REVIEW RESEARCH

THE EFFECT OF DIFFERENT TYPES OF SUGAR ON BACTERIAL GROWTH RATE：A REVIEW

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ABSTRACT

The proliferation of bacteria is significantly influenced by the sources and characteristics of carbon sources, with carbohydrates serving as essential nutrients for many organisms. The prioritisation of carbohydrate use, driven by carbon catabolite repression mechanisms, is essential for diauxic or multiaxial growth in the presence of multiple carbohydrates. *Escherichia coli* exhibits diauxic growth on glucose and lactose, whereas specific *Bifidobacterium* species utilise carbohydrates with more complex structures and exhibit multiphase growth kinetics. The sugar's structure affects growth rate and yield. Monosaccharides like Glucose and fructose are easier for bacteria to use, so they usually grow more quickly than polysaccharides like cellulose or inulin. These polysaccharides have more complex structures and require a range of depolymerising and hydrolytic enzymes to break them down into the appropriate mono- and oligosaccharides for the bacteria. The specific metabolic end products of bacterial activity during carbohydrate fermentation determine how acidic the environment becomes. This is very important for keeping food safe, maintaining gut health, and for use in industry. It is crucial to understand how carbohydrate structures affect bacterial growth, as this knowledge could be useful for making food, medicine, biofuels, and specialised microbial communities in basic and applied research.

Keywords: Bacterial Growth, Sugar Metabolism, Carbon Catabolite Repression, Glycolysis, Fermentation, Diauxic, Prebiotics, *Escherichia coli, Lactobacillus.*

INTRODUCTION

Bacteria are everywhere, and their growth and reproduction are important to many things, from global biogeochemical cycles to human health and disease. The rate of bacterial growth is an important factor influenced by a complex mix of genetic potential and environmental factors such as temperature, pH, oxygen availability, and nutrient availability (Madigan, 2021). Among these nutrients, carbon sources are the most important because they are the basic building blocks of biomass and the main source of metabolic energy.

Sugars, or saccharides, are the most easily used type of carbon source for a wide range of heterotrophic bacteria. They can range from monomers to polymers, and each has its own chemical properties that affect how bacteria recognizerecognise, move, and break them down. The main concern in microbial physiology is not only whether a sugar can be consumed, but how well it supports growth relative to other sugars that are accessible. We assess this efficiency using the growth rate (how many generations per hour), the growth yield (how much biomass is produced per substrate used), and the lag phase duration (how long it takes for metabolic adaptation to occur) (Gralka, Pollak, & Cordero, 2022). Research on sugar use is not simply an academic endeavour. It has strong effects:

Food Science & Safety: The amount of sugar in food directly affects how quickly it spoils and how quickly harmful germs develop (Mafe, 2024).

Gut Microbiome: The many glycans in the human diet change the makeup and metabolic output of the gut microbiota, which affects the health of the host (Makki, Deehan, Walter, & Bäckhed, 2018).

Industrial Biotechnology: To produce biofuels, organic acids, and medicines through fermentation in a cost-effective manner, it is important to optimizeoptimise sugar combinations (Singh et al., 2022).

Medical Microbiology: Comprehending the metabolic tendencies of bacteria may provide new treatment targets.

This review article seeks to integrate recent discoveries on the effects of various sugars on bacterial growth rates. It will examine the biochemical and genetic factors that influence sugar preference, analyze growth dynamics across different saccharides, and address the practical implications of this information.

Basic Principles of Bacterial Sugar Metabolism

The first step in bacterial sugar metabolism is moving the molecule across the cell membrane, which is not permeable. This happens in three ways: (1) phosphotransferase systems (PTS), which link transport to phosphorylation (for Glucose and mannose, for example); (2) ATP-binding cassette (ABC) transporters, which use ATP hydrolysis to bring in molecules (common for oligosaccharides); and (3) major facilitator superfamily (MFS) symporters, which use proton motive force (for example, for lactose import via LacY) (Jeckelmann & Erni, 2020).

After entering the cell, carbohydrates are directed into the main metabolic pathways. The goal is to convert the carbon skeleton into pyruvate, which produces ATP (via substrate-level phosphorylation) and NADH and NADPH, both of which are forms of energy (Xiao, Wang, Handy, & Loscalzo, 2018).

The Embden-Meyerhof-Parnas Pathway is the main pathway by which the body breaks down hexose carbohydrates such as glucose, fructose, and mannose. For every glucose molecule, it makes two pyruvate molecules, two ATP, and two NADH (Jojima et al., 2021).

The Pentose Phosphate Pathway (PPP) operates in parallel with glycolysis, especially for pentose sugars such as xylose and ribose. It is important for producing NADPH (for biosynthetic processes) and pentose precursors for nucleic acid synthesis (Bertels, Fernández Murillo, & Heinisch, 2021).

The Entner-Doudoroff Pathway: This pathway is found in *Pseudomonas* and other Gram-negative bacteria. It breaks down Glucose and gluconate in a different way, making one ATP, one NADH, and one NADPH for each Glucose (Chen et al, 2021)

The fate of pyruvate depends on the bacterial species and environmental conditions (aerobic versus anaerobic). When oxygen is present, pyruvate enters the TCA cycle, where it is fully oxidizedoxidised to CO_2. This process creates the most ATP by oxidative phosphorylation. When there is not enough oxygen, pyruvate is transported along other fermentation routes to turn NADH back into NAD^+. This is necessary for glycolysis to keep going. Lactate, acetate, ethanol, succinate, and butyrate are examples of the end products of these fermentations. They are unique to each bacterium type and to the sugar being fermented (El-Mansi, Nielsen, Mousdale, & Carlson, 2018; Eram & Ma, 2013).

How Sugar Preference Works: Carbon Catabolite Repression (CCR)

When there are many carbohydrates around, bacteria do not usually eat them all at once. Instead, they focus on the sugar that helps them grow the fastest. This is mostly controlled by Carbon Catabolite Repression (CCR). When a preferred carbon source is available, CCR is a global regulatory mechanism that represses the expression of genes and operons required for the transport and breakdown of less preferred sugars (Sonnleitner, 2023).

Escherichia coli and other *Enterobacteriaceae* prefer Glucose as their sugar. The PTS breaks it down, which sets off a chain reaction of events (Schubert & Unden, 2021):

1- When there is much Glucose, the $EIIA^{Glc}$ part of the glucose PTS does not get phosphorylated.
2- Unphosphorylated $EIIA^{Glc}$ binds to and stops non-PTS sugar transporters, like the lactose permease LacY. This is called "inducer exclusion."
3- At the same time, low levels of cAMP (which are caused by active glycolysis) stop the cAMP-CRP complex from forming. This complex is needed to initiate transcription of operons such as lac (lactose), mal (maltose), and ara (arabinose).

This leads to diauxic development: an initial phase of exponential growth on Glucose, followed by a lag phase during which the bacteria synthesize the enzymes required for the second sugar (e.g., β-galactosidase for lactose), and subsequently a second phase of exponential growth.

The hierarchy of sugar preference is species-specific. For example, in Bacillus subtilis, CCR is facilitated by an alternative protein, CcpA, which inhibits target genes in response to glycolytic intermediates (Fujita & Miwa, 1994). Some gut bacteria, including Bifidobacterium longum, have evolved to prefer complex plant-derived oligosaccharides over simple sugars. They achieve this by using specialised ABC transporters rather than standard CCR pathways for Glucose, which helps them fit into their biological niche (Veselovsky et al., 2022).

Ecological and Evolutionary Rationale for Sugar Preference

The evolutionary basis for hierarchical sugar consumption is the enhancement of fitness in competitive, dynamic environments. A bacterium can quickly exploit a nutrient patch, outcompete neighbouring microbes for the most energetically favourable resource, and maximize its population size before nutrients are depleted or environmental conditions change (Hibbing et al., 2010).

This "feast-or-famine" method is metabolically efficient because it eliminates the extra cost of producing enzymes for less-preferred sugars when a better one is available. Furthermore, preference consumption can influence ecological relationships. A bacterium that specializes in consuming a secondary sugar, such as a complex plant oligosaccharide, after a generalist has consumed the preferred Glucose, can carve out a distinct metabolic niche, promoting species coexistence and functional diversity within complex microbial communities like the gut microbiome (Cavaliere et al., 2017).

Growth on Simple Sugars

Monosaccharides are the simplest sugars, and the body usually breaks them down the fastest. However, growth rates might differ greatly even within this group, depending on the transport mechanism and metabolic pathway used.

- **Glucose** is the most common carbon source for most microorganisms. PTS moves it quickly to glycolysis, where it goes straight in. It helps organisms like *E. coli* grow the fastest. Coli and *Bacillus subtilis* (Chaudhry & Varacallo, 2018).
- **Fructose:** A hexose sugar that is commonly moved by a PTS. In many bacteria, it helps them grow at almost the same rate as Glucose. However, in some *Lactobacilli*, fructose can serve as an alternative electron acceptor, altering the ATP yield and slightly changing growth dynamics (Chaudhry & Varacallo, 2018; Gänzle & Follador, 2012).
- **Galactose** is broken down via the Leloir pathway, which means it must be converted to glucose-1-phosphate before it can enter glycolysis. This extra step usually makes the lag phase longer and the growth rate about 10–20% lower than when Glucose is added to E. coli. coli (Boulanger, Sabag-Daigle, Thirugnanasambantham, Gopalan, & Ahmer, 2021; Li et al., 2020; Mestrom et al., 2019).
- **Xylose** and Arabinose are two pentoses found in hemicellulose. The PPP breaks them down. Bacteria such as *E.coli*. It is possible to genetically modify *E. coli* to use pentoses more effectively. However, wild-type strains usually grow more slowly on xylose or arabinose than on Glucose because they transport them less efficiently, and the PPP produces less energy (Domingues et al., 2021; Woo et al., 2022).

Table 1: Representative Growth Rates of *E. coli* on Various Monosaccharides

Sugar	Mean Generation Time (min)	Relative Growth Rate (%)	Primary Pathway
Glucose	~45	100%	Glycolysis
Fructose	~48	94%	Glycolysis
Galactose	~55	82%	Leloir -> Glycolysis
Xylose	~120	38%	Pentose Phosphate Pathway

How Disaccharides Help Growth

Disaccharides need to be broken down into their individual monosaccharides through hydrolysis before the monomers can enter central metabolism. This extra step needs the production of certain hydrolase enzymes, which can often be turned on and off by CCR (Sun & You, 2021).

- Lactose (Glucose + Galactose): The standard disaccharide model for investigating gene regulation. In E. coli, the lac operon is activated when Glucose is not present. In *E. coli*, the lac operon is activated when Glucose is not present. When growing on lactose, there is a long lag phase while β-galactosidase is made. The growth rate that follows is usually slower than that of Glucose because it is limited by the rate at which galactose is hydrolysed and metabolised (Holden, Rayment, & Thoden, 2003).
- Sucrose (Glucose + fructose): Many bacteria that live in the mouth, such *as Streptococcus mutans*, use sucrose (Glucose + fructose). It is quickly broken down by the enzyme sucrase, which makes extracellular polysaccharides that help create dental biofilm (plaque). Adapted organisms can grow very quickly on sucrose (Kawada-Matsuo, Oogai, & Komatsuzawa, 2016).
- Maltose (Glucose + Glucose) is what happens when starch breaks down. An ABC transporter moves it, and maltase breaks it down. It provides two glucose molecules, but the energy cost of moving it and the fact that CCR controls the mal operon ensure it cannot be used until the preferred sugars run out (Mächtel, Narducci, Griffith, Cordes, & Orelle, 2019).
- Trehalose (Glucose + Glucose): A disaccharide that protects against stress. Certain dangerous bacteria, including Clostridium difficile, have developed effective trehalose metabolic pathways. Elevated dietary trehalose has been associated with the development of hypervirulent strains, functioning as a significant growth substrate, hence underscoring the clinical importance of disaccharide metabolism (Collins et al., 2018).

The growth rate of a disaccharide is contingent upon the efficacy of its transport system, the kinetics of its hydrolysis enzyme, and the metabolic pathways of its monomeric components.

Growing on Oligo- and Polysaccharides that are Complicated

Complex carbohydrates such as starches, cellulose, hemicellulose, and inulin cannot be absorbed directly. Specialized bacteria that make extracellular or cell-bound enzymes (CAZymes: Carbohydrate-Active Enzymes) use them to break down carbohydrates into smaller, more transportable components (Lapébie, Lombard, Drula, Terrapon, & Henrissat, 2019).

- Starch is a type of glucose polymer. In the gut, bacteria like Bacteroides thetaiotaomicron release amylases that break down starch into maltose and maltooligosaccharides. These are then brought in and further broken down. Growth on starch is usually slower than on Glucose because it needs more enzymatic processes, but it is faster than on polymers that are harder to break down (Anderson & Salyers, 1989; Tancula, Feldhaus, Bedzyk, & Salyers, 1992).

- Cellulose is a crystalline polymer of glucose with β-1,4 linkages and is very hard to break down. Only a few bacteria, such as Clostridium thermocellum and Cytophaga spp., have large enzyme complexes called cellulosomes that can break it down. Cellulose growth is very slow and typically requires complex interactions between soil microbes and the stomachs of ruminants (Hirano et al., 2016).
- Polymers containing fructose are inulin and fructooligosaccharides (FOS). These are called prebiotics because they help good gut bacteria, such as Bifidobacterium and Lactobacillus, flourish. These bacteria use unique β-fructosidases to import and hydrolyze FOS. Even though the absolute growth rate may not be very high, these sugars give probiotic species an edge against potential pathogens, thereby altering the organisation of the microbiome (Hughes, Alvarado, Swanson, & Holscher, 2022).
- Mucin O-Glycans: The glycoprotein parts of the mucus in the intestines. Certain bacteria that break down mucin, including *Akkermansia muciniphila*, use sialic acid and N-acetylglucosamine as carbon sources. They grow slowly on mucin, which is important for maintaining gut mucosal barrier health and has been linked to metabolic health (Tailford, Crost, Kavanaugh, & Juge, 2015).

A bacterium's ecological niche and its significance in a microbial community are typically determined by its capacity to absorb complex polysaccharides.

Environmental Feedback and Metabolic End-Products

The type of sugar eaten not only affects how fast things grow but also the metabolic end products, which then affect the growth environment. Making acid is the most important change. When carbohydrates ferment, they nearly always release organic acids (lactic, acetic, propionic, butyric, etc.), which lower the pH of the surrounding environment by a large amount (Zi et al., 2022). This acidification can:

1- Inhibit Further Growth: Metabolism slows and eventually stops when the external pH dips below the optimal level for growth. This self-limitation is an important idea behind fermentation as a means of preventing food spoilage (Yi, 2022).

2- Gain a Competitive Edge: Acid-tolerant species (like numerous Lactobacilli) can do better than acid-sensitive neighbours in places with much sugar. This is very important in the mouth, where Streptococcus mutans ferments carbohydrates from food, makes a low-pH environment, and causes cavities (Kawada-Matsuo et al., 2016).

3- Shape the Gut Microbiome: The short-chain fatty acids (SCFAs) acetate, propionate, and butyrate, generated by gut bacteria during the fermentation of dietary fibre, serve as both waste products and crucial signalling molecules for human health, impacting immunity and metabolism (Parada Venegas et al., 2019).

The acid profile depends on the sugar. For instance, when Lactobacillus plantarum ferments Glucose, it mostly makes lactate. However, when the same strain ferments the prebiotic fructo-oligosaccharide (FOS), it might make acetate and formate instead, depending on how the metabolism changes the environment (Hughes et al., 2022). So, the type of sugar that one species eats affects not just that species but the entire microbial ecosystem.

Uses and Effects

Many professions require precise knowledge of sugar-dependent growth kinetics.

- Industrial Microbiology and Biotechnology: The main purpose of most fermentation processes is to get the most product (such as bioethanol, citric acid, or antibiotics) and the fastest rate. This entails formulating appropriate sugar blends, frequently derived from economical plant hydrolysates that include both C6 (Glucose) and C5 (xylose) sugars. A major area of research is figuring out how to get around CCR in production strains (e.g., by making CRP mutants) so that sugars can be used together. This will speed up growth and productivity throughout the fermentation process (Singh et al., 2022).

- Probiotics and Prebiotics: The effectiveness of a probiotic supplement is contingent upon the bacteria's capacity to endure, colonize, and proliferate within the gastrointestinal tract. The provision of a specific prebiotic sugar (e.g., FOS, GOS) tailored for consumption by a particular probiotic strain—termed synbiotics—can preferentially promote its growth and viability, therefore conferring health benefits to the host (Sanders, Merenstein, Reid, Gibson, & Rastall, 2019).

- Food Safety and Preservation: To figure out how long food will last, you need models of how pathogens proliferate. Different types of sugar can either help or hurt the growth of microbes that cause rotting (Tarlak, 2023). For instance, the high sucrose content in jams keeps microbes from growing by lowering the water activity. However, if you add water, they become ideal places for microbes to grow. To ensure food is safe, you need to understand how these things work. The critical importance of controlling microbial growth is exemplified in high-risk food categories, such as dairy products, where sugars like lactose are readily available for fermentation by pathogens, a concern detailed in reviews on milk-borne diseases (Almashhadany et al., 2022).

- Medical Microbiology: The metabolic proclivities of infections present prospective therapeutic targets. For instance, the identification of hypervirulent C. Difficile bacteria shows better growth on the disaccharide trehalose, suggesting that changing what you eat or blocking the trehalose metabolic pathway could be new ways to help (Collins et al., 2018). The distinctive sugar metabolism of Pseudomonas aeruginosa in the cystic fibrosis lung is also a subject of ongoing research.

CONCLUSION

This review emphasizes that the influence of sugar type on bacterial growth rate is a multifaceted yet comprehensible phenomenon, grounded in the essential principles of transport, catabolism, and genetic regulation. There is a distinct order: Glucose is a monosaccharide that is quickly used up, and cellulose is a polysaccharide that is slowly broken down. The regulatory mechanism of Carbon Catabolite Repression ensures that this hierarchical consumption occurs, leading to well-known growth patterns such as diauxic.

Future studies will progressively transition from simplistic cultural studies in laboratory media to more intricate, ecologically pertinent environments. The correlation between sugar type and bacterial proliferation is fundamental to microbiology. We need to understand it to use bacteria for our own good, whether in medicine, industry, or to keep ourselves healthy.

Conflicts of Interest

The authors declare no conflicts of interest.

REFERENCES

- Almashhadany, D.A., Mohammed, H.I., Muslat, T.A.M., Hassan, R.R., Rashid, R.F. & Hassan, A.A. (2022). Milk-borne diseases. In: M. Sameed (ed.) Health Risks of Food Additives. Available at: https://doi.org/10.5772/intechopen.108796.
- Anderson, K.L. & Salyers, A.A. (1989). Biochemical evidence that starch breakdown by *Bacteroides thetaiotaomicron* involves outer membrane starch-binding sites and periplasmic starch-degrading enzymes. Journal of Bacteriology, 171(6), pp. 3192–3198. Available from: https://doi.org/10.1128/jb.171.6.3192-3198.1989.
- Bertels, L.-K., Fernández Murillo, L. & Heinisch, J.J. (2021). 'The pentose phosphate pathway in yeasts–more than a poor cousin of glycolysis', *Biomolecules*, 11(5), p. 725. Available at: https://doi.org/10.3390/biom11050725
- Boulanger, E.F., Sabag-Daigle, A., Thirugnanasambantham, P., Gopalan, V. & Ahmer, B.M.M. (2021). 'Sugar-phosphate toxicities', *Microbiology and Molecular Biology Reviews*, 85(4), pp. e00123-21. Available at: https://doi.org/10.1128/MMBR.00123-21
- Cavaliere, M., Feng, S., Soyer, O.S., & Jiménez, J.I. (2017). Cooperation in microbial communities and their biotechnological applications. Environmental Microbiology, 19(8), pp. 2949–2963. Available from: https://doi.org/10.1111/1462-2920.13767
- Chaudhry, R. & Varacallo, M. (2018). *Biochemistry, Glycolysis*. Treasure Island (FL): StatPearls Publishing. Available at: https://www.ncbi.nlm.nih.gov/books/NBK470170/
- Chen, X., Schreiber, K., Appel, J. and Hagemann, M., (2021). The Entner-Doudoroff pathway contributes to glycogen breakdown during high-to-low CO_2 shifts in the cyanobacterium Synechocystis sp. PCC 6803. Frontiers in Plant Science, 12, p.787943. https://doi.org/10.3389/fpls.2021.787943
- Collins, J., Robinson, C., Danhof, H., Knetsch, C.W., van Leeuwen, H.C., Lawley, T.D., Auchtung, J.M. and Britton, R.A. (2018). 'Dietary trehalose enhances virulence of epidemic *Clostridium difficile'*, *Nature*, 553(7688), pp. 291–294. Available at: https://doi.org/10.1038/nature25178
- Domingues, R., Bondar, M., Palolo, I., Queirós, O., de Almeida, C.D. and Cesário, M.T. (2021). 'Xylose metabolism in bacteria—opportunities and challenges towards efficient lignocellulosic biomass-based biorefineries', *Applied Sciences*, 11(17), p. 8112. Available at: https://doi.org/10.3390/app11178112
- El-Mansi, E., Nielsen, J., Mousdale, D. & Carlson, R.P. (eds.) (2018). *Fermentation Microbiology and Biotechnology*. 4th edn. Boca Raton: CRC Press.

- Eram, M.S. & Ma, K. (2013). 'Decarboxylation of pyruvate to acetaldehyde for ethanol production by hyperthermophiles', *Biomolecules*, 3(3), pp. 578–596. Available at: https://doi.org/10.3390/biom3030578
- Fujita, Y. and Miwa, Y. (1994). 'Catabolite repression of the *Bacillus subtilis* gnt operon mediated by the CcpA protein', *Journal of Bacteriology*, 176(2), pp. 511–513. Available at: https://doi.org/10.1128/jb.176.2.511-513.1994
- Gänzle, M.G. and Follador, R. (2012). 'Metabolism of oligosaccharides and starch in lactobacilli: a review', *Frontiers in Microbiology*, 3, p. 340. Available at: https://doi.org/10.3389/fmicb.2012.00340
- Gralka, M., Pollak, S. & Cordero, O.X. (2022). *Fundamental metabolic strategies of heterotrophic bacteria*. BioRxiv. Available at: https://doi.org/10.1101/2022.08.04.502823
- Hibbing, M.E., Fuqua, C., Parsek, M.R. & Peterson, S.B. (2010). Bacterial competition: surviving and thriving in the microbial jungle. Nature Reviews Microbiology, 8(1), pp. 15–25. Available from: https://doi.org/10.1038/nrmicro2259
- Hirano, K., Kurosaki, M., Nihei, S., Hasegawa, H., Shinoda, S., Haruki, M., & Hirano, N. (2016). 'Enzymatic diversity of the Clostridium thermocellum cellulosome is crucial for the degradation of crystalline cellulose and plant biomass', *Scientific Reports*, 6(1), p. 35709. Available at: https://doi.org/10.1038/srep35709
- Holden, H.M., Rayment, I. & Thoden, J.B. (2003). 'Structure and function of enzymes of the Leloir pathway for galactose metabolism', *Journal of Biological Chemistry*, 278(45), pp. 43885–43888. Available at: https://doi.org/10.1074/jbc.R300025200
- Hughes, R.L., Alvarado, D.A., Swanson, K.S. & Holscher, H.D. (2022). 'The prebiotic potential of inulin-type fructans: a systematic review', *Advances in Nutrition*, 13(2), pp. 492–529. Available at: https://doi.org/10.1093/advances/nmab119
- Jeckelmann, J.M. & Erni, B. (2020). Transporters of Glucose and other carbohydrates in bacteria. Pflügers Archiv - European Journal of Physiology, 472(9), pp. 1129–1153. Available from: https://doi.org/10.1007/s00424-020-02379-0
- Jojima, T., Igari, T., Noburyu, R., Watanabe, A., Suda, M., & Inui, M. (2021). 'Coexistence of the Entner–Doudoroff and Embden–Meyerhof–Parnas pathways enhances glucose consumption of ethanol-producing Corynebacterium glutamicum', *Biotechnology for Biofuels*, 14(1), p. 45. Available at: https://doi.org/10.1186/s13068-021-01896-z
- Kawada-Matsuo, M., Oogai, Y. & Komatsuzawa, H. (2016). 'Sugar allocation to metabolic pathways is tightly regulated and affects the virulence of Streptococcus mutans', *Genes*, 8(1), p. 11. Available at: https://doi.org/10.3390/genes8010011
- Lapébie, P., Lombard, V., Drula, E., Terrapon, N. & Henrissat, B. (2019). 'Bacteroidetes use thousands of enzyme combinations to break down glycans', *Nature Communications*, 10(1), p. 2043. Available at: https://doi.org/10.1038/s41467-019-10068-5
- Li, Y., Sun, Z., Xu, Y., Luan, Y., Xu, J., Liang, Q., Liu, D. and Wang, Q. (2020). 'Enhancing the glucose flux of an engineered EP-bifido pathway for high poly(hydroxybutyrate) yield production', *Frontiers in Bioengineering and Biotechnology*, 8, p. 517336. Available at: https://doi.org/10.3389/fbioe.2020.517336
- Mächtel, R., Narducci, A., Griffith, D.A., Cordes, T. and Orelle, C. (2019). 'An integrated transport mechanism of the maltose ABC importer', *Research in Microbiology*, 170(8), pp. 321–337. Available at: https://doi.org/10.1016/j.resmic.2019.09.004
- Madigan, M.T., Bender, K.S., Buckley, D.H., Sattley, W.M., & Stahl, D.A. (2021). *Brock Biology of Microorganisms*. 16th edn. Harlow: Pearson.
- Mafe, A.N. (2024). A review on food spoilage mechanisms, food-borne diseases, and the commercial dimensions of food preservation and packaging. Food Science & Technol. Reviews.Available at: https://doi.org/10.1016/j.focha.2024.100852
- Makki, K., Deehan, E.C., Walter, J. & Bäckhed, F. (2018). 'The impact of dietary fibre on gut microbiota in host health and disease', *Cell Host & Microbe*, 23(6), pp. 705–715. Available at: https://doi.org/10.1016/j.chom.2018.05.012
- Mestrom, L., Przypis, M., Kowalczykiewicz, D., Pollender, A., Kumpf, A., Marsden, S.R., Szymańska, K., Jarzębski, A.B. and Hagedoorn, P.L. (2019). 'Leloir glycosyltransferases in applied biocatalysis: A multidisciplinary approach', *International Journal of Molecular Sciences*, 20(21), p. 5263. Available at: https://doi.org/10.3390/ijms20215263
- Parada Venegas, D., De la Fuente, M.K., Landskron, G., González, M.J., Quera, R., Dijkstra, G., Harmsen, H.J.M., Faber, K.N. and Hermoso, M.A. (2019) 'Short chain fatty acids (SCFAs)-mediated gut epithelial and

immune regulation and its relevance for inflammatory bowel diseases', *Frontiers in Immunology*, 10, p. 277. Available at: https://doi.org/10.3389/fimmu.2019.00277

- Sanders, M.E., Merenstein, D.J., Reid, G., Gibson, G.R. & Rastall, R.A. (2019). 'Probiotics and prebiotics in intestinal health and disease: from biology to the clinic', *Nature Reviews Gastroenterology & Hepatology*, 16(10), pp. 605–616. Available at: https://doi.org/10.1038/s41575-019-0173-3
- Schubert, C. & Unden, G. (2021). 'Regulation of dctA and DctA by cAMP-CRP and EIIA Glc at the transcriptional and post-translational levels in E. coli: Consequences for aerobic uptake and metabolism of C4-dicarboxylates'. Available at: https://doi.org/10.1101/2021.11.24.469881
- Singh, S., Srivastava, P., Deep, S., Ashish, Shukla, P., Rizvi, H. & Sinha, R. (2022). 'Fermentation strategies for organic acid production', in P. Srivastava et al. (eds.) *Industrial Microbiology and Biotechnology*. Singapore: Springer, pp. 379–425. Available at: https://doi.org/10.1007/978-981-16-5214-1_13

- Sonnleitner, E., Abdou, L. & Haas, D. (2023). “Catabolite repression control protein antagonist, a novel player in *Pseudomonas aeruginosa* carbon catabolite repression control.” Frontiers in Microbiology. Available at: https://doi.org/10.3389/fmicb.2023.1195558
- Sun, S. and You, C. (2021) 'Disaccharide phosphorylases: structure, catalytic mechanisms and directed evolution', *Synthetic and Systems Biotechnology*, 6(1), pp. 23-31. Available at: https://doi.org/10.1016/j.synbio.2021.01.003
- Tailford, L.E., Crost, E.H., Kavanaugh, D., & Juge, N. (2015). 'Mucin glycan foraging in the human gut microbiome', *Frontiers in Genetics*, 6, p. 81. Available at: https://doi.org/10.3389/fgene.2015.00081
- Tancula, E., Feldhaus, M.J., Bedzyk, L.A. & Salyers, A.A. (1992). 'Location and characterization of genes involved in binding of starch to the surface of *Bacteroides thetaiotaomicron'*, *Journal of Bacteriology*, 174(17), pp. 5609–5616. Available at: https://doi.org/10.1128/jb.174.17.5609-5616.1992
- Tarlak, F. (2023). 'The Use of Predictive Microbiology for the Prediction of the Shelf Life of Food Products', *Foods*, 12(24), p. 4461. Available at: https://doi.org/10.3390/foods12244461
- Veselovsky, V.A., Dyachkova, M.S., Bespiatykh, D.A., Yunes, R.A., Shitikov, E.A., Polyaeva, P.S., Izhboldina, O.V., & Klimina, K.M. (2022). 'The gene expression profile differs in growth phases of the *Bifidobacterium longum* culture', *Microorganisms*, 10(8), p. 1683. Available at: https://doi.org/10.3390/microorganisms10081683
- Woo, S., Lim, H.G., Han, Y.H., Park, S., Noh, M.H., Baek, D., Lee, H., Seo, S.W. and Jung, G.Y. (2022). 'A Vibrio-based microbial platform for accelerated lignocellulosic sugar conversion', *Biotechnology for Biofuels and Bioproducts*, 15(1), p. 58. Available at: https://doi.org/10.1186/s13068-022-02157-3
- Xiao, W., Wang, R.-S., Handy, D.E., & Loscalzo, J. (2018). 'NAD(H) and NADP(H) redox couples and cellular energy metabolism', *Antioxidants & Redox Signalling*, 28(3), pp. 251-272. Available at: https://doi.org/10.1089/ars.2017.7216
- Yi, A. P. (2022). Principles and Case Studies of Fed Batch Fermentation and Continuous Fermentation, Journal of Clinical and Nursing Research, 6(2), pp. 99–104. Available at: https://doi.org/10.26689/jcnr.v6i2.3712.
- Zi, X., Liu, Y., Chen, T., Li, M., Zhou, H. & Tang, J., (2022). Effects of sucrose, Glucose and molasses on fermentation quality and bacterial community of stylo silage. Fermentation, 8(5), 191. https://doi.org/10.3390/fermentation8050191