type type NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) Formate--tetrahydrofolate ligase (EC 6.3.4.3) non-responder 3 untreated Glycogen biosynthesis protein GlgD, glucose–1–phosphate adenylyltransferase f... 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) Glycogen synthase, ADP–glucose transglucosylase (EC 2.4.1.21) Glucose–6–phosphate isomerase (EC 5.3.1.9) Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3) 2 Enolase (EC 4.2.1.11) N-acetylhexosamine 1-kinase Formyl-coenzyme A transferase (EC 2.8.3.16) Phosphoglycerate mutase (EC 5.4.2.1)
Acetyl–CoA acetyltransferase (EC 2.3.1.9)
Malate dehydrogenase (EC 1.1.1.37) Malate dehydrogenase (EC 1.1.1.37)
Alpha–xylosidase (EC 3.2.1.–)
2–oxoglutarate oxidoreductase, alpha subunit (EC 1.2.7.3) 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-denydro-3-deoxygluconage (EC 2.7.1.45) 6-phospho-beta-glucosidase (EC 3.2.1.86) Beta-xylosidase (EC 3.2.1.37) Uronate isomerase (EC 5.3.1.12) 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)
Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)
Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5) Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) Glucokinase (EC 2.7.1.2) D-mannonate oxidoreductase (EC 1.1.1.57) Methylglyoxal synthase (EC 4.2.3.3) rhamnogalacturonan acetylesterase 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) Carbon storage regulator Maltose operon transcriptional repressor MalR, LacI family Oligo–1,6–glucosidase (EC 3.2.1.10) Lactaldehyde reductase (EC 1.1.1.77) Altronate hydrolase (EC 4.2.1.7) L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) Peptidoglycan N-acetylglucosamine deacetylase (ÉC 3.5.1.-) Rhamnogalacturonides degradation protein RhiN Altronate oxidoreductase (EC 1.1.1.58)
Altronate oxidoreductase (EC 1.1.1.58)
Propanediol dehydratase large subunit (EC 4.2.1.28) Melibiose carrier protein, Na+/melibiose symporter CoA-acylating propionaldehyde dehydrogenase 5-keto-D-gluconate 5-reductase (EC 1.1.1.69) Hexuronate utilization operon transcriptional repressor ExuR Propanediol dehydratase reactivation factor large subunit Glycerol dehydratase reactivation factor large subunit Biotin carboxyl carrier protein of oxaloacetate decarboxylase Maltodextrin phosphorylase (EC 2.4.1.1) 2–oxoglutarate oxidoreductase, gamma subunit (EC 1.2.7.3) 2–oxoglutarate oxidoreductase, beta subunit (EC 1.2.7.3) 2–oxoglutarate oxidoreductase, beta subunit (EC 1.2.7.3) D–lactate dehydrogenase (EC 1.1.1.28) NADH-dependent butanol dehydrogenase A (EC 1.1.1.-) Chloride channel protein Alanine dehydrogenase (EC 1.4.1.1) Xylose isomerase (EC 5.3.1.5) Transcriptional repressor of the fructose operon, DeoR family Alpha–amylase (EC 3.2.1.1) Methylmalonyl–CoA decarboxylase, alpha chain (EC 4.1.1.41)
Rhamnulose–1–phosphate aldolase (EC 4.1.2.19)
Trehalose–6–phosphate hydrolase (EC 3.2.1.93) Glycerol dehydratase small subunit (EC 4.2.1.30)
Propanediol dehydratase small subunit (EC 4.2.1.28)
Fructose–6–phosphate phosphoketolase (EC 4.1.2.22) Propanediol utilization polyhedral body protein PduJ Glycerol uptake operon antiterminator regulatory protein Ethanolamine utilization polyhedral-body-like protein EutN Maltose phosphorylase (EC 2.4.1.8) Trehalose phosphorylase (EC 2.4.1.64) Outer surface protein of unknown function, cellobiose operon L-xylulose/3-keto-L-gulonate kinase (EC 2.7.1.-)
Predicted nucleoside ABC transporter, ATP-binding component
Putative aldolase Ydjl Putative aldolase Ydjl Transcriptional activator of maltose regulon, MalT Predicted rhamnogalacturonide–specific TRAP–type transporter, small transmemb... CoB–CoM heterodisulfide reductase subunit C (EC 1.8.98.1) Hypothetical oxidoreductase YdjG (EC 1.-.-.-)

Xylose oligosaccharides ABC transporter, ATP-binding protein 2

Phosphoenolpyruvate carboxylase (EC 4.1.1.31)

Beta-phosphoglucomutase (EC 5.4.2.6)

Putative oxidoreductase YdjL

Propagadial debydratase medium subunit (EC 4.3.1.28) Propanediol dehydratase medium subunit (EC 4.2.1.28) Cyclomaltodextrin glucanotransferase (EC 2.4.1.19) Glycerol dehydratase medium subunit (EC 4.2.1.30) Beta-galactosidase (EC 3.2.1.23), LacA family Seta-galactosidase (EC 3.2.1.23), LacA family

Xylose ABC transporter, periplasmic xylose-binding protein XylF

Propanediol utilization polyhedral body protein PduN

Beta-galactosidase small subunit (EC 3.2.1.23)

NAD(P)-dependent glyceraldehyde 3-phosphate dehydrogenase archaeal (EC 1.2.1.59)

Glucose oligosaccharide ABC transport system, sugar-binding protein

Xylose oligosaccharides ABC transporter, sugar-binding protein

PTS system, sucrose-specific IIA component (EC 2.7.1.69)

Predicted nucleoside ABC transporter, substrate-binding component

D-alapine aminotransferase (EC 2.6.1.21) D-alanine aminotransferase (EC 2.6.1.21) Acetoin dehydrogenase E1 component beta–subunit (EC 1.2.4.–) Alpha–amylase (Neopullulanase) SusA (EC 3.2.1.135) Alpha–amylase (Neopullulanase) SusA (EC 3.2.1.135) L-arabinose-specific 1-epimerase (mutarotase)
SusC, outer membrane protein involved in starch binding SusC, outer membrane protein involved in starch binding
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 Fucose permease 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) PrpF protein involved in 2–methylcitrate cycle Fumarate hydratase class I (EC 4.2.1.2) 2-methylisocitrate dehydratase (EC 4.2.1.99) Alpha–glucosidase, family 31 of glycosyl hydrolases, COG1501 Mlc, transcriptional repressor of MaIT (the transcriptional activator of malt... Oxidoreductase, short chain dehydrogenase/reductase family Fructose-bisphosphate aldolase, archaeal class I (EC 4.1.2.13)
Predicted L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit YkgF Hypothetical oxidoreductase YqhD (EC 1.1.-.-) Alpha–N–acetylglucosaminidase (EC 3.2.1.50)
Inositol–1–phosphate synthase (EC 5.5.1.4)
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) 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) 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 Ethanolamine utilization protein EutA Transcriptional antiterminator of lichenan operon, BglG family Glyoxylate reductase (EC 1.1.1.79) Regulatory protein SusR Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1) Putative glycogen debranching enzyme, archaeal type, TIGR01561 Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase comple... Fructoselysine 3-epimerase Two-component sensor histidine kinase, malate (EC 2.7.3.-) Novel Xylose regulator from LacI family Predicted alpha-L-rhamnosidase