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Identifying Hub Genes in Autism Spectrum Disorder: A Bioinformatics Approach Using GEO Data Set and GEO2R Tool

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Abstract—Autism Spectrum Disorder (ASD) is a complex neurodevelopmental condition characterized by impairments in social interaction, communication, and behaviour. This study examined the genetic foundations of ASD through the analysis of RNA-sequencing data from two datasets (GSE107867 and GSE117776) obtained from the Gene Expression Omnibus (GEO). Using GEO2R, differentially expressed genes (DEGs) were identified, and a protein-protein interaction (PPI) network was constructed using STRING analysis. Among the upregulated genes, FCGR3A emerged as a central hub gene, indicating its potential involvement in the immune responses and neuroinflammation associated with ASD pathophysiology. Enrichment analysis revealed significant associations between immune system processes, molecular signaling, and neurodevelopmental pathways. This investigation underscores the complex molecular nature of ASD, with immune-related genes, particularly FCGR3A, playing a crucial role in the manifestation of the disorder. These findings provide insights into the genetic and immune pathways of ASD and suggest that FCGR3A is a potential therapeutic target. However, further experimental validation is required to confirm its functional relevance.

Keywords: GEO (Gene Expression Omnibus) data set, GEO2R tool, Autism Spectrum Disorder, DEG (Differentially expressed gene).

I. INTRODUCTION

Autism spectrum disorder (ASD) constitutes a complex disorder of neurodevelopment that mainly impacts behavioral patterns, communicative abilities, and cognitive learning capacities in pediatric populations (Khasawneh et al. 2023, Bhat et al. 2021). The condition starts through various symptoms, including lack of eye contact, reduced or absent non-verbal communication, walking on the toes, and a lack of object-pointing (Lord et al. 2000, AlSalehi et al. 2020). Furthermore, children diagnosed with autism frequently engage in stereotypical behaviors such as hand flapping, repetitive verbal expressions, and echolalia, which refers to the repetition of verbal words or phrases (Melo et al. 2023, Kim et al. 2013). These attributes exhibit variability in their intensity and may adversely affect a child's capacity for social interaction and the achievement of linguistic skills (MacDonald et al. 2007). The causes of ASD are multifactorial, it can be environmental, epigenetic, cytogenetic, and molecular genetic factors. Environmental influences can play a significant role in the development of ASD, particularly factors that occur during birth (Almandil et al. 2019), for example, delayed crying and birth-related hypoxia, which is a lack of oxygen during delivery, have been linked to an increased risk of autism (Kurinczuk et al. 2010). These perinatal complications may contribute to alterations in brain development, potentially affecting neural connectivity and function (Gardener et al, 2011).

Cytogenetic anomalies are also implicated in autism spectrum disorder (ASD), with both numerical and structural chromosomal anomalies contributing to its clinical presentation (Bergbaum et al. 2016, El-Baz et al. 2016). The most common cytogenetic correlation with autism is the occurrence of trisomy 21, commonly referred to as Down syndrome (Ozkan et al. 2020). This genetic condition may be present in a complete form, as a mosaic variant, or through Robertsonian translocations involving chromosome 21 (Belkady et al. 2019). Additionally, chromosomal anomalies affecting various other genomic regions have been associated with ASD, thereby highlighting the complex nature of its genetic foundations (State, et al. 2011).

Beyond cytogenetics, molecular genetics play a crucial role in autism development (Zafeiriou et al, 2013). Several genes have been identified as being actively involved in the development of ASD symptoms (De Rubeis et al. 2015). These genes are responsible for various biological functions, including synaptic development, neural connectivity, and neurotransmitter regulation (Bourgeron 2015). Disruptions in these genetic pathways can lead to the behavioral and cognitive characteristics

observed in individuals with ASD (Masini et al. 2020). Genetic mutations and variations in specific loci may alter neural processing, resulting in the sensory sensitivities, repetitive behaviors, and communication difficulties that define the disorder (Miles 2011).

In this study, we focused on illuminating the genes that exhibit the most significant involvement in the development of autism spectrum disorder (ASD) symptoms. To perform this objective, we harnessed data from the National Centre for Biotechnology Information (NCBI) (NCBI database), which serves as an extensive repository of genetic and biomedical data. Subsequently, we analyzed gene expression patterns utilizing the GEO2R tool, a statistical analysis platform that enables the comparative assessment of gene expression across varying conditions. Through the application of this methodology, we sought to pinpoint essential genetic determinants of ASD and acquire insights into their functional implications in neurodevelopment.

Our study aims to add to the expanding quantity of knowledge on autism and advance our understanding of its genetic foundation. We aim to early diagnostic markers, and potential therapeutic approaches by identifying particular genes linked to ASD.

I.I. ABOUT GENE EXPRESSION OMNIBUS (GEO)

The National Center for Biotechnology Information (NCBI) manages the Gene Expression Omnibus (GEO) (Edgar et al. 2002), which serves as a publicly accessible repository for functional genomics information. Scholars globally contribute high-throughput sequencing datasets, including microarray data, RNA sequencing (RNA-Seq), and ChIP-Seq (Clark et al. 2024). Given the public availability of these databases, researchers are allowed to investigate gene expression patterns across various biological scenarios (Barrett et al. 2012). Incorporating tools for cluster analysis and differential gene expression (DEG) investigations, GEO provides accurately curated gene expression datasets, experimental series, and platform annotations (Barrett et al. 2010). Gene expression studies, which include a variety of fields of genetics, constitute approximately 90% of the data housed within GEO (Barrett et al. 2012). It is essential to the advancement of genomic research, the facilitation of data-driven discoveries, and the support of the scientific community in understanding complex biological processes, since it provides a large, well-structured database.

I.II. GEO2R TOOL

Through the utilization of the online interactive platform GEO2R (GEO2R dataset), researchers are enabled to conduct comparative analyses of two or more sample groups derived from one or multiple datasets that constitute a GEO series. This platform is instrumental in ascertaining whether specific genes exhibit activation or down-regulation across varied experimental conditions (Zamanian-Azodi et al. 2024). The software generates graphical representations that elucidate patterns of gene regulation, as well as providing a gene expression table that includes corresponding p-values (Katsiki et al. 2024). For data analysis, GEO2R uses a variety of R tools sourced from the Bioconductor project. Specifically, it uses DESeq2 for the analysis of RNA-seq datasets, it utilizes GEOquery and lima (Linear Models for Microarray Analysis) for microarray data (Amanatidou et al. 2020). Consequently, GEO2R emerges as a robust and accessible tool for the investigation of differential gene expression within the domain of functional genomics research (Niu et al. 2025).

This research used the GEO2R platform to investigate RNA-sequencing data about autism spectrum disorder, sourced from the Gene Expression Omnibus (GEO). The FunRich software was utilized to identify and conduct a comprehensive analysis of upregulated genes. Additionally, a network of protein-protein interactions was scrutinized via STRING analysis, and key hub genes were extracted utilizing Cytoscape tools to simplify a more in-depth examination of the network.

II. METHODS MATERIALS

II.I. SELECTION OF DATA FROM GEO

We have searched RNA-Seq data of autism spectrum disorder on the GEO data set and we discovered two data sets with the same analysis: Widespread RNA editing dysregulation in autism spectrum disorders and Widespread RNA editing dysregulation in autism spectrum disorders II. These data sets have accession IDs GSE107867 and GSE117776, respectively. We used the GEO2R tool to evaluate the data after it was selected.

II.II. ANALYSIS WITH GEO2R AND IDENTIFICATION OF DEG

We have used accession IDs GSE107867 and GSE117776 to analyze the Geo2R data collection. Since the data set GSE107867 solely contains carrier and case data, we grouped it in carrier versus case in this data set and case (fragile X) versus control in data set GSE117776, because case (fragile X) and control data are included in this dataset. Following the GEO2R study, we

created an Excel spreadsheet by the findings. Both data sets contain 250 genes that are differentially expressed; the data have been arranged according to the log fold chain value. After that, we used FunRich3.1.3 to evaluate all of the upregulated genes from both data sets in order to identify the common gene between them. We were able to identify just one common gene, so we took all upregulated genes from both data sets to form protein-protein interactions.

II.III. FORMATION OF PPI AND EXTRACTION OF HUB GENE

To create a network of protein-protein interactions, all upregulated genes from the two data sets were subjected to string analysis. To extract the hub gene, the PPI network's tsv file was downloaded, extracted to Excel, and examined using the Cytoscape tool.

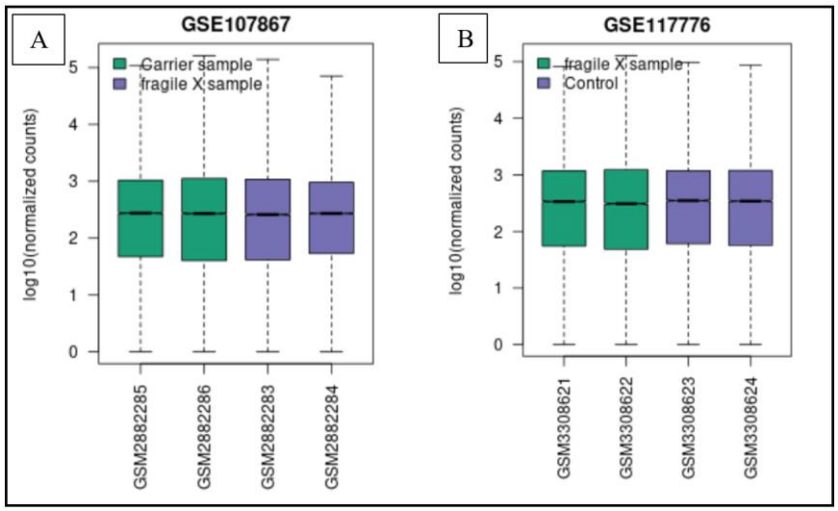

Figure 1. Figure showing a bar graph of GEO2R analysis, 1A shows GEO2R analysis of GSE107867 carrier versus case (fragile X) and 1B shows GEO2R analysis of GEO2R analysis of case (fragile X) versus Control.

III. RESULTS

Many genes are elevated in both datasets. The upregulated genes are mentioned in Table 1, data set-1 has 35 upregulated genes, and data set-2 has 11 upregulated genes. We have analyzed these upregulated genes from both data sets to form a PPI by using String. After analyzing with string, we find 15 proteins have PPI in string, namely, SERPINA5, CP, MATN3, SERPINA1, GIG25, S100A9, ALOX5AP, FCGR3A, LY75, VSIG4, RGS1, CD93, ELTD1, PECAM1, DLL4, proteins have protein-protein interaction network, shown in Figure 1. Then we downloaded the tsv file and analyzed it using the Cytoscape tool to find the hub gene of the PPI, as shown in Figure 2, the darkest color shows the hub gene, in our study, the hub gene is FCGR3A.

We have also performed enrichment analysis by using the FunRich3.1.3 tool, for cellular components, molecular functions, and biological processes for upregulated genes of both data sets. Enrichment analysis for cellular components is shown in Figure 3, for molecular functions is shown in Figure 4, and for biological processes is shown in Figure 5. In enrichment analysis, the translation products of genes of data set 1 are more expressed than data set 2.

Table 1. Showing upregulated genes of both data sets.

S.N.	Upregulated Gene data Set 1 (GSE107867)	Upregulated Gene data Set 2 (GSE117776)
1.	LINC01293	LDHC
2.	LOC105379417	HCG22
3.	S100A9	HLA-DQB2
4.	SERPINA5	OCLNP1
5.	SERPINA3	LINC00323
6.	OR7D2	PADI4

7.	LOC112268317	LOC101929237
8.	CLEC4E	LOC101929777
9.	APOL4	PP12613
10.	SLC1A7	TRIM58
11.	CP	LOC112267937
12.	LOC107984360	
13.	LOC105376081	
14.	CD93	
15.	ALOX5AP	
16.	HLA-DRB6	
17.	MPZL2	
18.	LOC101929777	
19.	VSIG4	
20.	DLL4	
21.	FCGR3A	
22.	SERPINA1	
23.	RGS1	
24.	MATN3	
25.	KIAA0040	
26.	ADGRL4	
27.	BAALC-AS1	
28.	APOLD1	
29.	BCL6B	
30.	ANGPTL4	
31.	ADGRG6	
32.	PECAM1	
33.	LY75	
34.	CLXN	
35.	DEPP1	

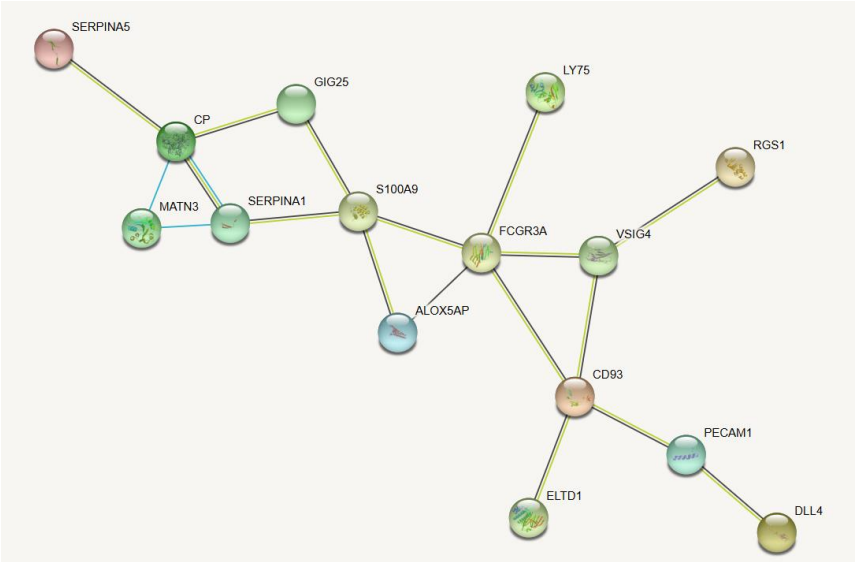

Figure 2. Shows the PPI network of string analysis of upregulated genes from both data sets.

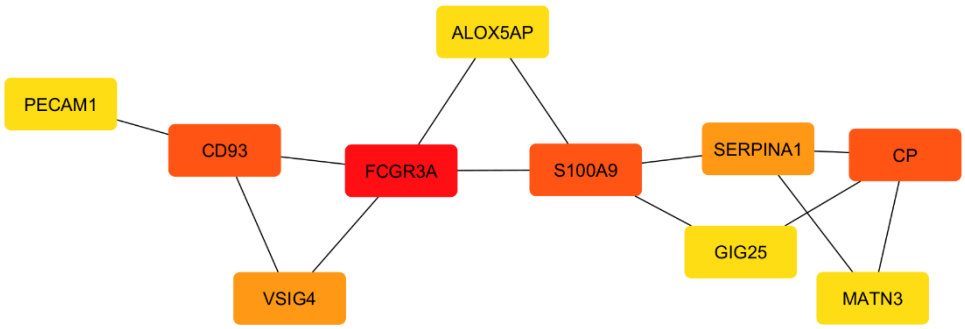

Figure 3. Shows the top 10 gene networks by analyzing with Cytoscape

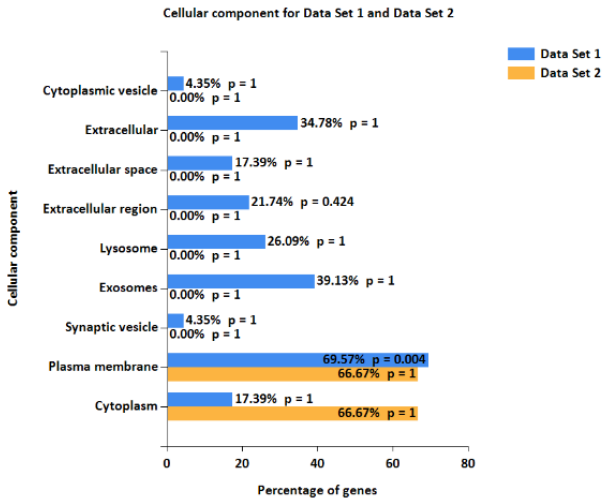

Figure 4. Show the enrichment analysis of cellular components for Data set 1 and Data set 2

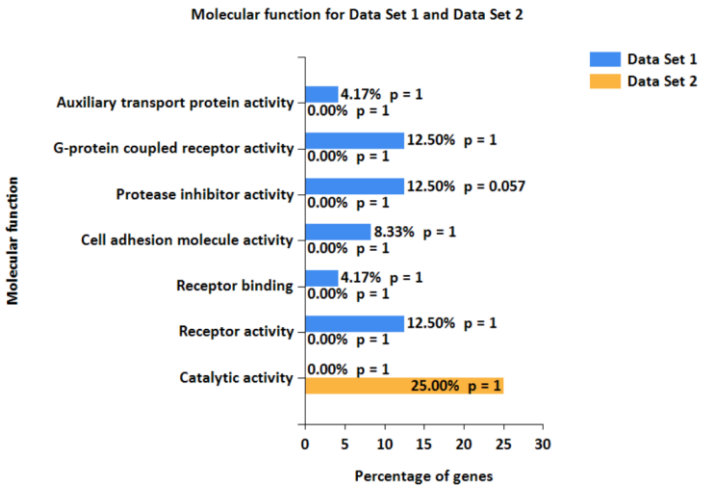

Figure 5. Show the enrichment analysis of the Molecular function for Data set 1 and Data se

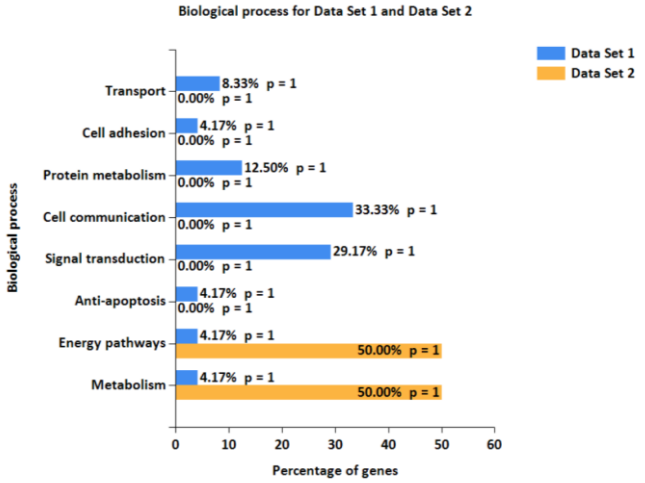

Figure 6. Show the enrichment analysis of the Biological process for Dataset 1 and Dataset 2

IV. DISCUSSION

In this study, we identified multiple upregulated genes in two separate autism datasets. The first dataset revealed 35 upregulated genes, while the second dataset identified 11. We utilized the STRING database to generate a protein-protein interaction (PPI) network, which highlighted connections among 15 proteins: SERPINA5, CP, MATN3, SERPINA1, GIG25, S100A9, ALOX5AP, FCGR3A, LY75, VSIG4, RGS1, CD93, ELTD1, PECAM1, and DLL4. Through Cytoscape (Shannon et al. 2003) analysis, we determined that FCGR3A was the hub gene, suggesting its possible key function in autism-associated molecular pathways.

The identifications of FCGR3A as a central gene indicates its crucial role in the underlying mechanisms of autism spectrum disorder (ASD). This gene encodes the low-affinity Fc gamma receptor III-A, which is primarily found in immune cells like natural killer (NK) cells and macrophages and has no direct connection to autism. Several studies have shown that immune system irregularities and neuroinflammation are associated central nervous system, lending support to our findings that genes involved in immune response processes may be integral to the disorder (Okun et al. 2010). Moreover, FCGR3A's function in regulating immune responses and neuroinflammatory (Ab Rajab et al. 2024) pathways hints at a potential connection between immune system dysfunction and the manifestation of ASD symptoms.

Our enrichment analysis using the FunRich3.1.3 tool (Pathan et al. 2015) revealed significant functional categorization of upregulated genes. Analysis of cellular components indicated that dataset-1 genes exhibited greater enrichment compared to dataset-2 genes, suggesting more substantial alterations in cellular localization within dataset-1 (Figure 3). Examination of molecular functions (Figure 4) underscored the role of these genes in protein binding, enzyme regulation, and interactions with

the immune system. Notably, the enrichment of biological processes (Figure 5) highlighted pathways linked to immune responses, cell signaling, and neurodevelopmental regulation. These findings align with previous studies that have emphasized the importance of these pathways in ASD.

The differential gene expression patterns noted between dataset-1 and dataset-2 indicated diversity in ASD-related gene expression, potentially stemming from variations in cohort selection, environmental influences, or genetic makeup. Dataset-1 showed a more extensive range of upregulated genes with elevated expression in signal transduction and intercellular adhesion processes. This variability highlights the intricate nature of ASD at the molecular level and implies that various biological pathways might play a role in its development.

Our finding underscores the vital importance of genes related to immune function in autism spectrum disorder (ASD) and identifies FCGR3A as a hub gene within the protein-protein interaction network. Subsequent research should aim to confirm these results in more extensive population samples and investigate the functional role of FCGR3A in ASD pathology through experimental work. Combining analyses of gene expression and protein levels may provide further insights into the molecular mechanisms underlying ASD, potentially leading to the identification of new therapeutic targets.

V. LIMITATION

This study has several constraints. The analysis was limited to 2 datasets from distinct cohorts, potentially introducing variability due to differences in sample handling, processing, and demographic characteristics. While powerful, the STRING (Snel et al. 2000) database and Cytoscape analysis are constrained by the completeness and quality of existing interaction data, possibly overlooking some relevant interactions that are not yet documented. The enrichment analysis using FunRich3.1.3 is based on predefined functional categories, which may not encompass novel or less-studied pathways related to ASD. Moreover, this research primarily focuses on transcriptomic data, necessitating further validation through proteomic and functional assays to confirm the biological significance of the identified hub genes. Although FCGR3A emerged as a crucial hub gene, its precise mechanistic role in ASD requires additional experimental validation. Future studies should aim to validate these findings through larger-scale research and functional assays to explore potential therapeutic interventions targeting key molecular pathways in ASD.

VI. CONCLUSION

In conclusion, our research uncovered crucial upregulated genes in autism datasets and developed a protein-protein interaction (PPI) network to identify significant protein relationships. The discovery of FCGR3A as a pivotal hub gene underscores its potential significance in immune-related pathways and the pathophysiology of Autism Spectrum Disorder (ASD). Functional enrichment analysis further substantiated the involvement of immune responses and molecular signaling in neurodevelopmental processes. The observed variations between dataset-1 and dataset-2 point to the heterogeneous nature of gene expression, highlighting the molecular intricacy of ASD.

VII. ACKNOWLEDGMENT

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REFERENCES

1. Khasawneh, M. A. S. (2023). Communication in children with autism spectrum disorder. *Onomázein hosts unpublished articles derived from scientific research*, 69-82.
2. Bhat, A. N. (2021). Motor impairment increases in children with autism spectrum disorder as a function of social communication, cognitive and functional impairment, repetitive behavior severity, and comorbid diagnoses: A SPARK study report. *Autism research*, *14*(1), 202-219. **https://doi.org/10.3390/ijms24031819**
3. Lord, C., Cook, E. H., Leventhal, B. L., & Amaral, D. G. (2000). Autism spectrum disorders. *Neuron*, *28*(2), 355-363. https://doi.org/10.1038/s41572-019-0138-4
4. AlSalehi, S. M., & Alhifthy, E. H. (2020). Autism spectrum disorder. *Clinical Child Neurology*, 275-292. https://doi.org/10.1007/978-3-319-43153-6_10

5. Melo, C., Ribeiro, T. P., Prior, C., Gesta, C., Martins, V., Oliveira, G., & Temudo, T. (2023). Motor stereotypies in autism spectrum disorder: Clinical randomized study and classification proposal. *Autism*, *27*(2), 456-471. https://doi.org/10.1177/1362361322110
6. Kim, S. H., & Lord, C. (2013). The behavioral manifestations of autism spectrum disorders. *The neuroscience of autism spectrum disorders*, (1978). http://dx.doi.org/10.1016/B978-0-12-391924-3.00002-8
7. MacDonald, R., Green, G., Mansfield, R., Geckeler, A., Gardenier, N., Anderson, J., ... & Sanchez, J. (2007). Stereotypy in young children with autism and typically developing children. *Research in developmental disabilities*, *28*(3), 266-277. https://doi.org/10.1016/j.ridd.2006.01.004
8. Almandil, N. B., Alkuroud, D. N., AbdulAzeez, S., AlSulaiman, A., Elaissari, A., & Borgio, J. F. (2019). Environmental and genetic factors in autism spectrum disorders: special emphasis on data from Arabian studies. *International journal of environmental research and public health*, *16*(4), 658. **https://doi.org/10.3390/ijerph16040658**
9. Kurinczuk, J. J., White-Koning, M., & Badawi, N. (2010). Epidemiology of neonatal encephalopathy and hypoxic–ischaemic encephalopathy. *Early human development*, *86*(6), 329-338. https://doi.org/10.1016/j.earlhumdev.2010.05.010
10. Gardener, H., Spiegelman, D., & Buka, S. L. (2011). Perinatal and neonatal risk factors for autism: a comprehensive meta-analysis. *Pediatrics*, *128*(2), 344-355. https://doi.org/10.1542/peds.2010-1036
11. Bergbaum, A., & Ogilvie, C. M. (2016). Autism and chromosome abnormalities—A review. *Clinical Anatomy*, *29*(5), 620-627. **https://doi.org/10.1002/ca.22719**
12. El-Baz, F., Zaghloul, M. S., El Sobky, E., Elhossiny, R. M., Salah, H., & Abdelaziz, N. E. (2016). Chromosomal abnormalities and autism. *Egyptian Journal of Medical Human Genetics*, *17*(1), 57-62. https://doi.org/10.1016/j.ejmhg.2015.05.002
13. Ozkan, E., & Lacerda, M. P. (2020). Genetics, cytogenetic testing and conventional karyotype.
14. Belkady, B., Elkhattabi, L., Elkarhat, Z., Zarouf, L., Razoki, L., Aboulfaraj, J., ... & Barakat, A. (2019). Chromosomal abnormalities in patients with intellectual disability: a 21-year retrospective study. *Human Heredity*, *83*(5), 274-282. https://doi.org/10.1159/000499710
15. State, M. W., & Levitt, P. (2011). The conundrums of understanding genetic risks for autism spectrum disorders. *Nature neuroscience*, *14*(12), 1499-1506. https://doi.org/10.1038/nn.2924
16. Zafeiriou, D. I., Ververi, A., Dafoulis, V., Kalyva, E., & Vargiami, E. (2013). Autism spectrum disorders: the quest for genetic syndromes. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, *162*(4), 327-366. **https://doi.org/10.1002/ajmg.b.32152**
17. De Rubeis, S., & Buxbaum, J. D. (2015). Genetics and genomics of autism spectrum disorder: embracing complexity. *Human molecular genetics*, *24*(R1), R24-R31. https://doi.org/10.1093/hmg/ddv273
18. 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
19. Masini, E., Loi, E., Vega-Benedetti, A. F., Carta, M., Doneddu, G., Fadda, R., & Zavattari, P. (2020). An overview of the main genetic, epigenetic and environmental factors involved in autism spectrum disorder focusing on synaptic activity. *International journal of molecular sciences*, *21*(21), 8290. **https://doi.org/10.3390/ijms21218290**
20. Miles, J. H. (2011). Autism spectrum disorders—a genetics review. *Genetics in Medicine*, *13*(4), 278-294. https://doi.org/10.1097/GIM.0b013e3181ff67ba
21. National Center for Biotechnology Information (NCBI)[Internet]. Bethesda (MD): National Library of Medicine (US), National Center for Biotechnology Information; [1988] – [cited 2025 March 08]. Available from: https://www.ncbi.nlm.nih.gov/
22. Edgar R, Domrachev M, Lash AE. Gene Expression Omnibus: NCBI gene expression and hybridization array data repository Nucleic Acids Res. 2002 Jan 1;30(1):207-10
23. Clark, A. J., & Lillard Jr, J. W. (2024). A comprehensive review of bioinformatics tools for genomic biomarker discovery driving precision oncology. *Genes*, *15*(8), 1036. **https://doi.org/10.3390/genes15081036**
24. Barrett, T., Wilhite, S. E., Ledoux, P., Evangelista, C., Kim, I. F., Tomashevsky, M., ... & Soboleva, A. (2012). NCBI GEO: archive for functional genomics data sets—update. *Nucleic acids research*, *41*(D1), D991-D995. https://doi.org/10.1093/nar/gks1193

25. Barrett, T., Troup, D. B., Wilhite, S. E., Ledoux, P., Evangelista, C., Kim, I. F., ... & Soboleva, A. (2010). NCBI GEO: archive for functional genomics data sets—10 years on. *Nucleic acids research*, *39*(suppl_1), D1005-D1010. https://doi.org/10.1093/nar/gkq1184
26. Barrett, T., Wilhite, S. E., Ledoux, P., Evangelista, C., Kim, I. F., Tomashevsky, M., ... & Soboleva, A. (2012). NCBI GEO: archive for functional genomics data sets—update. *Nucleic acids research*, *41*(D1), D991-D995. https://doi.org/10.1093/nar/gks1193
27. GEO2R, a web-based tool available on the Gene Expression Omnibus (GEO) database at NCBI. https://www.ncbi.nlm.nih.gov/geo/geo2r/
28. Zamanian-Azodi, M., Ahmadzadeh, A., Rezaei, M., & Robati, R. M. (2024). Considerations Regarding CHSY1 Knockdown and Its Influence on Gene Expression Profiles: A Perspective from Protein Interaction Network Analysis. *Asian Pacific Journal of Cancer Biology*, *9*(3), 323-328. **10.31557/apjcb.2024.9.3.323-328**
29. Katsiki, A. D., Karatzas, P. E., De Lastic, H. X., Georgakilas, A. G., Tsitsilonis, O., & Vorgias, C. E. (2024). DExplore: An Online Tool for Detecting Differentially Expressed Genes from mRNA Microarray Experiments. *Biology*, *13*(5), 351. **https://doi.org/10.3390/biology13050351**
30. Amanatidou, A. I., Nastou, K. C., Tsitsilonis, O. E., & Iconomidou, V. A. (2020). Visualization and analysis of the interaction network of proteins associated with blood-cell targeting autoimmune diseases. *Biochimica et Biophysica Acta (BBA)-Molecular Basis of Disease*, *1866*(5), 165714. https://doi.org/10.1016/j.bbadis.2020.165714
31. Niu, Y., Zhang, Y., Zha, Q., Shi, J., & Weng, Q. (2025). Bioinformatics to analyze the differentially expressed genes in different degrees of Alzheimer's disease and their roles in progress of the disease. *Journal of Applied Genetics*, *66*(1), 73-85. https://doi.org/10.1007/s13353-024-00827-6
32. Shannon, P., Markiel, A., Ozier, O., Baliga, N. S., Wang, J. T., Ramage, D., … Ideker, T. (2003). Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Research*, *13*(11), 2498–2504.
33. Okun, E., Mattson, M. P., & Arumugam, T. V. (2010). Involvement of Fc receptors in disorders of the central nervous system. *Neuromolecular medicine*, *12*, 164-178. 10.3389/fimmu.2019.00811
34. Ab Rajab, N. S., Yasin, M. A. M., Ghazali, W. S. W., Talib, N. A., Taib, W. R. W., & Sulong, S. (2024). Schizophrenia and Rheumatoid Arthritis Genetic Scenery: Potential Non-HLA Genes Involved in Both Diseases Relationship. *The Yale journal of biology and medicine*, *97*(3), 281. 10.59249/FBOT5313
35. Pathan, M., Keerthikumar, S., Ang, C., Gangoda, L., Quek, C., Williamson, N. A., … & Mathivanan, S. (2015). Funrich: an open access standalone functional enrichment and interaction network analysis tool. Proteomics, 15(15), 2597-2601. https://doi.org/10.1002/pmic.201400515 **https://doi.org/10.1002/pmic.201400515**
36. Snel, B., Jensen, L. J., Kuhn, M., et al. (2000). STRING: a web-server to retrieve and display the repeatedly occurring neighbourhood of a gene. Nucleic Acids Research, 28(18), 3442-3444.
37. Pathan, M., Keerthikumar, S., Ang, C., Gangoda, L., Quek, C., Williamson, N. A., … & Mathivanan, S. (2015). Funrich: an open access standalone functional enrichment and interaction network analysis tool. Proteomics, 15(15), 2597-2601. https://doi.org/10.1002/pmic.201400515 **https://doi.org/10.1002/pmic.201400515**
38. Snel, B., Jensen, L. J., Kuhn, M., et al. (2000). STRING: a web-server to retrieve and display the repeatedly occurring neighbourhood of a gene. Nucleic Acids Research, 28(18), 3442-3444.