Journal of Science Research International (JSRI)
ISSN: 2456-6365 (Online)

OPEN ACCESS

BIOINFORMATICS ANALYSIS OF AUTISM SPECTRUM DISORDER–ASSOCIATED GENES AND BIOLOGICAL PATHWAYS

Gopakumar Pillai* and Sakshi Salunke

Department of Biotechnology,

Pillai College of Arts, Commerce and Science (Empowered Autonomous), New Panvel, India

**Corresponding Author E-mail: gopakumar.pillai@mes.ac.in*

ORCID ID: 0000-0003-0060-6523

Received: 06 March 2026	Revised: 25 April 2026	Accepted: 10 May 2026	Published: 25 May 2026

DOI: https://doi.org/10.5281/zenodo.20374151

Abstract:

Autism Spectrum Disorder is characterised by numerous genetic and molecular components and is classified as a neurodevelopmental disorder. Although many potential contributors to ASD have already been identified at the gene level, the biological mechanisms behind Autism Spectrum Disorders are still not completely understood. Using an integrated bioinformatics approach to retrieve ASD-associated genes from the DisGeNET database, create protein-protein interaction networks (STRING), develop expanded gene interaction networks (GeneMANIA), perform and interpret functional enrichment analyses (Enrichr), and map biological pathways (Reactome), this study was undertaken. Several hub genes (PTEN, SHANK3, BDNF, NRXN1, and MECP2) showed very strong interactions with one another in the analysis, confirming that they are involved in the same molecular networks. Enrichment analyses found that these hub genes are primarily important for: synaptic organisation, neuronal communication, brain structure development, and gene expression regulation, suggesting that ASD results from disruptions in interconnected molecular networks and not from single mutations that cause defects. This research demonstrates how integrated bioinformatics approaches can provide insight into how ASD pathology occurs, in addition to establishing the first steps toward developing novel ASD biomarkers and identifying potential therapeutic targets.

Keywords: *Autism Spectrum Disorder, Bioinformatics, Gene Network Analysis, STRING, GeneMANIA, Enrichr, Reactome, Synaptic Organisation.*

Introduction

ASD is a neurodevelopmental disorder that negatively affects many aspects of communication (verbal and nonverbal), as well as other social and interpersonal skills throughout the person's life [1]. Typically, symptoms are first identified in childhood, but there may be some cases where the symptoms do not become evident until

later in life [2,3]. The process of developing ASD is quite complex, and there are a variety of biological, genetic, and environmental factors that contribute to its development [2,4,5].

While there are many genes implicated in neurodevelopmental disorders, the more difficult problem is understanding how different gene products (proteins) interact with one another to create an effective developmental process [6,7,8]. Interestingly, many of the genes that have been implicated in causing ASD have diverse biological functions, such as synapse formation, neuronal communication, and regulation of gene expression [9,10]. When taken as a whole, the combined effect of multiple genes on ASD suggests that a person with ASD does not have a single gene defect but rather an abnormality in connected biological systems that interfere with the normal functioning of the brain [11,12].

Due to the recent increase in available genetic information and the use of biological databases, bioinformatics and computational methods may now provide alternative ways for studying and understanding complex disorders such as ASD. Bioinformatics tools can assist scientists by allowing them to analyze gene interactions through the use of protein–protein interaction networks and biological pathway analysis. In this report, a variety of bioinformatics resources including STRING, GeneMANIA, DisGeNET, Reactome and Enrichr were utilized to analyze genes interactions and pathways [13,14,15,16,17].

Materials and Methods

DisGeNET analysis

The list of genes associated with Autism Spectrum Disorders (ASD) was obtained from the DisGeNET database, which is an aggregation of gene-disease associations from a variety of sources, including curated datasets, genome-wide association studies, and the published scientific literature [15]. The term "Autism Spectrum Disorder" was used to query the DisGeNET database and identify gene-disease associations within it. Initial screening of the genes returned from DisGeNET was based on the DisGeNET association score, and only genes with a minimum score of 0.80 (or 0.8) were selected for inclusion into the downstream analysis resulting in the top thirty ASD-associated genes for further analysis.

STRING analysis

The functional relationships of the selected gene set were evaluated using protein-protein interaction analysis with the STRING database [13]. The gene list was uploaded to the STRING database with the selected organism set to Homo sapiens. A high confidence interaction score of ≥0.70 was applied to filter for the most reliable protein-protein interactions. Both direct physical and indirect functional interactions were considered during the analysis. The resulting interaction network was examined for areas of high interaction density and for protein hubs, which could represent proteins that play critical roles in the biological processes associated with ASD.

GeneMANIA analysis

GeneMANIA was utilized for exploring gene-gene interactions and for discovering additional genes that are functionally related to the genes included in the input dataset [14]. This tool integrates different types of biological data, including but not limited to co-expression, physical interaction, genetic interaction, and shared biological pathways. The output network produced from GeneMANIA provided an illustration of the functional interactions between the genes studied and identified genes of central importance in biological pathways related to Autism Spectrum Disorders (ASD).

Enrichr analysis

Using Enrichr, a functional enrichment analysis was conducted to assess biological pathways and processes enriched within the gene set libraries including both the KEGG and Gene Ontology gene sets [17]. The enrichment terms were then evaluated against standard enrichment analysis criteria provided by Enrichr, as well as combined scores for the enriched pathways.

Reactome analysis

To expand on the biological function of the selected genes, a Reactome pathway analysis was performed [16]. The Reactome analysis allowed for mapping genes to corresponding and well-defined biological pathways for gene sets related to neuronal signaling, synaptic activity, and development. The results of this analysis illustrate how genes interact with one another to form larger biological systems and elucidate the molecular components that contribute towards Autism Spectrum Disorder.

Results

DisGeNET

Table 1: Thirty Autism Spectrum Disorder–associated genes were analyzed

Gene Symbol	Gene Description	Number of Diseases Associated	No. of Variants Associated	Score
PTEN	Phosphatase and tensin homolog	1945	1852	1.0
SHANK3	SH3 and multiple ankyrin repeat domains 3	336	152	0.95
CNTNAP2	Contactin associated protein 2	528	998	0.95
TCF4	Transcription factor 4	582	885	0.95
ARID1B	AT-rich interaction domain 1B	533	429	0.95
SLC6A4	Solute carrier family 6 member 4	621	129	0.9
BDNF	Brain derived neurotrophic factor	1487	108	0.9
AUTS2	Activator of transcription and developmental regulator AUTS2	288	705	0.9
DYRK1A	Dual specificity tyrosine phosphorylation regulated kinase 1A	477	383	0.9
FOXP1	Forkhead box P1	559	611	0.9
CUL3	Cullin 3	197	159	0.9
FOXP2	Forkhead box P2	348	462	0.9
SYN1	Synapsin I	135	227	0.9
CHD8	Chromodomain helicase DNA binding protein 8	237	190	0.85
NRXN1	Neurexin 1	268	1068	0.85
SCN2A	Sodium voltage-gated channel alpha subunit 2	518	1199	0.85
NLGN4X	Neuroligin 4 X-linked	84	59	0.85
TSC2	TSC complex subunit 2	665	4617	0.85
POGZ	Pogo transposable element derived with ZNF domain	298	214	0.85
SCN1A	Sodium voltage-gated channel alpha subunit 1	569	2549	0.85
CYFIP1	Cytoplasmic FMR1 interacting protein 1	86	23	0.85

GABRB3	GABA type A receptor subunit beta3	227	290	0.85
AVPR1A	Arginine vasopressin receptor 1A	97	3	0.85
MBD5	Methyl-CpG binding domain protein 5	257	715	0.85
KIRREL3	Kirre like nephrin family adhesion molecule 3	63	43	0.85
MEF2C	Myocyte enhancer factor 2C	314	302	0.85
SHANK2	SH3 and multiple ankyrin repeat domains 2	133	184	0.8
MECP2	Methyl-CpG binding protein 2	844	954	0.8
NLGN3	Neuroligin 3	76	35	0.8
ADNP	Activity dependent neuroprotector homeobox	348	134	0.8

Evidence of the involvement of the 30 most prominent genes associated with autism spectrum disorder (ASD), as determined by the DisGeNET analysis were identified to have a substantial association with disorders of acute neurological and/or developmental conditions, and that the identified genes play an important part in the pathogenesis of ASD (Table 1). The key genes of interest, including, PTEN, SHANK3, CNTNAP2, TCF4, and BDNF, exhibited high association scores, providing substantial evidence to suggest an association with ASD.

The identified autism spectrum disorder related genes have a primary function in the processes of synaptic organization, neuronal growth, signal transduction and neurotransmission. Furthermore, each of the associated variants evidenced by the number of genetic alterations suggested that genetic variants had a strong influence on brain growth/development and neuronal communication, and reflected in the clinical symptoms of ASD. The association scores also supported the strong confidence level, demonstrating the strength of evidence for each association.

STRING

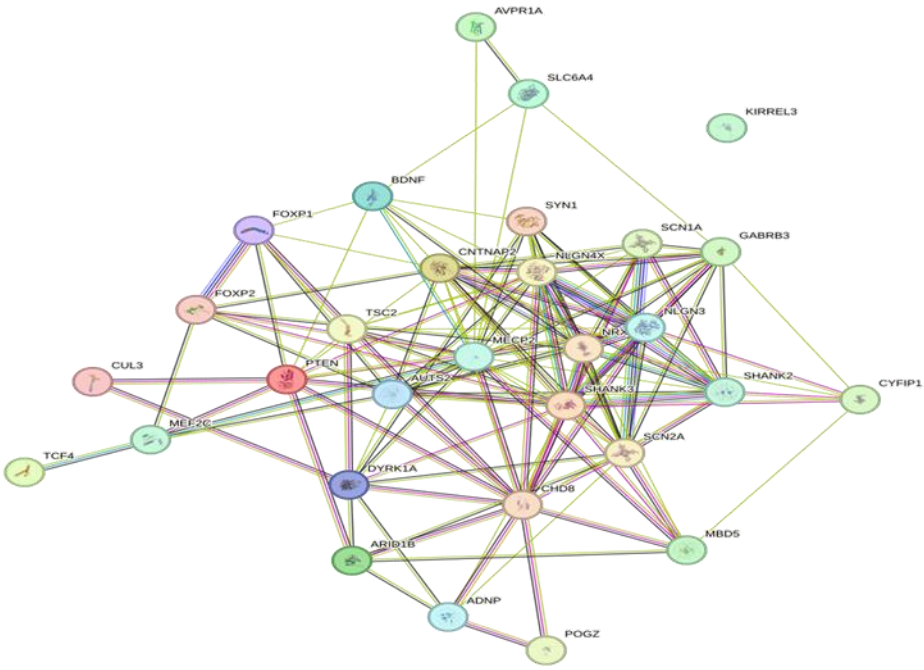

Figure 1: STRING protein–protein interaction network connectivity among Autism Spectrum Disorder genes

Table 2: Key Biological themes and representative GO processes in Autism Spectrum Disorder

Theme	Representative GO Biological Process Terms
Behavior & Cognitive Function	Learning, memory, cognition, behavioral regulation
Synaptic Structure & Plasticity	Synapse assembly, postsynaptic density organization, synaptic plasticity
Synaptic Transmission	Chemical synaptic transmission, regulation of neurotransmission, excitatory postsynaptic potential
Neuronal Development & Differentiation	Neuron differentiation, dendrite development, axon development
Brain Development	Telencephalon development, cerebellum development
Regulation of Neural Signaling	Regulation of membrane potential, ion transport regulation, receptor signaling regulation

The STRING database of protein-protein interactions shows how the genes associated with Autism Spectrum Disorder (ASD) interact with one another through protein interactions, thereby being integral players in a biological pathway that is comprised of multiple genes involved in shared biological processes (for example, the regulation of synaptic signaling and neuronal development). The enrichment analysis of Gene Ontology (GO) has shown that the majority of the genes listed here are involved in the biological functions of synaptic transmission, regulating neuronal signaling, neurogenesis, and regulating apoptosis, which are all vital to the development and function of a healthy brain (Table 2). In addition, these same genes have been found to be enriched in pathways involved in synaptic signaling and neuronal connectivity, which are key to how neurons communicate with one another and how cognitive processes occur. In addition, several genes here are also involved in the early development of the brain and synapse formation, and are critical for the establishment and maintenance of neural circuits that are often disrupted in individuals with ASD.

GeneMANIA

The genes that are associated with Autism Spectrum Disorder (ASD) form a highly interconnected gene network, suggesting a strong possibility that they will act via the same biological pathways, rather than independently (Fig. 2a and 2b). The degree of interconnectivity among these genes demonstrates the necessity for properly coordinated molecular interactions for the development of ASD and is critical to establishing the relationship of its genetic foundations. Within this network, the following genes have been identified as major central hub nodes in the network of genes related to ASD: PTEN, SHANK3, SCN1A, SCN2A, FOXP1, and MEF2C. In addition to having the ability to influence the biological developmental processes of neurons, these gene products also help to create and maintain the structure and function of synaptic connections.

The majority of connections seen in the network represent a connection between synaptic interactions, how neurons communicate, and how the brain develops. Other genes have also been implicated in critical processes including neurogenesis, signal transduction, and regulation of the expression of genes necessary for proper functioning of the neuronal network during normal operation. These genes provide evidence that they are key contributors to the preservation of synaptic transmission (communication) and the integrity of neural connections within the brain.

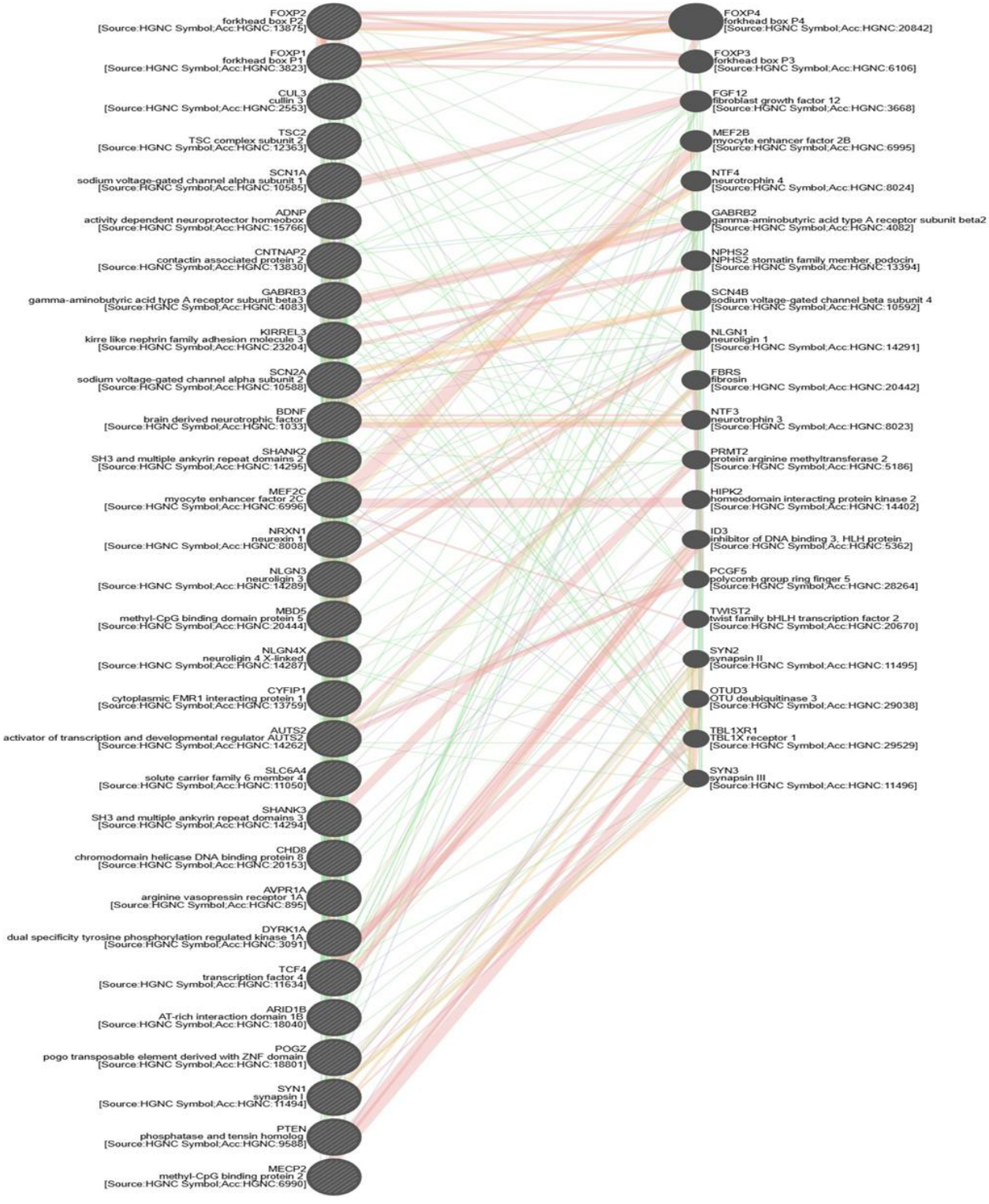

Figure 2a: GeneMANIA network showing functional associations between input Autism Spectrum Disorder (ASD)–associated genes (left panel) and predicted related genes (right panel). The connections represent co-expression, physical interactions, shared pathways, and genetic interactions, highlighting the expansion of the gene network based on functional similarity

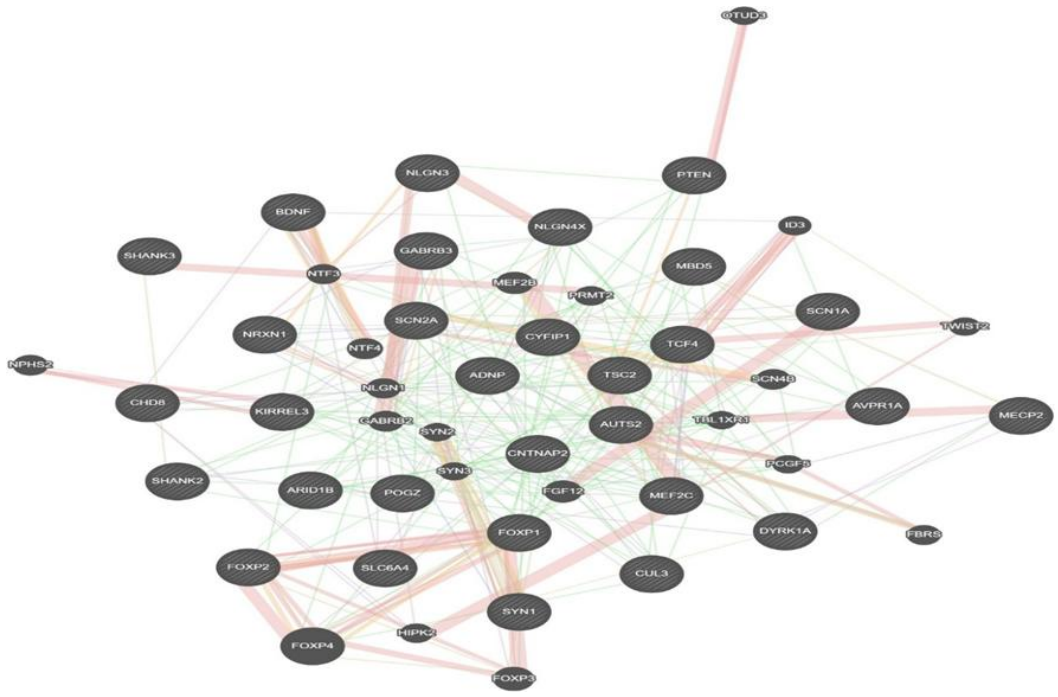

Figure 2b: Integrated GeneMANIA interaction network illustrating the complex connectivity among Autism Spectrum Disorder (ASD)–associated genes and their predicted partners. The dense network highlights key hub genes and their interactions, reflecting coordinated involvement in biological pathways relevant to ASD pathogenesis

Enrichr

A KEGG 2021 Human Pathway enrichment analysis indicated that ASD-associated Genes were primarily involved in the development of neurons, synaptic interactions, and overall function of the human brain. Examples of genes known to be associated with cellular signaling, neurodevelopmental processes and regulation of synapses include, but are not limited to, the following: PTEN; SHANK3; NRXN1; SCN1A; SCN2A; and BDNF (see Figure 3a and 3b). Moreover, the majority of gene-enriched pathways were related to synaptic interactions, neurodevelopment, apoptosis, and the transfer of signals from one cell to another. Together these genes act together via coordinated molecular pathways which support the neuronal connections and function of the brain as a whole, and disruption of these pathways may impair neuronal communication and contribute to ASD development.

Table 3: Hub-genes identified by multi database Enrichment Analysis

Gene	Reactome Pathways	KEGG Human	Wiki Pathways	Elsevier	ARCHS4 Kinases	PPI Hub Protein	Count
PTEN	YES	NO	YES	YES	YES	YES	6
SHANK3	YES	YES	YES	YES	YES	YES	6
NLGN3	NO	YES	YES	YES	NO	YES	5
BDNF	NO	YES	YES	YES	NO	NO	4
CNTNAP2	NO	YES	YES	YES	YES	NO	4
NRXN1	YES	NO	YES	YES	NO	YES	4
NLGN4X	YES	YES	YES	NO	YES	YES	5
GABRB3	NO	YES	YES	YES	YES	NO	4

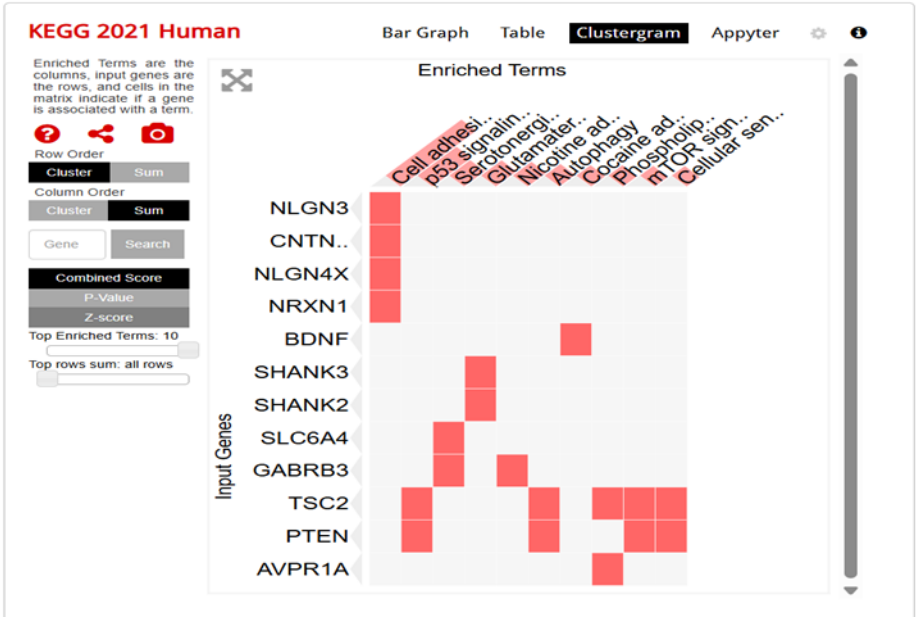

Figure 3a: Heatmap Representation of KEGG Pathway Enrichment in Autism Spectrum Disorder Genes

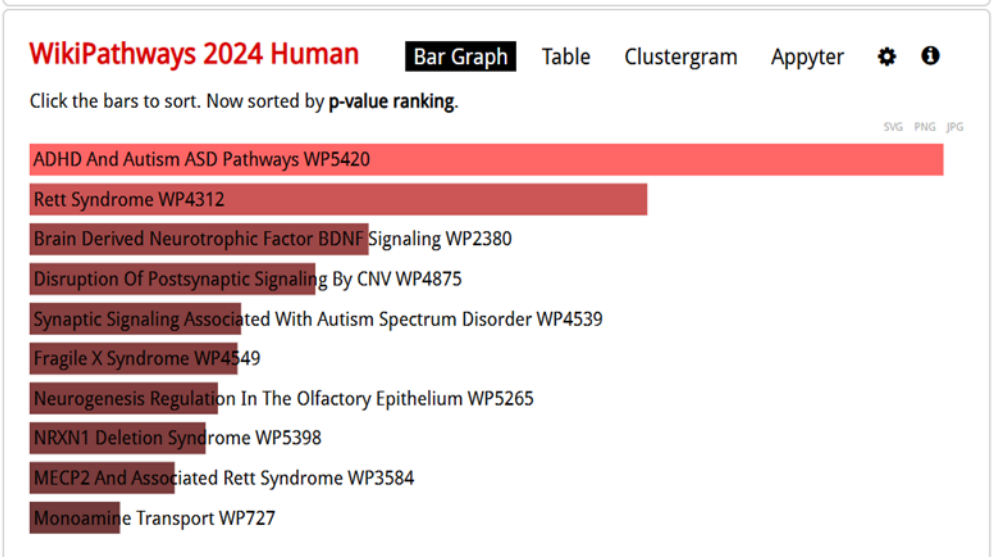

Figure 3b: Enrichr output showing enriched KEGG pathways and biological processes associated with Autism Spectrum Disorder (ASD)–related genes

Database comparisons showed a consistent association of numerous genes across multiple platforms of analysis, suggesting a significant contribution of these genes to Autism Spectrum Disorder (ASD) (Table 3). For example, PTEN and SHANK3 were among the most frequently detected genes across multiple databases, indicating they may serve as a common intracellular target/dependent component in the etiology of the disorder.

Similar to the above example, NLGN3 and NLGN4X represent other ASD related genes found in multiple databases, further supporting their role as contributing to functional organization of the synapse. However, BDNF, NRXN1,

GABRB3, and CNTNAP2 were present in less number of datasets providing evidence of potentially more specific or context-dependent functions of these genes with respect to the disorder.

The consistency of associations of these genes in multiple independent experiments, across different methods of analysis, supports the involvement of these genes in neuronal development and synaptic exchange.

Reactome

The Autism Spectrum Disorder (ASD) gene clustering example demonstrates multiple clusters of ASD-related genes clustered into distinct groups of genes with similar biological functions. As shown in the clustering example, many of the gene clusters functionally appear to be involved in the same major biological process/ cellular pathway, such as synaptic organization (e.g., formation/maintenance of the synapse), neuronal signaling, brain development and gene regulation. In addition, many of the ASD gene clusters are highly interrelated to one another indicating that the genes that affect synapse formation, neuronal communication and neural development likely do so in cooperation with one another. Also, some gene clusters are involved in controlling other genes (e.g., transcriptional regulation, etc.) and thus influence pathways associated with overall brain function. The branching nature of the gene network indicates that some of the gene clusters are related closer than other clusters.

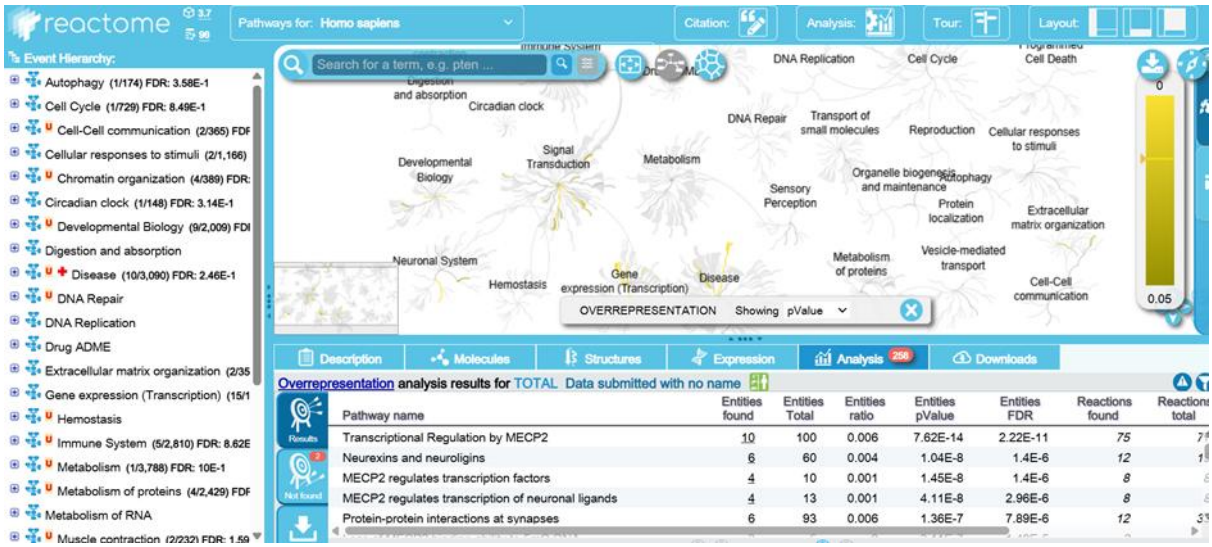

Figure 4: Reactome pathway clustering showing coordinated molecular mechanisms underlying Autism Spectrum Disorder (ASD)

Discussion

An integrated bioinformatics analysis was utilized to study the molecular basis of Autism Spectrum Disorder (ASD), concluding there is extensive functional connectivity between the genes identified. The gene hubs identified include PTEN, SHANK3, BDNF, NRXN1, and MECP2, which have critical roles in synaptic organization, neuronal signaling, development of the brain, and regulation of genes necessary for normal neural function. Moreover, recent advances in our understanding of the neurodevelopmental processes that contribute to ASD have revealed several different types of disruptions involving the regulatory mechanisms (e.g., signaling pathways, gene expression) that complicate the picture of ASD and confirm the findings in this study. We have expanded the ASD network by adding genome-wide analyses using the GeneMANIA and protein-protein interaction analysis with

STRING to illustrate that all of the ASD-associated genes exhibit strong protein-protein interaction among themselves, indicating that they operate as part of a single network, rather than exist as multiple, independent networks [12, 18, 19].

Therefore, studies supporting disrupted gene networks may provide insight into the role of disrupted gene networks in ASD. Enrichment analysis using Enrichr and Reactome identified significant enrichment of processes such as synaptic transmission, neuronal differentiation, signaling pathways, and gene regulation, which are all necessary for the normal development of the brain and communication between neurons. Using a combination of bioinformatics tools, we cross-validated important genes and pathways, which made our findings more trustworthy. DisGeNET provided the original gene–disease linkages, and later analysis helped to get a more comprehensive picture of the functional relationships between these genes as well as how they might act in pathways. All of these findings demonstrate that there are no single gene changes causing ASD, but rather molecular mechanisms that are complex and highly interconnected [12,18,19]. Autism Spectrum Disorder has a wide range of behavioral and developmentally based characteristics that require a multidimensional approach to management [20,21].

Conclusion

In summary, this work indicates that there are many complex interactions between various genes regulating synapse, neurons, brain development, etc. These interactions contribute to the development of Autism Spectrum Disorder (ASD). Using a combination of different bioinformatics methods, we identified the central genes of the molecular networks and their associated pathways. This indicates that ASD is not due to one gene causing the disorder, but rather by different molecular networks interacting with each other[12,18]. Overall, this paper provides a good starting point for further research/discovery of biomarkers and targeted therapies to help people with ASD in the future.

References

1. Lord, C., Brugha, T. S., Charman, T., Cusack, J., Dumas, G., Frazier, T., Jones, E. J. H., Jones, R. M., Pickles, A., State, M. W., Taylor, J. L., & Veenstra-VanderWeele, J. (2020). Autism spectrum disorder. *Nature Reviews Disease Primers*, *6*(1), Article 5. https://doi.org/10.1038/s41572-019-0138-4
2. Geschwind, D. H. (2011). Genetics of autism spectrum disorders. *Trends in Cognitive Sciences*, *15*(9), 409–416. https://doi.org/10.1016/j.tics.2011.07.003
3. McCracken, J. T., McGough, J., Shah, B., Cronin, P., Hong, D., Aman, M. G., Arnold, L. E., Lindsay, R., Nash, P., Hollway, J., McDougle, C. J., Posey, D. J., Swiezy, N. B., Kohn, A., Scahill, L., Martin, A., Koenig, K., Volkmar, F. R., Carroll, D. H., & Ritz, L. (2002). Clinical features and treatment approaches in autism spectrum disorder. *Journal of the American Academy of Child & Adolescent Psychiatry*, *41*(6), 654–662. https://doi.org/10.1097/00004583-200206000-00010
4. Bourgeron, T. (2015). From the genetic architecture to synaptic plasticity in autism spectrum disorder. *Nature Reviews Neuroscience*, *16*(9), 551–563. https://doi.org/10.1038/nrn3992
5. Grove, J., Ripke, S., Als, T. D., Mattheisen, M., Walters, R. K., Won, H., Pallesen, J., Agerbo, E., Andreassen, O. A., Askland, K., Boomsma, D. I., Børglum, A. D., Buitelaar, J. K., Burton, P., Bybjerg-Grauholm, J., Casas, M., Christensen, J. H., Daly, M. J., Derks, E. M., ... Werge, T. (2019). Identification of common genetic risk variants

for autism spectrum disorder. *Nature Genetics*, *51*(3), 431–444. https://doi.org/10.1038/s41588-019-0344-8

6. De Rubeis, S., He, X., Goldberg, A. P., Poultney, C. S., Samocha, K., Cicek, A. E., Kou, Y., Liu, L., Fromer, M., Walker, S., Singh, T., Klei, L., Kosmicki, J., Fu, S. C., Aleksic, B., Biscaldi, M., Bolton, P. F., Brownfeld, J. M., Cai, J., ... Buxbaum, J. D. (2014). Synaptic, transcriptional and chromatin genes disrupted in autism. *Nature*, *515*(7526), 209–215. https://doi.org/10.1038/nature13772
7. Sanders, S. J., He, X., Willsey, A. J., Ercan-Sencicek, A. G., Samocha, K. E., Cicek, A. E., Murtha, M. T., Bal, V. H., Bishop, S. L., Dong, S., Goldberg, A. P., Lalli, M. A., Walker, S. A., Markenscoff-Papadimitriou, E., Wright, M., Fu, S. C., Klei, L., Pelphrey, T., Li, J., ... State, M. W. (2015). Insights into autism spectrum disorder genomic architecture and biology from 71 risk loci. *Neuron*, *87*(6), 1215–1233. https://doi.org/10.1016/j.neuron.2015.09.016
8. Oliveira, M. M., Yadav, R., Erdin, S., & Talkowski, M. E. (2020). New gene discoveries highlight functional convergence in autism and related neurodevelopmental disorders. *Current Opinion in Genetics & Development, 65,* 195-206. https://doi.org/10.1016/j.gde.2020.07.001.
9. Parikshak, N. N., Luo, R., Zhang, A., Won, H., Lowe, J. K., Chandran, V., Horvath, S., & Geschwind, D. H. (2013). Integrative functional genomic analyses implicate specific molecular pathways and circuits in autism. *Cell*, *155*(5), 1008–1021. https://doi.org/10.1016/j.cell.2013.10.031
10. Manoli, D. S., & State, M. W. (2021). Autism spectrum disorder genetics and the search for pathological mechanisms. *American Journal of Psychiatry*, *178*(1), 30–38. https://doi.org/10.1176/appi.ajp.2020.20111608
11. Fang, W.-Q., Chen, W.-W., Fu, A. K. Y., & Ip, N. Y. (2013). Axin directs the amplification and differentiation of intermediate progenitors in the developing cerebral cortex. *Neuron*, *79*(4), 665–679. https://doi.org/10.1016/j.neuron.2013.06.017
12. Voineagu, I., Wang, X., Johnston, P., Lowe, J. K., Tian, Y., Horvath, S., Mill, J., Cantor, R. M., Blencowe, B. J., & Geschwind, D. H. (2011). Transcriptomic analysis of autistic brain reveals convergent molecular pathology. *Nature*, *474*(7351), 380–384. https://doi.org/10.1038/nature10110
13. Szklarczyk, D., Gable, A. L., Lyon, D., Junge, A., Wyder, S., Huerta-Cepas, J., Simonovic, M., Doncheva, N. T., Morris, J. H., Bork, P., Jensen, L. J., & von Mering, C. (2019). STRING v11: Protein–protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Research*, *47*(D1), D607–D613. https://doi.org/10.1093/nar/gky1131
14. Warde-Farley, D., Donaldson, S. L., Comes, O., Zuberi, K., Badrawi, R., Chao, P., Franz, M., Grouios, C., Kazi, F., Lopes, C. T., Maitland, A., Mostafavi, S., Montojo, J., Shao, Q., Wright, G., Bader, G. D., & Morris, Q. (2010). GeneMANIA prediction server: Biological network integration for gene prioritization and predicting gene function. *Nucleic Acids Research*, *38*(Suppl 2), W214–W220. https://doi.org/10.1093/nar/gkq537
15. Piñero, J., Bravo, À., Queralt-Rosinach, N., Gutiérrez-Sacristán, A., Deu-Pons, J., Centeno, E., García-García, J., Sanz, F., & Furlong, L. I. (2017). DisGeNET: A comprehensive platform integrating information on human disease-associated genes and variants. *Nucleic Acids Research*, *45*(D1), D833–D839. https://doi.org/10.1093/nar/gkw943

16. Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P., Haw, R., Jassal, B., Korninger, F., May, B., Milacic, M., Rocha, V., Tiheany, C., Roncaglia, P., Stein, L., & D'Eustachio, P. (2018). The Reactome pathway knowledgebase. *Nucleic Acids Research*, *46*(D1), D649–D655. https://doi.org/10.1093/nar/gkx1132
17. Kuleshov, M. V., Jones, M. R., Rouillard, A. D., Fernandez, N. F., Duan, Q., Wang, Z., Koplev, S., Jenkins, S. L., Jagodnik, K. M., Lachmann, A., McDermott, M. G., Monteiro, C. D., Gundersen, G. W., & Ma'ayan, A. (2016). Enrichr: A comprehensive gene set enrichment analysis web server 2016 update. *Nucleic Acids Research*, *44*(W1), W90–W97. https://doi.org/10.1093/nar/gkw377
18. Satterstrom, F. K., Kosmicki, J. A., Wang, J., Breen, M. S., De Rubeis, S., An, J.-Y., Peng, M., Collins, R., Grove, J., Klei, L., Stevens, C., Reichert, J., Mulhern, M. S., Artomov, M., Gerges, S., Sheppard, B., & Xu, X. (2020). Large-scale exome sequencing study implicates developmental and functional changes in autism. *Cell*, *180*(3), 568–584.e23. https://doi.org/10.1016/j.cell.2019.12.036
19. Jiang, C.-C., Lin, L.-S., Long, S., Ke, X.-Y., Fukunaga, K., Lu, Y.-M., & Han, F. (2022). Signalling pathways in autism spectrum disorder: Mechanisms and therapeutic implications. *Signal Transduction and Targeted Therapy*, *7*(1), Article 229. https://doi.org/10.1038/s41392-022-01081-0
20. Di Gregorio, F., Steinhauser, M., Maier, M. E., Thayer, J. F., & Battaglia, S. (2024). Error-related cardiac deceleration: Functional interplay between brain activity and autonomic nervous system in performance monitoring. *Neuroscience & Biobehavioral Reviews*, *157*, Article 105542. https://doi.org/10.1016/j.neubiorev.2024.105542
21. Hamp, N., Felice, L., Riva, V., Scattoni, M. L., & Fusar-Poli, P. (2023). Clinical and behavioral characteristics of autism spectrum disorder. *Frontiers in Psychiatry*, *14*, Article 1187654. https://doi.org/10.3389/fpsyt.2023.1187654