# 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). The intestinal tract is the body's largest immune system, interacting with antigens and mechanisms of both the immune system and the central nervous system (CNS) (Pelaseyed et al., 2014). It is estimated that around 70% of the immune system is generated in the gut (Hashemi et al., 2023; Hou et al., 2022a). 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., 2022b). Under balanced conditions, the gut microbiota contributes to stability, resilience and beneficial symbiosis for the host, acting as an additional organ, preventing uncontrolled absorption of toxic or pathogenic compounds, as well as in the regulation of the immune response (Hashemi et al., 2023; Hou et al., 2022a). 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 including or excluding specific microorganisms, can potentially 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, transcriptomic analysis was conducted on the cell lines Caco-2 and HT-29 treated with the probiotics *Bacillus subtilis* CW14 and *Propionibacterium freudenreichii* ITG P9, respectively. The objective of this analysis 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 two main axes: 1) the relationship with proteins associated with human diseases, and 2) the identification of possible gene modulation mechanisms linked to immune and physiological responses. This integrated approach will advance the understanding of how probiotics can modulate gene networks associated with human diseases, 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 S1](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 et al., 2016).

Principal Component Analysis (PCA) was conducted using the DESeq2 (version 1.38.1) (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 Collection (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 diseases.

Annotations were made to associate DEGs with human 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.

**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, 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 were visualized in Cytoscape v. 3.10.2 (Shannon et al., 2003) with a Padj ≤ 0.05

# 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.1)**. 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.

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 **(Fig. 1)**.



**Figure 1. PCA and Volcano Plot Analysis of Genomic Data in Probiotic-Treated Caco-2 and HT-29 Cells.** **(A and C)** Principal Component Analysis (PCA) of Genomic Data. In panel A (for *B. subtilis* CW14), PC1 accounts for 68% of the variance and PC2 for 18%. The points represent control samples (red) and treatment samples (blue) from Caco-2 cells. In panel C (for *P. freudenreichii* ITG P9), PC1 explains 94% of the variance and PC2 3%, with control samples depicted in red and treatment samples in blue from HT-29 cells. **(B and D)** Volcano Plots. In panel B (for *B. subtilis* CW14), the x-axis shows the logarithmic change in gene expression, and the y-axis displays the -log10 of the p-value. The red points represent genes with both significant log2FC and significant p-value; the blue points represent genes with only a significant p-value; the yellow points represent genes with only a significant log2FC; and the grey points represent non-significant genes. A cutoff of a log2FC of 1.333 and a p-value threshold of 10e-6 is applied for graphics. Panel D (for *P. freudenreichii* ITG P9) follows the same criteria.

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

Analysis of *B. subtilis* CW14-treated Caco-2 cells and *P. freudenreichii* ITG P9-treated HT-29 cells revealed significant modulation of DEGs through the implementation of expression change thresholds log2FC ≥ 2, an FDR value ≤ 0.05 and a Padj ≤ 0.05. These criteria allowed the selection of a set of genes associated with important biological processes, including cell cycle, immunity, adhesion, inflammation, and transport. In addition, key metabolic and signaling pathways were identified. All results obtained for gene ontology terms (Enrichr), metabolic and signaling pathways (KEGG and Elsevier Pathway Collection) can be viewed respectively in **Tables** [**S1**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S1_GO_Biological_Process_terms_sorted_with_FC.xlsx)**,** [**S2,**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S2_Elsevier_Pathway_Collection_terms_sorted_with_all.xlsx) and [**S3**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S3_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., 2022a). 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, regulatory T cells (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) 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* (-2.72) expression 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 (L. Chen et al., 2021; Neurath, 2014). Representative DEGs with a log2FC (LFC) doubling ≥ 2 for *B. subtilis* CW14 are shown in **Table 1**. All results obtained can be seen in **Tables** [**S1**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S1_GO_Biological_Process_terms_sorted_with_FC.xlsx)**,** [**S2,**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S2_Elsevier_Pathway_Collection_terms_sorted_with_all.xlsx) and [**S3**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S3_KEGG_2021_Human_terms_sorted_with_all.xlsx).

|  |  |  |  |
| --- | --- | --- | --- |
| 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 1. Functional enrichment of positively regulated genes in Caco-2 cells treated with *B. subtilis* CW14.** This table summarizes the key genes identified in the transcriptomic analysis, their associated enriched biological pathways, the adjusted p-values for these enrichments, and the corresponding log2FC in gene expression, highlighting their potential roles in immune signaling pathways and inflammatory responses.

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 suggesting mechanisms associated with cell arrest through the G1/S transition phase and thus in 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). All results obtained for *P. freudenreichii* ITG P9 can be found in **Tables** [**S1**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S1_GO_Biological_Process_terms_sorted_with_FC.xlsx)**,** [**S2,**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S2_Elsevier_Pathway_Collection_terms_sorted_with_all.xlsx) and [**S3**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S3_KEGG_2021_Human_terms_sorted_with_all.xlsx)**.**

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 to arrest 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 **(Table** [**S4**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S4_Genes_dysbiosis_diseases_with_FC_sorted_all.xlsx)**)**, neurological disorders **(Table** [**S5**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S5_Genes_neurological_diseases_with_FC_sorted_all.xlsx)**)**, and rare or orphan syndromes **(Table** [**S6**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S6_Genes_rare_diseases_with_FC_sorted_all.xlsx)**)** through log2FC (LFC) ≥ 2, an FDR value ≤ 0.05 and Padj filter ≤ 0.05. The results 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, positive regulation of several genes associated with proinflammatory and immunomodulatory pathways was observed, with log2FC values ranging from +2.10 to +5.23 **(Table** [**S1**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S1_GO_Biological_Process_terms_sorted_with_FC.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 Disease (PD), Alzheimer's Disease (AD)), rare disorders (amyloidosis, antibody-mediated glomerulonephritis) and gut dysbiosis, linked to metabolic disorders such as obesity, inflammatory bowel disease (IBD) and diabetes mellitus **(Table** [**S4**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S4_Genes_dysbiosis_diseases_with_FC_sorted_all.xlsx)**,** [**S5**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S5_Genes_neurological_diseases_with_FC_sorted_all.xlsx)**,** [**S6**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S6_Genes_rare_diseases_with_FC_sorted_all.xlsx)**),** suggesting a dual role in the activation of innate immunity and 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 (CNS) (Vida et al., 2024a). 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 (MS) or AD (Mayer et al., 2014).

Concerning the connection between dysbiosis and neuroinflammation, the results are reinforced when considering the role of genes such as *CXCL8* (+4,64), 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 **(Table** [**S7**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S7_diseases_rare_dysbiosis_neurological.xlsx)**)**, reinforcing the concept that the gut microbiota acts as a connector between the immune and nervous systems (Sarkar et al., 2016). A summary of the genes associated with different pathologies can be seen in **Fig. 2**.

Gráfico, Gráfico de barras

El contenido generado por IA puede ser incorrecto.**Figure 2. Association of genes with categories and Log2FoldChange in *B. subtilis* CW14.** This graph illustrates the association between regulated genes and various disease categories following treatment with *B. subtilis* CW14. On the x-axis, the analyzed genes are displayed, while the left y-axis indicates the number of disease categories linked to each gene. The stacked bars break down these counts by type: neurological diseases, pathogenic bacteria, cancer, rare diseases, dysbiosis, and viral diseases. Superimposed on the bars, a red line represents the logarithmic change in gene expression (Log2FoldChange), with its values shown on the right y-axis. A dotted horizontal line marks a reference value of Log2FoldChange = 0.

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** [**S1**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S1_GO_Biological_Process_terms_sorted_with_FC.xlsx)**)**. Enrichment analyses indicate that the *SH2D3C* (+6.80) and *CORO1A* (+3.79) both show an association with the polyhydramnios-megalencephaly-epilepsy symptomatic 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* (+4.52) gene has been associated with intellectual disability-obesity-brain malformations-facial deformity syndrome and AD. 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 the 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; M. 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 (H. Kim et al., 2024a). All the results obtained can be seen in **Tables** [**S4**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S4_Genes_dysbiosis_diseases_with_FC_sorted_all.xlsx)**,** [**S5**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S5_Genes_neurological_diseases_with_FC_sorted_all.xlsx)**,** and [**S6**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S6_Genes_rare_diseases_with_FC_sorted_all.xlsx). A summary of the genes associated with different pathologies can be seen in **Fig. 3**.

Gráfico, Gráfico de líneas

Descripción generada automáticamente**Figure 3. Association of genes with categories and Log2FoldChange in *P. freudenreichii* ITG P9.** This graph displays the association between regulated genes and various disease categories following treatment with *P. freudenreichii* ITG P9. It follows the same structure as the previous graph, with the x-axis showing the analyzed genes and the left y-axis indicating the number of disease categories linked to each gene. A red line overlays the bars to show the Log2FoldChange in gene expression (values on the right y-axis), while a dotted horizontal line marks a reference level of Log2FoldChange = 0.

Transcriptomic analyses also revealed a set of differentially expressed genes (DEGs) with multi-association profiles to various pathologies **(Table** [**S7**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S7_diseases_rare_dysbiosis_neurological.xlsx)**)**. Genes with pleiotropic roles were highlighted, simultaneously linked to dysbiosis, cancer, neurological diseases, bacterial infections, and rare and viral diseases **(Figure 4)**. In this regard, the genes *CCL4*, *CSF2*, *CSF3*, *CXCL8*, *CXCL10,* and *CCL5* emerged as central nodes, showing a significant positive Log2FC and being associated with the pathological categories analyzed **(Table** [**S7**](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Table_S7_diseases_rare_dysbiosis_neurological.xlsx)**)**. It is noteworthy that this group of genes exhibits a Log2FC that is twice the established (Log2FC ≥ 2), which may indicate a role as cross-cutting biomarkers in multiple pathophysiological pathways. Furthermore, *CCL4*, *TNF*, and *CSF2* genes also function as central nodes, connecting dysbiosis to neurological diseases including AD, PD, and epilepsy. For instance, *CSF2* (+5,03), associated with microglial activation in AD, and *TNF* (+3,88), implicated in neuroinflammation in amyotrophic lateral sclerosis (ALS), underscore the existence of shared mechanisms between gut inflammation and neuronal degeneration.

Gráfico de dispersión

El contenido generado por IA puede ser incorrecto.

**Figure 4. Heatmap of Log2FC in gene expression across diseases.** This heatmap illustrates the Log2FC in gene expression for a range of genes across several diseases. The vertical axis lists the diseases associated, while the horizontal axis displays the genes analyzed. Each cell’s color intensity represents the magnitude of the Log2FC, deeper blues indicate strong upregulation, whereas yellows reflect downregulation. Numerical values are overlaid on each cell for precise quantification.

## 2.3.4. Interacciones Proteína-Proteína (PPI)

En células Caco-2 tratadas con *B. subtilis* CW14, se destacó un grupo de genes con roles pleiotrópicos, descritos anteriormente. En la red, los genes CCL4, CSF2, CSF3, CXCL8, CXCL10 y CCL5 emergen como nodos centrales (véase [red CCL4](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/Cytoscape_network_ppi_go_biological_process.cys) en el material suplementario), se identificaron nuevas conexiones entre IL1B, IL1A y CCL20 mediante el análisis de PPI. La red resalta términos GO enriquecidos vinculados a la inflamación y a la quimiotaxis de leucocitos (linfocitos, monocitos, neutrófilos y eosinófilos). En este contexto, CCL4 desempeña un papel esencial en el reclutamiento inmunitario hacia sitios de infección o inflamación.

Asimismo, se identificaron términos que enfatizan la importancia de la vía ERK1/2 en la señalización celular, conectando la inflamación con procesos de proliferación, diferenciación y respuesta a citocinas (Chandiok, 2024). Adicionalmente, rutas mediadas por citoquinas y quimiocinas, que involucran a IL1A, IL1B, CXCLs, CCL20 y CCL5, indican respuestas a infecciones bacterianas, fúngicas y parasitarias. Finalmente, el nodo “Negative Regulation by Host of Viral Transcription” sugiere un componente antiviral, ampliando la función de CCL4 a mecanismos de defensa frente a infecciones virales.

En células HT-29 tratadas con *P. freudenreichii* ITG P9 se identificaron dos redes principales, cada una centrada en un gen clave: KIF20A y OASL (Figura 4). Aunque no se encontraron interacciones con términos de GO, el análisis de PPI reveló que ambas redes se derivan de PPI, vinculando a KIF20A y OASL con procesos como el ciclo celular y la respuesta antiviral.

Diagrama

El contenido generado por IA puede ser incorrecto.

**Figura 4. Redes PPI de KIF20A y OASL en células HT-29 tras tratamiento con *P. freudenreichii* ITG P9.**

KIF20A, con regulación negativa (-2,19), se posiciona como nodo central en la primera red. Este gen interactúa con ciclinas (CCNA2, CCNB1, CCNB2), quinasas (AURKA, PLK1, TTK) y componentes del centrómero (CENPA, INCENP, NCAPG, NUF2), lo que sugiere un rol esencial en la citocinesis, progresión del ciclo celular y estabilidad cromosómica. Su interacción con RACGAP1, clave para la citocinesis, indica que la regulación negativa inducida por *P. freudenreichii* ITG P9 puede provocar defectos en la división celular, inestabilidad genómica y apoptosis en células cancerosas, resaltando su potencial antitumoral (Eid et al., 2022).

Por otro lado, OASL (+2,03) emerge como un regulador central en la respuesta inmune antiviral. Este gen interactúa con IRF7, IFI44, IFIT3, ISG15 y RNASEL, lo que sugiere que activa RNASEL para degradar ARN viral e inhibir la replicación, además de modular la expresión de genes antivirales a través de IRF7 (Jung-Rodriguez et al., 2024; Lee et al., 2013). La regulación de OASL por *P. freudenreichii* ITG P9 podría potenciar la respuesta inmune innata, limitando la propagación viral y protegiendo las células epiteliales, fortaleciendo así la barrera inmune intestinal (Weiss, 2020).

# 2.4. 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. In contrast, 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.

## 2.4.1. 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). The hypothesis is supported by the fact that the over-expression of NFKBIZ, a regulator required for NF-κB-mediated modulation of transcription, is associated with cytokine release and amplification of the inflammatory response (Yamazaki et al., 2022b). Furthermore, the over-expression of chemokines such as CXCL8, CXCL10, CXCL11, and CX3CL2 indicates the activation of pathways that promote chemotaxis, resulting in the migration of neutrophils and NK cells to sites of infection or tissue damage. In particular, the importance of the proinflammatory factor, IL-8, in various inflammatory diseases is well-documented, with its role being to act via multiple signaling pathways, including PI3k/Akt, MAPK, and NF-κB (Y. Zhu et al., 2021).

In addition to the activation of immune pathways, modulation of chemokines and immune factors that could promote defense and repair mechanisms of the intestinal epithelium were also observed. Overexpression of CCL5 in association with CCL22 and CCL2 suggests the attraction of monocytes and Tregs, which would contribute to the polarization of macrophages towards a reparative and anti-inflammatory phenotype. This combination of effector and regulatory cell attraction is crucial for repairing epithelial damage and preventing inflammatory processes that can trigger gut barrier disruptions (Peng et al., 2019b). Thus, the activation of different pathways such as NF-κB, mediated by probiotics, through the overexpression of different genes, not only promotes the inflammatory response but can also trigger the production of growth and tissue repair factors. Indeed, the NF-κB pathway has been associated with the activation of repair mechanisms, which facilitates the reduction of inflammation and restoration of epithelial integrity (Liu et al., 2022).

Concurrently, alterations in genes linked to metabolic activity and stress were detected. Overexpression of CYP1B1, an enzyme categorized within the cytochrome P450 family, was observed to be implicated in the detoxification of xenobiotics, in addition to lipid and steroid hormone metabolism (Shah et al., 2019). In this context, CYP1B1 induction could be indicative of an adaptive response aimed at maintaining gut balance, thereby suggesting a mechanism of detoxification or metabolism of beneficial compounds derived from probiotics or microbiota. This contrasts with a promotion of proinflammatory signals, which would be consistent with a role in modulating pathways such as Ahr (aryl hydrocarbon receptor), which is key in the response to microbial metabolites (Schiering et al., 2017). For instance, the AhR/HIF1α pathway is activated by microbiota-derived ligands (e.g. tryptophan), which in turn induce CYP1A1/CPYP1B1, thereby facilitating the metabolism of these ligands and preventing immune overstimulation. This suggests that CPYP1B1 may function as a feedback regulator for immune homeostasis (Schiering et al., 2017).

Conversely, elevated BIRC3 expression and the negative regulation of RGS2 suggest the activation of anti-apoptotic mechanisms that promote epithelial cell survival under stress conditions (Hu & Shao, 2022). In this regard, BIRC3, a member of the inhibitor of apoptosis (IAP) family, through inactivation of CASP cascades, exerts this function, but in addition, it plays a crucial role in neuronal function through its NPD1-mediated positive regulation promoting neuronal cell survival (Martin-Gallausiaux et al., 2022). Furthermore, BIRC3 has been reported to be associated with crypt regeneration and, consequently, in the renewal and function of the intestinal epithelial barrier (Martin-Gallausiaux et al., 2022). Conversely, the study conducted by Hu & Shao (2022) revealed that positive regulation of BIRC3, mediated by the probiotic *Lactobacillus pentosus*, contributed to the inactivation of the NLRC4 inflammasome, which suppressed neuronal pyroptosis, suggesting it as an alternative strategy for the treatment of neurodegenerative diseases.

Concerning RGS2, it is a regulator of the G protein-coupled receptor (GPCR) signaling pathway, which belongs to the RGS superfamily of proteins. The expression of RGS2 is subject to epigenetic, transcriptional, and post-translational mechanisms (Pauletto et al., 2020). The negative regulation of RGS2 suggests a possible influence of this probiotic on the modulation of GPCR-mediated signaling in the intestinal epithelium; since RGS2 is involved in the regulation of T-cell immunity and antioxidant response, its downregulation could be related to a reduction of oxidative stress or inflammation in these cells. These findings are consistent with those reported by (Li et al., 2023), who have proposed that negative regulation of RGS2 contributes indirectly to gastrointestinal homeostasis.

Finally, the finding of reduced expression of HSPA6 is of interest, given that this gene encodes a chaperone of the heat shock protein (HSP) group. The induction of this gene is often observed in response to stress stimuli, such as exposure to toxins, oxidative stress, or heat conditions that compromise cellular integrity (H. Kim et al., 2024b; Song et al., 2022). Its functions include protein quality control, including correct protein folding, refolding, and control of subsequent protein degradation (Song et al., 2022). Modulation of heat shock proteins such as HSPA6 is closely associated with epithelial barrier function (Ohkawara et al., 2006). In this regard, the observed state of relaxation in the HSPA6 gene may be a consequence of the modulation exerted by the probiotic, as, in the absence of stressors, cells do not require its activity, thereby maintaining intestinal cell homeostasis.

## 2.4.2. Response of HT-29 cells treated with *P. freudenreichii* ITG P9.

Treatment of HT-29 cells with *P. freudenreichii* ITG P9 resulted in a transcriptional response focused on cell cycle modulation. Positive overexpression of genes such as CDKN1A, CDKN2B, and CDKN1C was observed (Table [S6](https://github.com/nicolasbroldan/Protocolo_Reposicionamiento_Probioticos/blob/main/8_Supplementary%20Material/ST6_KEGG_2021_Human_terms_sorted_with_all.xlsx)). These genes encode cyclin-dependent kinase inhibitors (CKIs) that play a critical role in cell cycle arrest at the G1/S transition (Cousin, Jouan-Lanhouet, Théret, Brenner, Jouan, Moigne-Muller, Dimanche-Boitrel, Jan, et al., 2016b; Y. Wang et al., 2012b). Their activation is crucial to prevent the proliferation of damaged and potentially cancerous cells, suggesting that *P. freudenreichii* may promote a protective arrest state that could prevent the spread of damaged cells or oxidative stress (Cousin et al., 2012; Cousin et al., 2016b). In this sense, the induction of cell arrest at critical stages of the cell cycle is interpreted as a protective mechanism against stress that would allow the cell to initiate repair processes or drive the cell toward apoptosis in the event of irreparable damage. Previous studies have shown that the induction of CDKN1A (p21) by compounds that alter histone acetylation, such as short-chain fatty acids, is a mechanism in the prevention of colon carcinogenesis. Indeed, down-regulation of these three genes has been associated with aberrant proliferation and thus the potential to trigger tumor transformation, as it has been suggested, for example, that CDKN1A may play a key role in inhibiting epithelial-mesenchymal transition (EMT), migration, and invasion (Bueno-Fortes et al., 2022; Tu et al., 2017; Yang et al., 2023).

Moreover, the regulation of genes involved in the G2/M transition, such as BRSK2 and NES, suggests that they may not only act in the G1/S phase but also modulate cycle progression in later phases. The coordination of these mechanisms may be crucial to arrest cell proliferation in response to a hostile environment, such as that generated in inflammatory conditions or in the presence of oxidative stress, thus preventing the accumulation of mutations and eventual malignant transformation (Cousin et al., 2016b; Y. Wang et al., 2012b). In this context, BRSK2 is known to be a serine/threonine protein kinase, a member of the *AMPK* family, which plays roles in apoptosis and cell polarity that are crucial for normal physiology (Z. Chen et al., 2025; Y. Wang et al., 2012b). In the context of pancreatic cancer, the study by (Saiyin et al., 2017) showed that pancreatic ductal adenocarcinoma (PDAC) neoplastic cells respond to nutrient deprivation by inducing BRSK2. This repression removes the feedback that mTORC1 normally exerts on Akt signaling, allowing Akt activity to increase, and giving cancer cells a survival advantage in an energetically unfavorable environment. However, BRSK2 is positively modulated after treatment with *P. freudenreichii* ITG P9. This finding suggests that metabolites or signals released by this probiotic could induce a state of metabolic stress like that of nutrient deprivation. Consequently, the activation of BRSK2 in intestinal cells (HT-29) could represent an adaptive response comparable to that observed in PDAC, with implications for the regulation of Akt/mTOR pathways. This is particularly relevant given that *P. freudenreichii* ITG P9 is known to produce short-chain fatty acids (e.g. propionate and acetate), compounds that can alter cellular metabolism and activate energy stress sensors such as AMP kinases (AMPKs) and their related members, including BRSK2. Thus, the positive modulation of BRSK2 in HT-29 cells following exposure to *P. freudenreichii* ITG P9 may be part of a cellular response aimed at coping with an environment of energy deprivation or metabolic stress-induced, for example, by bacterial metabolites.

## 2.4.3. Modulación probiótica de la respuesta inmune y su impacto en la salud neurológica.

La respuesta inmune en las células Caco-2 tras el tratamiento con *B. subtilis* CW14 evidenció un aumento en la expresión de quimioquinas inflamatorias, lo que plantea interrogantes sobre su impacto en la salud neurológica. Estudios recientes han evidenciado que la sobreexpresión de algunas de estas moléculas incide de manera significativa en la patogénesis de enfermedades neurodegenerativas, como el Alzheimer, caracterizado por deterioro cognitivo y neuroinflamación persistente. Por ejemplo, CCL4, regulado positivamente en contextos inflamatorios, se asocia con la activación de la vía NF-κB, lo que favorece la migración de microglía y la amplificación de la respuesta proinflamatoria en regiones cerebrales afectadas (J. Y. Kim et al., 2022). De manera similar, CXCL8 muestra un incremento en su expresión que potencia la activación glial y desencadena cascadas de señalización a través de las rutas PI3K/Akt y MAPK, agravando el daño neuronal (Lv et al., 2019; C. Wang et al., 2024). Asimismo, CSF2 y CSF3 se encuentran sobreexpresados; a través del receptor de GM-CSF que activa las vías JAK/STAT, MAPK, PI3K y NF-κB se estimula la proliferación y diferenciación de células inmunitarias, intensificando la respuesta inflamatoria. En modelos in vivo, GM-CSF, en interacción con IL-17, induce alteraciones progresivas en las oscilaciones gamma, lo que sugiere un papel específico en la disfunción neuronal y resalta su potencial como diana terapéutica (Dikmen et al., 2020) Por otro lado, CXCL10 y CCL5 facilitan la quimiotaxis y potencian los mecanismos inflamatorios, vinculándose estrechamente a procesos neurodegenerativos. Como lo señala el estudio de Guedes et al., 2018, es crucial profundizar en cómo estos mediadores afectan la deposición de Aβ, la hiperfosforilación de tau y la acumulación de microglía, para orientar el desarrollo de estrategias inmunoterapéuticas más eficaces.

Los genes KIFC2, ACAP3 y TUBGCP6 han sido implicados en la etiología de la distonía-parkinsonismo de inicio en la adultez. En nuestro estudio, el tratamiento con *P. freudenreichii* ITG P9 indujo la sobreexpresión de estos genes, sugiriendo que su modulación podría repercutir en la salud neurológica. Por ejemplo, KIFC2, miembro de la superfamilia de kinesinas, está relacionado con el transporte retrógrado axonal y la dinámica de microtúbulos, procesos críticos para la función neuronal (Hanlon et al., 1997). Asimismo, ACAP3 regula el equilibrio de Arf6, facilitando la transición de neuronas multipolares a bipolares y controlando el reciclaje de N-cadherina a través de la vía PIP5K/PI4,5P2, lo cual es esencial para la migración neuronal y la estabilidad sináptica (Miura & Kanaho, 2017). Por su parte, TUBGCP6 es fundamental para la duplicación de centriolos y la nucleación de microtúbulos, y su deficiencia se ha asociado con la microcefalia (J. Chen et al., 2022; Park et al., 2020). Aunque la literatura ha documentado la implicación de estos genes en la salud neurológica, aún no existen estudios que investiguen el impacto de tratamientos probióticos en enfermedades neurológicas, particularmente aquellos que involucren las vías descritas anteriormente. Nuestros hallazgos establecen un vínculo preliminar entre la modulación de KIFC2, ACAP3 y TUBGCP6 y la potencial mejora de la función neuronal, resaltando la necesidad de profundizar en este campo para desarrollar nuevas estrategias terapéuticas.

## 2.4.4. Modulación probiótica de marcadores metabólicos y genéticos relacionados con la disbiosis.

En nuestro estudio se evidenció una asociación entre la sobreexpresión de CCL4, inducida por el tratamiento probiótico con *B. subtilis* CW14, y marcadores de diabetes y obesidad, lo que sugiere que esta quimioquina podría influir en procesos metabólicos alterados. Este hallazgo cobra relevancia al contrastarlo con la literatura, donde se ha vinculado a CCL4 y a su receptor CCR5 con la inflamación crónica subyacente tanto a la diabetes mellitus como a las enfermedades cardiovasculares asociadas a la aterosclerosis. Aunque puede atraer macrófagos que destruyen las células de los islotes, se ha planteado que, en algunos modelos experimentales de diabetes, particularmente en el modelo NOD de diabetes tipo 1, CCL4 podría ejercer un papel protector, actuando más como un producto del proceso inmunológico que como un inductor inicial. Sin embargo, dada la diversidad de contextos patológicos, es crucial investigar a fondo su función para asegurar la traducción de estos hallazgos a ensayos clínicos, como concluyen Chang & Chen, 2016.

Adicionalmente, nuestros hallazgos sugieren que la sobreexpresión de CSF2 y CSF3, también inducida por el tratamiento probiótico con *B. subtilis* CW14, podría replicar, en parte, los efectos terapéuticos observados con la saponina CSF, ya que ambas condiciones activan las vías PI3K, NF-κB y MAPK. Según un estudio reportado por (Qin et al., 2023), interferir en estas cascadas, centradas en PI3K/Akt, MAPK y NF-κB, es uno de los mecanismos más críticos mediante los cuales la saponina CSF ejerce efectos protectores en enfermedades metabólicas como la obesidad, la hipertensión, la enfermedad del hígado graso no alcohólico, la diabetes y sus complicaciones cardiovasculares y cerebrovasculares. Además, la existencia de interacciones cruzadas entre estas vías, como la señalización MAPK–NF-κB, podría explicar en parte los efectos beneficiosos de la saponina CSF a dosis similares. Por ello, la modulación de CSF2 y CSF3 mediante tratamientos probióticos podría representar una estrategia novedosa para mejorar los procesos inflamatorios y metabólicos asociados a estas patologías.

En el tratamiento con *P. freudenreichii* ITG P9, observamos una sobreexpresión de HERC1 (+1.31), y en nuestro mapeo lo identificamos como un gen relacionado con la disbiosis, debido a su conexión con el síndrome de discapacidad intelectual, obesidad, malformaciones cerebrales y dismorfismo facial. Sin embargo, al contrastar estos hallazgos con la literatura, encontramos que HERC1 ha sido previamente asociado con discapacidad intelectual, megalencefalia y atrofia cerebelosa, lo que refuerza su papel en la regulación del desarrollo cerebral a través de la vía RTK/PI3K/mTOR. Además, su participación en la neurogénesis temprana, la regulación de la espinogénesis dendrítica postsináptica y la homeostasis de los terminales presinápticos sugiere un rol clave en la plasticidad sináptica y la conectividad neuronal. Estos resultados destacan la relevancia de HERC1 en la arquitectura cerebral y abren la posibilidad de explorar su implicación en los efectos de la microbiota sobre el sistema nervioso (Nguyen et al., 2015; Pérez-Villegas et al., 2020).

## 2.4.5. Modulación probiótica de la expresión génica y su relevancia en el cáncer.

En nuestro estudio, el tratamiento con *B. subtilis* CW14 indujo la sobreexpresión diferencial de CCL4, CSF2, CSF3, CXCL8 y CXCL10. CXCL8 está asociado con la proliferación, invasión y migración tumoral a través de PI3K/Akt, MAPK, STAT3 y ERK1/2 (Dobre et al., 2022). La sobreexpresión de CSF2 y CSF3, mediante la activación de GM-CSF, se relaciona con inflamación crónica y mal pronóstico; sin embargo, ciertos subgrupos de CSF2 (CSF2RA/CSF2RB) favorecen la respuesta inmunitaria, mientras que los de CSF3 (CSF3R) se asocian con inflamación y menor supervivencia (Huang et al., 2020). Por otro lado, CXCL10 podría desempeñar un papel antitumoral, ya que su alta expresión en el microambiente tumoral se asocia con mejor pronóstico, posiblemente por su capacidad para reforzar la inmunidad. En particular, CXCL10 activa CXCR3 en células CD8+ T, favoreciendo su respuesta citotóxica contra el tumor (Karin, 2020). CCL4, en cambio, tiene un rol dual: promueve la progresión tumoral al reclutar macrófagos pro-tumorigénicos y células T reguladoras, pero también puede potenciar la inmunidad al atraer linfocitos citotóxicos y macrófagos fagocíticos (Mukaida et al., 2020).

Asimismo, KIF20A, regulado negativamente (-2,19) tras el tratamiento con *P. freudenreichii* ITG P9, es clave en la citocinesis, progresión celular y estabilidad cromosómica. Su sobreexpresión en cáncer colorrectal se asocia con mal pronóstico, y su silenciamiento inhibe la proliferación y migración tumoral vía JAK/STAT3 (Zhang et al., 2020). La modulación negativa de KIF20A por P. freudenreichii ITG P9 sugiere un efecto antitumoral al atenuar JAK/STAT3, reduciendo la proliferación y migración celular. Estos hallazgos resaltan el valor terapéutico de modular KIF20A y JAK/STAT3, así como el potencial de los probióticos como estrategia adyuvante en el tratamiento del cáncer.

# 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

Bueno-Fortes, S., Muenzner, J. K., Berral-Gonzalez, A., Hampel, C., Lindner, P., Berninger, A., Huebner, K., Kunze, P., Bäuerle, T., Erlenbach-Wuensch, K., Sánchez-Santos, J. M., Hartmann, A., De Las Rivas, J., & Schneider-Stock, R. (2022). A gene signature derived from the loss of cdkn1a (P21) is associated with CMS4 colorectal cancer. *Cancers*, *14*(1), 136. https://doi.org/10.3390/CANCERS14010136/S1

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

Chandiok, T. (2024). ERK 1/2 Pathways: Discoveries in Disease Causation and Developments in Their Treatment. *International Journal of Research and Review*, *11*(6), 808–817. https://doi.org/10.52403/IJRR.20240687

Chang, T. T., & Chen, J. W. (2016). Emerging role of chemokine CC motif ligand 4 related mechanisms in diabetes mellitus and cardiovascular disease: friends or foes? *Cardiovascular Diabetology 2016 15:1*, *15*(1), 1–8. https://doi.org/10.1186/S12933-016-0439-9

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, J., Ying, L., Zeng, L., Li, C., Jia, Y., Yang, H., & Yang, G. (2022). The novel compound heterozygous rare variants may impact positively selected regions of TUBGCP6, a microcephaly associated gene. *Frontiers in Ecology and Evolution*, *10*, 1059477. https://doi.org/10.3389/FEVO.2022.1059477/PDF

Chen, L., Zhang, S., Wu, S., Ren, Z., Liu, G., & Wu, J. (2021). Synergistic Protective Effect of Konjac Mannan Oligosaccharides and Bacillus subtilis on Intestinal Epithelial Barrier Dysfunction in Caco-2 Cell Model and Mice Model of Lipopolysaccharide Stimulation. *Frontiers in Immunology*, *12*, 696148. https://doi.org/10.3389/FIMMU.2021.696148/BIBTEX

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., Dimanche-Boitrel, M. T., Corcos, L., & Jan, G. (2012). Milk Fermented by Propionibacterium freudenreichii Induces Apoptosis of HGT-1 Human Gastric Cancer Cells. *PLOS ONE*, *7*(3), e31892. https://doi.org/10.1371/JOURNAL.PONE.0031892

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. (2016a). 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. (2016b). 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

Dikmen, H. O., Hemmerich, M., Lewen, A., Hollnagel, J. O., Chausse, B., & Kann, O. (2020). GM-CSF induces noninflammatory proliferation of microglia and disturbs electrical neuronal network rhythms in situ. *Journal of Neuroinflammation*, *17*(1), 1–13. https://doi.org/10.1186/S12974-020-01903-4/FIGURES/5

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

Dobre, M., Trandafir, B., Milanesi, E., Salvi, A., Bucuroiu, I. A., Vasilescu, C., Niculae, A. M., Herlea, V., Hinescu, M. E., & Constantinescu, G. (2022). Molecular profile of the NF‐κB signalling pathway in human colorectal cancer. *Journal of Cellular and Molecular Medicine*, *26*(24), 5966–5975. https://doi.org/10.1111/JCMM.17545

Eid, R. A., Soltan, M. A., Eldeen, M. A., Shati, A. A., Dawood, S. A., Eissa, M., Zaki, M. S. A., Algahtani, M., Theyab, A., Abdel-Daim, M. M., & Kim, B. (2022). Assessment of RACGAP1 as a Prognostic and Immunological Biomarker in Multiple Human Tumors: A Multiomics Analysis. *International Journal of Molecular Sciences*, *23*(22), 14102. https://doi.org/10.3390/IJMS232214102/S1

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

Guedes, J. R., Lao, T., Cardoso, A. L., & El Khoury, J. (2018). Roles of microglial and monocyte chemokines and their receptors in regulating Alzheimer’s disease-associated amyloid-β and tau pathologies. *Frontiers in Neurology*, *9*(AUG). https://doi.org/10.3389/FNEUR.2018.00549/PDF

Hanlon, D. W., Yang, Z., & Goldstein, L. S. B. (1997). Characterization of KIFC2, a neuronal kinesin superfamily member in mouse. *Neuron*, *18*(3), 439–451. https://doi.org/10.1016/S0896-6273(00)81244-1/ASSET/9422B438-4343-42D4-804D-3D0C50D76EB0/MAIN.ASSETS/GR6.JPG

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

Hashemi, B., Abdollahi, M., Abbaspour-Aghdam, S., Hazrati, A., Malekpour, K., meshgi, S., Kafil, H. S., ghazi, F., Yousefi, M., Roshangar, L., & Ahmadi, M. (2023). The effect of probiotics on immune responses and their therapeutic application: A new treatment option for multiple sclerosis. *Biomedicine & Pharmacotherapy*, *159*, 114195. https://doi.org/10.1016/J.BIOPHA.2022.114195

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

Hu, M., & Shao, Z. (2022). Lactobacillus pentosus Alleviates Lipopolysaccharide-Induced Neuronal Pyroptosis via Promoting BIRC3-Mediated Inactivation of NLRC4. *Evidence-Based Complementary and Alternative Medicine*, *2022*(1), 2124876. https://doi.org/10.1155/2022/2124876

Huang, X., Hu, P., & Zhang, J. (2020). Genomic analysis of the prognostic value of colony-stimulating factors (CSFs) and colony-stimulating factor receptors (CSFRs) across 24 solid cancer types. *Annals of Translational Medicine*, *8*(16), 994–994. https://doi.org/10.21037/ATM-20-5363

Jung-Rodriguez, E., Barbault, F., Bignon, E., & Monari, A. (2024). Molecular bases and specificity behind the activation of the immune system OAS/RNAse L pathway by viral RNA. *BioRxiv*, 2024.07.08.602453. https://doi.org/10.1101/2024.07.08.602453

Karin, N. (2020). CXCR3 Ligands in Cancer and Autoimmunity, Chemoattraction of Effector T Cells, and Beyond. *Frontiers in Immunology*, *11*. https://doi.org/10.3389/FIMMU.2020.00976/PDF

Kim, H., Jo, J. H., Lee, H. G., Park, W., Lee, H. K., Park, J. E., & Shin, D. (2024a). 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

Kim, H., Jo, J. H., Lee, H. G., Park, W., Lee, H. K., Park, J. E., & Shin, D. (2024b). 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

Kim, J. Y., Kim, J., Huang, M., Kosonen, R., & Lee, J. E. (2022). CCR4 and CCR5 Involvement in Monocyte-Derived Macrophage Migration in Neuroinflammation. *Frontiers in Immunology*, *13*. https://doi.org/10.3389/FIMMU.2022.876033/PDF

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, B., Oh, G. T., & Kim, Y. J. (2013). OASL1 inhibits translation of the type I interferon–regulating transcription factor IRF7. *Nature Immunology 2013 14:4*, *14*(4), 346–355. https://doi.org/10.1038/ni.2535

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

Li, L., Xu, Q., & Tang, C. (2023). RGS proteins and their roles in cancer: friend or foe? *Cancer Cell International 2023 23:1*, *23*(1), 1–12. https://doi.org/10.1186/S12935-023-02932-8

Liu, Z., Zhao, J., Sun, R., Wang, M., Wang, K., Li, Y., Shang, H., Hou, J., & Jiang, Z. (2022). Lactobacillus plantarum 23-1 improves intestinal inflammation and barrier function through the TLR4/NF-κB signaling pathway in obese mice. *Food & Function*, *13*(11), 5971–5986. https://doi.org/10.1039/D1FO04316A

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

Lv, H., Li, J., & Che, Y. Q. (2019). CXCL8 gene silencing promotes neuroglial cells activation while inhibiting neuroinflammation through the PI3K/Akt/NF-κB-signaling pathway in mice with ischemic stroke. *Journal of Cellular Physiology*, *234*(5), 7341–7355. https://doi.org/10.1002/JCP.27493

Martin-Gallausiaux, C., Garcia-Weber, D., Lashermes, A., Larraufie, P., Marinelli, L., Teixeira, V., Rolland, A., Béguet-Crespel, F., Brochard, V., Quatremare, T., Jamet, A., Doré, J., Gray-Owen, S. D., Blottière, H. M., Arrieumerlou, C., & Lapaque, N. (2022). Akkermansia muciniphila upregulates genes involved in maintaining the intestinal barrier function via ADP-heptose-dependent activation of the ALPK1/TIFA pathway. *Gut Microbes*, *14*(1). https://doi.org/10.1080/19490976.2022.2110639

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

Miura, Y., & Kanaho, Y. (2017). ACAP3, the GTPase-activating protein specific to the small GTPase Arf6, regulates neuronal migration in the developing cerebral cortex. *Biochemical and Biophysical Research Communications*, *493*(2), 1089–1094. https://doi.org/10.1016/J.BBRC.2017.09.076

Mukaida, N., Sasaki, S. ichiro, & Baba, T. (2020). CCL4 Signaling in the Tumor Microenvironment. *Advances in Experimental Medicine and Biology*, *1231*, 23–32. https://doi.org/10.1007/978-3-030-36667-4\_3

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

Nguyen, L. S., Schneider, T., Rio, M., Moutton, S., Siquier-Pernet, K., Verny, F., Boddaert, N., Desguerre, I., Munich, A., Rosa, J. L., Cormier-Daire, V., & Colleaux, L. (2015). A nonsense variant in HERC1 is associated with intellectual disability, megalencephaly, thick corpus callosum and cerebellar atrophy. *European Journal of Human Genetics 2016 24:3*, *24*(3), 455–458. https://doi.org/10.1038/ejhg.2015.140

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

Ohkawara, T., Takeda, H., Nishiwaki, M., Nishihira, J., & Asaka, M. (2006). Protective effects of heat shock protein 70 induced by geranylgeranylacetone on oxidative injury in rat intestinal epithelial cells. *Scandinavian Journal of Gastroenterology*, *41*(3), 312–317. https://doi.org/10.1080/00365520500319427

*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

Park, E. M., Scott, P. M., Clutario, K., Cassidy, K. B., Zhan, K., Gerber, S. A., & Holland, A. J. (2020). WBP11 is required for splicing the TUBGCP6 pre-mRNA to promote centriole duplication. *Journal of Cell Biology*, *219*(1). https://doi.org/10.1083/JCB.201904203

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

Pelaseyed, T., Bergström, J. H., Gustafsson, J. K., Ermund, A., Birchenough, G. M. H., Schütte, A., van der Post, S., Svensson, F., Rodríguez-Piñeiro, A. M., Nyström, E. E. L., Wising, C., Johansson, M. E. V., & Hansson, G. C. (2014). The mucus and mucins of the goblet cells and enterocytes provide the first defense line of the gastrointestinal tract and interact with the immune system. *Immunological Reviews*, *260*(1), 8–20. https://doi.org/10.1111/IMR.12182

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

Pérez-Villegas, E. M., Pérez-Rodríguez, M., Negrete-Díaz, J. V., Ruiz, R., Rosa, J. L., de Toledo, G. A., Rodríguez-Moreno, A., & Armengol, J. A. (2020). HERC1 Ubiquitin Ligase Is Required for Hippocampal Learning and Memory. *Frontiers in Neuroanatomy*, *14*. https://doi.org/10.3389/FNANA.2020.592797/PDF

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

Qin, S., Chen, J., Zhong, K., Li, D., & Peng, C. (2023). Could Cyclosiversioside F Serve as a Dietary Supplement to Prevent Obesity and Relevant Disorders? *International Journal of Molecular Sciences*, *24*(18). https://doi.org/10.3390/IJMS241813762

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

Saiyin, H., Na, N., Han, X., Fang, Y., Wu, Y., Lou, W., Yang, X., Saiyin, H., Na, N., Han, X., Fang, Y., Wu, Y., Lou, W., & Yang, X. (2017). BRSK2 induced by nutrient deprivation promotes Akt activity in pancreatic cancer via downregulation of mTOR activity. *Oncotarget*, *8*(27), 44669–44681. https://doi.org/10.18632/ONCOTARGET.17965

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

Schiering, C., Wincent, E., Metidji, A., Iseppon, A., Li, Y., Potocnik, A. J., Omenetti, S., Henderson, C. J., Wolf, C. R., Nebert, D. W., & Stockinger, B. (2017). Feedback control of AHR signalling regulates intestinal immunity. *Nature 2017 542:7640*, *542*(7640), 242–245. https://doi.org/10.1038/nature21080

Shah, B. R., Xu, W., & Mraz, J. (2019). Cytochrome P450 1B1: role in health and disease and effect of nutrition on its expression. *RSC Advances*, *9*(36), 21050–21062. https://doi.org/10.1039/C9RA03674A

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

Song, B., Shen, S., Fu, S., & Fu, J. (2022). HSPA6 and its role in cancers and other diseases. *Molecular Biology Reports 2022 49:11*, *49*(11), 10565–10577. https://doi.org/10.1007/S11033-022-07641-5

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

Tu, Q., Hao, J., Zhou, X., Yan, L., Dai, H., Sun, B., Yang, D., An, S., Lv, L., Jiao, B., Chen, C., Lai, R., Shi, P., & Zhao, X. (2017). CDKN2B deletion is essential for pancreatic cancer development instead of unmeaningful co-deletion due to juxtaposition to CDKN2A. *Oncogene 2018 37:1*, *37*(1), 128–138. https://doi.org/10.1038/onc.2017.316

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. (2024a). Chemokines in neurodegenerative diseases. *Immunology and Cell Biology*, 1–18. https://doi.org/10.1111/IMCB.12843

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

Wang, C., Wang, J., Zhu, Z., Hu, J., & Lin, Y. (2024). Spotlight on pro-inflammatory chemokines: regulators of cellular communication in cognitive impairment. *Frontiers in Immunology*, *15*, 1421076. https://doi.org/10.3389/FIMMU.2024.1421076/PDF

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. (2012a). 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

Wang, Y., Wan, B., Li, D., Zhou, J., Li, R., Bai, M., Chen, F., & Yu, L. (2012b). 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

Weiss, S. R. (2020). Activation and Antagonism of the OAS–RNase L Pathway. *Proceedings 2020, Vol. 50, Page 14*, *50*(1), 14. https://doi.org/10.3390/PROCEEDINGS2020050014

Yamazaki, S., Inohara, N., Ohmuraya, M., Tsuneoka, Y., Yagita, H., Katagiri, T., Nishina, T., Mikami, T., Funato, H., Araki, K., & Nakano, H. (2022a). 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

Yamazaki, S., Inohara, N., Ohmuraya, M., Tsuneoka, Y., Yagita, H., Katagiri, T., Nishina, T., Mikami, T., Funato, H., Araki, K., & Nakano, H. (2022b). 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

Yang, R. Y., Tan, J. Y., Liu, Z., Shen, X. L., & Hu, Y. J. (2023). Lappaol F regulates the cell cycle by activating CDKN1C/p57 in human colorectal cancer cells. *Pharmaceutical Biology*, *61*(1), 337–344. https://doi.org/10.1080/13880209.2023.2172048

Zhang, Q., Di, J., Ji, Z., Mi, A., Li, Q., Du, X., Wang, A., Wang, A., & Qin, C. (2020). [Retracted] KIF20A Predicts Poor Survival of Patients and Promotes Colorectal Cancer Tumor Progression through the JAK/STAT3 Signaling Pathway. *Disease Markers*, *2020*(1), 2032679. https://doi.org/10.1155/2020/2032679

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

Zhu, Y., Yang, S., Zhao, N., Liu, C., Zhang, F., Guo, Y., & Liu, H. (2021). CXCL8 chemokine in ulcerative colitis. *Biomedicine & Pharmacotherapy*, *138*, 111427. https://doi.org/10.1016/J.BIOPHA.2021.111427

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