|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Supplementary Table 3.** Comparison of *Parageobacillus* genomes according to genes associated with carbohydrate utilization and exopolysaccharide production | | | | | | | | | | | | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| **M1** | ***Parageobacillus thermantarcticus* M1** |  |  |  |  |  |  |  |  |  |  |  |
| **CIC9** | ***Parageobacillus caldoxylosilyticus* CIC9** |  |  |  |  |  |  |  |  |  |  |  |
| **DSM 14590** | ***Parageobacillus toebii* DSM 14590** |  |  |  |  |  |  |  |  |  |  |  |
| **DSM 2542** | ***Parageobacillus thermoglucosidasius* DSM 2542** |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| ■ present in the genome □ not present in the genome   |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | | **Subsystem** | **Function** | **M1** | **CIC9** | **DSM 14590** | **DSM 2542** | | Beta-Glucoside Metabolism | Outer surface protein of unknown function, cellobiose operon | 0 |  |  |  | | Beta-Glucoside Metabolism | Transcriptional antiterminator of lichenan operon, BglG family | 0 |  |  |  | | Beta-Glucoside Metabolism | Cellobiose phosphotransferase system YdjC-like protein | 0 |  |  |  | | Biotin synthesis cluster | Competence protein F homolog, phosphoribosyltransferase domain |  |  |  |  | | Biotin synthesis cluster | Substrate-specific component BioY of biotin ECF transporter |  |  |  |  | | Biotin synthesis cluster | Biotin operon repressor |  |  |  |  | | Biotin synthesis cluster | Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62) |  |  |  |  | | Biotin synthesis cluster | 8-amino-7-oxononanoate synthase (EC 2.3.1.47) |  |  |  |  | | Biotin synthesis cluster | Dethiobiotin synthetase (EC 6.3.3.3) |  |  |  |  | | Biotin synthesis cluster | Biotin synthase (EC 2.8.1.6) |  |  |  |  | | Chitin and N-acetylglucosamine utilization | Glucosamine-6-phosphate deaminase (EC 3.5.99.6) |  |  |  |  | | Chitin and N-acetylglucosamine utilization | N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) |  |  |  |  | | Chitin and N-acetylglucosamine utilization | Predicted transcriptional regulator of N-Acetylglucosamine utilization, GntR family |  |  |  |  | | Chitin and N-acetylglucosamine utilization | N-Acetyl-D-glucosamine ABC transport system, permease protein 1 |  |  |  |  | | D-galactarate, D-glucarate and D-glycerate catabolism - gjo | Sugar diacid utilization regulator SdaR |  |  |  |  | | D-Galacturonate and D-Glucuronate Utilization | Transcriptional regulator KdgR, KDG operon repressor |  |  |  |  | | D-Galacturonate and D-Glucuronate Utilization | Mannonate dehydratase (EC 4.2.1.8) |  |  |  |  | | D-Galacturonate and D-Glucuronate Utilization | D-mannonate oxidoreductase (EC 1.1.1.57) |  |  |  |  | | D-Galacturonate and D-Glucuronate Utilization | Uronate isomerase (EC 5.3.1.12) |  |  |  |  | | D-Galacturonate and D-Glucuronate Utilization | Alpha-glucosidase (EC 3.2.1.20) |  |  |  |  | | D-Galacturonate and D-Glucuronate Utilization | 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14) |  |  |  |  | | D-Galacturonate and D-Glucuronate Utilization | 2-keto-3-deoxygluconate permease (KDG permease) |  |  |  |  | | D-gluconate and ketogluconates metabolism | Gluconate transporter family protein |  |  |  |  | | D-gluconate and ketogluconates metabolism | Gluconokinase (EC 2.7.1.12) |  |  |  |  | | D-ribose utilization | Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) |  |  |  |  | | D-ribose utilization | Ribose operon repressor |  |  |  |  | | D-ribose utilization | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) |  |  |  |  | | D-ribose utilization | Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1) |  |  |  |  | | dTDP-rhamnose synthesis | dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133) |  |  |  |  | | dTDP-rhamnose synthesis | dTDP-glucose 4,6-dehydratase (EC 4.2.1.46) |  |  |  |  | | dTDP-rhamnose synthesis | dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13) |  |  |  |  | | dTDP-rhamnose synthesis | Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24) |  |  |  |  | | Exopolysaccharide Biosynthesis | Manganese-dependent protein-tyrosine phosphatase (EC 3.1.3.48) |  |  |  |  | | Exopolysaccharide Biosynthesis | Tyrosine-protein kinase transmembrane modulator EpsC |  |  |  |  | | Exopolysaccharide Biosynthesis | Tyrosine-protein kinase EpsD (EC 2.7.10.2) |  |  |  |  | | Exopolysaccharide Biosynthesis | Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6) |  |  |  |  | | Fructooligosaccharides(FOS) and Raffinose Utilization | Multiple sugar ABC transporter, substrate-binding protein |  |  |  |  | | Fructooligosaccharides(FOS) and Raffinose Utilization | Multiple sugar ABC transporter, membrane-spanning permease protein MsmG |  |  |  |  | | Fructooligosaccharides(FOS) and Raffinose Utilization | Multiple sugar ABC transporter, membrane-spanning permease protein MsmF |  |  |  |  | | Fructose utilization | Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9) |  |  |  |  | | Fructose utilization | Transcriptional repressor of the fructose operon, DeoR family |  |  |  |  | | Fructose utilization | 1-phosphofructokinase (EC 2.7.1.56) |  |  |  |  | | Fructose utilization | PTS system, fructose-specific IIB component (EC 2.7.1.69) |  |  |  |  | | Fructose utilization | PTS system, fructose-specific IIC component (EC 2.7.1.69) |  |  |  |  | | Glycerate metabolism | Hydroxypyruvate isomerase (EC 5.3.1.22) |  |  |  |  | | Glycerate metabolism | 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) |  |  |  |  | | Glycerate metabolism | D-glycerate transporter (predicted) |  |  |  |  | | Glycerol and Glycerol-3-phosphate Uptake and Utilization | Glycerol-3-phosphate ABC transporter, permease protein UgpE (TC 3.A.1.1.3) |  |  |  |  | | Glycerol and Glycerol-3-phosphate Uptake and Utilization | Glycerophosphoryl diester phosphodiesterase, periplasmic (EC 3.1.4.46) |  |  |  |  | | Glycerol and Glycerol-3-phosphate Uptake and Utilization | Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) |  |  |  |  | | Glycerol and Glycerol-3-phosphate Uptake and Utilization | Glycerol-3-phosphate ABC transporter, permease protein UgpA (TC 3.A.1.1.3) |  |  |  |  | | Glycerol and Glycerol-3-phosphate Uptake and Utilization | Glycerol kinase (EC 2.7.1.30) |  |  |  |  | | Glycerol and Glycerol-3-phosphate Uptake and Utilization | Glycerol-3-phosphate responsive antiterminator (mRNA-binding) |  |  |  |  | | Glycerol and Glycerol-3-phosphate Uptake and Utilization | Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46) |  |  |  |  | | Glycerol and Glycerol-3-phosphate Uptake and Utilization | Glycerol-3-phosphate ABC transporter, ATP-binding protein UgpC (TC 3.A.1.1.3) |  |  |  |  | | Glycerol and Glycerol-3-phosphate Uptake and Utilization | GlpG protein (membrane protein of glp regulon) |  |  |  |  | | Glycogen metabolism | Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) |  |  |  |  | | Glycogen metabolism | 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18) |  |  |  |  | | Glycogen metabolism | Glycogen biosynthesis protein GlgD, glucose-1-phosphate adenylyltransferase family |  |  |  |  | | Glycogen metabolism | Glycogen phosphorylase (EC 2.4.1.1) |  |  |  |  | | Glycogen metabolism | Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21) |  |  |  |  | | Lactose and Galactose Uptake and Utilization | Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10) |  |  |  |  | | Lactose and Galactose Uptake and Utilization | Galactokinase (EC 2.7.1.6) |  |  |  |  | | Lactose and Galactose Uptake and Utilization | Aldose 1-epimerase (EC 5.1.3.3) |  |  |  |  | | L-Arabinose utilization | L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) |  |  |  |  | | L-Arabinose utilization | Ribulokinase (EC 2.7.1.16) |  |  |  |  | | L-Arabinose utilization | L-arabinose isomerase (EC 5.3.1.4) |  |  |  |  | | L-Arabinose utilization | Transcriptional repressor of arabinoside utilization operon, GntR family |  |  |  |  | | Mannose Metabolism | Phosphomannomutase (EC 5.4.2.8) |  |  |  |  | | Mannose Metabolism | Mannose-6-phosphate isomerase (EC 5.3.1.8) |  |  |  |  | | Mannose Metabolism | PTS system, mannose-specific IIB component (EC 2.7.1.69) |  |  |  |  | | Mannose Metabolism | PTS system, mannose-specific IIC component (EC 2.7.1.69) |  |  |  |  | | Mannose Metabolism | PTS system, mannose-specific IIA component (EC 2.7.1.69) |  |  |  |  | | Mannose Metabolism | Beta-mannosidase (EC 3.2.1.25) |  |  |  |  | | Mannose Metabolism | Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22) |  |  |  |  | | N-linked Glycosylation in Bacteria | UDP-N-acetylglucosamine 4,6-dehydratase (EC 4.2.1.-) |  |  |  |  | | N-linked Glycosylation in Bacteria | Lipid carrier : UDP-N-acetylgalactosaminyltransferase (EC 2.4.1.-) |  |  |  |  | | N-linked Glycosylation in Bacteria | 4-keto-6-deoxy-N-Acetyl-D-hexosaminyl-(Lipid carrier) aminotransferase |  |  |  |  | | None | ABC transporter, ATP-binding protein |  |  |  |  | | None | Phosphoglucomutase (EC 5.4.2.2) |  |  |  |  | | None | Undecaprenyl-diphosphatase (EC 3.6.1.27) |  |  |  |  | | None | UDP-glucose 6-dehydrogenase (EC 1.1.1.22) |  |  |  |  | | None | ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron) |  |  |  |  | | None | Glucose-6-phosphate isomerase (EC 5.3.1.9) |  |  |  |  | | None | Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19) |  |  |  |  | | None | putative sugar ABC transporter, permease protein |  |  |  |  | | None | Chitooligosaccharide deacetylase (EC 3.5.1.-) |  |  |  |  | | None | UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227) |  |  |  |  | | None | UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.3.1.98) |  |  |  |  | | None | ABC transporter, substrate-binding protein (cluster 2, ribose/xylose/arabinose/galactose) |  |  |  |  | | None | Polysaccharide deacetylase |  |  |  |  | | None | ABC transporter, permease protein 2 (cluster 1, maltose/g3p/polyamine/iron) |  |  |  |  | | None | Phosphatidylethanolamine N-methyltransferase (EC 2.1.1.17) |  |  |  |  | | None | Membrane protein of EXOQ family, involved in exopolysaccharide production |  |  |  |  | | None | Poly(glycerol-phosphate) alpha-glucosyltransferase (EC 2.4.1.52) |  |  |  |  | | None | N-acetylmannosaminyltransferase (EC 2.4.1.187) |  |  |  |  | | None | UDP-N-acetyl-D-mannosamine dehydrogenase (EC 1.1.1.336) |  |  |  |  | | None | Polysaccharide pyruvyl transferase |  |  |  |  | | None | Lipopolysaccharide biosynthesis |  |  |  |  | | None | ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron) |  |  |  |  | | None | ABC transporter, permease protein 1 (cluster 1, maltose/g3p/polyamine/iron) |  |  |  |  | | None | Glycerol-3-phosphate ABC transporter, substrate-binding protein UgpB |  |  |  |  | | None | SN-glycerol-3-phosphate transport ATP-binding protein UgpC (TC 3.A.1.1.3) |  |  |  |  | | None | sugar and carbohydrate transporters |  |  |  |  | | None | Sensory box/GGDEF family protein |  |  |  |  | | None | Maltose operon transcriptional repressor MalR, LacI family |  |  |  |  | | None | 6-phospho-3-hexuloisomerase (EC 5.3.1.27) |  |  |  |  | | None | D-arabino-3-hexulose 6-phosphate formaldehyde-lyase (EC 4.1.2.43) |  |  |  |  | | None | Glycosyl transferase, family 8 |  |  |  |  | | None | Glycosyltransferase |  |  |  |  | | None | Sorbitol dehydrogenase (EC 1.1.1.14) |  |  |  |  | | None | 6-phospho-beta-glucosidase (EC 3.2.1.86) |  |  |  |  | | None | Predicted beta-glucoside-regulated ABC transport system, sugar binding component, COG1653 |  |  |  |  | | None | Predicted beta-glucoside-regulated ABC transport system, permease component 1, COG1175 |  |  |  |  | | None | Predicted beta-glucoside-regulated ABC transport system, permease component 2, COG0395 |  |  |  |  | | None | Uncharacterized membrane protein YkoS |  |  |  |  | | None | Uncharacterized glycosyltransferase YkoT |  |  |  |  | | None | UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) |  |  |  |  | | None | Glycosyl transferase, family 2 |  |  |  |  | | None | Glycosyl transferase, group 1 |  |  |  |  | | None | Sugar-phosphate guanylyltransferase / Sugar-phosephate isomerase |  |  |  |  | | None | Probable polysaccharide deacetylase pdaB precursor |  |  |  |  | | None | PTS system, glucosamine-specific IIC component / PTS system, glucosamine-specific IIB component / PTS system, glucosamine-specific IIA component |  |  |  |  | | None | Trehalose-6-phosphate hydrolase (EC 3.2.1.93) |  |  |  |  | | None | PTS system, trehalose-specific IIB component (EC 2.7.1.201) / PTS system, trehalose-specific IIC component |  |  |  |  | | None | Phosphoglycerate/bisphosphoglycerate mutase |  |  |  |  | | None | carbohydrate kinase, FGGY( EC:2.7.1.17 ) |  |  |  |  | | None | Rhamnulokinase (EC 2.7.1.5) |  |  |  |  | | None | Maltodextrin ABC transporter, permease protein MdxG |  |  |  |  | | None | Maltodextrin ABC transporter, ATP-binding protein MsmX |  |  |  |  | | None | UDP-N-acetylglucosamine:L-malate glycosyltransferase |  |  |  |  | | None | FIG013069: hypothetical protein co-occurring with TPR domain protein |  |  |  |  | | None | FIG009300: TPR-repeat-containing protein |  |  |  |  | | None | PTS system, maltose-specific IIC component / PTS system, maltose-specific IIB component (EC 2.7.1.208) |  |  |  |  | | None | Maltose-6'-phosphate glucosidase (EC 3.2.1.122) |  |  |  |  | | None | PTS system, glucose-specific IIA component |  |  |  |  | | None | TPR repeat-containing protein YvcD |  |  |  |  | | None | Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.33) |  |  |  |  | | None | Fructose-1,6-bisphosphatase, GlpX type (EC 3.1.3.11) |  |  |  |  | | None | Uncharacterized glycosyltransferase YwdF |  |  |  |  | | None | GAF domain/HD domain protein |  |  |  |  | | None | ABC transport protein, sugar-binding component yneA |  |  |  |  | | None | 3-oxoacyl-[acyl-carrier protein] reductase paralog (EC 1.1.1.100) in cluster with unspecified monosaccharide transporter |  |  |  |  | | None | Mannosyltransferase |  |  |  |  | | None | D-galactose 1-dehydrogenase (EC 1.1.1.48) |  |  |  |  | | None | PTS system, fructose-specific IIA component (EC 2.7.1.202) / PTS system, fructose-specific IIB component (EC 2.7.1.202) / PTS system, fructose-specific IIC component |  |  |  |  | | None | Ferrous iron uptake system protein A |  |  |  |  | | None | 1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157); diglucosyldiacylglycerol synthase (LTA membrane anchor synthesis) |  |  |  |  | | None | Glucomannan utilization operon transcriptional regulator, GmuR |  |  |  |  | | None | PTS system, oligo-beta-mannoside-specific IIC component |  |  |  |  | | None | PTS system, oligo-beta-mannoside-specific IIA component (EC 2.7.1.205) |  |  |  |  | | None | PTS system, oligo-beta-mannoside-specific IIB component (EC 2.7.1.205) |  |  |  |  | | None | Endo-1,4-beta-xylanase (EC 3.2.1.8) |  |  |  |  | | None | Xylan 1,4-beta-xylosidase (EC 3.2.1.37) |  |  |  |  | | None | Xylan alpha-1,2-glucuronosidase (EC 3.2.1.131) |  |  |  |  | | None | Predicted beta-xyloside ABC transporter, permease component |  |  |  |  | | None | Putative sodium-glucose/galactose cotransporter |  |  |  |  | | None | Predicted xylanase/chitin deacetylase |  |  |  |  | | None | Maltose O-acetyltransferase (EC 2.3.1.79) |  |  |  |  | | None | Glucokinase (EC 2.7.1.2) |  |  |  |  | | None | Putative membrane peptidase, contains TPR repeat domain |  |  |  |  | | None | TPR repeat-containing protein YrrB |  |  |  |  | | None | TPR repeat protein |  |  |  |  | | None | 6-phosphofructokinase (EC 2.7.1.11) |  |  |  |  | | None | GGDEF domain protein |  |  |  |  | | None | Lipopolysaccharide 1,2-N-acetylglucosaminetransferase (EC 2.4.1.56) |  |  |  |  | | None | alpha-mannosidase (EC 3.2.1.24) |  |  |  |  | | None | alpha-L-rhamnosidase (EC 3.2.1.40) |  |  |  |  | | None | Predicted rhamnose oligosaccharide ABC transport system, permease component 2 |  |  |  |  | | None | Predicted rhamnose oligosaccharide ABC transport system, permease component |  |  |  |  | | None | Predicted rhamnose oligosaccharide ABC transport system, substrate-binding component |  |  |  |  | | None | L-rhamnose isomerase (EC 5.3.1.14) |  |  |  |  | | None | Predicted rhamnulose-1-phosphate aldolase (EC 4.1.2.19) / Predicted lactaldehyde dehydrogenase (EC 1.2.1.22) |  |  |  |  | | None | Predicted L-rhamnose mutarotase |  |  |  |  | | None | Predicted L-rhamnose permease RhaY |  |  |  |  | | None | TPR domain protein, putative component of TonB system |  |  |  |  | | None | alpha-L-arabinofuranosidase (EC 3.2.1.55) |  |  |  |  | | None | Alpha-arabinosides ABC transport system, permease protein AraQ |  |  |  |  | | None | Alpha-arabinosides ABC transport system, permease protein AraP |  |  |  |  | | None | Alpha-arabinosides ABC transport system, substrate-binding protein AraN |  |  |  |  | | None | L-arabinose ABC transporter, permease protein AraH |  |  |  |  | | None | L-arabinose ABC transporter, ATP-binding protein AraG |  |  |  |  | | None | L-arabinose ABC transporter, substrate-binding protein AraF |  |  |  |  | | None | Response regulator for an arabinose sensor |  |  |  |  | | None | Histidine kinase in an arabinose sensing sensor |  |  |  |  | | None | Arabinose sensor protein |  |  |  |  | | None | N-acetyl-D-glucosamine ABC transporter, permease protein 2 |  |  |  |  | | None | PTS system, cellobiose-specific IIA component (EC 2.7.1.205) |  |  |  |  | | None | PTS system, cellobiose-specific IIC component |  |  |  |  | | None | PTS system, cellobiose-specific IIB component (EC 2.7.1.205) |  |  |  |  | | None | PTS system, N-acetylglucosamine-specific IIC component / PTS system, N-acetylglucosamine-specific IIB component (EC 2.7.1.193) |  |  |  |  | | None | Maltodextrin ABC transporter, substrate-binding protein MdxE |  |  |  |  | | None | Maltodextrin ABC transporter, permease protein MdxF |  |  |  |  | | None | UDP-galactose:(galactosyl) LPS alpha1,2-galactosyltransferase WaaW (EC 2.4.1.-) |  |  |  |  | | None | Polysaccharide deacetylase, possible chitooligosaccharide deacetylase (EC 3.5.1.41) |  |  |  |  | | None | alpha-galactosidase (EC 3.2.1.22) |  |  |  |  | | None | beta-galactosidase (EC 3.2.1.23) |  |  |  |  | | None | O antigen biosynthesis rhamnosyltransferase rfbN (EC 2.4.1.-) |  |  |  |  | | None | PTS system, glucose-specific IIA component (EC 2.7.1.199) |  |  |  |  | | None | PTS system, mannose-specific IIB component (EC 2.7.1.191) / PTS system, mannose-specific IIC component / PTS system, mannose-specific IIA component (EC 2.7.1.191) |  |  |  |  | | None | PTS system, mannitol-specific IIC component / PTS system, mannitol-specific IIB component (EC 2.7.1.197) |  |  |  |  | | None | Mannitol operon activator, BglG family |  |  |  |  | | None | PTS system, mannitol-specific IIA component (EC 2.7.1.197) |  |  |  |  | | None | Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17) |  |  |  |  | | None | Mannosylglycerate hydrolase (EC 3.2.1.170) |  |  |  |  | | None | PTS system, 2-O-alpha-mannosyl-D-glycerate-specific IIA component (EC 2.7.1.195) / PTS system, 2-O-alpha-mannosyl-D-glycerate-specific IIB component (EC 2.7.1.195) / PTS system, 2-O-alpha-mannosyl-D-glycerate-specific IIC component |  |  |  |  | | None | PTS system, lactose/cellobiose specific IIB subunit |  |  |  |  | | None | beta-N-acetylglucosaminidase (EC 3.2.1.52) |  |  |  |  | | None | beta-glucosidase (EC 3.2.1.21) |  |  |  |  | | None | 1,2-beta-oligoglucan phosphorylase (EC 2.4.1.333) |  |  |  |  | | None | Sugar ABC transporter, permease protein precursor |  |  |  |  | | None | Putative glycosyl transferase |  |  |  |  | | None | Possible sporulation protein SpoIID precursor |  |  |  |  | | None | Succinoglycan biosynthesis protein | 0 | 0 |  |  | | None | Uncharacterized sugar epimerase YhfK | 0 | 0 |  |  | | None | Spore coat polysaccharide biosynthesis protein SpsF | 0 | 0 |  |  | | None | UDP-N-acetylglucosamine 4,6-dehydratase (inverting) (EC 4.2.1.115) | 0 | 0 |  |  | | None | UDP-galactopyranose mutase (EC 5.4.99.9) | 0 | 0 |  |  | | None | Glycerol-3-phosphate cytidylyltransferase (EC 2.7.7.39) | 0 | 0 |  |  | | None | Glycosyltransferase (EC 2.4.1.-) | 0 | 0 |  |  | | None | Lipopolysaccharide biosynthesis protein RffA | 0 | 0 |  |  | | None | capsular polysaccharide biosynthesis protein | 0 | 0 |  |  | | None | D-ribose pyranase (EC 5.4.99.62) | 0 | 0 |  |  | | None | GGDEF/HD domain protein | 0 | 0 |  |  | | None | Uncharacterized glycosyltransferase YcjM | 0 | 0 |  |  | | None | N-acetylglucosaminyltransferase | 0 | 0 |  |  | | None | Rhamnulose-1-phosphate aldolase (EC 4.1.2.19) | 0 | 0 |  |  | | None | L-rhamnose mutarotase (EC 5.1.3.32) | 0 | 0 |  |  | | None | PTS system, galactitol-specific IIA component (EC 2.7.1.200) | 0 | 0 |  |  | | None | PTS system, galactitol-specific IIB component (EC 2.7.1.200) | 0 | 0 |  |  | | None | PTS system, galactitol-specific IIC component | 0 | 0 |  |  | | None | Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251) | 0 | 0 |  |  | | None | Glycerol uptake operon antiterminator regulatory protein | 0 | 0 |  |  | | None | PTS system, glucitol/sorbitol-specific IIA component (EC 2.7.1.198) | 0 | 0 |  |  | | None | PTS system, glucitol/sorbitol-specific IIB component (EC 2.7.1.198) / PTS system, glucitol/sorbitol-specific IIC component 2 | 0 | 0 |  |  | | None | PTS system, glucitol/sorbitol-specific IIC component | 0 | 0 |  |  | | None | Sorbitol-6-phosphate 2-dehydrogenase (EC 1.1.1.140) | 0 | 0 |  |  | | Osmoregulation | Glycerol uptake facilitator protein |  |  |  |  | | Sucrose utilization | Fructokinase (EC 2.7.1.4) |  |  |  |  | | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158) |  |  |  |  | | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157) |  |  |  |  | | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) |  |  |  |  | | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | Phosphoglucosamine mutase (EC 5.4.2.10) |  |  |  |  | | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | N-acetylglucosamine-1-phosphate uridyltransferase (EC 2.7.7.23) |  |  |  |  | | Xylose utilization | Xylose ABC transporter, substrate-binding component |  |  |  |  | | Xylose utilization | Xylose isomerase (EC 5.3.1.5) |  |  |  |  | | Xylose utilization | Xylose ABC transporter, ATP-binding component |  |  |  |  | | Xylose utilization | Xylulose kinase (EC 2.7.1.17) |  |  |  |  | | Xylose utilization | Xylose-responsive transcription regulator, ROK family |  |  |  |  | | Xylose utilization | Xylose ABC transporter, permease component |  |  |  |  | | Xylose utilization | Xylose ABC transporter, permease protein XylH |  |  |  |  | | | | | | | | | | | | | |