type type Fumarate hydratase class I (EC 4.2.1.2) Alpha–glucosidase, family 31 of glycosyl hydrolases, COG1501 2–methylisocitrate dehydratase (EC 4.2.1.99) PrpF protein involved in 2–methylcitrate cycle non-responder 3 untreated Trimethylamine methyltransferase corrinoid protein Fructose-bisphosphate aldolase, archaeal class I (EC 4.1.2.13) 2 Predicted L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit YkgF Hypothetical oxidoreductase YqhD (EC 1.1.-.-)
Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5) Pyruvate oxidase [ubiquinone, cytochrome] (EC 1.2.2.2)
Acetyl-CoA synthetase (ADP-forming) alpha and beta chains, putative 1 Fucose perméase Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (... Succinyl–CoA ligase [ADP–forming] beta chain (EC 6.2.1.5) 2–oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) Chondroitinase (chondroitin lyase) Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4) Mlc, transcriptional repressor of MalT (the transcriptional activator of malt... Transcriptional repressor of the fructose operon, DeoR family Alpha–amylase (EC 3.2.1.1) Chloride channel protein Alanine dehydrogenase (EC 1.4.1.1) Alpha-amylase (Neopullulanase) SúsA (EC 3.2.1.135) SusC, outer membrane protein involved in starch binding L-arabinose-specific 1-epimerase (mutarotase) Fructoselysine 3-epimerase Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1) Putative glycogen debranching enzyme, archaeal type, TIGR01561 Rhamnulose–1–phosphate aldolase (EC 4.1.2.19)
Unknown pentose isomerase TM0951 Methylmalonyl-CoA decarboxylase, alpha chain (EC 4.1.1.41) Two-component sensor histidine kinase, malate (EC 2.7.3.-) Predicted alpha-L-rhamnosidase Novel Xylose regulator from LacI family Ethanolamine utilization protein EutA Glyoxylate reductase (EC 1.1.1.79) N-Acetyl-D-glucosamine permease 2, possible Alpha-glucosidase SusB (EC 3.2.1.20)
Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)
Fructose-bisphosphate aldolase class I (EC 4.1.2.13)
Uncharacterized protein YphG, TPR-domain containing
Fumarate hydratase class I, anaerobic (EC 4.2.1.2) SusD, outer membrane protein
Regulatory protein SusR
Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) Alpha–N–acetylglucosaminidase (EC 3.2.1.50) Inositol–1–phosphate synthase (EC 5.5.1.4) D–alanine aminotransferase (EC 2.6.1.21) Fructoselysine kinase (EC 2.7.1.–) Predicted rhamnogalacturonan lyase in rhamnose utilization cluster Propanediol dehydratase large subunit (EC 4.2.1.28) Melibiose carrier protein, Na+/melibiose symporter Hexuronate utilization operon transcriptional repressor ExuR Propanediol dehydratase reactivation factor large subunit Glycerol dehydratase reactivation factor large subunit Propanediol utilization polyhedral body protein PduJ Glycerol uptake operon antiterminator regulatory protein Maltodextrin phosphorylase (EC 2.4.1.1) Carbon storage regulator
Biotin carboxyl carrier protein of oxaloacetate decarboxylase CoA-acylating propionaldehyde dehydrogenase Oligo-1,6-glucosidase (EC 3.2.1.10) rhamnogalacturonan acetylesterase 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) Fructose–6–phosphate phosphoketolase (EC 4.1.2.22)
Outer surface protein of unknown function, cellobiose operon PTS system, sucrose-specific IIA component (EC 2.7.1.69) Propanediol utilization polyhedral body protein PduN CoB--CoM heterodisulfide reductase subunit C (EC 1.8.98.1) Hypothetical oxidoreductase YdjG (EC 1.-.-.) Hypothetical oxidoreductase YdjG (EC 1.-.-.-)
Methanol:corrinoid methyltransferase
Transcriptional activator of maltose regulon, MalT
Predicted L-arabinose isomerase (EC 5.3.1.4)
Phosphoenolpyruvate carboxylase (EC 4.1.1.31)
Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8)
Beta-galactosidase (EC 3.2.1.23), LacA family
Betaine reductase component B alpha subunit (EC 1.21.4.4)
Maltose phosphorylase (EC 2.4.1.8)
Trehalose phosphorylase (EC 2.4.1.64)
Propagediol dehydratase medium subunit (EC 4.2.1.28) Propanediol dehydratase medium subúnit (EC 4.2.1.28) Glycorol dehydratase medium subunit (EC 4.2.1.30)
Cyclomaltodextrin glucanotransferase (EC 2.4.1.19)
NAD(P)-dependent glyceraldehyde 3-phosphate dehydrogenase archaeal (EC 1.2.1.59)
Glucose oligosaccharides ABC transporter system, sugar-binding protein Xylose oligosaccharides ABC transporter, sugar–binding protein Predicted nucleoside ABC transporter, substrate–binding component Predicted nucleoside ABC transporter, ATP–binding component L–xylulose/3–keto–L–gulonate kinase (EC 2.7.1.–) Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)
NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
Malate dehydrogenase (EC 1.1.1.37) Acetyl-CoA acetyltransferase (EC 2.3.1.9) Enolase (EC 4.2.1.11) N-acetylhexosamine 1-kinase Formate—tetrahydrofolate ligase (EC 6.3.4.3) Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18) Methylglyoxal synthase (EC 4.2.3.3) Altronate hydrolase (EC 4.2.1.7) Polygalacturonase (EC 3.2.1.15) Altronate oxidoreductase (EC 1.1.1.58)
Rhamnogalacturonides degradation protein RhiN L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) Peptidoglycan N-acetylglucosamine deacetylase (ÉC 3.5.1.-) 2-oxoglutarate oxidoreductase, alpha subunit (EC 1.2.7.3) NADP-dependent malic enzyme (EC 1.1.1.40) Alpha–mannosidase (EC 3.2.1.24) 2–dehydro–3–deoxygluconate kinase (EC 2.7.1.45) Beta-xylosidase (EC 3.2.1.37) Galactose–1–phosphate uridylyltransferase (EC 2.7.7.10) Glucokinase (EC 2.7.1.2) Formyl-coenzyme A transferase (EC 2.8.3.16) D-lactate dehydrogenase (EC 1.1.1.28) Alfa-L-rhamnosidase (EC 3.2.1.40) 2-oxoglutarate oxidoreductase, beta subunit (EC 1.2.7.3) 2-oxoglutarate oxidoreductase, gamma subunit (EC 1.2.7.3) D1D29 B2D29 B1D29 D2D29 C7D29 C6D29 A5D29