



HKG *epi* THERAPEUTICS Ltd.
Harnessing the epigenome

epiPsych Personalized Methylation Report

Your Barcode:

Date:

Testing Laboratory:
HKG epiTherapeutics Limited

Introduction

Welcome to your personalized methylation report. This report provides insights into the methylation levels of key genes involved in stress response and psychiatric disorders: NR3C1, FKBP5, BDNF, IL6, and OXTR. Changes in methylation of these genes has been associated by several studies with mental health status particularly stress and depression.

Understanding DNA Methylation

The DNA in every cell of our body functions like a sophisticated minicomputer, managing cellular operations to ensure our body performs necessary tasks throughout our lives. This DNA, inherited from our parents, acts as the operating system for this minicomputer. Although we possess the same DNA in every cell, it operates differently across various cell types and organs.

The Role of DNA Methylation

Like a computer requiring software to execute specific functions, our DNA needs programming to operate effectively. This programming is largely achieved through a chemical modification known as DNA methylation. DNA methylation involves the addition of a methyl group (a chemical cap) to the DNA molecule, particularly at cytosine bases in the context of CpG dinucleotides.

DNA methylation serves as a critical part of the "software" that dictates how our genetic code is expressed. This process begins as we develop in the womb, guided by a highly precise plan that has evolved over millions of years. This plan ensures that each cell type receives the appropriate methylation pattern, allowing our organs to function correctly.



Introduction

DNA Methylation as a Gene Regulator

The positioning of methyl groups on DNA can act as an on/off switch for genes. When a gene's promoter region (the part of a gene which turns on its activity) is heavily methylated, the gene is typically silenced, meaning it is not expressed. Conversely, when the promoter region is unmethylated, the gene can be active and expressed. This regulation is essential for maintaining the proper function of cells and organs.

Importance of DNA Methylation

Proper DNA methylation is crucial for normal development and health. It ensures that genes are expressed at the right times and in the right cells. For instance, genes necessary for liver function are switched on in liver cells, but those same genes are switched off in brain cells. This precise regulation helps prevent diseases, maintain cellular identity, and respond to environmental changes.

In summary, DNA methylation is a vital component of our genetic programming, ensuring that our body's "minicomputer" functions smoothly and efficiently. This intricate system of on/off switches allows our cells and organs to perform their designated roles, ultimately safeguarding our health and well-being.

Understanding Your Results

Methylation Percentage Explanation:

The methylation percentage in your report indicates the proportion of cells analyzed that have a methylation mark at a specific CpG site within a gene. When we refer to the percentage of methylation, it reflects the balance between methylated (silenced) and unmethylated (active) cells. This balance is crucial because it determines how genes are regulated within different cells. For instance, if a high percentage of cells have methylation marks at a particular gene site, it means that gene is likely silenced in those cells (Razin & Riggs, 1980). Conversely, lower methylation percentages suggest that the gene is active in more cells.

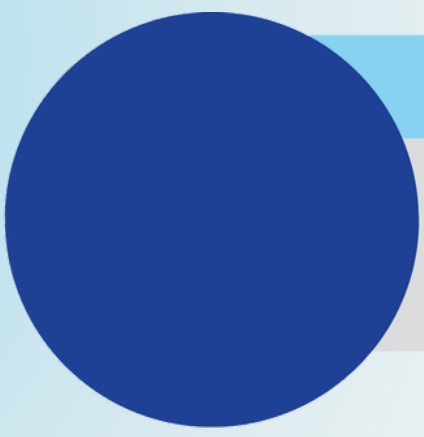
Hyper- and Hypomethylation:

Hypermethylation: When we observe high methylation percentages at certain critical positions that regulate gene function, it generally means the gene is being silenced. This can prevent the gene from performing its normal function and may be associated with certain health conditions.

Hypomethylation: Low methylation percentages at critical position indicate that the gene is more likely to be active under the right conditions or in response to the right triggers. This can be beneficial or harmful depending on the gene's function and the context in which it is active.

External factors such as stress, environmental influences, and lifestyle choices can shift this balance, leading to changes in gene expression (Weaver et al., 2004). Increased stress, for example, might result in more cells becoming methylated at stress-related gene sites, potentially impacting overall health and well-being.

DNA methylation differs between tissues. However, although genes regulating mental health are expressed and regulated in the brain, which we can't measure in living people, studies showed that methylation of the sites that we selected for the epiPsych test associate with mental health states in blood and saliva.



Your Results

Gene Methylation Table

Gene	95% Confidence Interval*	Your Methylation Results (Average)	Your 95% Confidence Interval	Your Standard Deviation
NR3C1	0.19 - 0.32 %			
BDNF	2.34 - 3.58 %			
IL6	4.55 - 13.97 %			
OXTR	3.82 - 5.35 %			
FKBP5 CG1	65.76 - 84.88 %			
FKBP5 CG2	50.82 - 67.26 %			
FKBP5 CG3	77.06 - 94.21 %			
FKBP5 CG4	77.00 - 90.33 %			
FKBP5 CG5	64.15 - 72.73 %			
FKBP5 CG6	50.13 - 57.59 %			
FKBP5 CG7	48.03 - 55.85 %			

- **95% Confidence Interval:** This interval indicates the range of DNA methylation for a specific gene position in the healthy control group we examined at a 95% confidence level. The two numbers represent the lower and upper bounds of this range.
- **Your Methylation Results (Average):** This column shows your specific average methylation level.
- **Your 95% Confidence Interval:** This interval provides a range within which your true average methylation level is likely to fall.
- **Your Standard Deviation:** This value shows how much variation there is in your triplicate measurements.



Have Some Questions?

Gene-Specific Information

Understanding NR3C1 and Its Importance

What is NR3C1?

NR3C1 stands for **Nuclear Receptor Subfamily 3 Group C Member 1**, also known as the glucocorticoid receptor gene. This gene plays a crucial role in regulating the body's response to stress by controlling the effects of glucocorticoids, which are stress hormones like cortisol.

Why is Methylation of NR3C1 Important?

Proper regulation of NR3C1 is essential for maintaining normal stress responses. Changes in NR3C1 methylation have been linked to various mental health conditions, including depression, anxiety, schizophrenia, and Post-Traumatic Stress Disorder (PTSD). Monitoring NR3C1 methylation can provide insights into an individual's stress response and potential risks for these conditions (de Assis Pinheiro et al., 2021; Misiak et al., 2021).

Research has shown that the glucocorticoid receptor NR3C1 gene can become more methylated ("switched off") in response to early adversity, such as childhood trauma. This change is linked to long-term alterations in stress reactivity and increased susceptibility to depression in adulthood (Brown, 2021; Chou, Huang, & Yu, 2024; Dieckmann & Czamara, 2024; Melas et al., 2013).

Hypermethylation of NR3C1 has been associated with reduced expression of the glucocorticoid receptor, impairing the body's ability to regulate stress effectively and might be associated with increased anxiety (Brown, 2021; Chou et al., 2024).



NR3C1

Interpretation of Your Methylation Results

Below Lower Bound

Your methylation level is below the typical range for healthy individuals.

Within Range

Your methylation level is within the normal range, suggesting typical regulation of the NR3C1 gene.

Above Upper Bound

Your methylation level is above the typical range, which may indicate hypermethylation. This might be related to increased risk of stress-related conditions such as depression and anxiety.

Recommendations

Maintain a Healthy Lifestyle

Regular physical activity, a balanced diet, and sufficient sleep can support overall stress management and NR3C1 levels.

Manage Stress

Practices such as mindfulness, meditation, and yoga can help reduce stress.

Seek Professional Guidance

If you are concerned, consulting with a healthcare provider for personalized advice and interventions is crucial.

Understanding BDNF and Its Importance

What is BDNF?

BDNF stands for **Brain-Derived Neurotrophic Factor**. It is a protein that plays a crucial role in the growth, development, and maintenance of neurons in the brain. BDNF is essential for brain health, supporting learning, memory, and overall cognitive function.

Why is Methylation of BDNF Important?

The methylation status of the BDNF gene can significantly impact its expression levels. When BDNF is properly expressed, it supports healthy brain function and resilience to stress. However, changes in BDNF methylation levels have been linked to various mental health conditions, including depression, anxiety, and borderline personality disorder (Arosio, Guerini, Voshaar, & Aprahamian, 2021; Januar, Ancelin, Ritchie, Saffery, & Ryan, 2015; Velasquez et al., 2021).

Monitoring BDNF methylation can provide insights into an individual's mental health and potential risks for these conditions. Specifically, methylation changes in the promoter region of the BDNF gene can lead to altered BDNF expression, which may affect brain function and mental health. Studying this specific promoter helps us understand how gene regulation might contribute to conditions like borderline personality disorder and other stress-related issues.

By understanding the methylation status of the BDNF promoter, we can gain valuable insights into the genetic factors influencing mental health and develop strategies to mitigate the associated risks.



BDNF

Interpretation of Your Methylation Results

Below Lower Bound

Your methylation level is below the typical range for healthy individuals. While this does not necessarily indicate a problem, it suggests that your BDNF expression is likely within a healthy range, as this was the lower bound observed in healthy individuals.

Within Range

Your methylation level is within the normal range, suggesting typical regulation of the BDNF gene and normal brain function.

Above Upper Bound

Your methylation level is above the typical range, which may indicate hypermethylation. This might be associated with reduced expression of the BDNF gene, potentially affecting brain health and increasing the risk of conditions such as depression, anxiety, and borderline personality disorder.

Recommendations

Maintain a Healthy Lifestyle

Regular physical activity, a balanced diet rich in omega-3 fatty acids, and sufficient sleep can support overall brain health and BDNF levels.

Manage Stress

Practices such as mindfulness, meditation, and yoga can help reduce stress and support healthy BDNF expression.

Seek Professional Guidance

If you are concerned, consulting with a healthcare provider for personalized advice and interventions is crucial.

Understanding IL6 and Its Importance

What is IL6?

IL6 stands for **Interleukin-6**, a cytokine or small protein important in inflammation and the immune response. It is produced by various cells, including T cells, B cells, monocytes, and fibroblasts, and plays a crucial role in the body's defense mechanisms against infections and injuries.

Why is Methylation of IL6 Important?

The methylation status of the IL6 gene is associated with its expression levels. Proper regulation of IL6 is essential for maintaining a balanced immune response. Changes in IL6 methylation have been linked to various inflammatory and autoimmune conditions, including depression, rheumatoid arthritis, and Behcet's disease. Monitoring IL6 methylation can provide insights into an individual's immune function and potential risks for these conditions (Ryan et al., 2017)(Alipour et al., 2020).

Methylation changes in the IL6 can lead to altered gene expression, affecting how the body responds to inflammation. Hypomethylation of the IL6 can lead to increased expression of IL6, which may result in chronic inflammation has also been associated with depression.



IL6

Interpretation of Your Methylation Results

Lower Bound of IL6 Methylation

If your methylation level is below the lower bound, it indicates hypomethylation. This may be associated with higher IL6 expression, which might contribute to chronic inflammation and an increased risk of depression and other inflammatory conditions (Mao et al., 2017).

Within Range

If your IL6 methylation levels are within the established range, it suggests that your IL6 gene expression is likely balanced, supporting a healthy immune response. This balance is crucial for preventing chronic inflammation and associated health issues.

Above Upper Bound of IL6 Methylation

If your methylation level is above the upper bound, it suggests hypermethylation. This can lead to the silencing of the IL6 gene, potentially reducing IL6 expression and impacting the body's ability to manage inflammation effectively.

Recommendations

Maintain a Healthy Lifestyle

Engage in regular physical activity, consume a balanced diet rich in anti-inflammatory foods (such as fruits, vegetables, and omega-3 fatty acids), and ensure you get sufficient sleep. These habits can support overall immune function and help regulate IL6 levels.

Manage Stress

Incorporate practices such as mindfulness, meditation, and yoga into your routine. These activities can help reduce stress and lower inflammation.

Seek Professional Guidance

If your methylation levels indicate potential health risks, consulting with a healthcare provider for personalized advice and interventions is crucial.

Understanding OXTR and Its Importance

What is OXTR?

OXTR stands for **Oxytocin Receptor**, a gene that encodes the receptor for oxytocin, a hormone involved in social bonding, emotional regulation, and various social behaviors. Oxytocin and its receptor play key roles in social interactions, maternal behavior, and stress responses.

Why is Methylation of OXTR Important?

The methylation status of the OXTR gene in critical positions is associated with its expression levels. Proper regulation of OXTR is essential for normal social and emotional functioning. Changes in OXTR methylation have been linked to various psychiatric conditions, including depression, anxiety, and obsessive-compulsive disorder (OCD). Methylation changes in these regions can lead to altered gene expression, affecting how the body responds to social and emotional stimuli. Monitoring OXTR methylation can provide insights into an individual's social behaviors and potential risks for these conditions (Ludwig et al., 2022) (Bajou et al., 2004; Maud, Ryan, McIntosh, & Olsson, 2018).

Increased methylation in the OXTR promoter region is associated with reduced expression of the oxytocin receptor. This reduction can impair social bonding and emotional regulation, contributing to conditions such as autism, depression, and social anxiety (Park, Kim, Jeon, Kang, & Kim, 2020) (Danoff et al., 2021).

Decreased methylation can result in increased expression of the oxytocin receptor, which has been associated with conditions like OCD (Park et al., 2020).

Interpretation of Your Methylation Results

Below Lower Bound

Your methylation level is below the typical range for healthy individuals. This usually indicates hypomethylation, which may be linked to increased OXTR expression and potentially higher social and emotional functioning.

Within Range

Your methylation level is within the normal range, suggesting typical regulation of the OXTR gene and normal social and emotional responses.

Above Upper Bound

Your methylation level is above the typical range, which may indicate hypermethylation. This might be associated with the expression of the OXTR gene, potentially impairing social bonding and emotional regulation, and increasing the risk of stress-related conditions such as autism, depression and social anxiety.

Recommendations

Maintain a Healthy Lifestyle

Regular physical activity, a balanced diet, and sufficient sleep can support overall mental health and OXTR levels.

Manage Stress

Practices such as mindfulness, meditation, and yoga can help reduce stress and support healthy OXTR expression.

Seek Professional Guidance

If you are concerned, consulting with a healthcare provider for personalized advice and interventions is crucial.

Understanding FKBP5 and Its Importance

What is FKBP5?

FKBP5 stands for FK506 Binding Protein 5, a gene encoding a protein that plays a critical role in regulating the stress hormone system. FKBP5 influences the glucocorticoid receptor (GR) function, which is pivotal in the body's response to stress. Dysregulation of FKBP5 can impact stress reactivity and is implicated in several psychiatric conditions (Binder, 2017; Sabbagh et al., 2014).

Why is Methylation of FKBP5 Important?

Methylation status of the FKBP5 gene can significantly impact its expression levels and, consequently, the body's stress response. Proper regulation of FKBP5 is essential for maintaining a balanced stress response. Changes in FKBP5 methylation have been linked to conditions such as depression, anxiety, PTSD, and other stress-related disorders (Klengel et al., 2013) (Womersley et al., 2022). Monitoring FKBP5 methylation provides insights into an individual's stress reactivity and potential risks for these conditions (Klengel et al., 2013; Sabbagh et al., 2014).

Hypermethylation: Increased methylation in specific regions of the FKBP5 gene, such as intron 7, has been associated with protective effects against stress-related conditions due to reduced gene expression and lower stress hormone system reactivity, potentially leading to better psychological resilience (Klengel et al., 2013).

Hypomethylation: Decreased methylation can lead to increased FKBP5 expression, contributing to prolonged stress responses and higher susceptibility to psychiatric disorders, including PTSD, depression, and anxiety (Klengel et al., 2013; Womersley et al., 2022).



FKBP5

Interpretation of Your Methylation Results

Below Lower Bound

Your methylation level is below the typical range for healthy individuals. This usually indicates hypomethylation, which may be linked to increased FKBP5 expression and potentially higher sensitivity to stress, making you more susceptible to stress-related conditions such as PTSD, depression, and anxiety.

Within Range

Your methylation level is within the normal range, suggesting typical regulation of the FKBP5 gene and a normal stress response.

Above Upper Bound

This typically indicates reduced FKBP5 expression. Hypermethylation can sometimes be protective against stress-related disorders by reducing sensitivity to stress. However, in certain contexts, it may also impair the regulation of stress hormones, potentially increasing the risk of conditions like depression. The relationship between hypermethylation and stress-related conditions is complex and context-dependent.

Recommendations

Maintain a Healthy Lifestyle

Engage in regular physical activity, maintain a balanced diet, and ensure sufficient sleep to support overall stress management and FKBP5 levels.

Manage Stress

Practice mindfulness, meditation, and yoga to reduce stress and support healthy FKBP5 expression.

Seek Professional Guidance

If you are concerned, consult with a healthcare provider for personalized advice and interventions.



Conclusion

Your methylation levels provide a valuable window into your epigenetic predispositions related to stress responses and psychiatric conditions. Understanding these patterns allows you to tailor your lifestyle to improve your mental well-being. Key takeaways from your results include:

Importance of Methylation

Your methylation profile influences how your body manages stress and regulates emotional responses. Both hypo- and hypermethylation of key genes like NR3C1, BDNF, IL6, OXTR, and FKBP5 can impact your mental health.

Personalized Lifestyle Adjustments

Engaging in regular physical activity, maintaining a balanced diet, ensuring sufficient sleep, and incorporating stress-reducing practices such as mindfulness, meditation, and yoga can support healthy gene expression and overall mental well-being.

Seeking Professional Guidance

For personalized advice and a deeper understanding of your methylation results, consulting with a healthcare provider is crucial. They can help you develop targeted strategies to manage potential health risks and enhance your mental health.



Next Steps

Implement Lifestyle Changes

Begin incorporating the recommended lifestyle adjustments to support your genetic health.

Monitor Your Progress

Keep track of any changes in your mental and physical health as you adjust your lifestyle.

Consult with a Healthcare Provider

Schedule an appointment with your healthcare provider to discuss your methylation results in detail and develop a comprehensive plan tailored to your needs.

Re-test with epiPsych

Consider re-testing your methylation levels with epiPsych after a certain period (e.g., 6-12 months) to monitor changes and evaluate the effectiveness of your lifestyle adjustments.

References

1. Alipour, S., Sakhinia, E., Khabbazi, A., Samadi, N., Babaloo, Z., Azad, M., . . . Nouri, M. (2020). Methylation status of interleukin-6 gene promoter in patients with Behcet's disease. *Reumatol Clin (Engl Ed)*, 16(3), 229-234. doi:10.1016/j.reuma.2018.06.006
2. Arosio, B., Guerini, F. R., Voshaar, R. C. O., & Aprahamian, I. (2021). Blood Brain-Derived Neurotrophic Factor (BDNF) and Major Depression: Do We Have a Translational Perspective? *Front Behav Neurosci*, 15, 626906. doi:10.3389/fnbeh.2021.626906
3. Bajou, K., Maillard, C., Jost, M., Lijnen, R. H., Gils, A., Declerck, P., . . . Noel, A. (2004). Host-derived plasminogen activator inhibitor-1 (PAI-1) concentration is critical for in vivo tumoral angiogenesis and growth. *Oncogene*, 23(41), 6986-6990. doi:10.1038/sj.onc.1207859
4. Binder, E. B. (2017). Dissecting the molecular mechanisms of gene x environment interactions: implications for diagnosis and treatment of stress-related psychiatric disorders. *Eur J Psychotraumatol*, 8(sup5), 1412745. doi:10.1080/20008198.2017.1412745
5. Brown, V. (2021). Methylation of the glucocorticoid receptor gene NR3C1: a summary for clinicians working with children and families. Cambridge University Press, 7, 5241.
6. Chou, P. C., Huang, Y. C., & Yu, S. (2024). Mechanisms of Epigenetic Inheritance in Post-Traumatic Stress Disorder. *Life (Basel)*, 14(1). doi:10.3390/life14010098
7. Danoff, J. S., Wroblewski, K. L., Graves, A. J., Quinn, G. C., Perkeybile, A. M., Kenkel, W. M., . . . Connelly, J. J. (2021). Genetic, epigenetic, and environmental factors controlling oxytocin receptor gene expression. *Clin Epigenetics*, 13(1), 23. doi:10.1186/s13148-021-01017-5
8. de Assis Pinheiro, J., Freitas, F. V., Borcoi, A. R., Mendes, S. O., Conti, C. L., Arpini, J. K., . . . Alvares-da-Silva, A. M. (2021). Alcohol consumption, depression, overweight and cortisol levels as determining factors for NR3C1 gene methylation. *Sci Rep*, 11(1), 6768. doi:10.1038/s41598-021-86189-z
9. Dieckmann, L., & Czamara, D. (2024). Epigenetics of prenatal stress in humans: the current research landscape. *Clin Epigenetics*, 16(1), 20. doi:10.1186/s13148-024-01635-9
10. Januar, V., Ancelin, M. L., Ritchie, K., Saffery, R., & Ryan, J. (2015). BDNF promoter methylation and genetic variation in late-life depression. *Transl Psychiatry*, 5(8), e619. doi:10.1038/tp.2015.114
11. Klengel, T., Mehta, D., Anacker, C., Rex-Haffner, M., Pruessner, J. C., Pariante, C. M., . . . Binder, E. B. (2013). Allele-specific FKBP5 DNA demethylation mediates gene-childhood trauma interactions. *Nat Neurosci*, 16(1), 33-41. doi:10.1038/nn.3275
12. Ludwig, B., Carlberg, L., Kienesberger, K., Swoboda, P., Swoboda, M. M. M., Bernegger, A., . . . Schosser, A. (2022). Oxytocin receptor gene methylation as a molecular marker for severity of depressive symptoms in affective disorder patients. *BMC Psychiatry*, 22(1), 381. doi:10.1186/s12888-022-04031-w
13. Mao, S. Q., Sun, J. H., Gu, T. L., Zhu, F. B., Yin, F. Y., & Zhang, L. N. (2017). Hypomethylation of interleukin-6 (IL-6) gene increases the risk of essential hypertension: a matched case-control study. *J Hum Hypertens*, 31(8), 530-536. doi:10.1038/jhh.2017.7
14. Maud, C., Ryan, J., McIntosh, J. E., & Olsson, C. A. (2018). The role of oxytocin receptor gene (OXTR) DNA methylation (DNAm) in human social and emotional functioning: a systematic narrative review. *BMC Psychiatry*, 18(1), 154. doi:10.1186/s12888-018-1740-9
15. Melas, P. A., Wei, Y., Wong, C. C., Sjoholm, L. K., Aberg, E., Mill, J., . . . Lavebratt, C. (2013). Genetic and epigenetic associations of MAOA and NR3C1 with depression and childhood adversities. *Int J Neuropsychopharmacol*, 1-16. doi:10.1017/S1461145713000102
16. Misiak, B., Samochowiec, J., Konopka, A., Gawronska-Szklarz, B., Beszlej, J. A., Szmidka, E., & Karpinski, P. (2021). Corrigendum to: Clinical Correlates of the NR3C1 Gene Methylation at Various Stages of Psychosis. *Int J Neuropsychopharmacol*, 24(9), 758. doi:10.1093/ijnp/pyab048
17. Park, C. I., Kim, H. W., Jeon, S., Kang, J. I., & Kim, S. J. (2020). Reduced DNA methylation of the oxytocin receptor gene is associated with obsessive-compulsive disorder. *Clin Epigenetics*, 12(1), 101. doi:10.1186/s13148-020-00890-w
18. Razin, A., & Riggs, A. D. (1980). DNA methylation and gene function. *Science*, 210(4470), 604-610. Retrieved from <http://www.ncbi.nlm.nih.gov/htbin-post/Entrez/query?db=m&form=6&dopt=r&uid=0006254144>
19. Ryan, J., Pilkington, L., Neuhaus, K., Ritchie, K., Ancelin, M. L., & Saffery, R. (2017). Investigating the epigenetic profile of the inflammatory gene IL-6 in late-life depression. *BMC Psychiatry*, 17(1), 354. doi:10.1186/s12888-017-1515-8
20. Sabbagh, J. J., O'Leary, J. C., 3rd, Blair, L. J., Klengel, T., Nordhues, B. A., Fontaine, S. N., . . . Dickey, C. A. (2014). Age-associated epigenetic upregulation of the FKBP5 gene selectively impairs stress resiliency. *PLoS One*, 9(9), e107241. doi:10.1371/journal.pone.0107241
21. Velasquez, M. M., Gomez-Maquet, Y., Ferro, E., Cardenas, W., Gonzalez-Nieves, S., & Lattig, M. C. (2021). Multidimensional Analysis of Major Depression: Association Between BDNF Methylation, Psychosocial and Cognitive Domains. *Front Psychiatry*, 12, 768680. doi:10.3389/fpsyt.2021.768680
22. Weaver, I. C., Cervoni, N., Champagne, F. A., D'Alessio, A. C., Sharma, S., Seckl, J. R., . . . Meaney, M. J. (2004). Epigenetic programming by maternal behavior. *Nat Neurosci*, 7(8), 847-854. Retrieved from http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&dopt=Citation&list_uids=15220929
23. Womersley, J. S., Roeh, S., Martin, L., Ahmed-Leitao, F., Sauer, S., Rex-Haffner, M., . . . Seedat, S. (2022). FKBP5 intron 7 methylation is associated with higher anxiety proneness and smaller right thalamus volume in adolescents. *Brain Struct Funct*, 227(8), 2809-2820. doi:10.1007/s00429-022-02577-9

The Company

HKG epiTherapeutics Limited Pioneering Advances in Genetic Testing

Accredited Excellence

HKG epiTherapeutics Limited, established in 2016, is renowned for its cutting-edge approach to healthcare, particularly in epigenetic research and testing. Our laboratory, situated within the prestigious HKG Science Park, has earned accreditations from the United States' College of American Pathologists (CAP) and the Clinical Laboratory Improvement Amendments (CLIA), signifying our commitment to the highest standards in laboratory testing and research integrity.



Professor Moshe Szyf: Visionary Founder

The founding of HKG epiTherapeutics Limited was inspired and led by Professor Moshe Szyf, a luminary in the field of epigenetics from McGill University's Department of Pharmacology and Therapeutics. Professor Szyf's pioneering work includes:

- Being an inventor of the first broad patents in the field of epigenetics and the first patents linking DNA methylation and cancer.
- Founding the field of behavioral and psychiatry epigenetics.
- Publishing over 300 papers, significantly contributing to the advancement of epigenetics.
- Serving as a Fellow of the Royal Society of Canada and the Canadian Academy of Health Sciences.

Professor Szyf's illustrious career extends beyond research and innovation. He has authored more than 300 peer-reviewed articles, solidifying his role as a key figure in epigenetics. He founded and served as the inaugural chief editor of a leading journal in the field, is an associate editor for Clinical Epigenetics, and holds a position on the Editorial Board of Environmental Epigenetics. His contributions have been instrumental in shaping the understanding and application of epigenetic science in medicine.



The Company

Our Collective Mission and Expansion

HKG epiTherapeutics is dedicated to harnessing the power of epigenetics combined with state-of-the-art sequencing technologies. We are committed to early disease detection and prevention, with our expertise spanning across various aspects of personalized medicine. Our expansion plans aim to replicate the success of our Hong Kong laboratory in North America and beyond.

Conclusion

Customers of HKG epiTherapeutics can rest assured that they are receiving services backed by pioneering research, accredited facilities, and a team of experts led by one of the foremost authorities in epigenetics, Prof. Moshe Szyf. Our mission is to bring innovative health solutions to the forefront of medical science, improving healthcare outcomes worldwide.



Contact Us

For more information or to discuss your results, please contact us at info@hkgepitherapeutics.com.

Global Headquarters

- **EpiMedTechGlobal (EMTG)**
60 Paya Lebar Road,
#08-06 Paya Lebar Square,
Singapore 409051

Testing Laboratory

- **HKG epiTherapeutics Limited**
Unit 313-315, 3/F Biotech Centre 2,
11 Science Park West Ave,
Hong Kong Science Park
Phone: +(852) 2354 8297

Disclaimer

This report is for informational purposes only and should not be considered medical advice. Always consult a healthcare provider for medical advice and treatment.