# Abstract

# 2.1 Introduction.

The human gut is home to a complex ecosystem of more than 100 trillion symbiotic microorganisms, which far exceeds the number of host cells. (Dekaboruah et al., 2020). This ecosystem, known as the gut microbiota, plays a fundamental role in human health, participating in essential biological processes such as nutrient extraction, metabolism, vitamin synthesis, and regulation of the immune system (Bouskra et al., 2008; Hou et al., 2022a). Under balanced conditions, the gut microbiota contributes to stability, resilience, and beneficial symbiosis for the host, acting as an additional metabolic organ (Hou et al., 2022b). However, dysbiosis, or disruption of this balance, has been associated with a wide range of diseases, from gastrointestinal disorders to metabolic, autoimmune, and neurological conditions. (Richard & Sokol, 2019).

In this context, modulation of gut microbiota using probiotics has emerged as a promising strategy for preventing and treating different pathologies. (Cremon et al., 2018; Sanders et al., 2019). Probiotics, defined as live microorganisms administered in adequate amounts that confer health benefits, have demonstrated their ability to protect against pathogens, inhibit colonization by harmful bacteria, strengthen the intestinal barrier, and modulate the immune response. (Ley et al., 2006; Richard & Sokol, 2019). Among the most widely used probiotics are lactic acid bacteria (LAB), which are considered GRAS (Generally Recognised as Safe) due to their well-established safety profile. (McFarland et al., 2018). Some of the most studied strains include *Propionibacterium freudenreichii, Lactobacillus subtilis, Lactobacillus acidophilus*, *Lacticaseibacillus casei*, *Limosilactobacillus reuteri*, *Lactiplantibacillus plantarum*, *Bifidobacterium brevis*, *Streptococcus salivaris subespecie thermophilus*, *Enterococcus faecalis*, *Enterococcus faecium*, *Lactococcus* y *Escherichia coli Nissle* 1917, among others (Kumari et al., 2020).

Consequently, modification of gut microbial communities, whether by the inclusion or exclusion of specific microorganisms, has the potential to prevent the development of diverse diseases. (Cani and Delzenne 2009). This phenomenon is closely related to the colonization of the intestinal tract by the microbiota, which can trigger immune responses mediated by the recognition of microbial signals through innate receptors. (Cerdó et al., 2019; Trejo & Sanz, 2013). These receptors, in addition, modulate the function of intestinal immune cells, thereby influencing immune homeostasis and inflammatory response. (Lee & Kim, 2007; Zmora et al., 2019). Therefore, the identification and characterization of the effect of a specific probiotic on the expression and modulation of genes associated with human pathologies are essential to understanding the underlying mechanisms of these diseases and developing more precise therapeutic interventions.

In this study, a transcriptomic analysis of HT-29 and Caco-2 cell lines treated with probiotic strains was conducted. The probiotic strains used in this study were *Propionibacterium freudenreichii* and *Bacillus subtilis* CW14. The objective of the study was to identify differentially expressed genes (DEGs) and to explore their protein-protein interactions (PPIs). These interactions were analyzed in a relevant biological context, focusing on three main axes: 1) interaction with viral proteins, 2) relationship with human disease-associated proteins, and 3) identification of possible gene modulation mechanisms related to immune and physiological response. This comprehensive approach will advance our understanding of how probiotics can modulate gene networks associated with human disease, opening new avenues for the development of gut microbiota-based therapies.

# 2.2. Materials and methods.

## 2.2.1. Differential expression analysis and data collection.

A comprehensive search of the Gene Expression Omnibus database was performed to obtain differential gene expression data related to probiotics' effect on colon cells. (GEO) (Clough & Barrett, 2016). A series of keywords, detailed in the [supplementary material](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/7_Selection%20criteria%20and%20search/README.md), were used to filter for relevant studies. From the results obtained, two studies were selected that met the following inclusion criteria: 1) colorectal adenocarcinoma cells as an experimental model, 2) evaluation of effect on the colon, and 3) probiotic-based treatments. The selected data includes Caco-2 cells treated with ***B. subtilis* CW14** (GSE115081) (Peng et al., 2019a), and HT-29 cells treated with ***P. freudenreichii* ITG P9** (GSE67033) (Cousin, Jouan-Lanhouet, Théret, Brenner, Jouan, Moigne-Muller, Dimanche-Boitrel, & Jan, 2016).

Principal Component Analysis (PCA) was conducted using the DESeq2 (Love et al., 2014) package to distinguish between the different groups and their respective controls. Differential expression analysis was performed with DESeq2 (version 1.38.1) (Love et al., 2014), to normalize the expression counts for each experiment. A base 2 logarithmic transformation of the fold change (log2FC (FC) ≥ 2 and an FDR value ≤ 0.05) was performed to interpret the results to account for differentially expressed genes. For better integration of the results, the names of the DEGs were converted to Entrez IDs using the Ensemble database. (Harrison et al., 2024) and **UniProt** (Consortium et al., 2025) through specific APIs. These identifiers facilitated querying and cross-annotation across different databases.

## 2.2.2. Functional enrichment and pathway analysis.

Gene ontology (GO) functional analysis was performed using Enrichr (E. Y. Chen et al., 2013), focusing on three main categories: GO Biological Process 2023 (Carbon et al., 2019). The identification of biological pathways associated with DEGs was performed using the following databases: KEGG 2021 Human (Ogata et al., 1999)and Elsevier Pathway Collectio (Nesterova et al., 2019). These databases enabled the mapping of DEGs into metabolic pathways and signaling processes. As a result, a comprehensive biological context of probiotic-induced alterations in colon cells was established. It is important to note that the threshold for enrichment analyses was set at Padj ≤ 0.05.

## 2.2.3. Association of DEGs with human pathogens and genetic diseases.

Annotations were performed to associate DEGs with human pathogens and genetic diseases, using specialized databases, such as DisGeNet (Piñero et al., 2020), GeDiNet 2023 (Kundu et al., 2023), Jensen DISEASES (Pletscher-Frankild et al., 2015), Virus-Host PPI P-HIPSTer 2020 (Lasso et al., 2019), Orphanet Augmented (Orphanet, 2025). This analysis enabled the identification of potential associations between affected genes and human diseases. The thresholds established for the enrichment analyses were Padj ≤ 0.05 or a score ≥ 0.85.

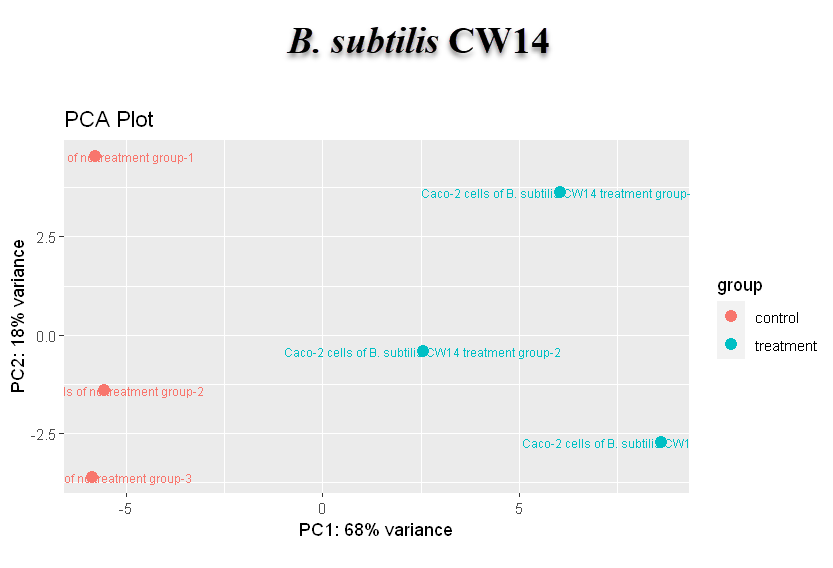
**2.2.4. Protein-Protein Interactions (PPIs) and visualization of Results.**

The exploration of protein-protein interactions (PPIs) of differentially expressed genes (DEGs), as well as their interaction with proteins associated with human diseases, viruses, and bacteria, was carried out using the following databases: **STRING** (Szklarczyk et al., 2023), BioGRID (Oughtred et al., 2021), IntAct (del Toro et al., 2022), the thresholds established for the PPI analyses were a combined score, quantitative score, and confidence value of ≥ 0.9, respectively. These networks and biological pathways were generated using Cytoscape v. 3.10.2 (Shannon et al., 2003), the DEGs are represented by green, the interacting proteins by blue, and the biological terms associated with GO Biological Process with a Padj ≤ 0.05 by purple. These networks provide a clear and comprehensive representation of the molecular interactions and pathways affected by DEGs in response to probiotic treatments.

# 2.3. Results.

## 2.3.1. HT-29 and Caco-2 cell lines treated with various probiotics show differentially expressed mRNA.

PCA analysis revealed marked transcriptional responses in both probiotics. (**Fig.2)**. For *P. freudenreichii* ITG P9 showed exceptionally high variance, with a PC1 of 94%, reflecting a clear separation between treatments and controls. While PC1 of *B. subtilis* CW14 explained 68% of the variance, suggesting that this axis contributes significantly to the separation of the groups. These results suggest that the treatment effect varies by probiotic, with a more pronounced response by *P. freudenreichii* *ITG P9* and indicating high mRNA heterogeneity as observed in the spatial distribution of treatments, which is evidence of intra-group variability.

Tabla

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**Figure 2. PCA analysis showing transcriptional responses in *P. freudenreichii* ITG P9 and *B. subtilis* CW14 probiotics.**

Following filtration of transcripts with a log2FC ≥ 2 and an FDR ≤ 0.05, a total of 2,337 genes were obtained from the *P. freudenreichii* treatment, of which 1457 (62.34 %) were positively regulated and 880 (37.66 %) were negatively regulated. This suggests a broad and robust transcriptional response. In the case of *B. subtilis* CW14, 198 genes were obtained, 136 (68.69%) were positively regulated and 62 (31.31%) were negatively regulated. In both cases, a trend towards gene activation was observed.

## 2.3.2. Functional enrichment analysis of biological processes and pathways

The present study analyzed the data obtained from *B. subtilis* CW14-treated Caco-2 cells and *P. freudenreichii* ITG P9-treated HT-29 cells, revealing significant modulation of DEGs through the implementation of expression change thresholds (log2FC ≥ 2), an FDR value ≤ 0.05 and a Padj ≤ 0.05. The implementation of these criteria enabled the selection of a set of genes associated with critical biological processes, including cell cycle, immunity, adhesion, inflammation, and transport. Furthermore, pathway analysis identified key metabolic and signaling pathways (KEGG and Elsevier Pathway Collection). The results obtained can be viewed in tables [ST1](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST1_Elsevier_Pathway_Collection_terms_sorted_with_all.xlsx) and [ST2](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST2_KEGG_2021_Human_terms_sorted_with_all.xlsx).

Transcriptomic analysis of *B. subtilis* CW14-treated Caco-2 cells revealed a coordinated and simultaneous response of immune signaling pathways and defense mechanisms. Overexpression of chemokines and immunostimulatory factors was observed, as reflected by increased expression of genes such as CCL4 (+5.24), CSF2 (+5.03), CSF3 (+4.95), NFKBIZ (+2.28), LTB-TNFSF3 (+3.07) and PLAU (+3.36). This observation suggests the activation of the *NF-κB* pathway, which likely facilitates the recruitment of T lymphocytes, neutrophils, and the differentiation of macrophages and granulocytes. This, in turn, promotes both the elimination of pathogens and the promotion of reparative processes in the intestinal epithelium (Anderson, 2023; Peng et al., 2019b; Upadhyay & Fu, 2013; Yamazaki et al., 2022). Furthermore, the increased expression of chemokines such as CXCL8 (+4.65), CXCL10 (+4.34), CXCL11 (+2.82), and CX3CL2 (+3.01) indicates the activation of pathways that promote neutrophil chemotaxis and migration and mast cell activation, contributing to a coordinated immune response to microbial pathogens (Kochumon et al., 2020). Similarly, the increased expression of CCL5 (+4.16) together with the modulation of CCL22 (+2.51) and CCL2 (+2.55) points to the attraction of monocytes, Tregs and the polarization of macrophages towards a reparative phenotype, which could contribute to mitigating epithelial damage under inflammatory conditions. Other genes such as TNFAPI3 (+2.31) and TNFSF14 (+2.95) could contribute to the control of intestinal inflammation, either by blocking *NF-κB* signaling or by apoptosis (Kolodziej et al., 2011; Krause et al., 2014). Concurrently, effects on genes associated with stress response and metabolic activity were identified. Overexpression of the CYP1B1 (+2.61) gene suggests the activation of detoxification pathways involved in the neutralization of xenobiotic compounds (such as mycotoxins), while the upregulation of BIRC3 (+2.51) and downregulation of RGS2 (-2.11) would indicate the involvement of anti-apoptotic mechanisms that favor the survival of epithelial cells against oxidative stress (Pauletto et al., 2020). In contrast, the reduction in HSPA6 expression (-2.72) may indicate an adaptation of the cellular system to stress conditions by optimizing resources in the face of a gastrointestinal environment that demands immune and repair responses (Z. Chen et al., 2025; Neurath, 2014).

Transcriptomic analysis of HT-29 cells treated with *P. freudenreichii* ITG P9 revealed a coordinated response of CDKN1A (+4.21), CDKN2B (+2.84), and CDKN1C (+2.43) genes, which are associated with cell cycle regulation. This suggests mechanisms associated with cell arrest through the G1/S transition phase thus reducing the proliferation of damaged cells (Abbas & Dutta, 2009). The BRSK2 (+2.64) and NES (+2.02) genes, which are involved in cycle transitions (G2/M), were also identified, suggesting the possibility of modulating the cell cycle under stress conditions (Cousin et al., 2016; Wang et al., 2012).

In a unified manner, changes in gene expression indicate that *B. subtilis* CW14 exerts a dual impact on intestinal cells. Firstly, it activates a controlled proinflammatory response by modulating chemokines and factors that promote the recruitment and activation of immune cells. Secondly, it modulates protective and detoxification mechanisms that contribute to the protection of epithelial integrity. In contrast, *P. freudenreichii* ITG P9 instigates cell cycle reprogramming with the objective of arresting cells in critical phases, such as G1/S and G2/M, whilst concurrently promoting defense mechanisms against stress.

## 2.3.3. Differentially expressed genes (DEGs) modulated by probiotics are repositioned as modulators in different pathologies having pluri-employment annotations.

**Modulation of *B. subtilis* CW14 in Caco-2 cells and *P. freudenreichii* ITG P9 in HT-29 cells on genes associated with diseases, neurological, dysbiosis and rare syndromes.**

The analysis of DEGs in intestinal cells following probiotic treatment has revealed a complex gene regulatory network associated with dysbiosis, metabolic diseases (obesity, diabetes), neurological disorders, cancer, and rare syndromes through log2FC (LFC) ≥ 2, an FDR value ≤ 0.05 and Padj filter ≤ 0.05 (Table [ST3](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST3_Genes_dysbiosis_diseases_with_FC_sorted_all.xlsx), [ST4](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST4_Genes_neurological_diseases_with_FC_sorted_all.xlsx), [ST5](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST5_Genes_rare_diseases_with_FC_sorted_all.xlsx)). The results obtained underline the critical role of the microbiota in modulating cross-cutting pathophysiological pathways, mediated by the regulation of chemokines, cytokines, and growth factors.

In Caco-2 cells treated with *B. subtilis* CW14, a positive regulation of several genes associated with proinflammatory and immunomodulatory pathways was observed, with log2FC values ranging from +2.10 to +5.23 (Table [ST6](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST6_KEGG_2021_Human_terms_sorted_with_all.xlsx)). Among these, CCL4 (+5.23), CSF2 (+5.02), CSF3 (+4.95), CXCL8 (+4.64) and CXCL10 (+4.34) genes stood out for their enrichment. These genes, according to enrichment analyses (Table 2), are associated not only with local inflammatory processes, but also with neurological diseases (epilepsy, Parkinson's, Alzheimer's), rare disorders (amyloidosis, antibody-mediated glomerulonephritis) and gut dysbiosis, linked to metabolic disorders such as obesity, inflammatory bowel disease (IBD) and diabetes mellitus (Table [ST7](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST7_Genes_neurological_diseases_with_FC_sorted_Bacilus.xlsx), [ST8](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST8_Genes_rare_diseases_with_FC_sorted_Bacilus.xlsx), [ST9](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST9_Genes_dysbiosis_diseases_with_FC_sorted_Bacilus.xlsx)), suggesting a dual role in the activation of innate immunity and in pleiotropic mechanisms beyond the gut environment. In the context of the gut-brain axis, these findings become pertinent, as previous studies have demonstrated that probiotic strains, such as B. subtilis, can modulate the gut immune response. This, in turn, may have the capacity to influence neuroinflammatory processes and central nervous system homeostasis (Vida et al., 2024). For instance, the over-expression of genes such as CXCL10 and CCL4, which have been linked to autoimmune and neurodegenerative diseases, supports the hypothesis that the gut microbiota may play a role in mediating neuroprotection and maintaining blood-brain barrier integrity by regulating these genes in a controlled manner (Vida et al., 2024). Concurrently, modulation of CSF2 and CSF3, regulators of immune cell proliferation and differentiation, suggests that B. subtilis strain CW14 could promote a controlled inflammatory response in diseases such as multiple sclerosis or Alzheimer's disease (Mayer et al., 2014).

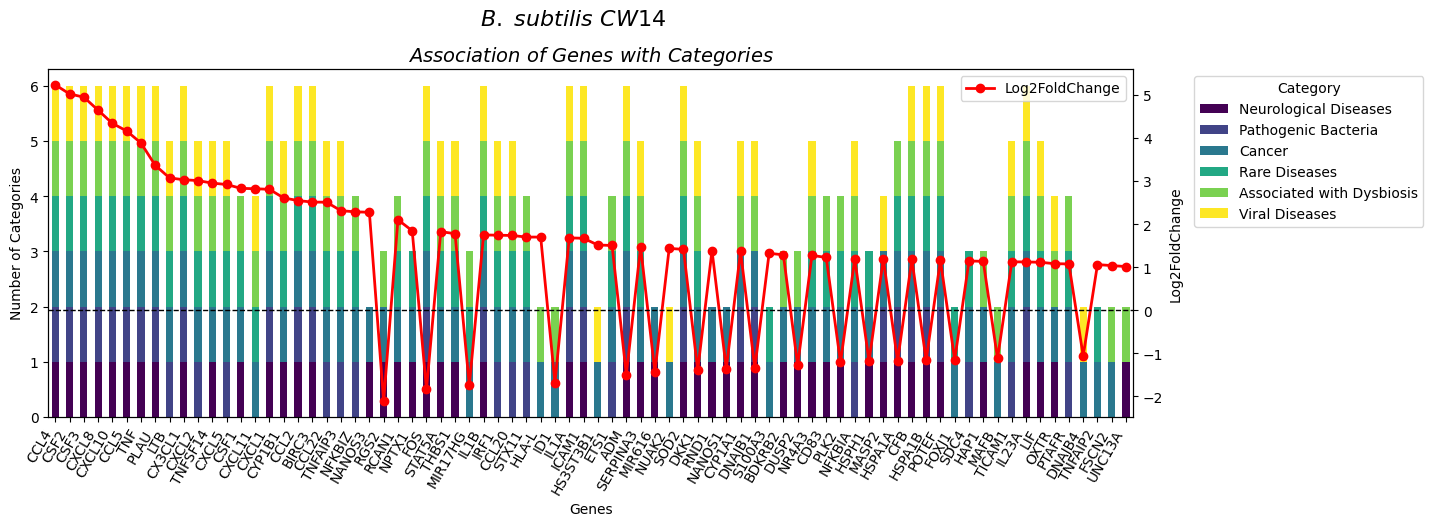
|  |  |  |  |
| --- | --- | --- | --- |
| **Genes** | **Term** | **Adjusted P-value** | **Log2FoldChange** |
| CCL4 | Cytokine-cytokine receptor interaction, Viral protein interaction with cytokine and cytokine receptor. | 1.86e-17, 3.08e-16 | 5.23 |
| CSF2 | TNF signaling pathway, Rheumatoid arthritis, Cytokine-cytokine receptor interaction. | 7.38e-21, 5.01e-18, 1.86e-17 | 5.02 |
| CSF3 | Cytokine-cytokine receptor interaction, IL-17 signaling pathway, Malaria, Coronavirus disease. | 1.86e-17, 2.86e-15, 4.92e-07 | 4.95 |
| CXCL8 | Rheumatoid arthritis, Cytokine-cytokine receptor interaction, Viral protein interaction with cytokine and cytokine receptor, IL-17 signaling pathway, NF-kappa B signaling pathway. | 5.01e-18, 1.86e-17, 3.08e-16, 2.86e-15, 1.15e-14 | 4.64 |
| CXCL10 | TNF signaling pathway, Cytokine-cytokine receptor interaction, Viral protein interaction with cytokine and cytokine receptor, IL-17 signaling pathway, Chemokine signaling pathway, Toll-like receptor signaling pathway. | 7.38e-21, 1.86e-17, 3.08e-16, 2.86e-15, 1.02e-09, 3.49e-08 | 4.34 |

**Table 2. Functional enrichment of positively regulated genes in Caco-2 cells treated with *B. subtilis* CW14.**

In relation to the connection between dysbiosis and neuroinflammation, the results are reinforced when considering the role of genes such as CXCL8, which is associated with the intestinal inflammatory response. Its regulation by *B. subtilis* CW14 points to a mechanism by which this probiotic could regulate intestinal homeostasis, mitigating systemic inflammation and its impact on neurological disorders (Mayer et al., 2014). This finding is consistent with the evidence linking dysbiosis to alterations in the gut-brain axis, increasing susceptibility to metabolic and neurodegenerative pathologies (Bercik et al., 2011; Cryan et al., 2019). Taken together, the results emphasize the potential of *B. subtilis* CW14 as a modulator of gut immunity and its cross-cutting effect on neurological and metabolic diseases, reinforcing the concept that the gut microbiota acts as a connector between the immune and nervous systems (Sarkar et al., 2016).

Treatment of HT-29 cells with *P. freudenreichii* ITG P9 resulted in evidence of dual modulation of gene expression, characterized by both positive and negative regulation of specific genes (Table [S10](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST10_Genes_multiple_categories_with_FC_sorted_Propionibacterium.xlsx)). Enrichment analyses indicate that the SH2D3C (+6.80) and CORO1A (+3.79) genes are associated with symptomatic polyhydramnios-megalencephalic-epilepsy syndrome. Similarly, KIFC2 (+2.14) has been linked to diseases such as Charcot-Marie-Tooth disease type 2P, type 4B3 and adult-onset dystonia-parkinsonism. The KIAA0513 gene (+4.52) has been associated with intellectual disability-obesity-brain malformations-facial deformity syndrome and Alzheimer's disease. This group of genes has been linked to synaptic plasticity, suggesting a potential role in maintaining the structure of the nervous system and thus a neuroprotective effect. This effect could be mediated by up-regulation of genes involved in stabilizing the neuronal cytoskeleton, thereby strengthening the hypothesis of a connection between gut microbiota modulation and neurological pathways (Biggs et al., 2025; Gerik-Celebi et al., 2023; Herbin et al., 2016; Shimojima et al., 2017; Zheng et al., 2022; Zhu et al., 2020). In contrast, down-regulation of KIF20A (-2,19), a gene enriched in citrullinemia type II, a primary immunodeficiency with natural killer cell deficiency and adrenal insufficiency, was observed. Research has indicated a correlation between this gene and the suppression of glioblastoma cell invasion and proliferation, suggesting a potential tumor suppressor mechanism (Saadh et al., 2025). These findings are pertinent in the context of the gut-brain axis, as they suggest the modulation of an intestinal immune response, which influences neuroinflammatory processes and central nervous system homeostasis (Kim et al., 2024).

Transcriptomic analyses also revealed a set of differentially expressed genes (DEGs) with multi-association profiles to various pathologies (Table [S11](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST11.xlsx)). Among these, genes with pleiotropic roles were highlighted, simultaneously linked to dysbiosis, cancer, neurological diseases, bacterial infections, and rare and viral diseases (Figure 3). In this regard, the genes *CCL4*, *CSF2*, *CSF3*, *CXCL8*, *CXCL10, and CCL5* emerged as central nodes, showing a significant positive LFC and being associated with the five pathological categories analyzed (Table [S11](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST11.xlsx)). It is noteworthy that this group of genes exhibits an LFC that is twice the established (LFC ≥ 2) **(Figure 3)**, which may indicate a role as cross-cutting biomarkers in multiple pathophysiological pathways. Furthermore, genes such as *CCL4*, *TNF,* and *CSF2* also function as central nodes, connecting dysbiosis to neurological diseases including Alzheimer's, Parkinson's, and epilepsy. For instance, *CSF2* (LFC +5,03), associated with microglial activation in Alzheimer's disease, and *TNF* (LFC +3,88), implicated in neuroinflammation in amyotrophic lateral sclerosis (ALS), underscore the existence of shared mechanisms between gut inflammation and neuronal degeneration.

 Gráfico, Gráfico de líneas

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**Figure 3. Association of genes with categories and Log2FoldChange in *B. subtilis* CW14 and *P. freudenreichii* ITG P9.**

# 3. Discussion.

The modulation of the intestinal cellular response through the implementation of probiotics has attracted the attention of researchers in recent years, especially for its potential to influence intestinal epithelial homeostasis, activation of immune pathways, reprogramming of the cell cycle by modulating critical phase arrests in damaged cells and the prevention of inflammatory, neoplastic and other human pathologies (Q. Wang et al., 2021). Previous studies have shown that the interaction between probiotics and intestinal epithelium promotes the modulation of local responses, which can lead to the improvement of the intestinal barrier, the inhibition of pathogens, the modulation and maturation of the immune system, and the reduction of inflammation and carcinogenic processes (Do Carmo et al., 2017; Foligné et al., 2010; Peng et al., 2019a).

The results obtained show significant differences in the differential mRNA expression of Caco-2 cells treated with *B. subtilis* CW14 and HT-29 cells treated with *P. freudenreichii* ITG P9. In the former, a coordinated immune response was observed through the overexpression of chemokines and inflammatory factors, whereas in the latter, a transcriptional response characterized by the modulation of genes related to cell cycle control and stress was observed. The diversity observed suggests that the effects of probiotics on intestinal cells may be strain-specific and may be related to molecular mechanisms regulating epithelial homeostasis, inflammation, cell adhesion, stress response, and cell cycle arrest.

## 3.1. Response of Caco-2 cells to Bacillus subtilis CW14 treatment.

Transcriptomic analysis revealed overexpression of chemokines and immunostimulatory factors (Table [ST2](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST2_KEGG_2021_Human_terms_sorted_with_all.xlsx)). These genes are involved in the recruitment of T lymphocytes, neutrophils, and macrophage differentiation, suggesting activation of the NF-κB signaling pathway, a central axis in the inflammatory response and defense against pathogens (Peng et al., 2019b). In this context, the chemokine CCL4 is known to attract immune cells expressing the CCR5 receptor, and its overexpression has been associated with inflammatory states in the gut and immune regulation (R. Chen et al., 2022). Asimismo, factores de estimulantes de colonias como CSF2 (GM-CSF) y CSF3 (G-CSF) modulan la proliferación, diferenciación, supervivencia, maduración y activación funcional de células hematopoyéticas, incluidos de granulocitos y macrófagos, reforzando la respuesta innata, y mediante 4 vías de señalización diferentes PI3K/Akt, ERK1/2, JAK2/STAT5 y NF-kB (Bhattacharya et al., 2015).

# References

Abbas, T., & Dutta, A. (2009). p21 in cancer: intricate networks and multiple activities. *Nature Reviews Cancer 2009 9:6*, *9*(6), 400–414. https://doi.org/10.1038/nrc2657

Anderson, G. (2023). Gut Microbiome and Circadian Interactions with Platelets Across Human Diseases, including Alzheimer’s Disease, Amyotrophic Lateral Sclerosis, and Cancer. *Current Topics in Medicinal Chemistry*, *23*(28), 2699–2719. https://doi.org/10.2174/0115680266253465230920114223

Bercik, P., Denou, E., Collins, J., Jackson, W., Lu, J., Jury, J., Deng, Y., Blennerhassett, P., MacRi, J., McCoy, K. D., Verdu, E. F., & Collins, S. M. (2011). The intestinal microbiota affect central levels of brain-derived neurotropic factor and behavior in mice. *Gastroenterology*, *141*(2), 599-609.e3. https://doi.org/10.1053/J.GASTRO.2011.04.052/ASSET/046D7D52-9F74-4709-98C4-98202C5684C3/MAIN.ASSETS/GRE2.JPG

Bhattacharya, P., Thiruppathi, M., Elshabrawy, H. A., Alharshawi, K., Kumar, P., & Prabhakar, B. S. (2015). GM-CSF: An immune modulatory cytokine that can suppress autoimmunity. *Cytokine*, *75*(2), 261–271. https://doi.org/10.1016/J.CYTO.2015.05.030

Biggs, K. E., Fikse, E. N., Anderson, F. L., Kettenbach, A. N., & Havrda, M. C. (2025). Coronin1A regulates the trafficking of alpha synuclein in microglia. *Journal of Neuroscience*, e1337242025. https://doi.org/10.1523/JNEUROSCI.1337-24.2025

Bouskra, D., Brézillon, C., Bérard, M., Werts, C., Varona, R., Boneca, I. G., & Eberl, G. (2008). Lymphoid tissue genesis induced by commensals through NOD1 regulates intestinal homeostasis. *Nature 2008 456:7221*, *456*(7221), 507–510. https://doi.org/10.1038/nature07450

Cani, P., & Delzenne, N. (2009). The Role of the Gut Microbiota in Energy Metabolism and Metabolic Disease. *Current Pharmaceutical Design*, *15*(13), 1546–1558. https://doi.org/10.2174/138161209788168164

Carbon, S., Douglass, E., Dunn, N., Good, B., Harris, N. L., Lewis, S. E., Mungall, C. J., Basu, S., Chisholm, R. L., Dodson, R. J., Hartline, E., Fey, P., Thomas, P. D., Albou, L. P., Ebert, D., Kesling, M. J., Mi, H., Muruganujan, A., Huang, X., … Westerfield, M. (2019). The Gene Ontology Resource: 20 years and still GOing strong. *Nucleic Acids Research*, *47*(D1), D330–D338. https://doi.org/10.1093/NAR/GKY1055

Cerdó, T., García-Santos, J. A., Bermúdez, M. G., & Campoy, C. (2019). The Role of Probiotics and Prebiotics in the Prevention and Treatment of Obesity. *Nutrients*, *11*(3). https://doi.org/10.3390/NU11030635

Chen, E. Y., Tan, C. M., Kou, Y., Duan, Q., Wang, Z., Meirelles, G. V., Clark, N. R., & Ma’ayan, A. (2013). Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. *BMC Bioinformatics*, *14*. https://doi.org/10.1186/1471-2105-14-128

Chen, R., Ma, L., Jiang, C., & Zhang, S. (2022). Expression and potential role of CCL4 in CD8+T cells in NSCLC. *Clinical and Translational Oncology*, *24*(12), 2420–2431. https://doi.org/10.1007/S12094-022-02913-9/METRICS

Chen, Z., Tang, M., Wang, N., Liu, J., Tan, X., Ma, H., Luo, J., & Xie, K. (2025). Genetic variation reveals the therapeutic potential of BRSK2 in idiopathic pulmonary fibrosis. *BMC Medicine*, *23*(1), 22. https://doi.org/10.1186/S12916-025-03848-Y/FIGURES/4

Clough, E., & Barrett, T. (2016). The Gene Expression Omnibus Database. *Methods in Molecular Biology (Clifton, N.J.)*, *1418*, 93–110. https://doi.org/10.1007/978-1-4939-3578-9\_5

Consortium, T. U., Bateman, A., Martin, M.-J., Orchard, S., Magrane, M., Adesina, A., Ahmad, S., Bowler-Barnett, E. H., Bye-A-Jee, H., Carpentier, D., Denny, P., Fan, J., Garmiri, P., Gonzales, L. J. da C., Hussein, A., Ignatchenko, A., Insana, G., Ishtiaq, R., Joshi, V., … Zhang, J. (2025). UniProt: the Universal Protein Knowledgebase in 2025. *Nucleic Acids Research*, *53*(D1), D609–D617. https://doi.org/10.1093/NAR/GKAE1010

Cousin, F. J., Jouan-Lanhouet, S., Théret, N., Brenner, C., Jouan, E., Moigne-Muller, G. L., Dimanche-Boitrel, M.-T., & Jan, G. (2016). The probiotic Propionibacterium freudenreichii as a new adjuvant for TRAIL-based therapy in colorectal cancer. *Oncotarget*, *7*(6), 7161–7178. https://doi.org/10.18632/oncotarget.6881

Cousin, F. J., Jouan-Lanhouet, S., Théret, N., Brenner, C., Jouan, E., Moigne-Muller, G. Le, Dimanche-Boitrel, M.-T., Jan, G., Cousin, F. J., Jouan-Lanhouet, S., Théret, N., Brenner, C., Jouan, E., Le Moigne-Muller, G., Dimanche-Boitrel, M.-T., & Jan, G. (2016). The probiotic  Propionibacterium freudenreichii  as a new adjuvant for TRAIL-based therapy in colorectal cancer. *Oncotarget*, *7*(6), 7161–7178. https://doi.org/10.18632/ONCOTARGET.6881

Cremon, C., Barbaro, M. R., Ventura, M., & Barbara, G. (2018). Pre- and probiotic overview. *Current Opinion in Pharmacology*, *43*, 87–92. https://doi.org/10.1016/J.COPH.2018.08.010

Cryan, J. F., O’riordan, K. J., Cowan, C. S. M., Sandhu, K. V., Bastiaanssen, T. F. S., Boehme, M., Codagnone, M. G., Cussotto, S., Fulling, C., Golubeva, A. V., Guzzetta, K. E., Jaggar, M., Long-Smith, C. M., Lyte, J. M., Martin, J. A., Molinero-Perez, A., Moloney, G., Morelli, E., Morillas, E., … Dinan, T. G. (2019). The microbiota-gut-brain axis. *Physiological Reviews*, *99*(4), 1877–2013. https://doi.org/10.1152/PHYSREV.00018.2018/ASSET/IMAGES/LARGE/Z9J0041929160006.JPEG

Dekaboruah, E., Suryavanshi, M. V., Chettri, D., & Verma, A. K. (2020). Human microbiome: an academic update on human body site specific surveillance and its possible role. *Archives of Microbiology 2020 202:8*, *202*(8), 2147–2167. https://doi.org/10.1007/S00203-020-01931-X

del Toro, N., Shrivastava, A., Ragueneau, E., Meldal, B., Combe, C., Barrera, E., Perfetto, L., How, K., Ratan, P., Shirodkar, G., Lu, O., Mészáros, B., Watkins, X., Pundir, S., Licata, L., Iannuccelli, M., Pellegrini, M., Martin, M. J., Panni, S., … Hermjakob, H. (2022). The IntAct database: efficient access to fine-grained molecular interaction data. *Nucleic Acids Research*, *50*(D1), D648–D653. https://doi.org/10.1093/NAR/GKAB1006

Do Carmo, F. L. R., Rabah, H., Huang, S., Gaucher, F., Deplanche, M., Dutertre, S., Jardin, J., Loir, Y. Le, Azevedo, V., & Jan, G. (2017). Propionibacterium freudenreichii surface protein SlpB is involved in adhesion to intestinal HT-29 cells. *Frontiers in Microbiology*, *8*(JUN), 269595. https://doi.org/10.3389/FMICB.2017.01033/BIBTEX

Foligné, B., Deutsch, S. M., Breton, J., Cousin, F. J., Dewulf, J., Samson, M., Pot, B., & Jan, G. (2010). Promising immunomodulatory effects of selected strains of dairy propionibacteria as evidenced in vitro and in vivo. *Applied and Environmental Microbiology*, *76*(24), 8259–8264. https://doi.org/10.1128/AEM.01976-10/SUPPL\_FILE/FIGURE\_S1\_AND\_LEGEND.PPT

Gerik-Celebi, H. B., Aydin, H., Bolat, H., & Unsel-Bolat, G. (2023). Clinical and Genetic Characteristics of Patients with Unexplained Intellectual Disability/Developmental Delay without Epilepsy. *Molecular Syndromology*, *14*(3), 208–218. https://doi.org/10.1159/000529018

Harrison, P. W., Amode, M. R., Austine-Orimoloye, O., Azov, A. G., Barba, M., Barnes, I., Becker, A., Bennett, R., Berry, A., Bhai, J., Bhurji, S. K., Boddu, S., Lins, P. R. B., Brooks, L., Ramaraju, S. B., Campbell, L. I., Martinez, M. C., Charkhchi, M., Chougule, K., … Yates, A. D. (2024). Ensembl 2024. *Nucleic Acids Research*, *52*(D1), D891–D899. https://doi.org/10.1093/NAR/GKAD1049

Herbin, O., Regelmann, A. G., Ramkhelawon, B., Weinstein, E. G., Moore, K. J., & Alexandropoulos, K. (2016). Monocyte adhesion and plaque recruitment during atherosclerosis development is regulated by the adapter protein chat-H/SHEP1. *Arteriosclerosis, Thrombosis, and Vascular Biology*, *36*(9), 1791–1801. https://doi.org/10.1161/ATVBAHA.116.308014/SUPPL\_FILE/ATVB\_ATVB-2016-308014D\_SUPP2.PDF

Hou, K., Wu, Z. X., Chen, X. Y., Wang, J. Q., Zhang, D., Xiao, C., Zhu, D., Koya, J. B., Wei, L., Li, J., & Chen, Z. S. (2022a). Microbiota in health and diseases. *Signal Transduction and Targeted Therapy 2022 7:1*, *7*(1), 1–28. https://doi.org/10.1038/s41392-022-00974-4

Hou, K., Wu, Z. X., Chen, X. Y., Wang, J. Q., Zhang, D., Xiao, C., Zhu, D., Koya, J. B., Wei, L., Li, J., & Chen, Z. S. (2022b). Microbiota in health and diseases. *Signal Transduction and Targeted Therapy 2022 7:1*, *7*(1), 1–28. https://doi.org/10.1038/s41392-022-00974-4

Kim, H., Jo, J. H., Lee, H. G., Park, W., Lee, H. K., Park, J. E., & Shin, D. (2024). Inflammatory response in dairy cows caused by heat stress and biological mechanisms for maintaining homeostasis. *PLOS ONE*, *19*(3), e0300719. https://doi.org/10.1371/JOURNAL.PONE.0300719

Kochumon, S., Madhoun, A. Al, Al-Rashed, F., Azim, R., Al-Ozairi, E., Al-Mulla, F., & Ahmad, R. (2020). Adipose tissue gene expression of CXCL10 and CXCL11 modulates inflammatory markers in obesity: implications for metabolic inflammation and insulin resistance. *Therapeutic Advances in Endocrinology and Metabolism*, *11*. https://doi.org/10.1177/2042018820930902/ASSET/IMAGES/LARGE/10.1177\_2042018820930902-FIG2.JPEG

Kolodziej, L. E., Lodolce, J. P., Chang, J. E., Schneider, J. R., Grimm, W. A., Bartulis, S. J., Zhu, X., Messer, J. S., Murphy, S. F., Reddy, N., Turner, J. R., & Boone, D. L. (2011). TNFAIP3 Maintains Intestinal Barrier Function and Supports Epithelial Cell Tight Junctions. *PLOS ONE*, *6*(10), e26352. https://doi.org/10.1371/JOURNAL.PONE.0026352

Krause, P., Zahner, S. P., Kim, G., Shaikh, R. B., Steinberg, M. W., & Kronenberg, M. (2014). The tumor necrosis factor family member TNFSF14 (LIGHT) is required for resolution of intestinal inflammation in mice. *Gastroenterology*, *146*(7), 1752-1762.e4. https://doi.org/10.1053/j.gastro.2014.02.010

Kumari, R., Singh, A., Yadav, A. N., Mishra, S., Sachan, A., & Ghosh Sachan, S. (2020). *Probiotics, prebiotics, and synbiotics: Current status and future uses for human health* (pp. 173–190). https://doi.org/10.1016/B978-0-12-820528-0.00012-0

Kundu, I., Sharma, M., Barai, R. S., Pokar, K., & Idicula-Thomas, S. (2023). GeDiPNet: Online resource of curated gene-disease associations for polypharmacological targets discovery. *Genes & Diseases*, *10*(3), 647–649. https://doi.org/10.1016/J.GENDIS.2022.05.034

Lasso, G., Mayer, S. V., Winkelmann, E. R., Chu, T., Elliot, O., Patino-Galindo, J. A., Park, K., Rabadan, R., Honig, B., & Shapira, S. D. (2019). A Structure-Informed Atlas of Human-Virus Interactions. *Cell*, *178*(6), 1526-1541.e16. https://doi.org/10.1016/J.CELL.2019.08.005

Lee, M. S., & Kim, Y.-J. (2007). Signaling Pathways Downstream of Pattern-Recognition Receptors and Their Cross Talk. *Annual Review of Biochemistry*, *76*(Volume 76, 2007), 447–480. https://doi.org/https://doi.org/10.1146/annurev.biochem.76.060605.122847

Ley, R. E., Turnbaugh, P. J., Klein, S., & Gordon, J. I. (2006). Microbial ecology: human gut microbes associated with obesity. *Nature*, *444*(7122), 1022–1023. https://doi.org/10.1038/4441022A

Love, M. I., Huber, W., & Anders, S. (2014). Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biology*, *15*(12), 1–21. https://doi.org/10.1186/S13059-014-0550-8/FIGURES/9

Mayer, E. A., Knight, R., Mazmanian, S. K., Cryan, J. F., & Tillisch, K. (2014). Gut Microbes and the Brain: Paradigm Shift in Neuroscience. *Journal of Neuroscience*, *34*(46), 15490–15496. https://doi.org/10.1523/JNEUROSCI.3299-14.2014

McFarland, L. V., Evans, C. T., & Goldstein, E. J. C. (2018). Strain-Specificity and Disease-Specificity of Probiotic Efficacy: A Systematic Review and Meta-Analysis. *Frontiers in Medicine*, *5*(MAY). https://doi.org/10.3389/FMED.2018.00124

Nesterova, A. P., Klimov, E. A., Zharkova, M., Sozin, S., Sobolev, V., Ivanikova, N. V., Shkrob, M., & Yuryev, A. (2019). Disease Pathways: An Atlas of Human Disease Signaling Pathways. *Disease Pathways: An Atlas of Human Disease Signaling Pathways*, 1–704. https://doi.org/10.1016/C2018-0-00586-1

Neurath, M. F. (2014). Cytokines in inflammatory bowel disease. *Nature Reviews Immunology 2014 14:5*, *14*(5), 329–342. https://doi.org/10.1038/nri3661

Ogata, H., Goto, S., Sato, K., Fujibuchi, W., Bono, H., & Kanehisa, M. (1999). KEGG: Kyoto Encyclopedia of Genes and Genomes. *Nucleic Acids Research*, *27*(1), 29–34. https://doi.org/10.1093/NAR/27.1.29

*Orphadata – Orphanet datasets*. (n.d.). Retrieved January 30, 2025, from https://www.orphadata.com/

Oughtred, R., Rust, J., Chang, C., Breitkreutz, B. J., Stark, C., Willems, A., Boucher, L., Leung, G., Kolas, N., Zhang, F., Dolma, S., Coulombe-Huntington, J., Chatr-aryamontri, A., Dolinski, K., & Tyers, M. (2021). The BioGRID database: A comprehensive biomedical resource of curated protein, genetic, and chemical interactions. *Protein Science : A Publication of the Protein Society*, *30*(1), 187–200. https://doi.org/10.1002/PRO.3978

Pauletto, M., Elgendy, R., Ianni, A., Marone, E., Giantin, M., Grotta, L., Ramazzotti, S., Bennato, F., Dacasto, M., & Martino, G. (2020). Nutrigenomic Effects of Long-Term Grape Pomace Supplementation in Dairy Cows. *Animals 2020, Vol. 10, Page 714*, *10*(4), 714. https://doi.org/10.3390/ANI10040714

Peng, M., Liu, J., & Liang, Z. (2019a). Probiotic Bacillus subtilis CW14 reduces disruption of the epithelial barrier and toxicity of ochratoxin A to Caco-2 cells. *Food and Chemical Toxicology*, *126*, 25–33. https://doi.org/10.1016/j.fct.2019.02.009

Peng, M., Liu, J., & Liang, Z. (2019b). Probiotic Bacillus subtilis CW14 reduces disruption of the epithelial barrier and toxicity of ochratoxin A to Caco-2 cells. *Food and Chemical Toxicology*, *126*, 25–33. https://doi.org/10.1016/J.FCT.2019.02.009

Piñero, J., Ramírez-Anguita, J. M., Saüch-Pitarch, J., Ronzano, F., Centeno, E., Sanz, F., & Furlong, L. I. (2020). The DisGeNET knowledge platform for disease genomics: 2019 update. *Nucleic Acids Research*, *48*(D1), D845–D855. https://doi.org/10.1093/NAR/GKZ1021

Pletscher-Frankild, S., Pallejà, A., Tsafou, K., Binder, J. X., & Jensen, L. J. (2015). DISEASES: Text mining and data integration of disease–gene associations. *Methods*, *74*, 83–89. https://doi.org/10.1016/J.YMETH.2014.11.020

Richard, M. L., & Sokol, H. (2019). The gut mycobiota: insights into analysis, environmental interactions and role in gastrointestinal diseases. *Nature Reviews Gastroenterology & Hepatology 2019 16:6*, *16*(6), 331–345. https://doi.org/10.1038/s41575-019-0121-2

Saadh, M. J., Ghnim, Z. S., Mahdi, M. S., Chandra, M., Ballal, S., Bareja, L., Chaudhary, K., Sharma, R. S. K., Gupta, S., Taher, W. M., Alwan, M., Jawad, M. J., & Hamad, A. K. (2025). Decoding the Role of Kinesin Superfamily Proteins in Glioma Progression. *Journal of Molecular Neuroscience 2025 75:1*, *75*(1), 1–28. https://doi.org/10.1007/S12031-025-02308-9

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 2019 16:10*, *16*(10), 605–616. https://doi.org/10.1038/s41575-019-0173-3

Sarkar, A., Lehto, S. M., Harty, S., Dinan, T. G., Cryan, J. F., & Burnet, P. W. J. (2016). Psychobiotics and the Manipulation of Bacteria–Gut–Brain Signals. *Trends in Neurosciences*, *39*(11), 763–781. https://doi.org/10.1016/J.TINS.2016.09.002/ASSET/47E1F62D-43C1-4C20-8C37-7040FF227529/MAIN.ASSETS/GR1.JPG

Shannon, P., Markiel, A., Ozier, O., Baliga, N. S., Wang, J. T., Ramage, D., Amin, N., Schwikowski, B., & Ideker, T. (2003). Cytoscape: A Software Environment for Integrated Models of Biomolecular Interaction Networks. *Genome Research*, *13*(11), 2498–2504. https://doi.org/10.1101/GR.1239303

Shimojima, K., Okamoto, N., Goel, H., Ondo, Y., & Yamamoto, T. (2017). Familial 9q33q34 microduplication in siblings with developmental disorders and macrocephaly. *European Journal of Medical Genetics*, *60*(12), 650–654. https://doi.org/10.1016/J.EJMG.2017.08.017

Szklarczyk, D., Kirsch, R., Koutrouli, M., Nastou, K., Mehryary, F., Hachilif, R., Gable, A. L., Fang, T., Doncheva, N. T., Pyysalo, S., Bork, P., Jensen, L. J., & Von Mering, C. (2023). The STRING database in 2023: protein-protein association networks and functional enrichment analyses for any sequenced genome of interest. *Nucleic Acids Research*, *51*(1 D), D638–D646. https://doi.org/10.1093/nar/gkac1000

Trejo, F., & Sanz, Y. (2013). 10 - Intestinal bacteria and probiotics: effects on the immune system and impacts on human health. In P. C. Calder & P. Yaqoob (Eds.), *Diet, Immunity and Inflammation* (pp. 267–291). Woodhead Publishing. https://doi.org/https://doi.org/10.1533/9780857095749.3.267

Upadhyay, V., & Fu, Y. X. (2013). Linking the microbiota and metabolic disease with lymphotoxin. *International Immunology*, *25*(7), 397–403. https://doi.org/10.1093/INTIMM/DXT018

Vida, H., Sahar, M., Nikdouz, A., & Arezoo, H. (2024). Chemokines in neurodegenerative diseases. *Immunology and Cell Biology*, 1–18. https://doi.org/10.1111/IMCB.12843

Wang, Q., Wu, H., Hu, J., Fu, H., Qu, Y., Yang, Y., Cai, Q., Efimov, A., Wu, M., Yen, T., Wang, Y., & Yang, Z. J. (2021). Nestin is required for spindle assembly and cell cycle progression in glioblastoma cells. *Molecular Cancer Research*, *19*(10), 1651–1665. https://doi.org/10.1158/1541-7786.MCR-20-0994/672984/AM/NESTIN-IS-REQUIRED-FOR-SPINDLE-ASSEMBLY-AND-CELL

Wang, Y., Wan, B., Li, D., Zhou, J., Li, R., Bai, M., Chen, F., & Yu, L. (2012). BRSK2 is regulated by ER stress in protein level and involved in ER stress-induced apoptosis. *Biochemical and Biophysical Research Communications*, *423*(4), 813–818. https://doi.org/10.1016/J.BBRC.2012.06.046

Yamazaki, S., Inohara, N., Ohmuraya, M., Tsuneoka, Y., Yagita, H., Katagiri, T., Nishina, T., Mikami, T., Funato, H., Araki, K., & Nakano, H. (2022). IκBζ controls IL-17-triggered gene expression program in intestinal epithelial cells that restricts colonization of SFB and prevents Th17-associated pathologies. *Mucosal Immunology*, *15*(6), 1321–1337. https://doi.org/10.1038/S41385-022-00554-3/ATTACHMENT/3FB6A419-770A-43B8-9568-F84985B28667/MMC2.PDF

Zheng, R., Du, Y., Wang, X., Liao, T., Zhang, Z., Wang, N., Li, X., Shen, Y., Shi, L., Luo, J., Xia, J., Wang, Z., & Xu, J. (2022). KIF2C regulates synaptic plasticity and cognition in mice through dynamic microtubule depolymerization. *ELife*, *11*. https://doi.org/10.7554/ELIFE.72483

Zhu, M., Jia, L., Li, F., & Jia, J. (2020). Identification of KIAA0513 and Other Hub Genes Associated With Alzheimer Disease Using Weighted Gene Coexpression Network Analysis. *Frontiers in Genetics*, *11*, 552414. https://doi.org/10.3389/FGENE.2020.00981/BIBTEX

Zmora, N., Suez, J., & Elinav, E. (2019). You are what you eat: diet, health and the gut microbiota. *Nature Reviews. Gastroenterology & Hepatology*, *16*(1), 35–56. https://doi.org/10.1038/S41575-018-0061-2