

Fagron

genomics

Gene Comprehensive Nutrigenomic Report

Accession Number: #####

Specimen Collected: ###/###/####

Specimen Received: ###/###/####

Report Generated: February 27, 2025

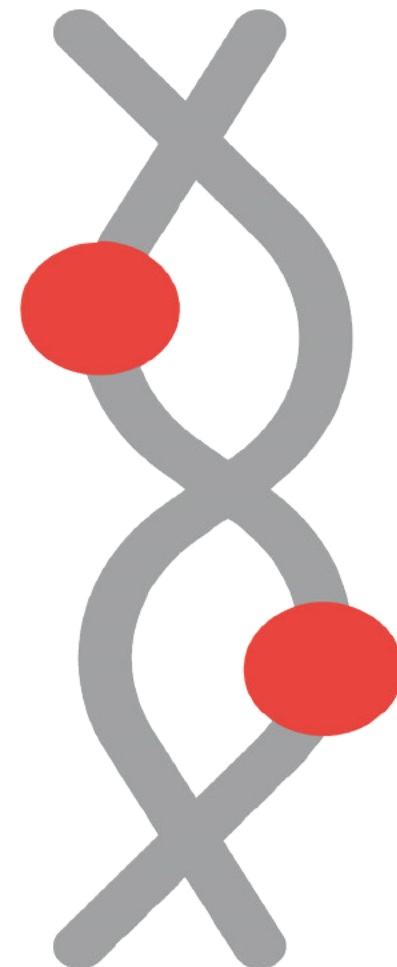
Specimen Type: Buccal Swab

Provider: #####

Patient Name: #####

Patient DOB: ###/###/####

Patient Gender: Female



Do not make any decisions about your health solely based on the information contained in this report.
Always consult with a licensed and experienced health practitioner when you receive this report.

– 36 – Female

(-/-) Normal Risk (-/+) Medium Risk (+/+) High Risk

rsID	Gene	Genetic Result	Therapeutics Associated With Positive Result	Highly Recommended Therapeutics - Designs for Health Formulas	Provider Discretion: As Needed Formula Recommendations	Lifestyle Recommendations	Laboratory Recommendations
Chronic Pain							
Inflammation Control							
	C3	T/C (+/-)	Anti-Inflammatory Therapy: Curcumin, Omega-3 Fatty Acids, Resveratrol, Quercetin, Low Dose Naltrexone (LDN), CBD Oil	Inflammatone™ SPM Supreme™ ImmunoMod-A™ OR Curcum-Evail® OmegaAvail™ Hi-Po		Consider Anti-inflammatory Diet and Lifestyle	General Inflammatory Markers: Serum High Sensitivity C-Reactive Protein, Serum Iron and Ferritin, Erythrocyte Sedimentation Rate, Serum Complement C3, Serum Interleukin 6 Lymphocyte Profile AND/OR Antibody Testing Additional Options: Adrenal Stress Profile, Sex Hormone Panel, Full Thyroid Panel, Food Allergy Panel, Comprehensive Micronutrient Testing, Microbial Titer (Candida, Epstein-Barr Virus, etc.), Toxic Metal Testing, Environmental Allergy Testing
	CD14	A/A (+/+)					
	IL5	A/G (+/-)					
	IL13	C/C (-/-)					
	STAT4	C/C (-/-)					
	IL1B	G/G (-/-)					
	IL6	C/G (+/-)					
	TNF	G/G (-/-)					
	CTLA4	A/G (+/-)					
	DRD2	C/C (-/-)	Increased Efficacy of Naltrexone				

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rsID	Gene	Genetic Result	Therapeutics Associated With Positive Result	Highly Recommended Therapeutics - Designs for Health Formulas	Provider Discretion: As Needed Formula Recommendations	Lifestyle Recommendations	Laboratory Recommendations
Chronic Pain							
Chemical Detoxification							
	AHCY	G/G (-/-)	N-Acetyl Cysteine (NAC)				Plasma Homocysteine
	CBS	G/A (+/-)	Methyltetrahydrofolate, Methylcobalamin, Pyridoxal 5'-Phosphate (B6), Choline, Trimethylglycine, Serine, N-Acetyl Cysteine		Homocysteine Supreme™ if Homocysteine Levels Are High N-Acetyl-L-Cysteine OR S-Acetyl Glutathione Synergy if Homocysteine Levels Are Low		
	CTH	G/G (-/-)	N-Acetyl Cysteine, Glutathione, Pyridoxal 5'-Phosphate				
	NFE2L2	G/G (-/-)	Pterostilbene, Green Tea (Epigallocatechin Gallate), Turmeric, Sulforaphane, Endurance Exercise				
	GCLC	A/G (+/-)	Glutathione	Liposomal Glutathione		Avoid Herbicides and Pesticides	Whole Blood Glutathione
	GSTP1	A/A (-/-)	N-Acetyl Cysteine (NAC), Glutathione			Consider Pre-Anesthesia Glutathione Treatment	

– 36 – Female

(-/-) Normal Risk (-/+) Medium Risk (+/+) High Risk

rsID	Gene	Genetic Result	Therapeutics Associated With Positive Result	Highly Recommended Therapeutics - Designs for Health Formulas	Provider Discretion: As Needed Formula Recommendations	Lifestyle Recommendations	Laboratory Recommendations
Chronic Pain							
Neurotransmitters/Pain Control							
	COMT	A/A (+/+)	Riboflavin (B2), Taurine, Choline, Trimethylglycine (TMG), Dimethylglycine (DMG), Methionine, SAMe, Inositol, L-Methionine		NeuroRenew™ if Experiencing Pain NeuroCalm™ OR CatecholaCalm™ if Chronic Anxiety or Depression Present	Be Cautious with Natural <u>COMT</u> Inhibitors, like Epigallocatechin, Caffeic Acid, and Quercetin as They Can Further Reduce COMT Activity	Consider Neurotransmitter Testing Consider PGx Testing
	GAD1	C/G (+/-)	Prescription Amantadine, Ketamine, Glycine, N-Acetyl-Cysteine (NAC), Zinc, Magnesium, Oxaloacetate, Elderberry, L-Theanine, Melatonin	May Benefit from StressArrest™ if Anxiety Is Present		Be Cautious with MSG (Monosodium Glutamate) Exposure and Glutamine Supplementation	Consider Neurotransmitter Testing
	GAD1	C/T (+/-)		May Benefit from Insomnitol™ if Sleep Initiation Is Problematic			
	ABCB1	A/A (+/+)	Defines Sensitivity to Opiates		Lower Doses of Opiates for Pain Control	Patient Should Need <u>Lower Dose</u> of Morphine Derivatives for Pain Control	Consider PGx Testing
	OPRM1	A/A (-/-)					

Summary for Chronic Pain

Highly Recommended Therapeutics - Designs for Health Formulas

Provider Discretion: As Needed Formula Recommendations

Lifestyle Recommendations

Laboratory Recommendations

Inflammation Control

- Inflammation™
- SPM Supreme™
- ImmunoMod-ATM OR Curcum-Evail®
- OmegaAvail™ Hi-Po

- Consider Anti-inflammatory Diet and Lifestyle

- General Inflammatory Markers: Serum High Sensitivity C-Reactive Protein, Serum Iron and Ferritin, Erythrocyte Sedimentation Rate, Serum Complement C3, Serum Interleukin 6
- Lymphocyte Profile AND/OR Antibody Testing
- Additional Options: Adrenal Stress Profile, Sex Hormone Panel, Full Thyroid Panel, Food Allergy Panel, Comprehensive Micronutrient Testing, Microbial Titer (Candida, Epstein-Barr Virus, etc.), Toxic Metal Testing, Environmental Allergy Testing

Chemical Detoxification

- Homocysteine Supreme™ if Homocysteine Levels Are High
- N-Acetyl-L-Cysteine OR S-Acetyl Glutathione Synergy if Homocysteine Levels Are Low

- Plasma Homocysteine

- Liposomal Glutathione

- Avoid Herbicides and Pesticides
- Consider Pre-Anesthesia Glutathione Treatment

- Whole Blood Glutathione

Neurotransmitters/Pain Control

- NeuroRenew™ if Experiencing Pain
- NeuroCalm™ OR CatecholaCalm™ if Chronic Anxiety or Depression Present

- Be Cautious with Natural COMT Inhibitors, like Epigallocatechin, Caffeic Acid, and Quercetin as They Can Further Reduce COMT Activity

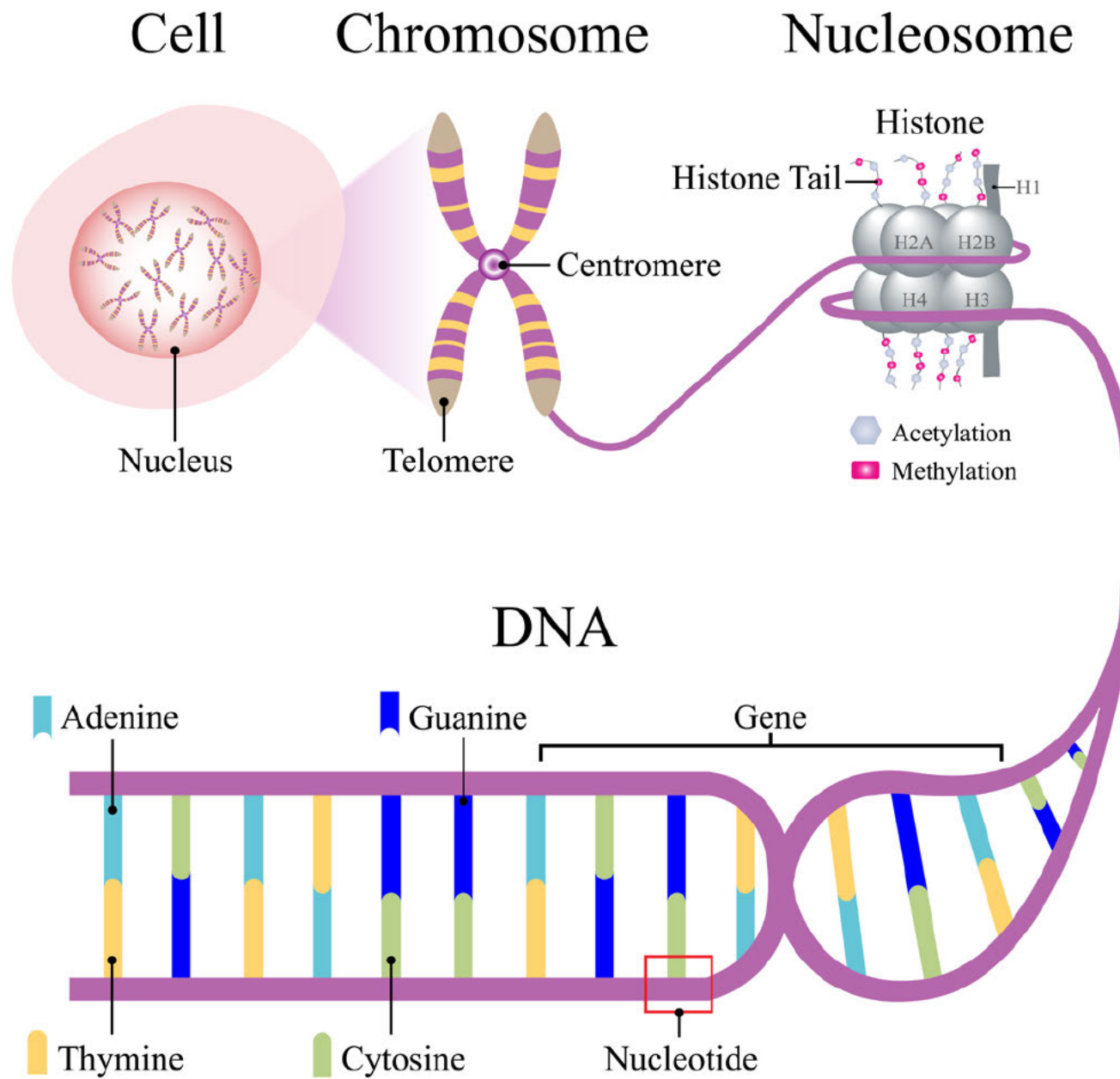
- Consider Neurotransmitter Testing
- Consider PGx Testing

- May Benefit from StressArrest™ if Anxiety Is Present
- May Benefit from Insomnitrol™ if Sleep Initiation Is Problematic

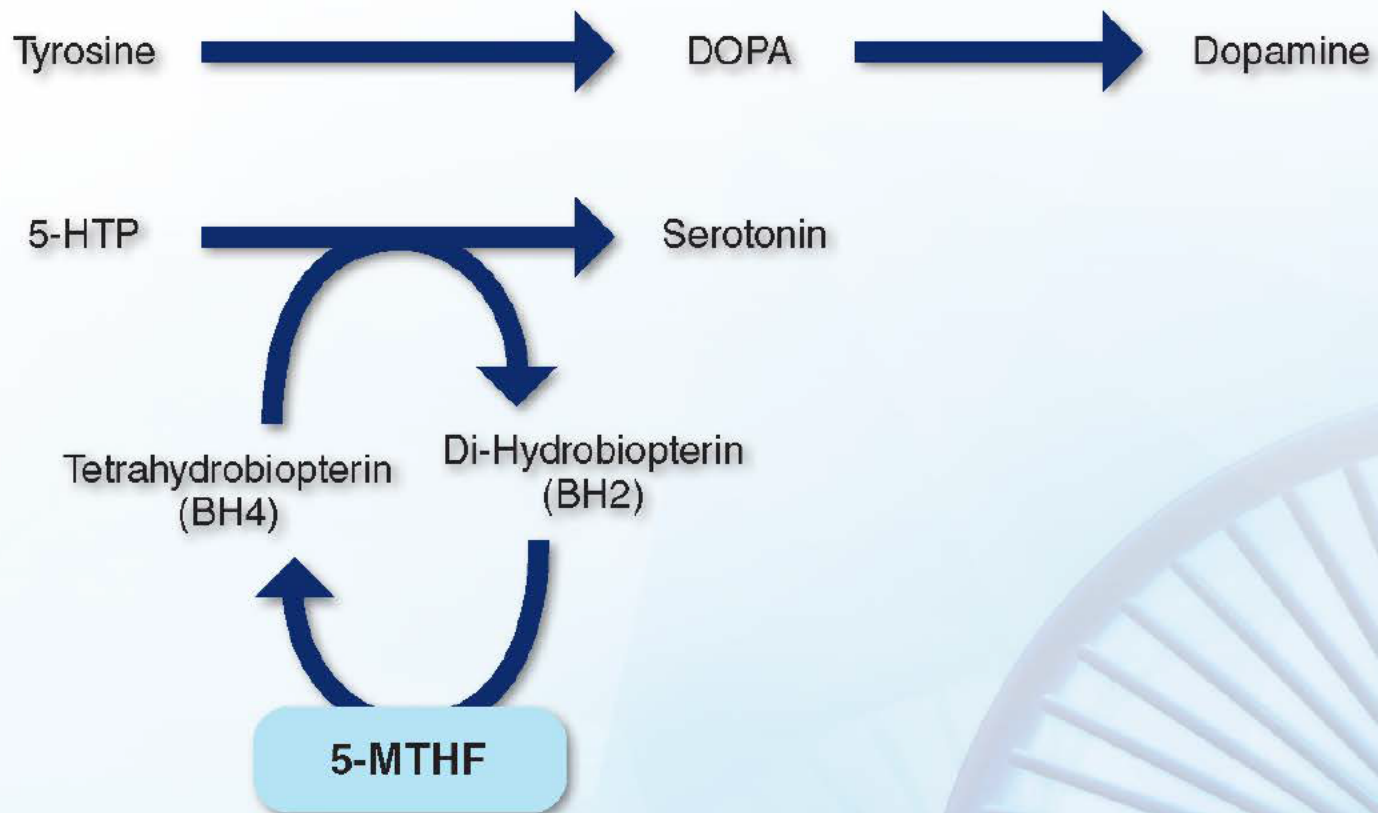
- Be Cautious with MSG (Monosodium Glutamate) Exposure and Glutamine Supplementation

- Lower Doses of Opiates for Pain Control

- Patient Should Need Lower Dose of Morphine Derivatives for Pain Control

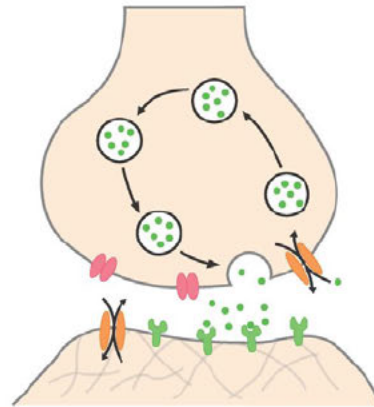


5-MTHF & Neurotransmitter Production



NEUROTRANSMITTERS & PATHWAY

TRANSMIT INFORMATION FOR ESSENTIAL PROCESSES SUCH AS DIGESTION, BREATHING, HEARTBEAT, MOVEMENT, PAIN REGULATION ETC.



RELEVANT GENES

- **HTR2, TPH2, SLC6A4, MAO-A** genes are important in the synthesis, breakdown, transport and/or functioning of serotonin
- **COMT, MAO-A, MAO-B** genes are important for the breakdown of serotonin, norepinephrine and/or dopamine
- The **DBH** gene is important for norepinephrine synthesis
- The **GAD1** gene is important for GABA synthesis
- Variants in **COMT, MAO-A, MAO-B and GAD1** genes have been associated with mood, anxiety and focus issues

WAYS TO INCREASE LEVELS



Aerobic Exercise



Dietary Factors



Mediation/Yoga

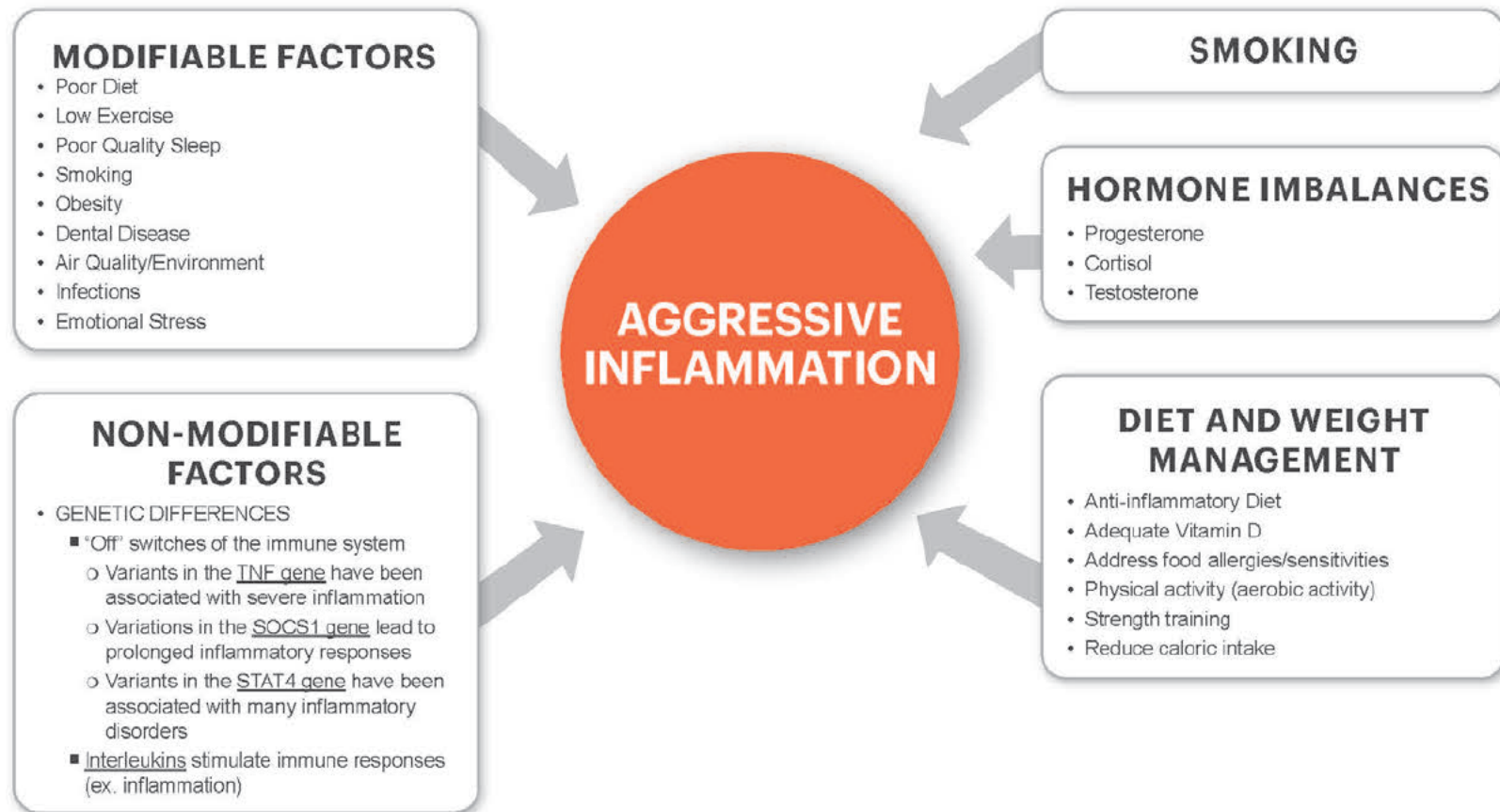


Increase Sun Exposure

ANTI-INFLAMMATORY

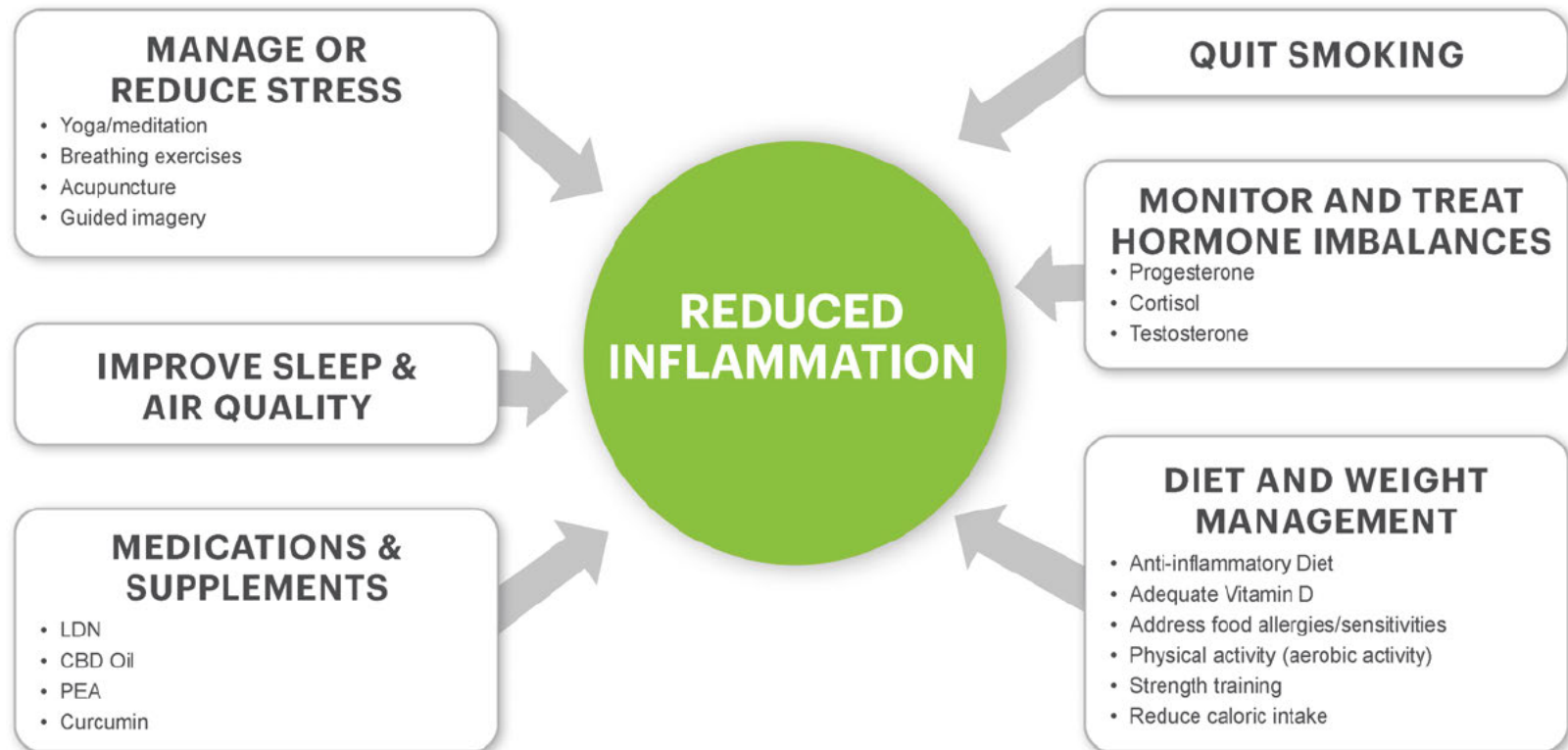
AN IMMUNE SYSTEM RESPONSE TRIGGERED BY HARMFUL STIMULI
(EX. PATHOGENS, DAMAGED CELLS, TOXIC COMPOUNDS, IRRADIATION)

DRIVERS OF INFLAMMATION



ANTI-INFLAMMATORY

WAYS TO REDUCE INFLAMMATION

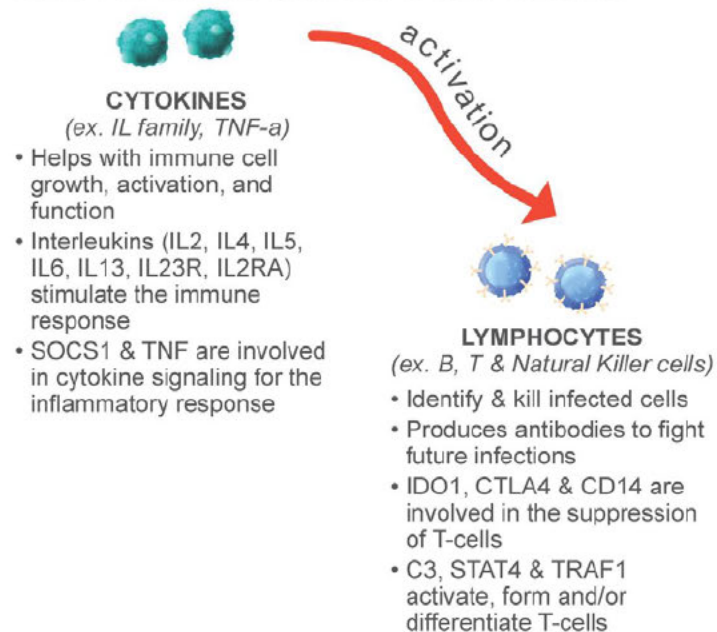


THE IMMUNE SYSTEM & AUTOIMMUNITY

WHAT DOES THE IMMUNE SYSTEM DO?

Prevent or limit infections by distinguishing between healthy and unhealthy cells

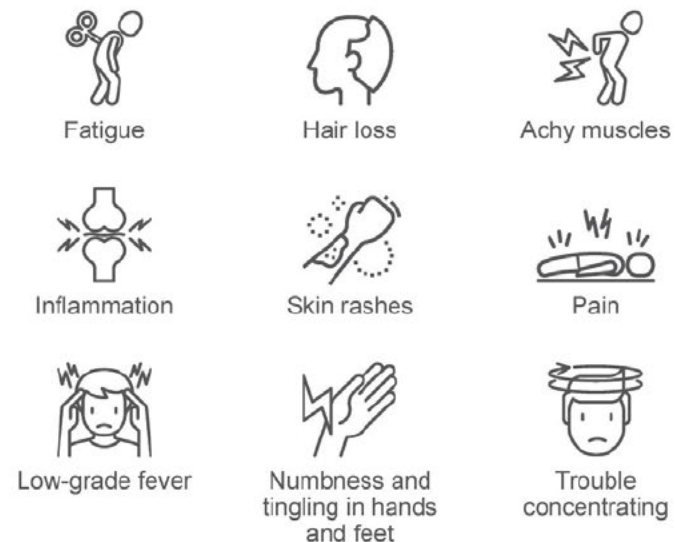
KEY PLAYERS & RELEVANT GENES



IMMUNE AGGRESSION

The immune system begins to attack healthy tissue

COMMON SYMPTOMS



MALFUNCTIONS LEAD TO

- Chronic inflammation
- Allergic reactions
- Immune aggressive diseases (Inflammatory bowel disease, skin & neurological disorders)

LOW-INFLAMMATORY

FOODS TO EAT



Fruits: strawberries, blueberries, cherries, oranges



Fatty fish: salmon, mackerel, tuna, sardines



Spices - turmeric, ginger



Green leafy vegetables & tomatoes



Dark chocolate



Olive oil



LOW-INFLAMMATORY DIET

FOODS TO AVOID



Soda & other sugar-sweetened drinks



Dairy products



Fried foods



Red & Processed meats (hotdogs, sausage)



Refined carbohydrates: white bread, pastries



Margarine, shortening, lard

BENEFITS



Reduces inflammation



Reduces risk for cardiovascular disease & Type II diabetes

DETOXIFICATION

GLUTATHIONE IN DETOXIFICATION

Relevant genes for production are AHCY, CTH, GSTP1, GSTM1, GSTM3, GSR, MTRR & MTR

WHY IS IT IMPORTANT?



Maintains health by protecting the body from toxins



Regulates cell production and programmed cell death



Critical role in chemical detoxification



Vital for proper mitochondrial function

DEFICIENCY CAUSES

- Auto-immune diseases
- Cardiovascular diseases
- Neurodegenerative diseases
- Cell death
- Poor mitochondrial function



WAYS TO INCREASE GLUTATHIONE

- Limit alcohol intake
- N-acetyl-cysteine (NAC)
- Glutathione therapies
- (ie. IV Glutathione, Glutathione suppository, Liposomal Glutathione)
- Include whey in diet, unless allergic or intolerant
- Methylation Support - if necessary

SUPEROXIDES & ANTIOXIDANTS

- SOD1, SOD2, SOD3 genes are important to transform superoxides to protect against mitochondrial damage
- Reactive Oxygen Species (ROS) can damage mitochondria and cause cell death.
- Antioxidants such as Vitamin A, Vitamin C and Vitamin E act as a defense against ROS

Gene Information Key

rsID	Gene	"_" variant	"_+" variant
	ABCB1	G	A
	AHCY	G	A
	C3	C	T
	CBS	A	G
	CD14	G	A
	COMT	G	A
	CTH	G	T
	CTLA4	A	G
	DRD2	C	A
	GAD1	C	T
	GAD1	G	C
	GCLC	G	A
	GSTP1	A	G
	IL13	C	T
	IL1B	G	A
	IL5	A	G
	IL6	C	G
	NFE2L2	G	T
	OPRM1	A	G
	STAT4	C	G
	TNF	G	A

Disclaimers

TESTING:

Testing Performed By: AC

METHODOLOGY AND LIMITATIONS DISCLAIMER:

Testing for genetic variation/mutation on listed genes was performed using ProFlex PCR and Real-Time PCR with TaqMan® allele-specific probes on the QuantStudio 12K Flex. All genetic testing is performed by GX Sciences, LLC d/b/a Fagron Genomics US ("Fagron Genomics US") (807 Las Cimas Pkwy, Suite 145, Austin, TX. 78746). This test will not detect all the known alleles that result in altered or inactive tested genes. This test does not account for all individual variations in the individual tested. Test results do not rule out the possibility that this individual could be a carrier of other mutations/variations not detected by this gene mutation/variation panel. Rare mutations surrounding these alleles may also affect our detection of genetic variations. Thus, the interpretation is given as a probability. Therefore, this genetic information shall be interpreted in conjunction with other clinical findings and familial history for the administration of specific nutrients. Patients should receive appropriate genetic counseling to explain the implications of these test results. Details of assay performance and algorithms leading to clinical recommendations are available upon request. The analytical and performance characteristics of this laboratory developed test (LDT) were determined by Fagron Genomics US's laboratory (Laboratory Director: James Jacobson, PhD) pursuant to Clinical Laboratory Improvement Amendments (CLIA) requirements (CLIA #: 45D2144988).

MEDICAL DISCLAIMER:

This test was developed and its performance characteristics determined by Fagron Genomics US. It has not been cleared or approved by the FDA. The laboratory is regulated under CLIA and qualified to perform high-complexity testing. This test is used for clinical and educational purposes. It should not be regarded as investigational or for research. The Reference SNP Cluster IDs (rsIDs) for the alleles being tested were obtained from the Single Nucleotide Polymorphism Database (dbSNP) (Build 142). These products are not approved by the Food and Drug Administration and are not intended to diagnose, treat, cure, or prevent disease. These recommendations are for report purposes only and an individual is not required to use such products. These are recommendations only and do not replace the advisement of your own healthcare practitioner.

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UND RESULT DISCLAIMER:

If you have received the result variant Undetermined (UND) this indicates that we were not able to determine your carrier status based on your raw data. You may request your sample to be run again by emailing info@fagrongenomicsus.com

Fagron Genomics US SNP References

C3

• Asteris, P. G., Gavrilaki, E., Touloumenidou, T., Koravou, E.-E., Koutra, M., Papayanni, P. G., Pouleres, A., Karali, V., Lemonis, M. E., Mamou, A., Skentou, A. D., Papalexandri, A., Varelas, C., Chatzopoulou, F., Chatzidimitriou, M., Chatzidimitriou, D., Veleni, A., Rapti, E., Kioumis, I., ... Anagnostopoulos, A. (2022). Genetic prediction of ICU hospitalization and mortality in COVID-19 patients using artificial neural networks. *Journal of Cellular and Molecular Medicine*, 26(5), 1445–1455. <https://doi.org/10.1111/jcmm.17098> • Phillips, C. M., Goumide, L., Bertrai, S., Ferguson, J. F., Field, M. R., Kelly, E. D., Peloso, G. M., Cupples, L. A., Shen, J., Ordovas, J. M., McManus, R., Hercberg, S., Portugal, H., Lairon, D., Planells, R., & Roche, H. M. (2009). Complement component 3 polymorphisms interact with polyunsaturated fatty acids to modulate risk of metabolic syndrome. *The American Journal of Clinical Nutrition*, 90(6), 1665–1673. <https://doi.org/10.3945/ajcn.2009.28101>

CD14

• Kamel, M. A., Selim, E. S., Tantawy, E. A., Elgendy, A., Abdulmageed, A., & Anis, R. H. (2023). Association of serum CD14 level and functional polymorphism C-159T in the promoter region of CD14 gene with allergic rhinitis. *Clinical and Experimental Medicine*, 23(8), 4861–4869. <https://doi.org/10.1007/s10238-023-01097-y> • Mertens, J., Bregadze, R., Mansur, A., Askar, E., Bieckhöller, H., Ramadori, G., & Mihm, S. (2009). Functional impact of endotoxin receptor CD14 polymorphisms on transcriptional activity. *Journal of Molecular Medicine* (Berlin, Germany), 87(8), 815–824. <https://doi.org/10.1007/s00109-009-0479-7> • Wang, Z., Hu, J., Fan, R., Zhou, J., & Zhong, J. (2012). Association between CD14 gene C-260T polymorphism and inflammatory bowel disease: A meta-analysis. *PloS One*, 7(9), e45144. <https://doi.org/10.1371/journal.pone.0045144> • Williams, L. K., McPhee, R. A., Ownby, D. R., Peterson, E. L., James, M., Zoratti, E. M., & Johnson, C. C. (2006). Gene-environment interactions with CD14 C-260T and their relationship to total serum IgE levels in adults. *The Journal of Allergy and Clinical Immunology*, 118(4), 851–857. <https://doi.org/10.1016/j.jaci.2006.07.007> • Xu, J.-J., Liu, K.-Q., Ying, Z.-M., Zhu, X.-W., Xu, X.-J., Zhao, P.-P., Bai, W.-Y., Qiu, M.-C., Zhang, X.-W., & Zheng, H.-F. (2019). Effect of CD14 polymorphisms on the risk of cardiovascular disease: Evidence from a meta-analysis. *Lipids in Health and Disease*, 18(1), 74. <https://doi.org/10.1186/s12944-019-1018-3>

IL5

• Ganesh, B. B., Bhattacharya, P., Gopisetty, A., & Prabhakar, B. S. (2011). Role of Cytokines in the Pathogenesis and Suppression of Thyroid Autoimmunity. *Journal of Interferon & Cytokine Research*, 31(10), 721–731. <https://doi.org/10.1089/jir.2011.0049> • Ishigaki, K., Akiyama, M., Kanai, M., Takahashi, A., Kawakami, E., Sugishita, H., Sakaue, S., Matoba, N., Low, S.-K., Okada, Y., Terao, C., Amariuta, T., Gazal, S., Kochi, Y., Honkoshi, M., Suzuki, K., Ito, K., Koyama, S., Ozaki, K., ... Kamatani, Y. (2020). Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. *Nature Genetics*, 52(7), 669–679. <https://doi.org/10.1038/s41588-020-0640-3> • Kabisch, M., Depner, M., Dahmen, I., Weiland, S. K., Vogelberg, C., Niggemann, B., Lau, S., Illig, T., Klopp, N., Wahn, U., Reinhardt, D., von Mutius, E., & Nickel, R. (2007). Polymorphisms in eosinophil pathway genes, asthma and atopy. *Allergy*, 62(4), 423–428. <https://doi.org/10.1111/j.1365-9695.2006.01300.x> • Mestri, S., Zaaber, I., Inoubil, O., Abid, N., Omrani, A., Nejehi, H., & Marmouch, H. (2020). Association of cytokine Th2 gene polymorphisms with autoimmune thyroid diseases in Tunisian population. *International Journal of Immunogenetics*, 47(3), 294–308. <https://doi.org/10.1111/iji.12472> • Principe, S., Porsbjerg, C., Balm Ditlev, S., Kjærsgaard Klein, D., Golebski, K., Dyhre?Petersen, N., van Dijk, Y. E., van Bragt, J. J. M. H., Dankelman, L. L. H., Dahlen, S., Brightling, C. E., Vijverberg, S. J. H., & Maitland?van der Zee, A. H. (2021). Treating severe asthma: Targeting the IL?5 pathway. *Clinical and Experimental Allergy*, 51(8), 992–1005. <https://doi.org/10.1111/cea.13885> • Zhu, W., Liu, N., Zhao, Y., Jia, H., Cui, B., & Ning, G. (2010). Association analysis of polymorphisms in IL-3, IL-4, IL-5, IL-9, and IL-13 with Graves' disease. *Journal of Endocrinological Investigation*, 33(10), 751–755. <https://doi.org/10.1007/BF03346882>

IL-13

• Cameron, L., Webster, R. B., Stempel, J. M., Kiesler, P., Kabisch, M., Ramachandran, H., Yu, L., Stern, D. A., Graves, P. E., Lohman, I. C., Wright, A. L., Halonen, M., Klimecki, W. T., & Vercelli, D. (2006). Th2 cell-selective enhancement of human IL13 transcription by IL13-1112C>T, a polymorphism associated with allergic inflammation. *Journal of Immunology* (Baltimore, Md.: 1950), 177(12), 8633–8642. <https://doi.org/10.4049/jimmunol.177.12.8633> • Dimberg, J., Rubér, M., Skarstedt, M., Andersson, M., & Andersson, R. E. (2020). Genetic polymorphism patterns suggest a genetic driven inflammatory response as pathogenesis in appendicitis. *International Journal of Colorectal Disease*, 35(2), 277–284. <https://doi.org/10.1007/s00384-019-03473-1> • Liao, N., Zhao, H., Chen, M.-L., & Xie, Z.-F. (2017). Association of the IL-13 polymorphisms rs1800925 and rs20541 with chronic obstructive pulmonary disease risk: An updated meta-analysis. *Medicine*, 96(47), e8558. <https://doi.org/10.1097/MD.00000000000008558> • Omraninava, M., Eslami, M. M., Aslani, S., Razi, B., Imani, D., & Feyzinia, S. (2022). Interleukin 13 gene polymorphism and susceptibility to asthma: A meta-regression and meta-analysis. *European Annals of Allergy and Clinical Immunology*, 54(4), 150–167. <https://doi.org/10.23822/EurAnnACI.1764-1489.180>

STAT4

• Jiang, Y., Zhang, R., Zheng, J., Liu, P., Tang, G., Lv, H., Zhang, L., Shang, Z., Zhan, Y., Lv, W., Shi, M., & Zhang, R. (2012). Meta-analysis of 125 rheumatoid arthritis-related single nucleotide polymorphisms studied in the past two decades. *PloS One*, 7(12), e51571. <https://doi.org/10.1371/journal.pone.0051571> • Lee, H.-S., Park, H., Yang, S., Kim, D., & Park, Y. (2008). STAT4 polymorphism is associated with early-onset type 1 diabetes, but not with late-onset type 1 diabetes. *Annals of the New York Academy of Sciences*, 1150, 93–98. <https://doi.org/10.1196/annals.1447.013> • Lee, H.-S., Remmers, E. F., Le, J. M., Kastner, D. L., Bae, S.-C., & Gregersen, P. K. (2007). Association of STAT4 with rheumatoid arthritis in the Korean population. *Molecular Medicine* (Cambridge, Mass.), 13(9–10), 455–460. <https://doi.org/10.2119/2007-00072.Lee> • Namjou, B., Sestak, A. L., Armstrong, D. L., Zidovetzki, R., Kelly, J. A., Jacob, N., Ciobanu, V., Kaufman, K. M., Ojwang, J. O., Ziegler, J., Quismorio, F., Reiff, A., Myones, B. L., Guthridge, J. M., Nath, S. K., Bruner, G. R., Mehrian-Shai, R., Silverman, E., Klein-Gitelman, M., ... Jacob, C. O. (2008). High density genotyping of STAT4 gene reveals multiple haplotypic associations with Systemic Lupus Erythematosus in different racial groups. *Arthritis and Rheumatism*, 60(4), 1085–1095. <https://doi.org/10.1002/art.24387> • Sigurdsson, S., Nordmark, G., Garnier, S., Grundberg, E., Kwan, T., Nilsson, O., Eloranta, M.-L., Gunnarsson, I., Svenungsson, E., Sturfelt, G., Bengtsson, A. A., Jönson, A., Truedsson, L., Rantapää-Dahlqvist, S., Eriksson, C., Alm, G., Göring, H. H. H., Pastinen, T., Sävänen, A.-C., & Rönnblom, L. (2008). A risk haplotype of STAT4 for systemic lupus erythematosus is over-expressed, correlates with anti-dsDNA and shows additive effects with two risk alleles of IRF5. *Human Molecular Genetics*, 17(18), 2868–2876. <https://doi.org/10.1093/hmg/ddn184> • Yan, N., Meng, S., Zhou, J., Xu, J., Muhali, F. S., Jiang, W., Shi, L., Shi, X., & Zhang, J. (2014). Association between STAT4 gene polymorphisms and autoimmune thyroid diseases in a Chinese population. *International Journal of Molecular Sciences*, 15(7), 12280–12293. <https://doi.org/10.3390/ijms150712280>

IL1B

• Bucho, N., di Giovine, F. S., Silvestri, T., Vannier, E., Duff, G. W., & Miossec, P. (2001). IL-1B and IL-1Ra gene polymorphisms and disease severity in rheumatoid arthritis: Interaction with their plasma levels. *Genes and Immunity*, 2(4), 222–228. <https://doi.org/10.1038/sj.gene.6363766> • Carter, K. W., Hung, J., Powell, B. L., Wiltshire, S., Foo, B. T. X., Leow, Y. C., McQuillan, B. M., Jennens, M., McCaskie, P. A., Thompson, P. L., Beilby, J. P., & Palmer, L. J. (2008). Association of Interleukin-1 gene polymorphisms with central obesity and metabolic syndrome in a coronary heart disease population. *Human Genetics*, 124(3), 199–208. <https://doi.org/10.1007/s00430-008-0540-6> • Fang, Y., Xie, H., & Lin, Z. (2018). Association between IL-1? + 3954C/T polymorphism and myocardial infarction risk: A meta-analysis. *Medicine*, 97(30), e11645. <https://doi.org/10.1097/MD.00000000000011645> • Galbraith, G. M., Palesch, Y., Gore, E. A., & Pandey, J. P. (1999). Contribution of interleukin 1beta and KM loci to alopecia areata. *Human Heredity*, 49(2), 85–98. <https://doi.org/10.1159/000022850> • Huang, D., Pirskanen, R., Hjeltnström, P., & Lefvert, A. K. (1998). Polymorphisms in IL-1beta and IL-1 receptor antagonist genes are associated with myasthenia gravis. *Journal of Neuroimmunology*, 81(1–2), 76–81. [https://doi.org/10.1016/s0165-5728\(97\)00161-6](https://doi.org/10.1016/s0165-5728(97)00161-6) • Samad, T. A., Moore, K. A., Sapirstein, A., Billet, S., Alchorn, A., Poole, S., Bonventre, J. V., & Woolf, C. J. (2001). Interleukin-1beta-mediated induction of Cox-2 in the CNS contributes to inflammatory pain hypersensitivity. *Nature*, 410(6827), 471–475. <https://doi.org/10.1038/35088566> • Solovieva, S., Leino-Arjas, P., Saarela, J., Luoma, K., Raitinko, R., & Riihimäki, H. (2004). Possible association of interleukin 1 gene locus polymorphisms with low back pain. *Pain*, 109(1–2), 8–19. <https://doi.org/10.1016/j.pain.2003.10.020> • Yilmaz, I. A., Ozge, A., Erdal, M. E., Edgünlü, T. G., Cakmak, S. E., & Yalin, O. O. (2010). Cytokine polymorphism in patients with migraine: Some suggestive clues of migraine and inflammation. *Pain Medicine* (Malden, Mass.), 11(4), 492–497. <https://doi.org/10.1111/j.1526-4637.2009.00791.x>

IL6

• Zhu, S., Wang, B., Jia, Q., & Duan, L. (2019). Candidate single nucleotide polymorphisms of irritable bowel syndrome: A systemic review and meta-analysis. *BMC Gastroenterology*, 19(1), 165. <https://doi.org/10.1186/s12876-019-1084-z> • Carini, M., Fredi, M., Cavazzana, I., Bresciani, R., Ferrari, F., Monti, E., Franceschini, F., & Biasiotto, G. (2023). Frequency Evaluation of the Interleukin-6 ?174G>C Polymorphism and Homeostatic Iron Regulator (HFE) Mutations as Disease Modifiers in Patients Affected by Systemic Lupus Erythematosus and Rheumatoid Arthritis. *International Journal of Molecular Sciences*, 24(22), 16300. <https://doi.org/10.3390/ijms242216300> • Chen, L., Zhang, Z., Huang, J., & Jin, M. (2018). Association between rs1800795 polymorphism in the interleukin-6 gene and the risk of polycystic ovary syndrome: A meta-analysis. *Medicine*, 97(29), e11558. <https://doi.org/10.1097/MD.00000000000011558> • Cheng, H., Zhu, W., Zhu, M., Sun, Y., Sun, X., Jia, D., Yang, C., Yu, H., & Zhang, C. (2021). Meta-analysis: Interleukin 6 gene -174G/C polymorphism associated with type 2 diabetes mellitus and interleukin 6 changes. *Journal of Cellular and Molecular Medicine*, 25(12), 5628–5639. <https://doi.org/10.1111/jcmm.16575> • Fishman, D., Faulds, G., Jeffery, R., Mohamed-Ali, V., Yudkin, J. S., Humphries, S., & Woo, P. (1998). The effect of novel polymorphisms in the interleukin-6 (IL-6) gene on IL-6 transcription and plasma IL-6 levels, and an association with systemic-onset juvenile chronic arthritis. *Journal of Clinical Investigation*, 102(7), 1369–1376. • Nie, G., Xie, C. L., Cao, Y. J., Xu, M. M., Shi, X., Zou, A. L., & Qi, J. H. (2016). Meta-analysis of IL-6 -174G/C polymorphism and psoriasis risk. *Genetics and Molecular Research: GMR*, 15(2). <https://doi.org/10.4238/gmr.15028255> • Tanaka, T., Narazaki, M., & Kishimoto, T. (2014). IL-6 in Inflammation, Immunity, and Disease. *Cold Spring Harbor Perspectives in Biology*, 6(10), a016295. <https://doi.org/10.1101/cshperspect.a016295> • Wang, X., Yan, Z., & Ye, Q. (2019). Interleukin-6 gene polymorphisms and susceptibility to liver diseases: A meta-analysis. *Medicine*, 98(50), e18408. <https://doi.org/10.1097/MD.00000000000018408> • Wu, W., Clark, E. A. S., Stoddard, G. J., Watkins, W. S., Esplin, M. S., Manuck, T. A.,

TNF-?

• Chen, L., Huang, Z., Liao, Y., Yang, B., & Zhang, J. (2019). Association between tumor necrosis factor polymorphisms and rheumatoid arthritis as well as systemic lupus erythematosus: A meta-analysis. Brazilian Journal of Medical and Biological Research = Revista Brasileira De Pesquisas Medicas E Biologicas, 52(3), e7927. <https://doi.org/10.1590/1414-431X20187927> • de Luis, D. A., Aller, R., Izaola, O., Gonzalez Sagrado, M., & Conde, R. (2013). Role of G308 promoter variant of tumor necrosis factor alpha gene on weight loss and metabolic parameters after a high monounsaturated versus a high polyunsaturated fat hypocaloric diets. Medicina Clinica, 141(5), 189–193. <https://doi.org/10.1016/j.medcli.2012.12.021> • Kilpeläinen, T. O., Laaksonen, D. E., Laikka, T. A., Herder, C., Koenig, W., Lindström, J., Eriksson, J. G., Uusitupa, M., Kolb, H., Laakso, M., Tuomilehto, J., & Finnish Diabetes Prevention Study. (2010). The rs1800629 polymorphism in the TNF gene interacts with physical activity on the changes in C-reactive protein levels in the Finnish Diabetes Prevention Study. Experimental and Clinical Endocrinology & Diabetes: Official Journal, German Society of Endocrinology [and] German Diabetes Association, 118(10), 757–759. <https://doi.org/10.1055/s-0030-1249688> • Kroeger, K. M., Canville, K. S., & Abraham, L. J. (1997). The -308 tumor necrosis factor-alpha promoter polymorphism effects transcription. Molecular Immunology, 34(5), 391–399. [https://doi.org/10.1016/s0161-5890\(97\)00052-7](https://doi.org/10.1016/s0161-5890(97)00052-7) • Loures, M. A. R., Alves, H. V., de Moraes, A. G., Santos, T. da S., Lara, F. F., Neves, J. S. F., Macedo, L. C., Teixeira, J. J. V., Sell, A. M., & Visentainer, J. E. L. (2019). Association of TNF, IL12, and IL23 gene polymorphisms and psoriatic arthritis: Meta-analysis. Expert Review of Clinical Immunology, 15(3), 303–313. <https://doi.org/10.1080/1744806X.2019.1564039> • Song, G. G., Seo, Y. H., Kim, J.-H., Choi, S. J., Ji, J. D., & Lee, Y. H. (2015). Association between TNF-? (-308 A/G, -238 A/G, -857 C/T) polymorphisms and responsiveness to TNF-? blockers in spondyloarthritis, psoriasis and Crohn's disease: A meta-analysis. Pharmacogenomics, 16(12), 1427–1437. <https://doi.org/10.2217/pgs.15.90> • Tu, Y., Fan, G., Zeng, T., Cai, X., & Kong, W. (2018). Association of TNF-? promoter polymorphism and Graves' disease: An updated systematic review and meta-analysis. Bioscience Reports, 38(2), BSR20180143. <https://doi.org/10.1042/BSR20180143> • Yang, G., Chen, J., Xu, F., Bao, Z., Yao, Y., & Zhou, J. (2014). Association between Tumor Necrosis Factor-? rs1800629 Polymorphism and Risk of Asthma: A Meta-Analysis. PLoS ONE, 9(8), e99982. <https://doi.org/10.1371/journal.pone.0099982>

CTLA4

• Chen, M., & Li, S. (2019). Associations between cytotoxic T-lymphocyte-associated antigen 4 gene polymorphisms and diabetes mellitus: A meta-analysis of 78 case-control studies. Bioscience Reports, 39(5), BSR20190309. <https://doi.org/10.1042/BSR20190309> • Chen, Y., Chen, S., Gu, Y., Feng, Y., Shi, Y., Fu, Q., Wang, Z., Cai, Y., Dai, H., Zheng, S., Sun, M., Zhang, M., Xu, X., Chen, H., Xu, K., & Yang, T. (2018). CTLA-4 +49 G/A, a functional T1D risk SNP, affects CTLA-4 level in Treg subsets and IA-2A positivity, but not beta-cell function. Scientific Reports, 8(1), 10074. <https://doi.org/10.1038/s41598-018-28423-9> • Fathima, N., Name, P., & Ishaq, M. (2018). Association and gene-gene interaction analyses for polymorphic variants in CTLA-4 and FOXP3 genes: Role in susceptibility to autoimmune thyroid disease. Endocrine, 64(3), 591–604. <https://doi.org/10.1007/s12020-019-01859-3> • Mäurer, M., Loserth, S., Kolb-Mäurer, A., Ponath, A., Wiese, S., Kruse, N., & Rieckmann, P. (2002). A polymorphism in the human cytotoxic T-lymphocyte antigen 4 (CTLA4) gene (exon 1 +49) alters T-cell activation. Immunogenetics, 54(1), 1–8. <https://doi.org/10.1007/s00251-002-0429-0> • Mousavi, M. J., Shayesteh, M. R. H., Jamalzehi, S., Alimohammadi, R., Rahimi, A., Aslani, S., & Rezaei, N. (2021). Association of the genetic polymorphisms in inhibiting and activating molecules of immune system with rheumatoid arthritis: A systematic review and meta-analysis. Journal of Research in Medical Sciences: The Official Journal of Isfahan University of Medical Sciences, 26, 22. https://doi.org/10.4103/jrms.JRMS_567_20 • Patel, H., Mansuri, M. S., Singh, M., Begum, R., Shastri, M., & Misra, A. (2016). Association of Cytotoxic T-Lymphocyte Antigen 4 (CTLA4) and Thyroglobulin (TG) Genetic Variants with Autoimmune Hypothyroidism. PloS One, 11(3), e0149441. <https://doi.org/10.1371/journal.pone.0149441>

DRD2

• Clarke, T.-K., Weiss, A. R. D., Ferraro, T. N., Kampman, K. M., Dackis, C. A., Pettinati, H. M., O'brien, C. P., Oslin, D. W., Lohoff, F. W., & Berrettini, W. H. (2014). The dopamine receptor D2 (DRD2) SNP rs1076560 is associated with opioid addiction. Annals of Human Genetics, 78(1), 33–39. <https://doi.org/10.1111/ahg.12046> • Gluskin, B. S., & Mickey, B. J. (2016). Genetic variation and dopamine D2 receptor availability: A systematic review and meta-analysis of human in vivo molecular imaging studies. Translational Psychiatry, 6(3), e747. <https://doi.org/10.1038/tp.2016.22> • Sasabe, T., Furukawa, A., Matsuita, S., Higuchi, S., & Ishiura, S. (2007). Association analysis of the dopamine receptor D2 (DRD2) SNP rs1076560 in alcoholic patients. Neuroscience Letters, 412(2), 139–142. <https://doi.org/10.1016/j.neulet.2006.10.084> • Tunbridge, E. M., Narajos, M., Harrison, C. H., Beresford, C., Cipriani, A., & Harrison, P. J. (2019). Which Dopamine Polymorphisms Are Functional? Systematic Review and Meta-analysis of COMT, DAT, DBH, DDC, DRD1-5, MAOA, MAOB, TH, VMAT1, and VMAT2. Biological Psychiatry, 86(8), 608–620. <https://doi.org/10.1016/j.biopsych.2019.05.014> • Zheng, C., Shen, Y., & Xu, Q. (2012). Rs1076560, a functional variant of the dopamine D2 receptor gene, confers risk of schizophrenia in Han Chinese. Neuroscience Letters, 518(1), 41–44. <https://doi.org/10.1016/j.neulet.2012.04.052>

AHCY

• Feng, Q., Keshtgarpour, M., Pellemounter, L. L., Moon, I., Kalari, K. R., Eckloff, B. W., Wieben, E. D., & Weinshilboum, R. M. (2009). Human S-adenosylhomocysteine hydrolase: Common gene sequence variation and functional genomic characterization. Journal of Neurochemistry, 110(6), 1806–1817. <https://doi.org/10.1111/j.1471-4159.2009.06276.x> • Fumi?, K., Beluzzi?, R., Cuk, M., Pavkov, T., Kloor, D., Bari?, I., Miji?, I., & Vugrek, O. (2007). Functional analysis of human S-adenosylhomocysteine hydrolase isoforms SAHH-2 and SAHH-3. European Journal of Human Genetics: EJHG, 15(3), 347–351. <https://doi.org/10.1038/sj.ejhg.5201757>

CBS

• Aras, O., Hanson, N. Q., Yang, F., & Tsai, M. Y. (2000). Influence of 699C→T and 1080C→T polymorphisms of the cystathionine beta-synthase gene on plasma homocysteine levels. Clinical Genetics, 58(6), 455–459. <https://doi.org/10.1034/j.1399-0004.2000.580605.x> • De Stefano, V., Dekou, V., Nicaud, V., Chasse, J. F., London, J., Stansbie, D., Humphries, S. E., & Gudnason, V. (1998). Linkage disequilibrium at the cystathionine beta synthase (CBS) locus and the association between genetic variation at the CBS locus and plasma levels of homocysteine. The Ears II Group. European Atherosclerosis Research Study. Annals of Human Genetics, 62(Pt 6), 481–490. <https://doi.org/10.1046/j.1469-1809.1998.6260481.x> • Fredriksen, A., Meyer, K., Ueland, P. M., Vollset, S. E., Grotmol, T., & Schneede, J. (2007). Large-scale population-based metabolic phenotyping of thirteen genetic polymorphisms related to one-carbon metabolism. Human Mutation, 28(9), 856–865. <https://doi.org/10.1002/humu.20522> • Kruger, W. D., Evans, A. A., Wang, L., Malinow, M. R., Duell, P. B., Anderson, P. H., Block, P. C., Hess, D. L., Graf, E. E., & Upson, B. (2000). Polymorphisms in the CBS gene associated with decreased risk of coronary artery disease and increased responsiveness to total homocysteine lowering by folic acid. Molecular Genetics and Metabolism, 70(1), 53–60. <https://doi.org/10.1008/mgme.2000.2993>

CTH

• Wenstrom, K. D., Johanning, G. L., Owen, J., Johnston, K. E., Acton, S., & Tamura, T. (2000). Role of amniotic fluid homocysteine level and of fetal 5, 10-methylenetetrahydrofolate reductase genotype in the etiology of neural tube defects. American Journal of Medical Genetics, 90(1), 12–18. [https://doi.org/10.1002/\(sici\)1096-8628\(20000103\)90:112::aid-ajmg3>3.0.co;2-h](https://doi.org/10.1002/(sici)1096-8628(20000103)90:112::aid-ajmg3>3.0.co;2-h)

NFE2L2

• Marzec, J. M., Christie, J. D., Reddy, S. P., Jedlicka, A. E., Vuong, H., Lanken, P. N., Aplenc, R., Yamamoto, T., Yamamoto, M., Cho, H.-Y., & Kleeberger, S. R. (2007). Functional polymorphisms in the transcription factor NRF2 in humans increase the risk of acute lung injury. FASEB Journal: Official Publication of the Federation of American Societies for Experimental Biology, 21(9), 2237–2246. <https://doi.org/10.1096/fj.06-7759com> • Reuland, D. J., McCord, J. M., & Hamilton, K. L. (2013). The role of Nr1f2 in the attenuation of cardiovascular disease. Exercise and Sport Sciences Reviews, 41(3), 162–168. <https://doi.org/10.1097/JES.0b013e3182948a1e> • Satta, S., Mahmoud, A. M., Wilkinson, F. L., Yvonne Alexander, M., & White, S. J. (2017). The Role of Nr1f2 in Cardiovascular Function and Disease. Oxidative Medicine and Cellular Longevity, 2017, 9237263. <https://doi.org/10.1155/2017/9237263> • Shimizu, S., Mimura, J., Hasegawa, T., Shimizu, E., Imoto, S., Tsushima, M., Kasai, S., Yamazaki, H., Ushida, Y., Suganuma, H., Tomita, H., Yamamoto, M., Nakaji, S., & Itoh, K. (2020). Association of single nucleotide polymorphisms in the NRF2 promoter with vascular stiffness with aging. PloS One, 15(8), e0236834. <https://doi.org/10.1371/journal.pone.0236834> • Wang, X., Chen, H., Liu, J., Ouyang, Y., Wang, D., Bao, W., & Liu, L. (2015). Association between the NF-E2 Related Factor 2 Gene Polymorphism and Oxidative Stress, Anti-Oxidative Status, and Newly-Diagnosed Type 2 Diabetes Mellitus in a Chinese Population. International Journal of Molecular Sciences, 16(7), 16483–16498. <https://doi.org/10.3390/ijms160716483>

GCLC

• Azarova, I., Klyosova, E., Lazarenko, V., Konoplya, A., & Polonikov, A. (2020). Genetic variants in glutamate cysteine ligase confer protection against type 2 diabetes. Molecular Biology Reports, 47(8), 5793–5805. <https://doi.org/10.1007/s11033-020-05647-5> • Koide, S., Kugiyama, K., Sugiyama, S., Nakamura, S., Fukushima, H., Honda, O., Yoshimura, M., & Ogawa, H. (2003). Association of polymorphism in glutamate-cysteine ligase catalytic subunit gene with coronary vasomotor dysfunction and myocardial infarction. Journal of the American College of Cardiology, 41(4), 539–545. [https://doi.org/10.1016/s0735-1067\(02\)02866-8](https://doi.org/10.1016/s0735-1067(02)02866-8) • Zuo, H., Xu, W., Luo, M., Zhu, Z., & Zhu, G. (2007). [The glutamate-cysteine ligase catalytic subunit gene C-129T and modifier subunit gene G-23T polymorphisms and risk for coronary diseases]. Zhonghua Xin Xue Guan Bing Za Zhi, 35(7), 637–640.

GSTP1

• Dai, X., Bui, D. S., & Lodge, C. (2021). Glutathione S-Transferase Gene Associations and Gene-Environment Interactions for Asthma. Current Allergy and Asthma Reports, 21(5), 31. <https://doi.org/10.1007/s11882-021-01005-y> • do Nascimento, M. R., Silva de Souza, R. O., Silva, A. L., Lima, E. S., Gonçalves, M. S., & de Moura Neto, J. P. (2021). GSTP1 rs1695 and rs1871042, and SOD2 rs4880 as molecular markers of lipid peroxidation in blood storage. Blood Transfusion = Trasfusione Del Sangue, 19(4), 309–316. <https://doi.org/10.2450/2020.0062-20> • Hollman, A. L., Tchounwou, P. B., & Huang, H.-C. (2016). The Association between Gene-Environment Interactions and Diseases Involving the Human GST Superfamily with SNP Variants. International Journal of Environmental Research and Public Health, 13(4), 379. <https://doi.org/10.3390/ijerph13040379> • Katsarou, M.-S., Giakoumaki, M., Papadimitriou, A., Demertzis, N., Androutsopoulos, V., & Drakoulis, N. (2018). Genetically driven antioxidant capacity in a Caucasian Southeastern European population. Mechanisms of Ageing and Development, 172, 1–5. <https://doi.org/10.1016/j.mad.2017.08.010> • Melén, E., Nyberg, F., Lindgren, C. M., Berglind, N., Zucchelli, M., Nordling, E., Hallberg, J., Svartengren, M., Morgenstern, R., Kere, J., Bellander, T., Wickman, M., & Pershagen, G. (2008). Interactions between glutathione S-transferase P1, tumor necrosis factor, and traffic-related air pollution for development of childhood allergic disease. Environmental Health Perspectives, 116(8), 1077–1084. <https://doi.org/10.1289/ehp.11117> • Moyer, A. M., Salavaggione, O. E., Wu, T.-Y., Moon,

I., Eckloff, B. W., Hildebrandt, M. A. T., Schaid, D. J., Wieben, E. D., & Weinshilboum, R. M. (2008). Glutathione S-Transferase P1: Gene Sequence Variation and Functional Genomic Studies. *Cancer Research*, 68(12), 4791–4801. <https://doi.org/10.1158/0008-5472.CAN-07-0724> • Mukhammadiyeva, G. F., Bakirov, A. B., Karimov, D. O., Ziatdinova, M. M., Valova, Y. V., Borisova, A. I., & Distanova, A. A. (2022). Analysis of the GSTP1 rs1695 polymorphism association with the development of asthma and phenotypic manifestations. *The Journal of Asthma: Official Journal of the Association for the Care of Asthma*, 59(6), 1065–1069. <https://doi.org/10.1080/02770903.2021.1910295> • Palmer, C. N. A., Doney, A. S. F., Lee, S. P., Murrie, I., Ismail, T., Macgregor, D. F., & Mukhopadhyay, S. (2006). Glutathione S-transferase M1 and P1 genotype, passive smoking, and peak expiratory flow in asthma. *Pediatrics*, 118(2), 710–716. <https://doi.org/10.1542/peds.2005-3030> • Scafró, M., Sciandra, C., Ruberto, S., & Santovito, A. (2021). GSTT1, GSTP1 and XPC genes are associated with longevity in an Italian cohort. *Annals of Human Biology*, 48(5), 443–447. <https://doi.org/10.1080/03014460.2021.1985170> • Simeunovic, D., Odanovic, N., Pljesa-Eroegovac, M., Radic, T., Radovanovic, S., Coric, V., Milinkovic, I., Matic, M., Djukic, T., Ristic, A., Risimic, D., Seferovic, P., Simic, T., Simic, D., & Savic-Radojevic, A. (2019). Glutathione Transferase P1 Polymorphism Might Be a Risk Determinant in Heart Failure. *Disease Markers*, 2019, 6984845. <https://doi.org/10.1155/2019/6984845> • Tamer, L., Calikoğlu, M., Ates, N. A., Yıldırım, H., Eroan, B., Saritas, E., Unlü, A., & Atik, U. (2004). Glutathione-S-transferase gene polymorphisms (GSTT1, GSTM1, GSTP1) as increased risk factors for asthma. *Respirology (Carlton, Vic.)*, 9(4), 493–498. <https://doi.org/10.1111/j.1440-1843.2004.00657.x>

COMT

• Dawling, S., Roodi, N., Mernaugh, R. L., Wang, X., & Parl, F. F. (2001). Catechol-O-methyltransferase (COMT)-mediated metabolism of catechol estrogens: Comparison of wild-type and variant COMT isoforms. *Cancer Research*, 61(18), 6716–6722. • Eriksson, A.-L., Suuriniemi, M., Mahonen, A., Cheng, S., & Ohlsson, C. (2005). The COMT val158met polymorphism is associated with early pubertal development, height and cortical bone mass in girls. *Pediatric Research*, 58(1), 71–77. <https://doi.org/10.1203/01.PDR.0000163383.49747.B5> • Kumar, P., & Rai, V. (2020). Catechol-O-methyltransferase gene Val158Met polymorphism and obsessive compulsive disorder susceptibility: A meta-analysis. *Metabolic Brain Disease*, 35(2), 241–251. <https://doi.org/10.1007/s11011-019-00495-0> • Lachman, H. M., Papolos, D. F., Saito, T., Yu, Y. M., Szumlanski, C. L., & Weinshilboum, R. M. (1996). Human catechol-O-methyltransferase pharmacogenetics: Description of a functional polymorphism and its potential application to neuropsychiatric disorders. *Pharmacogenetics*, 6(3), 243–250. <https://doi.org/10.1097/00008571-199606000-00007> • Sardahae, F. S., Holmen, T. L., Micali, N., & Kvale, K. (2017). Effects of single genetic variants and polygenic obesity risk scores on disordered eating in adolescents—The HUNT study. *Appetite*, 118, 8–16. <https://doi.org/10.1016/j.appet.2017.07.003> • Scanlon, P. D., Raymond, F. A., & Weinshilboum, R. M. (1979). Catechol-O-methyltransferase: Thermolabile enzyme in erythrocytes of subjects homozygous for allele for low activity. *Science (New York, N.Y.)*, 203(4375), 63–65. <https://doi.org/10.1126/science.758679> • Stein, D. J., Newman, T. K., Savitz, J., & Ramesar, R. (2006). Warriors versus worriers: The role of COMT gene variants. *CNS Spectrums*, 11(10), 745–748. <https://doi.org/10.1017/s1092852900014863> • Stein, M. B., Fallin, M. D., Schork, N. J., & Gelernter, J. (2005). COMT polymorphisms and anxiety-related personality traits. *Neuropsychopharmacology: Official Publication of the American College of Neuropsychopharmacology*, 30(11), 2092–2102. <https://doi.org/10.1038/sj.npp.1300787> • Tunbridge, E. M., Harrison, P. J., Warden, D. R., Johnston, C., Refsum, H., & Smith, A. D. (2008). Polymorphisms in the catechol-O-methyltransferase (COMT) gene influence plasma total homocysteine levels. *American Journal of Medical Genetics. Part B, Neuropsychiatric Genetics: The Official Publication of the International Society of Psychiatric Genetics*, 147B(6), 996–999. <https://doi.org/10.1002/ajmg.b.30700> • Tunbridge, E. M., Narajos, M., Harrison, C. H., Beresford, C., Cipriani, A., & Harrison, P. J. (2019). Which Dopamine Polymorphisms Are Functional? Systematic Review and Meta-analysis of COMT, DAT, DBH, DDC, DRD1-5, MAOA, MAOB, TH, VMAT1, and VMAT2. *Biological Psychiatry*, 86(8), 608–620. <https://doi.org/10.1016/j.biopsych.2019.05.014> • Wichers, M., Aguilera, M., Kenis, G., Krabbendam, L., Myin-Germeyns, I., Jacobs, N., Peeters, F., Derom, C., Vlietinck, R., Mengelers, R., Delespaul, P., & van Os, J. (2008). The catechol-O-methyl transferase Val158Met polymorphism and experience of reward in the flow of daily life. *Neuropsychopharmacology: Official Publication of the American College of Neuropsychopharmacology*, 33(13), 3030–3038. <https://doi.org/10.1038/sj.npp.1301520>

GAD1

• Ulge, S. et al. A population-based association study of candidate genes for depression and sleep disturbance. *Am J Med Genet B Neuropsychiatr Genet* 153B, 468–476 (2010). • Hettema, J. M. et al. Association between glutamic acid decarboxylase genes and anxiety disorders, major depression, and neuroticism. *Mol Psychiatry* 11, 752–762 (2006). • Barakat, A. K. et al. Citalopram-induced pathways regulation and tentative treatment-outcome-predicting biomarkers in lymphoblastoid cell lines from depression patients. *Transl Psychiatry* 10, 210 (2020). • Weber, H. et al. Gender Differences in Associations of Glutamate Decarboxylase 1 Gene (GAD1) Variants with Panic Disorder. *PLoS One* 7, e37851 (2012).

GAD1

• Lim, S. W. et al. Genetic Prediction of Antidepressant Drug Response and Nonresponse in Korean Patients. *PLoS One* 9, e107098 (2014). • Darrah, S. D. et al. Genetic Variability in Glutamic Acid Decarboxylase Genes: Associations with Post-traumatic Seizures after Severe TBI. *Epilepsy Res* 103, 180–194 (2013).

ABCB1:C3435T

• Enabakh, D., El Baz, H., & Moselhy, H. (2014). Higher frequency of C.3435 of the ABCB1 gene in patients with tramadol dependence disorder. *The American Journal of Drug and Alcohol Abuse*, 40(4), 317–320. <https://doi.org/10.3109/00952990.2014.925468> • Hoffmeyer, S., Burk, O., von Richter, O., Arnold, H. P., Brockmüller, J., John, A., Cascorbi, I., Gerloff, T., Roots, I., Eichelbaum, M., & Brinkmann, U. (2000). Functional polymorphisms of the human multidrug-resistance gene: Multiple sequence variations and correlation of one allele with P-glycoprotein expression and activity in vivo. *Proceedings of the National Academy of Sciences of the United States of America*, 97(7), 3473–3478. <https://doi.org/10.1073/pnas.97.7.3473> • Hooten, W. M., Hu, D., & Cunningham, J. M. (2021). Effects of the ABCB1 c.3435C>T (rs1045642) Polymorphism on Heat Pain Perception in Opioid-Free Adults With Chronic Pain. *Anesthesia and Analgesia*, 133(4), 1028–1035. <https://doi.org/10.1213/ANE.00000000000005829> • Horvat, C. M., Au, A. K., Conley, Y. P., Kochanek, P. M., Li, L., Poloyac, S. M., Empey, P. E., & Clark, R. S. B. (2017). ABCB1 genotype is associated with fentanyl requirements in critically ill children. *Pediatric Research*, 82(1), 29–35. <https://doi.org/10.1038/pr.2017.103> • Iwersen-Bergmann, S., Plattner, S., Hischke, S., Müller, A., Andresen-Streichert, H., Jungen, H., Erb, R., & Beer-Sandner, B. (2021). Brain/blood ratios of methadone and ABCB1 polymorphisms in methadone-related deaths. *International Journal of Legal Medicine*, 135(2), 473–482. <https://doi.org/10.1007/s00414-021-02502-5> • Levran, O., O'Hara, K., Peles, E., Li, D., Barral, S., Ray, B., Borg, L., Ott, J., Adelson, M., & Kreek, M. J. (2008). ABCB1 (MDR1) genetic variants are associated with methadone doses required for effective treatment of heroin dependence. *Human Molecular Genetics*, 17(14), 2219–2227. <https://doi.org/10.1093/hmg/ddn122>

OPRM1:A118G

• Frangakis, S. G., MacEachern, M., Akbar, T. A., Bolton, C., Lin, V., Smith, A. V., Brummett, C. M., & Bicket, M. C. (2023). Association of Genetic Variants with Postsurgical Pain: A Systematic Review and Meta-analyses. *Anesthesiology*, 139(6), 827–839. <https://doi.org/10.1097/ALN.0000000000004677> • Lee, M. G., Kim, H. J., Lee, K. H., & Choi, Y. S. (2016). The Influence of Genotype Polymorphism on Morphine Analgesic Effect for Postoperative Pain in Children. *The Korean Journal of Pain*, 29(1), 34–39. <https://doi.org/10.3344/kjp.2016.29.1.34> • Lötsch, J., Skarke, C., Grösch, S., Darimont, J., Schmidt, H., & Geisslinger, G. (2002). The polymorphism A118G of the human mu-opioid receptor gene decreases the pupil constrictory effect of morphine-6-glucuronide but not that of morphine. *Pharmacogenetics*, 12(1), 3–9. <https://doi.org/10.1097/00008571-200201000-00002> • Oertel, B. G., Schmidt, R., Schneider, A., Geisslinger, G., & Lötsch, J. (2006). The mu-opioid receptor gene polymorphism 118A>G depletes alfentanil-induced analgesia and protects against respiratory depression in homozygous carriers. *Pharmacogenetics and Genomics*, 16(9), 625–636. <https://doi.org/10.1097/01.fpc.0000220568.90466.a2> • Zhang, Y., Wang, D., Johnson, A. D., Papp, A. C., & Sadée, W. (2005). Allelic expression imbalance of human mu opioid receptor (OPRM1) caused by variant A118G. *The Journal of Biological Chemistry*, 280(38), 32618–32624. <https://doi.org/10.1074/jbc.M504942200>