## Justin M O'sullivan

List of Publications by Year in descending order

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Ιμετιν Μ.Ο'εμιμναν

#	Article	IF	CITATIONS
1	Assigning function to SNPs: Considerations when interpreting genetic variation. Seminars in Cell and Developmental Biology, 2022, 121, 135-142.	5.0	13
2	3D genome organization, genetic variation and disease. Seminars in Cell and Developmental Biology, 2022, 121, 133-134.	5.0	0
3	Transcription shifts in gut bacteria shared between mothers and their infants. Scientific Reports, 2022, 12, 1276.	3.3	7
4	Establishing gene regulatory networks from Parkinson's disease risk loci. Brain, 2022, 145, 2422-2435.	7.6	10
5	A de novo <scp><i>ACTB</i></scp> gene pathogenic variant in identical twins with phenotypic variation for hydrops and jejunal atresia. American Journal of Medical Genetics, Part A, 2022, 188, 1299-1306.	1.2	3
6	Redefining the hypotheses driving Parkinson's diseases research. Npj Parkinson's Disease, 2022, 8, 45.	5.3	7
7	Can adult polygenic scores improve prediction of body mass index in childhood?. International Journal of Obesity, 2022, 46, 1375-1383.	3.4	7
8	Low tolerance for transcriptional variation at cohesin genes is accompanied by functional links to disease-relevant pathways. Journal of Medical Genetics, 2021, 58, 534-542.	3.2	3
9	Lower insulin sensitivity remains a feature of children born very preterm. Pediatric Diabetes, 2021, 22, 161-167.	2.9	3
10	Population epidemiology and concordance for plasma amino acids and precursors in 11–12-year-old children and their parents. Scientific Reports, 2021, 11, 3619.	3.3	8
11	Plasma B Vitamers: Population Epidemiology and Parent-Child Concordance in Children and Adults. Nutrients, 2021, 13, 821.	4.1	5
12	Strain engraftment competition and functional augmentation in a multi-donor fecal microbiota transplantation trial for obesity. Microbiome, 2021, 9, 107.	11.1	55
13	Intronic Haplotypes in <scp>GBA</scp> Modify Age at Diagnosis of Parkinson's: Replication in a Subgroup. Movement Disorders, 2021, 36, 1468-1470.	3.9	1
14	Oral administration of maternal vaginal microbes at birth to restore gut microbiome development in infants born by caesarean section: A pilot randomised placebo-controlled trial. EBioMedicine, 2021, 69, 103443.	6.1	58
15	Untangling the genetic link between type 1 and type 2 diabetes using functional genomics. Scientific Reports, 2021, 11, 13871.	3.3	6
16	Transcriptional Regulation of RUNX1: An Informatics Analysis. Genes, 2021, 12, 1175.	2.4	4
17	Understanding the impact of SNPs associated with autism spectrum disorder on biological pathways in the human fetal and adult cortex. Scientific Reports, 2021, 11, 15867.	3.3	15
18	Unravelling the Shared Genetic Mechanisms Underlying 18 Autoimmune Diseases Using a Systems Approach. Frontiers in Immunology, 2021, 12, 693142.	4.8	14

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19	Identifying the lungs as a susceptible site for allele-specific regulatory changes associated with type 1 diabetes risk. Communications Biology, 2021, 4, 1072.	4.4	2
20	Trimethylamine N-oxide (TMAO) Is not Associated with Cardiometabolic Phenotypes and Inflammatory Markers in Children and Adults. Current Developments in Nutrition, 2021, 5, nzaa179.	0.3	15
21	Machine Learning Identifies Six Genetic Variants and Alterations in the Heart Atrial Appendage as Key Contributors to PD Risk Predictivity. Frontiers in Genetics, 2021, 12, 785436.	2.3	4
22	Hi-C detects novel structural variants in HL-60 and HL-60/S4 cell lines. Genomics, 2020, 112, 151-162.	2.9	15
23	GWAS SNPs Impact Shared Regulatory Pathways Amongst Multimorbid Psychiatric Disorders and Cognitive Functioning. Frontiers in Psychiatry, 2020, 11, 560751.	2.6	7
24	Desacetyl-α-MSH and α-MSH have sex specific interactions with diet to influence mouse gut morphology, metabolites and microbiota. Scientific Reports, 2020, 10, 18957.	3.3	3
25	A period of 10 weeks of increased protein consumption does not alter faecal microbiota or volatile metabolites in healthy older men: a randomised controlled trial. Journal of Nutritional Science, 2020, 9, e25.	1.9	10
26	Plasma Trimethylamine N-Oxide and Its Precursors: Population Epidemiology, Parent–Child Concordance, and Associations with Reported Dietary Intake in 11- to 12-Year-Old Children and Their Parents. Current Developments in Nutrition, 2020, 4, nzaa103.	0.3	18
27	Maternal bacteria to correct abnormal gut microbiota in babies born by C-section. Medicine (United) Tj ETQq1	1 0.784314 1.0	4 rg <mark>BT</mark> /Overlo
28	High prevalence of undiagnosed comorbidities among adolescents with obesity. Scientific Reports, 2020, 10, 20101.	3.3	10
29	Shared Regulatory Pathways Reveal Novel Genetic Correlations Between Grip Strength and Neuromuscular Disorders. Frontiers in Genetics, 2020, 11, 393.	2.3	5
30	The microbial biogeography of the gastrointestinal tract of preterm and term lambs. Scientific Reports, 2020, 10, 9113.	3.3	8
31	Differences in Compositions of Gut Bacterial Populations and Bacteriophages in 5–11 Year-Olds Born Preterm Compared to Full Term. Frontiers in Cellular and Infection Microbiology, 2020, 10, 276.	3.9	9
32	Common Variants Coregulate Expression of <scp><i>GBA</i></scp> and Modifier Genes to Delay Parkinson's Disease Onset. Movement Disorders, 2020, 35, 1346-1356.	3.9	30
33	Genetic variants associated with alcohol dependence co-ordinate regulation of ADH genes in gastrointestinal and adipose tissues. Scientific Reports, 2020, 10, 9897.	3.3	1
34	Gut microbiome transfer—Finding the perfect fit. Clinical Endocrinology, 2020, 93, 3-10.	2.4	6
35	Robotic automation of a UHPLC/MS-MS method profiling one-carbon metabolites, amino acids, and precursors in plasma. Analytical Biochemistry, 2020, 592, 113558.	2.4	15
36	Genomic dissection of 43 serum urate-associated loci provides multiple insights into molecular mechanisms of urate control. Human Molecular Genetics, 2020, 29, 923-943.	2.9	40

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37	Reconstructing the blood metabolome and genotype using long-range chromatin interactions. Metabolism Open, 2020, 6, 100035.	2.9	6
38	Randomised Double-Blind Placebo-Controlled Trial of Inulin with Metronidazole in Non-Alcoholic Fatty Liver Disease (NAFLD). Nutrients, 2020, 12, 937.	4.1	35
39	Effects of Fecal Microbiome Transfer in Adolescents With Obesity. JAMA Network Open, 2020, 3, e2030415.	5.9	76
40	Gut Microbial Predictors of Type 2 Diabetes Remission Following Bariatric Surgery. Obesity Surgery, 2020, 30, 3536-3548.	2.1	25
41	Transcriptional profiling of the zebrafish proximal tubule. American Journal of Physiology - Renal Physiology, 2019, 317, F478-F488.	2.7	17
42	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	10.3	86
43	The Super-Donor Phenomenon in Fecal Microbiota Transplantation. Frontiers in Cellular and Infection Microbiology, 2019, 9, 2.	3.9	262
44	Perspective: Advancing Understanding of Population Nutrient–Health Relations via Metabolomics and Precision Phenotypes. Advances in Nutrition, 2019, 10, 944-952.	6.4	14
45	Protocol for the Gut Bugs Trial: a randomised double-blind placebo-controlled trial of gut microbiome transfer for the treatment of obesity in adolescents. BMJ Open, 2019, 9, e026174.	1.9	16
46	Machine Learning SNP Based Prediction for Precision Medicine. Frontiers in Genetics, 2019, 10, 267.	2.3	142
47	Changes in long-range rDNA-genomic interactions associate with altered RNA polymerase II gene programs during malignant transformation. Communications Biology, 2019, 2, 39.	4.4	33
48	Altered gut microbiome after bariatric surgery and its association with metabolic benefits: A systematic review. Surgery for Obesity and Related Diseases, 2019, 15, 656-665.	1.2	58
49	TNF-α Differentially Regulates Cell Cycle Genes in Promyelocytic and Granulocytic HL-60/S4 Cells. G3: Genes, Genomes, Genetics, 2019, 9, 2775-2786.	1.8	3
50	Cohesin facilitates zygotic genome activation in zebrafish. Development (Cambridge), 2018, 145, .	2.5	47
51	GWAS on prolonged gestation (post-term birth): analysis of successive Finnish birth cohorts. Journal of Medical Genetics, 2018, 55, 55-63.	3.2	23
52	Genome organization: connecting the developmental origins of disease and genetic variation. Journal of Developmental Origins of Health and Disease, 2018, 9, 260-265.	1.4	0
53	Type 1 Diabetes Mellitus-Associated Genetic Variants Contribute to Overlapping Immune Regulatory Networks. Frontiers in Genetics, 2018, 9, 535.	2.3	39
54	Chromatin interactions and expression quantitative trait loci reveal genetic drivers of multimorbidities. Nature Communications, 2018, 9, 5198.	12.8	64

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55	Migration through a small pore disrupts inactive chromatin organization in neutrophil-like cells. BMC Biology, 2018, 16, 142.	3.8	37
56	The Impact of Nutritional Interventions in Pregnant Women on DNA Methylation Patterns of the Offspring: A Systematic Review. Molecular Nutrition and Food Research, 2018, 62, e1800034.	3.3	11
57	Identification of human skeletal muscle miRNA related to strength by high-throughput sequencing. Physiological Genomics, 2018, 50, 416-424.	2.3	27
58	Factors Affecting Gastrointestinal Microbiome Development in Neonates. Nutrients, 2018, 10, 274.	4.1	176
59	A non-coding genetic variant maximally associated with serum urate levels is functionally linked to HNF4A-dependent PDZK1 expression. Human Molecular Genetics, 2018, 27, 3964-3973.	2.9	26
60	The genetic architecture of type 1 diabetes mellitus. Molecular and Cellular Endocrinology, 2018, 477, 70-80.	3.2	51
61	Functional Urate-Associated Genetic Variants Influence Expression of lincRNAs LINC01229 and MAFTRR. Frontiers in Genetics, 2018, 9, 733.	2.3	18
62	Nutritional Intervention Preconception and During Pregnancy to Maintain Healthy Glucose Metabolism and Offspring Health ("NiPPeRâ€): study protocol for a randomised controlled trial. Trials, 2017, 18, 131.	1.6	53
63	Linkages between changes in the 3D organization of the genome and transcription during myotube differentiation in vitro. Skeletal Muscle, 2017, 7, 5.	4.2	45
64	Long-term stability in the gut microbiome over 46â€ <sup>−</sup> years in the life of Billy Apple®. Human Microbiome Journal, 2017, 5-6, 7-10.	3.8	9
65	A DNA Contact Map for the Mouse Runx1 Gene Identifies Novel Haematopoietic Enhancers. Scientific Reports, 2017, 7, 13347.	3.3	9
66	A Memory of Early Life Physical Activity Is Retained in Bone Marrow of Male Rats Fed a High-Fat Diet. Frontiers in Physiology, 2017, 8, 476.	2.8	5
67	Physical Interactions and Expression Quantitative Traits Loci Identify Regulatory Connections for Obesity and Type 2 Diabetes Associated SNPs. Frontiers in Genetics, 2017, 8, 150.	2.3	84
68	The New Era of Treatment for Obesity and Metabolic Disorders: Evidence and Expectations for Gut Microbiome Transplantation. Frontiers in Cellular and Infection Microbiology, 2016, 6, 15.	3.9	60
69	A diffusion model for the coordination of DNA replication in Schizosaccharomyces pombe. Scientific Reports, 2016, 6, 18757.	3.3	15
70	A potential role for genome structure in the translation of mechanical force during immune cell development. Nucleus, 2016, 7, 462-475.	2.2	2
71	Interactions between mitochondrial and nuclear DNA in mammalian cells are non-random. Mitochondrion, 2016, 30, 187-196.	3.4	16
72	Intergenic GWAS SNPs are key components of the spatial and regulatory network for human growth. Human Molecular Genetics, 2016, 25, 3372-3382.	2.9	36

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73	Connecting SNPs in Diabetes: A Spatial Analysis of Meta-GWAS Loci. Frontiers in Endocrinology, 2015, 6, 102.	3.5	18
74	Different Short-Term Mild Exercise Modalities Lead to Differential Effects on Body Composition in Healthy Prepubertal Male Rats. BioMed Research International, 2015, 2015, 1-9.	1.9	5
75	Different exercise modalities have distinct effects on the integrin-linked kinase (ILK) and Ca2+signaling pathways in the male rat bone. Physiological Reports, 2015, 3, e12568.	1.7	6
76	Cohesin modulates transcription of estrogen-responsive genes. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2015, 1849, 257-269.	1.9	18
77	Data for chromosome contacts and matched transcription profiles at three cell cycle phases in the fission yeast. Genomics Data, 2015, 4, 12-16.	1.3	0
78	A Sequence-Specific Interaction between the Saccharomyces cerevisiae rRNA Gene Repeats and a Locus Encoding an RNA Polymerase I Subunit Affects Ribosomal DNA Stability. Molecular and Cellular Biology, 2015, 35, 544-554.	2.3	7
79	Biochar in Co-Contaminated Soil Manipulates Arsenic Solubility and Microbiological Community Structure, and Promotes Organochlorine Degradation. PLoS ONE, 2015, 10, e0125393.	2.5	45
80	Insights from Space: Potential Role of Diet in the Spatial Organization of Chromosomes. Nutrients, 2014, 6, 5724-5739.	4.1	4
81	Genes and post-term birth: late for delivery. BMC Research Notes, 2014, 7, 720.	1.4	11
82	Chromosome conformation maps in fission yeast reveal cell cycle dependent sub nuclear structure. Nucleic Acids Research, 2014, 42, 12585-12599.	14.5	26
83	Potential roles for interactions between the mitochondrial and nuclear DNA throughout the cell cycle of Schizosaccharomyces pombe. Mitochondrion, 2014, 17, 141-149.	3.4	4
84	Cohesin mutations in myeloid malignancies: underlying mechanisms. Experimental Hematology and Oncology, 2014, 3, 13.	5.0	54
85	The missing story behind Genome Wide Association Studies: single nucleotide polymorphisms in gene deserts have a story to tell. Frontiers in Genetics, 2014, 5, 39.	2.3	51
86	Genome conformation capture reveals that the Escherichia coli chromosome is organized by replication and transcription. Nucleic Acids Research, 2013, 41, 6058-6071.	14.5	115
87	The statistical-mechanics of chromosome conformation capture. Nucleus, 2013, 4, 390-398.	2.2	47
88	The nucleolus: a raft adrift in the nuclear sea or the keystone in nuclear structure?. Biomolecular Concepts, 2013, 4, 277-286.	2.2	24
89	Mitochondrial-Nuclear DNA Interactions Contribute to the Regulation of Nuclear Transcript Levels as Part of the Inter-Organelle Communication System. PLoS ONE, 2012, 7, e30943.	2.5	21
90	tRNA Gene Identity Affects Nuclear Positioning. PLoS ONE, 2011, 6, e29267.	2.5	11

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91	Chromosome organizaton in simple and complex unicellular organisms. Current Issues in Molecular Biology, 2011, 13, 37-42.	2.4	1
92	Yeast chromosomal interactions and nuclear architecture. Current Opinion in Cell Biology, 2010, 22, 298-304.	5.4	5
93	Nucleolar structure: It's all in a tangle. Cell Cycle, 2010, 9, 4609-4609.	2.6	1
94	Repeated elements coordinate the spatial organization of the yeast genome. Yeast, 2009, 26, 125-138.	1.7	33
95	Global identification of yeast chromosome interactions using Genome conformation capture. Fungal Genetics and Biology, 2009, 46, 879-886.	2.1	109
96	Gene loops juxtapose promoters and terminators in yeast. Nature Genetics, 2004, 36, 1014-1018.	21.4	321
97	Regulation of Elongating RNA Polymerase II by Forkhead Transcription Factors in Yeast. Science, 2003, 300, 492-495.	12.6	62
98	Isw1 Chromatin Remodeling ATPase Coordinates Transcription Elongation and Termination by RNA Polymerase II. Cell, 2003, 115, 425-435.	28.9	160
99	Lab Ref: a recipe for every occasion. Journal of Cell Science, 2003, 116, 762-762.	2.0	0
100	Promoter proximal splice sites enhance transcription. Genes and Development, 2002, 16, 2792-2799.	5.9	234
101	A Role for Chromatin Remodeling in Transcriptional Termination by RNA Polymerase II. Molecular Cell, 2002, 10, 1441-1452.	9.7	137
102	Polyadenylation: A tail of two complexes. Current Biology, 2002, 12, R855-R857.	3.9	96
103	The Candida albicans gene encoding the cytoplasmic leucyl-tRNA synthetase: implications for the evolution of CUG codon reassignment. Gene, 2001, 275, 133-140.	2.2	7
104	Seryl-tRNA synthetase is not responsible for the evolution of CUG codon reassignment inCandida albicans. Yeast, 2001, 18, 313-322.	1.7	7
105	Codon reassignment and the evolving genetic code: problems and pitfalls in post-genome analysis. Trends in Genetics, 2001, 17, 20-22.	6.7	8
106	Candida albicans : adherence, signaling and virulence. Medical Mycology, 2000, 38, 125-137.	0.7	55
107	Adhesion of Candida albicans to oral streptococci is promoted by selective adsorption of salivary proteins to the streptococcal cell surface. Microbiology (United Kingdom), 2000, 146, 41-48.	1.8	84
108	Identification of salivary basic proline-rich proteins as receptors for Candida albicans adhesion. Microbiology (United Kingdom), 1997, 143, 341-348.	1.8	40

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109	A Review of Feature Selection Methods for Machine Learning-Based Disease Risk Prediction. Frontiers in Bioinformatics, 0, 2, .	2.1	128