Faisal I Rezwan

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Integration of Genomic Risk Scores to Improve the Prediction of Childhood Asthma Diagnosis. Journal of Personalized Medicine, 2022, 12, 75.	2.5	8
2	Predicting Pulmonary Function From the Analysis of Voice: A Machine Learning Approach. Frontiers in Digital Health, 2022, 4, 750226.	2.8	12
3	Meta-analysis of epigenome-wide association studies in newborns and children show widespread sex differences in blood DNA methylation. Mutation Research - Reviews in Mutation Research, 2022, 789, 108415.	5.5	24
4	Placental uptake and metabolism of 25(OH)vitamin D determine its activity within the fetoplacental unit. ELife, 2022, 11, .	6.0	31
5	Nonlinear effects of environment on childhood asthma susceptibility. Pediatric Allergy and Immunology, 2022, 33, e13777.	2.6	0
6	Reply to Owora et al Pediatric Allergy and Immunology, 2021, 32, 393-395.	2.6	0
7	Pre-adolescence DNA methylation is associated with BMI status change from pre- to post-adolescence. Clinical Epigenetics, 2021, 13, 64.	4.1	3
8	Preconceptional smoking alters spermatozoal miRNAs of murine fathers and affects offspring's body weight. International Journal of Obesity, 2021, 45, 1623-1627.	3.4	16
9	Gaussian Bayesian network comparisons with graph ordering unknown. Computational Statistics and Data Analysis, 2021, 157, 107156.	1.2	4
10	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
11	Development of childhood asthma prediction models using machine learning approaches. Clinical and Translational Allergy, 2021, 11, e12076.	3.2	17
12	Epigenome wide comparison of DNA methylation profile between paired umbilical cord blood and neonatal blood on Guthrie cards. Epigenetics, 2020, 15, 454-461.	2.7	14
13	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. Genome Medicine, 2020, 12, 105.	8.2	41
14	Prediction of Lung Function in Adolescence Using Epigenetic Aging: A Machine Learning Approach. Methods and Protocols, 2020, 3, 77.	2.0	3
15	Genome-Wide DNA Methylation in Peripheral Blood and Long-Term Exposure to Source-Specific Transportation Noise and Air Pollution: The SAPALDIA Study. Environmental Health Perspectives, 2020, 128, 67003.	6.0	56
16	Role of DNA methylation in the association of lung function with body mass index: a two-step epigenetic Mendelian randomisation study. BMC Pulmonary Medicine, 2020, 20, 171.	2.0	3
17	Prediction models for childhood asthma: A systematic review. Pediatric Allergy and Immunology, 2020, 31, 616-627.	2.6	46
18	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. Genome Medicine, 2020, 12, 25.	8.2	81

FAISAL I REZWAN

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19	Changes of DNA methylation are associated with changes in lung function during adolescence. Respiratory Research, 2020, 21, 80.	3.6	12
20	Association of adult lung function with accelerated biological aging. Aging, 2020, 12, 518-542.	3.1	23
21	Epigenome-Wide Association Study Reveals Duration of Breastfeeding Is Associated with Epigenetic Differences in Children. International Journal of Environmental Research and Public Health, 2020, 17, 3569.	2.6	12
22	Epigenome-wide association study of asthma and wheeze characterizes loci within HK1. Allergy, Asthma and Clinical Immunology, 2019, 15, 43.	2.0	10
23	Effect of gestational oily fish intake on the risk of allergy in children may be influenced by FADS1/2, ELOVL5 expression and DNA methylation. Genes and Nutrition, 2019, 14, 20.	2.5	16
24	DNA methylation links prenatal smoking exposure to later life health outcomes in offspring. Clinical Epigenetics, 2019, 11, 97.	4.1	88
25	Epigenome-wide association study of lung function level and its change. European Respiratory Journal, 2019, 54, 1900457.	6.7	49
26	Duration of breastfeeding is associated with leptin (LEP) DNA methylation profiles and BMI in 10-year-old children. Clinical Epigenetics, 2019, 11, 128.	4.1	36
27	Reply. Journal of Allergy and Clinical Immunology, 2019, 144, 624-625.	2.9	0
28	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	2.1	64
29	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 2062-2074.	2.9	147
30	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. Hypertension, 2019, 74, 375-383.	2.7	73
31	Growth disrupting mutations in epigenetic regulatory molecules are associated with abnormalities of epigenetic aging. Genome Research, 2019, 29, 1057-1066.	5.5	38
32	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. Nature Communications, 2019, 10, 1893.	12.8	140
33	<scp>DNA</scp> methylation and allergic sensitizations: A genomeâ€scale longitudinal study during adolescence. Allergy: European Journal of Allergy and Clinical Immunology, 2019, 74, 1166-1175.	5.7	28
34	Changes in DNA methylation from pre- to post-adolescence are associated with pubertal exposures. Clinical Epigenetics, 2019, 11, 176.	4.1	35
35	The phenotypic variations of multi-locus imprinting disturbances associated with maternal-effect variants of NLRP5 range from overt imprinting disorder to apparently healthy phenotype. Clinical Epigenetics, 2019, 11, 190.	4.1	22
36	Genetic Analyses in Small-for-Gestational-Age Newborns. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 917-925.	3.6	38

FAISAL I REZWAN

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37	Maternal variants in <i>NLRP</i> and other maternal effect proteins are associated with multilocus imprinting disturbance in offspring. Journal of Medical Genetics, 2018, 55, 497-504.	3.2	126
38	Transgenerational and intergenerational epigenetic inheritance in allergic diseases. Journal of Allergy and Clinical Immunology, 2018, 142, 765-772.	2.9	70
39	Changes of DNA methylation and their association with changes in lung function during adolescence - an epigenome-wide study. Journal of Allergy and Clinical Immunology, 2018, 141, AB202.	2.9	0
40	SERPINA1 methylation and lung function in tobacco-smoke exposed European children and adults: a meta-analysis of ALEC population-based cohorts. Respiratory Research, 2018, 19, 156.	3.6	11
41	Epigenome-Wide Assessment on DNA Methylation Change with Asthma Transition in Adolescence. Journal of Allergy and Clinical Immunology, 2018, 141, AB182.	2.9	0
42	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. Human Molecular Genetics, 2017, 26, 4067-4085.	2.9	211
43	Systematic review of lung function and COPD with peripheral blood DNA methylation in population based studies. BMC Pulmonary Medicine, 2017, 17, 54.	2.0	28
44	Tetanus vaccination is associated with differential DNA-methylation: Reduces the risk of asthma in adolescence. Vaccine, 2016, 34, 6493-6501.	3.8	14
45	Association of season of birth with <scp>DNA</scp> methylation and allergic disease. Allergy: European Journal of Allergy and Clinical Immunology, 2016, 71, 1314-1324.	5.7	61
46	A statistical method for single sample analysis of HumanMethylation450 array data: genome-wide methylation analysis of patients with imprinting disorders. Clinical Epigenetics, 2015, 7, 48.	4.1	18
47	Identifying CpG sites associated with eczema via random forest screening of epigenome-scale DNA methylation. Clinical Epigenetics, 2015, 7, 68.	4.1	19
48	Very small deletions within the NESP55 gene in pseudohypoparathyroidism type 1b. European Journal of Human Genetics, 2015, 23, 494-499.	2.8	20
49	Mutations in NLRP5 are associated with reproductive wastage and multilocus imprinting disorders in humans. Nature Communications, 2015, 6, 8086.	12.8	134
50	Congenital imprinting disorders: Application of multilocus and high throughput methods to decipher new pathomechanisms and improve their management. Molecular and Cellular Probes, 2015, 29, 282-290.	2.1	12
51	Genome-wide DNA methylation analysis of patients with imprinting disorders identifies differentially methylated regions associated with novel candidate imprinted genes. Journal of Medical Genetics, 2014, 51, 229-238.	3.2	91
52	The interplay of DNA methylation over time with Th2 pathway genetic variants on asthma risk and temporal asthma transition. Clinical Epigenetics, 2014, 6, 8.	4.1	47
53	Improving Transcription Factor Binding Site Predictions by Using Randomised Negative Examples. Lecture Notes in Computer Science, 2012, , 225-237.	1.3	0
54	MAGETabulator, a suite of tools to support the microarray data format MAGE-TAB. Bioinformatics, 2009, 25, 279-280.	4.1	14

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55	ArrayExpress updatefrom an archive of functional genomics experiments to the atlas of gene expression. Nucleic Acids Research, 2009, 37, D868-D872.	14.5	380
56	Combining experts in order to identify binding sites in yeast and mouse genomic data. Neural Networks, 2008, 21, 856-861.	5.9	4