

# Seyma Katrinli

## List of Publications by Year in descending order

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21  
papers

357  
citations

1040056

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888059

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#	ARTICLE	IF	CITATIONS
1	Epigenome-wide meta-analysis of PTSD symptom severity in three military cohorts implicates DNA methylation changes in genes involved in immune system and oxidative stress. <i>Molecular Psychiatry</i> , 2022, 27, 1720-1728.	7.9	21
2	Methylation quantitative trait loci are largely consistent across disease states in Crohn's disease. <i>Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	2
3	Transcriptome-wide association study of post-trauma symptom trajectories identified GRIN3B as a potential biomarker for PTSD development. <i>Neuropsychopharmacology</i> , 2021, 46, 1811-1820.	5.4	15
4	Immune system regulation and role of the human leukocyte antigen in posttraumatic stress disorder. <i>Neurobiology of Stress</i> , 2021, 15, 100366.	4.0	10
5	Critical evaluation of copy number variant calling methods using DNA methylation. <i>Genetic Epidemiology</i> , 2020, 44, 148-158.	1.3	12
6	Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies methylation changes in AHRH. <i>Nature Communications</i> , 2020, 11, 5965.	12.8	84
7	Evaluating the impact of trauma and PTSD on epigenetic prediction of lifespan and neural integrity. <i>Neuropsychopharmacology</i> , 2020, 45, 1609-1616.	5.4	63
8	Association of HLA locus alleles with posttraumatic stress disorder. <i>Brain, Behavior, and Immunity</i> , 2019, 81, 655-658.	4.1	30
9	EPIGENOME-WIDE META-ANALYSES OF PTSD HIGHLIGHT THE ROLE OF SEX AND TRAUMA-TYPE AS A POTENTIAL SOURCE OF HETEROGENEITY. <i>European Neuropsychopharmacology</i> , 2019, 29, S42.	0.7	0
10	S15ASSOCIATION OF DIFFERENTIALLY METHYLATED REGIONS WITH PTSD IN A TRAUMATIZED CIVILIAN COHORT. <i>European Neuropsychopharmacology</i> , 2019, 29, S121.	0.7	0
11	F95. Effect of HLA Alleles on Suicide Attempts and Chronic Pain in Women. <i>Biological Psychiatry</i> , 2019, 85, S249-S250.	1.3	2
12	S152. Genetic Risk for Hospitalization in Serious Mental Illness. <i>Biological Psychiatry</i> , 2019, 85, S355-S356.	1.3	0
13	The association of variations in TLR genes and spontaneous immune control of hepatitis B virus. <i>Clinics and Research in Hepatology and Gastroenterology</i> , 2018, 42, 139-144.	1.5	7
14	Host genetic factors affecting hepatitis B infection outcomes: Insights from genome-wide association studies. <i>World Journal of Gastroenterology</i> , 2018, 24, 3347-3360.	3.3	52
15	Integrating Personalized Genomics To Turkish Health Care System: A Cancer Oriented Pilot Activity of Istanbul Northern Anatolian Public Hospitals with GLAB. <i>İstanbul Kuzey Klinikleri</i> , 2017, 4, 1-3.	0.3	7
16	Determination of Stage Specific Markers for Liver Fibrosis in Hepatitis B: A Comparative Tissue Proteomic Study. <i>Journal of Hepatology</i> , 2016, 64, S446.	3.7	0
17	Proteomic profiling of HBV infected liver biopsies with different fibrotic stages. <i>Proteome Science</i> , 2016, 15, 7.	1.7	18
18	Effect of HLA-DPA1 Alleles on Chronic Hepatitis B Prognosis and Treatment Response. <i>İstanbul Kuzey Klinikleri</i> , 2016, 3, 168-174.	0.3	2

#	ARTICLE	IF	CITATIONS
19	HLA DQB1 alleles are related with nonalcoholic fatty liver disease. Molecular Biology Reports, 2014, 41, 7937-7943.	2.3	11
20	Association of human leukocyte antigen DQB1 and DRB1 alleles with chronic hepatitis B. World Journal of Gastroenterology, 2014, 20, 8179.	3.3	16
21	The effect of HLA-DQB1 alleles on virologic breakthroughs during chronic hepatitis B treatment with genetically low barrier drugs. Clinics and Research in Hepatology and Gastroenterology, 2013, 37, 359-364.	1.5	5