

Faisal I Rezwan

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

2,674
citations

236925

25
h-index

197818

49
g-index

61
all docs

61
docs citations

61
times ranked

5057
citing authors

#	ARTICLE	IF	CITATIONS
1	Integration of Genomic Risk Scores to Improve the Prediction of Childhood Asthma Diagnosis. <i>Journal of Personalized Medicine</i> , 2022, 12, 75.	2.5	8
2	Predicting Pulmonary Function From the Analysis of Voice: A Machine Learning Approach. <i>Frontiers in Digital Health</i> , 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. <i>Mutation Research - Reviews in Mutation Research</i> , 2022, 789, 108415.	5.5	24
4	Placental uptake and metabolism of 25(OH)vitamin D determine its activity within the fetoplacental unit. <i>ELife</i> , 2022, 11, .	6.0	31
5	Nonlinear effects of environment on childhood asthma susceptibility. <i>Pediatric Allergy and Immunology</i> , 2022, 33, e13777.	2.6	0
6	Reply to Owora et al.. <i>Pediatric Allergy and Immunology</i> , 2021, 32, 393-395.	2.6	0
7	Pre-adolescence DNA methylation is associated with BMI status change from pre- to post-adolescence. <i>Clinical Epigenetics</i> , 2021, 13, 64.	4.1	3
8	Preconceptional smoking alters spermatozoal miRNAs of murine fathers and affects offspring's body weight. <i>International Journal of Obesity</i> , 2021, 45, 1623-1627.	3.4	16
9	Gaussian Bayesian network comparisons with graph ordering unknown. <i>Computational Statistics and Data Analysis</i> , 2021, 157, 107156.	1.2	4
10	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
11	Development of childhood asthma prediction models using machine learning approaches. <i>Clinical and Translational Allergy</i> , 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. <i>Epigenetics</i> , 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. <i>Genome Medicine</i> , 2020, 12, 105.	8.2	41
14	Prediction of Lung Function in Adolescence Using Epigenetic Aging: A Machine Learning Approach. <i>Methods and Protocols</i> , 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. <i>Environmental Health Perspectives</i> , 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. <i>BMC Pulmonary Medicine</i> , 2020, 20, 171.	2.0	3
17	Prediction models for childhood asthma: A systematic review. <i>Pediatric Allergy and Immunology</i> , 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. <i>Genome Medicine</i> , 2020, 12, 25.	8.2	81

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19	Changes of DNA methylation are associated with changes in lung function during adolescence. <i>Respiratory Research</i> , 2020, 21, 80.	3.6	12
20	Association of adult lung function with accelerated biological aging. <i>Aging</i> , 2020, 12, 518-542.	3.1	23
21	Epigenome-Wide Association Study Reveals Duration of Breastfeeding Is Associated with Epigenetic Differences in Children. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 3569.	2.6	12
22	Epigenome-wide association study of asthma and wheeze characterizes loci within HK1. <i>Allergy, Asthma and Clinical Immunology</i> , 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. <i>Genes and Nutrition</i> , 2019, 14, 20.	2.5	16
24	DNA methylation links prenatal smoking exposure to later life health outcomes in offspring. <i>Clinical Epigenetics</i> , 2019, 11, 97.	4.1	88
25	Epigenome-wide association study of lung function level and its change. <i>European Respiratory Journal</i> , 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. <i>Clinical Epigenetics</i> , 2019, 11, 128.	4.1	36
27	Reply. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 624-625.	2.9	0
28	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. <i>Epigenomics</i> , 2019, 11, 1487-1500.	2.1	64
29	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 2062-2074.	2.9	147
30	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. <i>Hypertension</i> , 2019, 74, 375-383.	2.7	73
31	Growth disrupting mutations in epigenetic regulatory molecules are associated with abnormalities of epigenetic aging. <i>Genome Research</i> , 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. <i>Nature Communications</i> , 2019, 10, 1893.	12.8	140
33	<sc>DNA</sc> methylation and allergic sensitizations: A genome-scale longitudinal study during adolescence. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2019, 74, 1166-1175.	5.7	28
34	Changes in DNA methylation from pre- to post-adolescence are associated with pubertal exposures. <i>Clinical Epigenetics</i> , 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. <i>Clinical Epigenetics</i> , 2019, 11, 190.	4.1	22
36	Genetic Analyses in Small-for-Gestational-Age Newborns. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 917-925.	3.6	38

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37	Maternal variants in <i>NLRP1</i> and other maternal effect proteins are associated with multilocus imprinting disturbance in offspring. <i>Journal of Medical Genetics</i> , 2018, 55, 497-504.	3.2	126
38	Transgenerational and intergenerational epigenetic inheritance in allergic diseases. <i>Journal of Allergy and Clinical Immunology</i> , 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. <i>Journal of Allergy and Clinical Immunology</i> , 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. <i>Respiratory Research</i> , 2018, 19, 156.	3.6	11
41	Epigenome-Wide Assessment on DNA Methylation Change with Asthma Transition in Adolescence. <i>Journal of Allergy and Clinical Immunology</i> , 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. <i>Human Molecular Genetics</i> , 2017, 26, 4067-4085.	2.9	211
43	Systematic review of lung function and COPD with peripheral blood DNA methylation in population based studies. <i>BMC Pulmonary Medicine</i> , 2017, 17, 54.	2.0	28
44	Tetanus vaccination is associated with differential DNA-methylation: Reduces the risk of asthma in adolescence. <i>Vaccine</i> , 2016, 34, 6493-6501.	3.8	14
45	Association of season of birth with CpG DNA methylation and allergic disease. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 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. <i>Clinical Epigenetics</i> , 2015, 7, 48.	4.1	18
47	Identifying CpG sites associated with eczema via random forest screening of epigenome-scale DNA methylation. <i>Clinical Epigenetics</i> , 2015, 7, 68.	4.1	19
48	Very small deletions within the NESP55 gene in pseudohypoparathyroidism type 1b. <i>European Journal of Human Genetics</i> , 2015, 23, 494-499.	2.8	20
49	Mutations in NLRP5 are associated with reproductive wastage and multilocus imprinting disorders in humans. <i>Nature Communications</i> , 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. <i>Molecular and Cellular Probes</i> , 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. <i>Journal of Medical Genetics</i> , 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. <i>Clinical Epigenetics</i> , 2014, 6, 8.	4.1	47
53	Improving Transcription Factor Binding Site Predictions by Using Randomised Negative Examples. <i>Lecture Notes in Computer Science</i> , 2012, , 225-237.	1.3	0
54	MAGETabulator, a suite of tools to support the microarray data format MAGE-TAB. <i>Bioinformatics</i> , 2009, 25, 279-280.	4.1	14

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