Richard W Francis

List of Publications by Year in descending order

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35 papers

2,158 citations

331670 21 h-index 395702 33 g-index

36 all docs 36 does citations

36 times ranked 4947 citing authors

#	Article	IF	CITATIONS
1	Common and Rare Genetic Variants That Could Contribute to Severe Otitis Media in an Australian Aboriginal Population. Clinical Infectious Diseases, 2021, 73, 1860-1870.	5.8	4
2	Optimal interpregnancy interval in autism spectrum disorder: A multiâ€national study of a modifiable risk factor. Autism Research, 2021, 14, 2432-2443.	3.8	6
3	Reference exome data for a Northern Brazilian population. Scientific Data, 2020, 7, 360.	5. 3	O
4	Association of Genetic and Environmental Factors With Autism in a 5-Country Cohort. JAMA Psychiatry, 2019, 76, 1035.	11.0	319
5	Birth seasonality and risk of autism spectrum disorder. European Journal of Epidemiology, 2019, 34, 785-792.	5.7	28
6	Recurrence Risk of Autism in Siblings and Cousins: AÂMultinational, Population-Based Study. Journal of the American Academy of Child and Adolescent Psychiatry, 2019, 58, 866-875.	0.5	41
7	Apgar score and risk of autism. European Journal of Epidemiology, 2019, 34, 105-114.	5.7	26
8	An in silico pipeline to filter the Toxoplasma gondii proteome for proteins that could traffic to the host cell nucleus and influence host cell epigenetic regulation. Memorias Do Instituto Oswaldo Cruz, 2018, 113, e170471.	1.6	4
9	A platform for discovery of functional cell-penetrating peptides for efficient multi-cargo intracellular delivery. Scientific Reports, 2018, 8, 12538.	3.3	50
10	Caesarean section and risk of autism across gestational age: a multi-national cohort study of 5 million births. International Journal of Epidemiology, 2017, 46, dyw336.	1.9	44
11	Official ERS technical standards: Global Lung Function Initiative reference values for the carbon monoxide transfer factor for Caucasians. European Respiratory Journal, 2017, 50, 1700010.	6.7	394
12	Reference genotype and exome data from an Australian Aboriginal population for health-based research. Scientific Data, 2016, 3, 160023.	5. 3	19
13	ViPAR: a software platform for the Virtual Pooling and Analysis of Research Data. International Journal of Epidemiology, 2016, 45, 408-416.	1.9	42
14	Autism risk associated with parental age and with increasing difference in age between the parents. Molecular Psychiatry, 2016, 21, 693-700.	7.9	178
15	First Genome-Wide Association Study in an Australian Aboriginal Population Provides Insights into Genetic Risk Factors for Body Mass Index and Type 2 Diabetes. PLoS ONE, 2015, 10, e0119333.	2.5	35
16	DataSHIELD: taking the analysis to the data, not the data to the analysis. International Journal of Epidemiology, 2014, 43, 1929-1944.	1.9	188
17	Genetic and functional evidence for a locus controlling otitis media at chromosome 10q26.3. BMC Medical Genetics, 2014, 15, 18.	2.1	10
18	The International Collaboration for Autism Registry Epidemiology (iCARE): Multinational Registry-Based Investigations of Autism Risk Factors and Trends. Journal of Autism and Developmental Disorders, 2013, 43, 2650-2663.	2.7	30

#	Article	IF	Citations
19	Genetic and functional evidence for a role for SLC11A1 in susceptibility to otitis media in early childhood in a Western Australian population. Infection, Genetics and Evolution, 2013, 16, 411-418.	2.3	7
20	GOLink: Finding Cooccurring Terms across Gene Ontology Namespaces. International Journal of Genomics, 2013, 2013, 1-10.	1.6	3
21	Novel BRD4–NUT fusion isoforms increase the pathogenic complexity in NUT midline carcinoma. Oncogene, 2013, 32, 4664-4674.	5.9	41
22	Application of Population-Based Linked Data to the Study of Intellectual Disability and Autism. International Review of Research in Developmental Disabilities, 2013, , 281-327.	0.8	10
23	S-086. Epidemiology, 2012, 23, 1.	2.7	0
24	FusionFinder: A Software Tool to Identify Expressed Gene Fusion Candidates from RNA-Seq Data. PLoS ONE, 2012, 7, e39987.	2.5	46
25	Predominance of nontypeable Haemophilus influenzae in children with otitis media following introduction of a 3+0 pneumococcal conjugate vaccine schedule. Vaccine, 2011, 29, 5163-5170.	3.8	95
26	FBXO11, a regulator of the TGF \hat{l}^2 pathway, is associated with severe otitis media in Western Australian children. Genes and Immunity, 2011, 12, 352-359.	4.1	63
27	Genetic and Functional Evidence Implicating DLL1 as the Gene That Influences Susceptibility to Visceral Leishmaniasis at Chromosome 6q27. Journal of Infectious Diseases, 2011, 204, 467-477.	4.0	15
28	Validation of a mouse xenograft model system for gene expression analysis of human acute lymphoblastic leukaemia. BMC Genomics, 2010, 11, 256.	2.8	16
29	A Screen for Endocytic Motifs. Traffic, 2010, 11, 843-855.	2.7	89
30	Classification and Regression Tree and Spatial Analyses Reveal Geographic Heterogeneity in Genome Wide Linkage Study of Indian Visceral Leishmaniasis. PLoS ONE, 2010, 5, e15807.	2.5	29
31	The d subunit plays a central role in human vacuolar H+-ATPases. Journal of Bioenergetics and Biomembranes, 2008, 40, 371-380.	2.3	11
32	TCF7L2 Polymorphisms Modulate Proinsulin Levels and Â-Cell Function in a British Europid Population. Diabetes, 2007, 56, 1943-1947.	0.6	154
33	Evolution of Differences in Transport Function in Slc11a Family Members. Journal of Biological Chemistry, 2007, 282, 35646-35656.	3.4	38
34	Genes at human chromosome 5q31.1 regulate delayed-type hypersensitivity responses associated with Leishmania chagasi infection. Genes and Immunity, 2007, 8, 539-551.	4.1	47
35	From genome to vaccines for leishmaniasis: Screening 100 novel vaccine candidates against murine Leishmania major infection. Vaccine, 2006, 24, 2602-2616.	3.8	76