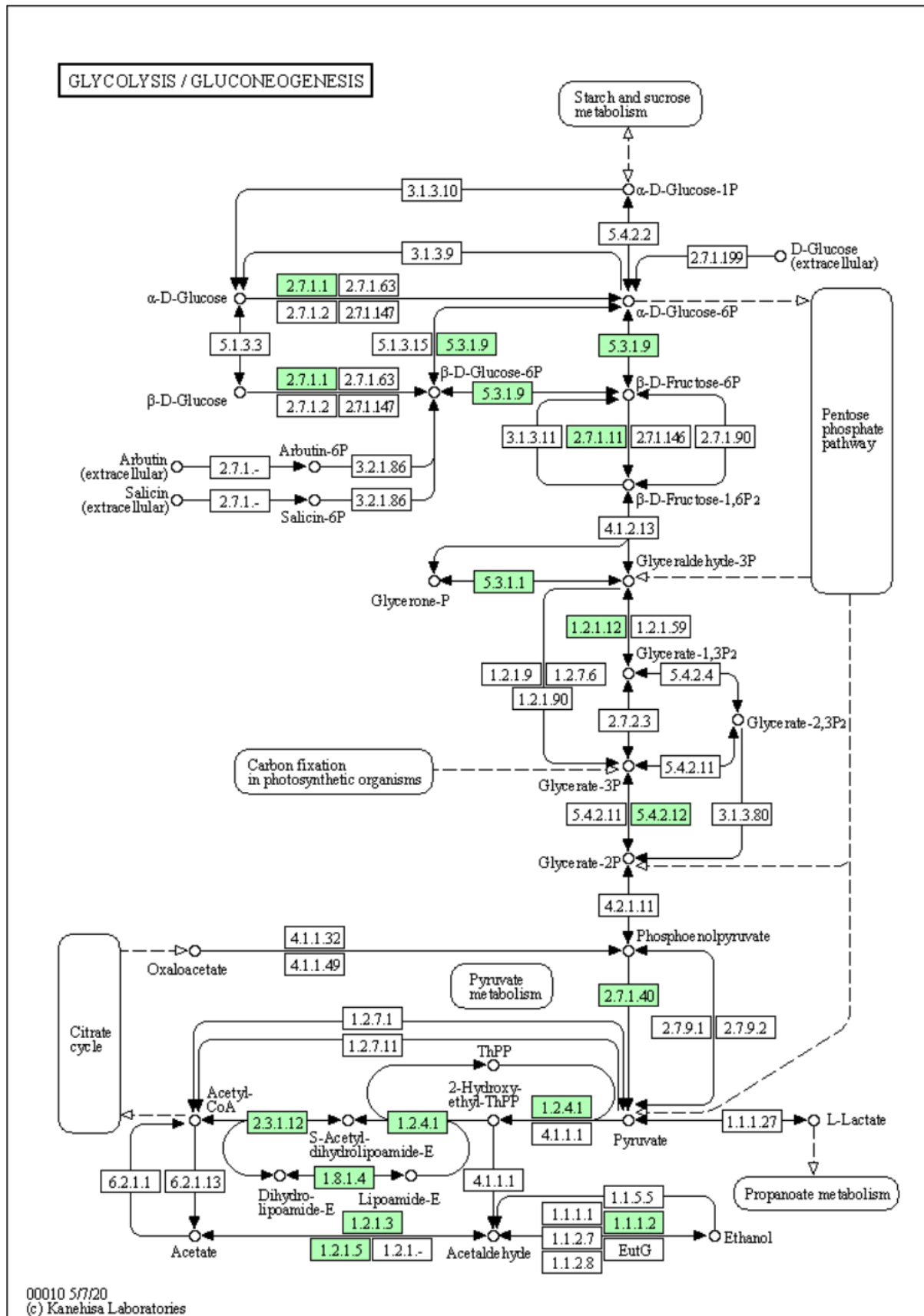
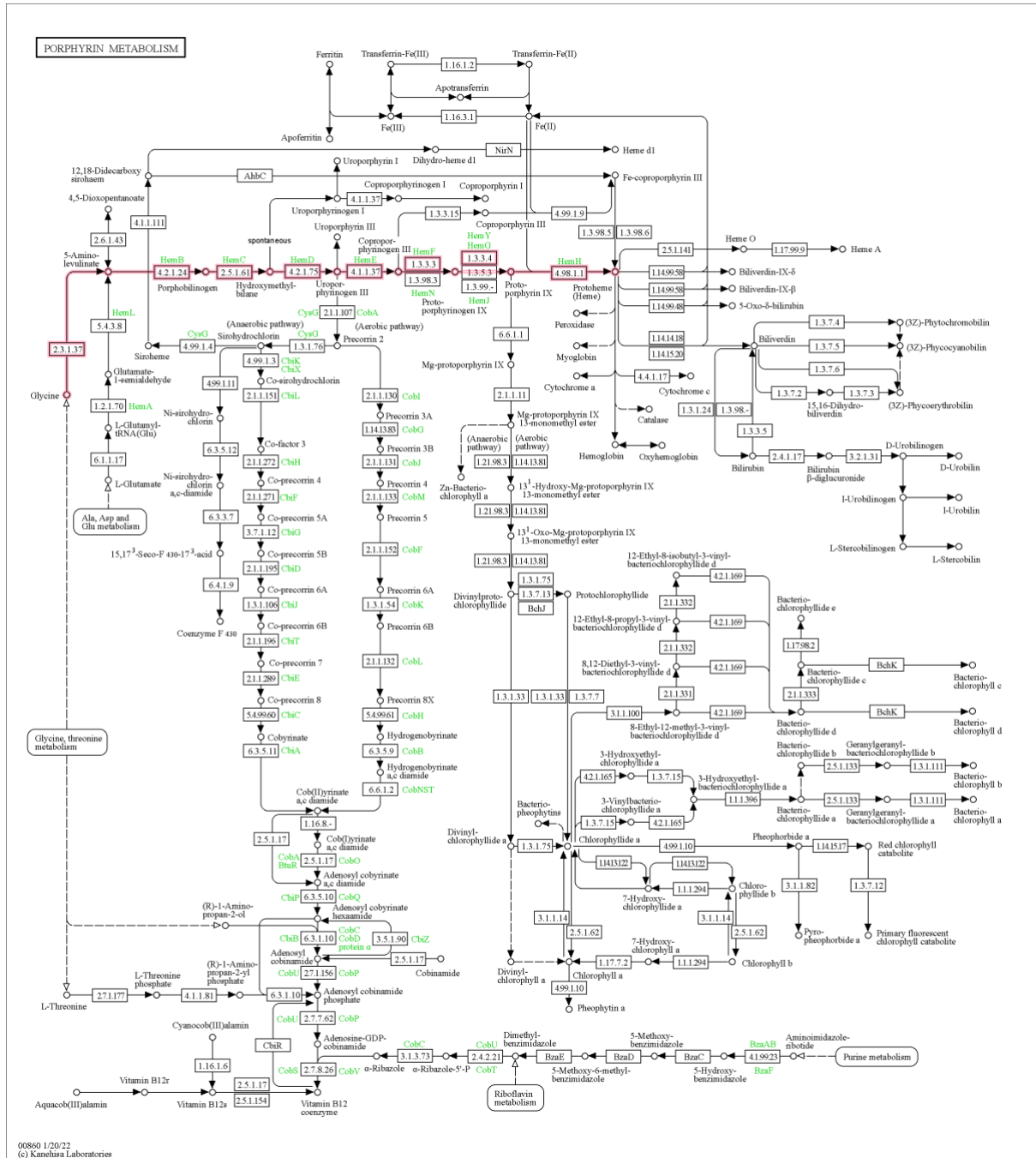


A



KO	geneid	annotation	reaction
K00002	GG_SM_NEW_LIB10227	alcohol dehydrogenase (NADP+) [EC:1.1.1.2]	a primary alcohol + NADP+ = an aldehyde + NADPH + H+
K00128	GG_SM_NEW_LIB1972	aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]	an aldehyde + NAD+ + H2O = a carboxylate + NADH + H+
K00129	GG_SM_NEW_LIB197	aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]	an aldehyde + NAD(P)+ + H2O = a carboxylate + NAD(P)H + H+
K00134	GG_SM_NEW_LIB15548, GG_SM_NEW_LIB15547, GG_SM_NEW_LIB15544, GG_SM_NEW_LIB20798	glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [EC:1.2.1.12]	D-glyceraldehyde-3-phosphate:NAD+ oxidoreductase (phosphorylating) Also acts very slowly on D-glyceraldehyde and some other aldehydes; thiols can replace phosphate
K00149	GG_SM_NEW_LIB17448	aldehyde dehydrogenase family 9 member A1 [EC:1.2.1.47 1.2.1.3]	4-trimethylammonibutanal + NAD+ + H2O = 4-trimethylammonibutanoate + NADH + 2 H+
K00161	GG_SM_NEW_LIB17024, GG_SM_NEW_LIB17025	pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	pyruvate + [dihydrolipoyllysine-residue acetyltransferase] lipoyllysine = [dihydrolipoyllysine-residue acetyltransferase] S-acetyldihydrolipoyllysine + CO2
K00162	GG_SM_NEW_LIB6758, GG_SM_NEW_LIB6759, GG_SM_NEW_LIB6761, GG_SM_NEW_LIB6756, GG_SM_NEW_LIB6755	pyruvate dehydrogenase E1 component beta subunit [EC:1.2.4.1]	pyruvate + [dihydrolipoyllysine-residue acetyltransferase] lipoyllysine = [dihydrolipoyllysine-residue acetyltransferase] S-acetyldihydrolipoyllysine + CO2
K00382	GG_SM_NEW_LIB19429	dihydrolipoamide dehydrogenase [EC:1.8.1.4]	protein N6-(dihydrolipoyl)lysine + NAD+ = protein N6-(lipoyl)lysine + NADH + H+
K00627	GG_SM_NEW_LIB366	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	acetyl-CoA + enzyme N6-(dihydrolipoyl)lysine = CoA + enzyme N6-(S-acetyldihydrolipoyl)lysine
K00844	GG_SM_NEW_LIB11096, GG_SM_NEW_LIB21111	hexokinase [EC:2.7.1.1]	ATP + D-hexose = ADP + D-hexose 6-phosphate ATP + D-glucose = ADP + D-glucose 6-phosphate ATP + D-hexose = ADP + D-hexose 6-phosphate
K00850	GG_SM_NEW_LIB4896	6-phosphofructokinase 1 [EC:2.7.1.11]	ATP + beta-D-fructofuranose 6-phosphate = ADP + beta-D-fructofuranose 1,6-bisphosphate

K00873	GG_SM_NEW_LIB20909	pyruvate kinase [EC:2.7.1.40]	ATP + pyruvate = ADP + phosphoenolpyruvate
K01803	GG_SM_NEW_LIB11800	triosephosphate isomerase (TIM) [EC:5.3.1.1]	D-Glyceraldehyde 3-phosphate = glyceralone phosphate
K01810	GG_SM_NEW_LIB12661	glucose-6-phosphate isomerase [EC:5.3.1.9]	alpha-D-glucose 6-phosphate = beta-D-fructofuranose 6-phosphate
K15633	GG_SM_NEW_LIB1862	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12]	2-phospho-D-glycerate = 3-phospho-D-glycerate



KO	geneid	annotation	reaction
K00228	GG_SM_NEW_LIB10092	coproporphyrinogen III oxidase [EC:1.3.3.3]	coproporphyrinogen III + O ₂ + 2 H ⁺ = protoporphyrinogen-IX + 2 CO ₂ + 2 H ₂ O
	GG_SM_NEW_LIB10093		
K00231	GG_SM_NEW_LIB16792	protoporphyrinogen/coproporphyrinogen III oxidase [EC:1.3.3.4; 1.3.3.15]	protoporphyrinogen IX + 3 O ₂ = protoporphyrin IX + 3 H ₂ O ₂
	GG_SM_NEW_LIB14530		
	GG_SM_NEW_LIB14531		

K00643	GG_SM_NEW_LIB20208	5-aminolevulinate synthase [EC:2.3.1.37]	succinyl-CoA + glycine = 5-aminolevulinate + CoA + CO ₂
K01599	GG SM NEW LIB377	uroporphyrinogen decarboxylase [EC:4.1.1.37]	uroporphyrinogen III = coproporphyrinogen III + 4 CO ₂
	GG SM NEW LIB376		
	GG SM NEW LIB374		
K01698	GG SM NEW LIB3984	porphobilinogen synthase [EC:4.2.1.24]	2 5-aminolevulinate = porphobilinogen + 2 H ₂ O
	GG SM NEW LIB3326		
	GG SM NEW LIB3985		
K01749	GG_SM_NEW_LIB12658	hydroxymethylbilane synthase [EC:2.5.1.61]	4 porphobilinogen + H ₂ O = hydroxymethylbilane + 4 NH ₃
K01772	GG SM NEW LIB15955	protoporphyrin/ coproporphyrin ferrochelatase [EC:4.98.1.1; 4.99.1.9]	protoheme + 2 H ⁺ = protoporphyrin + Fe ²⁺
	GG SM NEW LIB15956		
	GG_SM_NEW_LIB6112		