Reiner A Veitia

List of Publications by Year
in descending order

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106 papers	6,362 citations	53794 45 h-index	71685 76 g-index
109 all docs	109 docs citations	109 times ranked	7602 citing authors

#	Article	IF	Citations
1	Gene-dosage issues: a recurrent theme in whole genome duplication events. Trends in Genetics, 2022, 38, 1-3.	6.7	8
2	Pathogenic â€œgermlineâ€•variants associated with myeloproliferative disorders in apparently normal individuals: Inherited or acquired genetic alterations?. Clinical Genetics, 2022, 101, 371-374.	2.0	2
3	Who ever thought genetic mutations were random?. Trends in Plant Science, 2022, , .	8.8	1
4	A truncating variant of RAD51B associated with primary ovarian insufficiency provides insights into its meiotic and somatic functions. Cell Death and Differentiation, 2022, 29, 2347-2361.	11.2	2
5	Forkhead Transcription Factors in Health and Disease. Trends in Genetics, 2021, 37, 460-475.	6.7	65
6	A reply to: Longitudinal changes in the frequency of mosaic chromosome Y loss in peripheral blood cells of aging men varies profoundlyÂbetween individuals. European Journal of Human Genetics, 2021, 29, 1321-1322.	2.8	0
7	Predictable increase in female reproductive window: A simple model connecting age of reproduction, menopause, and longevity. BioEssays, 2021, 43, 2000233.	2.5	1
8	Insights into the pathogenicity of missense variants in the forkhead domain of FOX proteins underlying Mendelian disorders. Human Genetics, 2021, 140, 999-1010.	3.8	2
9	Genomic exploration of the targets of FOXL2 and ESR2 unveils their implication in cell migration, invasion, and adhesion. FASEB Journal, 2021, 35, e21355.	0.5	10
10	Precocious pseudo-puberty in a 2-year-old girl, presenting with bilateral ovarian enlargement and progressing to unilateral juvenile granulosa cell tumour. JCRPE Journal of Clinical Research in Pediatric Endocrinology, 2021, .	0.9	0
11	Reply to â€œAn alternative miRISC targets a cancerâ€associated coding sequence mutation in FOXL2â€• EMBO Journal, 2021, 40, e107517.	7.8	3
12	FOXL2 in adultâ€type granulosa cell tumour of the ovary: oncogene or tumour suppressor gene?. Journal of Pathology, 2021, 255, 225-231.	4.5	10
13	Clinical Genetics paving the way to the future. Clinical Genetics, 2021, 99, 217-218.	2.0	0
14	One Hundred Years of Gene Balance: How Stoichiometric Issues Affect Gene Expression, Genome Evolution, and Quantitative Traits. Cytogenetic and Genome Research, 2021, 161, 529-550.	1.1	28
15	Insights into the loss of the Y chromosome with age in control individuals and in patients with age-related macular degeneration using genotyping microarray data. Human Genetics, 2020, 139, 401-407.	3.8	18
16	Genetic and epigenetic Mullerâ€™s ratchet as a mechanism of frailty and morbidity during aging: a demographic genetic model. Human Genetics, 2020, 139, 409-420.	3.8	6
17	Conventional and unconventional interactions of the transcription factor FOXL2 uncovered by a proteomeâ€wide analysis. FASEB Journal, 2020, 34, 571-587.	0.5	11
18	Primary ovarian insufficiency, meiosis and DNA repair. Biomedical Journal, 2020, 43, 115-123.	3.1	30

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19	DHH pathogenic variants involved in 46,XY disorders of sex development differentially impact protein self-cleavage and structural conformation. Human Genetics, 2020, 139, 1455-1470.	3.8	2
20	An exomeâ€wide exploration of cases of primary ovarian insufficiency uncovers novel sequence variants and candidate genes. Clinical Genetics, 2020, 98, 293-298.	2.0	11
21	Special issue on â€œMolecular genetics of aging and longevityâ€: a critical time in the field of geroscience. Human Genetics, 2020, 139, 275-276.	3.8	0
22	The Mullerâ€™s Ratchet and Aging. Trends in Genetics, 2020, 36, 395-402.	6.7	12
23	A missense in HSF2BP causing primary ovarian insufficiency affects meiotic recombination by its novel interactor C19ORF57/BRME1. ELife, 2020, 9, .	6.0	29
24	Genomic Balance and Speciation. Epigenetics Insights, 2019, 12, 251686571984029.	2.0	4
25	MIRAGE Syndrome: Phenotypic Rescue by Somatic Mutation and Selection. Trends in Molecular Medicine, 2019, 25, 937-940.	6.7	2
26	Further quantitative insights into the decrease of heteroplasmy of m.3243A>G with age in leukocytes. Clinical Genetics, 2019, 95, 542-543.	2.0	3
27	Causes and effects of haploinsufficiency. Biological Reviews, 2019, 94, 1774-1785.	10.4	40
28	DNA Content, Cell Size, and Cell Senescence. Trends in Biochemical Sciences, 2019, 44, 645-647.	7.5	16
29	A truncating MEIOB mutation responsible for familial primary ovarian insufficiency abolishes its interaction with its partner SPATA22 and their recruitment to DNA double-strand breaks. EBioMedicine, 2019, 42, 524-531.	6.1	50
30	High-throughput Exploration of the Network Dependent on AKT1 in Mouse Ovarian Granulosa Cells. Molecular and Cellular Proteomics, 2019, 18, 1307-1319.	3.8	10
31	Darwinian selection within an individual or somatic selection: facts and models. Journal of Molecular Cell Biology, 2019, 11, 719-722.	3.3	4
32	AFF3: a new player in maintaining XIST monoallelic expression. Journal of Molecular Cell Biology, 2019, 11, 723-724.	3.3	1
33	Threeâ€dimensional genome architecture in health and disease. Clinical Genetics, 2019, 95, 189-198.	2.0	6
34	High-throughput Exploration of the Network Dependent on AKT1 in Mouse Ovarian Granulosa Cells. Molecular and Cellular Proteomics, 2019, 18, 1307-1319.	3.8	8
35	How the most common mitochondrial DNA mutation (m.3243A>G) vanishes from leukocytes: a mathematical model. Human Molecular Genetics, 2018, 27, 1565-1571.	2.9	7
36	Gene Expression Dominance in Allopolyploids: Hypotheses and Models. Trends in Plant Science, 2018, 23, 393-402.	8.8	81

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37	Advances in the Molecular Pathophysiology, Genetics, and Treatment of Primary Ovarian Insufficiency. Trends in Endocrinology and Metabolism, 2018, 29, 400-419.	7.1	118
38	Mechanisms of Mendelian dominance. Clinical Genetics, 2018, 93, 419-428.	2.0	70
39	Dosage effects in morphogenetic gradients of transcription factors: insights from a simple mathematical model. Journal of Genetics, 2018, 97, 365-370.	0.7	2
40	On the loss of human sex chromosomes in lymphocytes with age: a quantitative treatment. European Journal of Human Genetics, 2018, 26, 1875-1878.	2.8	5
41	Hill functionâ€based models of transcriptional switches: impact of specific, nonspecific, functional and nonfunctional binding. Biological Reviews, 2017, 92, 953-963.	10.4	23
42	Gene Duplicates: Agents of Robustness or Fragility?. Trends in Genetics, 2017, 33, 377-379.	6.7	18
43	A homozygous donor splice-site mutation in the meiotic gene MSH4 causes primary ovarian insufficiency. Human Molecular Genetics, 2017, 26, 3161-3166.	2.9	50
44	A homozygous mutation of GNRHR in a familial case diagnosed with polycystic ovary syndrome. European Journal of Endocrinology, 2017, 176, K9-K14.	3.7	20
45	Aging: Somatic Mutations, Epigenetic Drift and Gene Dosage Imbalance. Trends in Cell Biology, 2017, 27, 299-310.	7.9	27
46	A novel variant of <scp>DHH</scp> in a familial case of 46,<scp>XY</scp> disorder of sex development: Insights from molecular dynamics simulations. Clinical Endocrinology, 2017, 87, 539-544.	2.4	19
47	Gene Duplicates: Agents of Fragility? â€“ A Reply to Landry and Diss. Trends in Genetics, 2017, 33, 658-660.	6.7	1
48	A Fresh Look at â€˜Agingâ€™ Proteins. Trends in Biochemical Sciences, 2017, 42, 86-89.	7.5	0
49	The genetic makeâ€up of ovarian development and function: the focus on the transcription factor <scp>FOXL2</scp>. Clinical Genetics, 2017, 91, 173-182.	2.0	45
50	NR5A1 is a novel disease gene for 46,XX testicular and ovotesticular disorders of sex development. Genetics in Medicine, 2017, 19, 367-376.	2.4	87
51	A homozygous FANCM mutation underlies a familial case of non-syndromic primary ovarian insufficiency. ELife, 2017, 6, .	6.0	56
52	A nonâ€sense <scp>MCM9</scp> mutation in a familial case of primary ovarian insufficiency. Clinical Genetics, 2016, 89, 603-607.	2.0	60
53	Identification of Multiple Gene Mutations Accounts for a new Genetic Architecture of Primary Ovarian Insufficiency. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 4541-4550.	3.6	99
54	Kinetics genetics: Incorporating the concept of genomic balance into an understanding of quantitative traits. Plant Science, 2016, 245, 128-134.	3.6	43

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55	Le facteur de transcription FOXL2 : un acteur clÃ© de la diffÃ©renciation de lâ€™ovaire, de son maintien et de la fertilitÃ©. Bulletin De L'Academie Nationale De Medecine, 2016, 200, 1115-1127.	0.0	0
56	Models of buffering of dosage imbalances in protein complexes. Biology Direct, 2015, 10, 42.	4.6	18
57	A Hot-spot of In-frame Duplications Activates the Oncoprotein AKT1 in Juvenile Granulosa Cell Tumors. EBioMedicine, 2015, 2, 421-431.	6.1	61
58	X chromosome inactivation and active X upregulation in therian mammals: facts, questions, and hypotheses. Journal of Molecular Cell Biology, 2015, 7, 2-11.	3.3	46
59	Molecular analyses of juvenile granulosa cell tumors bearingAKT1mutations provide insights into tumor biology and therapeutic leads. Human Molecular Genetics, 2015, 24, 6687-6698.	2.9	51
60	Dominance and interloci interactions in transcriptional activation cascades: Models explaining compensatory mutations and inheritance patterns. BioEssays, 2014, 36, 84-92.	2.5	14
61	FOXL2: a central transcription factor of the ovary. Journal of Molecular Endocrinology, 2014, 52, R17-R33.	2.5	125
62	STAG3 is a strong candidate gene for male infertility. Human Molecular Genetics, 2014, 23, 3421-3431.	2.9	69
63	Transcription factors: specific DNA binding and specific gene regulation. Trends in Genetics, 2014, 30, 211-219.	6.7	145
64	Mutant Cohesin in Premature Ovarian Failure. New England Journal of Medicine, 2014, 370, 943-949.	27.0	244
65	FOXL2, GATA4, and SMAD3 Co-Operatively Modulate Gene Expression, Cell Viability and Apoptosis in Ovarian Granulosa Cell Tumor Cells. PLoS ONE, 2014, 9, e85545.	2.5	55
66	The transcription factor FOXL2 mobilizes estrogen signaling to maintain the identity of ovarian granulosa cells. ELife, 2014, 3, .	6.0	96
67	Gene dosage effects: nonlinearities, genetic interactions, and dosage compensation. Trends in Genetics, 2013, 29, 385-393.	6.7	111
68	Discovery of novel protein partners of the transcription factor FOXL2 provides insights into its physiopathological roles. Human Molecular Genetics, 2012, 21, 3264-3274.	2.9	41
69	Gene balance hypothesis: Connecting issues of dosage sensitivity across biological disciplines. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14746-14753.	7.1	491
70	Genome-Wide Linkage in a Highly Consanguineous Pedigree Reveals Two Novel Loci on Chromosome 7 for Non-Syndromic Familial Premature Ovarian Failure. PLoS ONE, 2012, 7, e33412.	2.5	28
71	SUMOylation of the Forkhead Transcription Factor FOXL2 Promotes Its Stabilization/Activation through Transient Recruitment to PML Bodies. PLoS ONE, 2011, 6, e25463.	2.5	24
72	Forkhead transcription factors: key players in health and disease. Trends in Genetics, 2011, 27, 224-232.	6.7	267

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73	Transcription factor FOXL2 protects granulosa cells from stress and delays cell cycle: role of its regulation by the SIRT1 deacetylase. Human Molecular Genetics, 2011, 20, 1673-1686.	2.9	81
74	Mutational probing of the forkhead domain of the transcription factor FOXL2 provides insights into the pathogenicity of naturally occurring mutations. Human Molecular Genetics, 2011, 20, 3376-3385.	2.9	21
75	The forkhead factor FOXL2: A novel tumor suppressor?. Biochimica Et Biophysica Acta: Reviews on Cancer, 2010, 1805, 1-5.	7.4	13
76	FOXL2 versus SOX9: A lifelong â€œbattle of the sexesâ€• BioEssays, 2010, 32, 375-380.	2.5	82
77	A generalized model of gene dosage and dominant negative effects in macromolecular complexes. FASEB Journal, 2010, 24, 994-1002.	0.5	43
78	FOXL2 mutations lead to different ovarian phenotypes in BPES patients: Case Report. Human Reproduction, 2010, 25, 235-243.	0.9	53
79	Generic binding sites, generic DNAâ€binding domains: where does specific promoter recognition come from?. FASEB Journal, 2010, 24, 346-356.	0.5	74
80	Whole Genome Duplications and a â€˜Functionâ€™ for Junk DNA? Facts and Hypotheses. PLoS ONE, 2009, 4, e8201.	2.5	10
81	Towards a functional classification of pathogenic FOXL2 mutations using transactivation reporter systems. Human Molecular Genetics, 2009, 18, 3324-3333.	2.9	41
82	Positive and negative feedback regulates the transcription factor FOXL2 in response to cell stress: evidence for a regulatory imbalance induced by disease-causing mutations. Human Molecular Genetics, 2009, 18, 632-644.	2.9	56
83	Dominant negative factors in health and disease. Journal of Pathology, 2009, 218, 409-418.	4.5	28
84	Differential functional effects of novel mutations of the transcription factor FOXL2 in BPES patients. Human Mutation, 2008, 29, E123-E131.	2.5	27
85	FOXO3a variants in patients with premature ovarian failure. Clinical Endocrinology, 2008, 68, 495-497.	2.4	26
86	Cellular reactions to gene dosage imbalance: genomic, transcriptomic and proteomic effects. Trends in Genetics, 2008, 24, 390-397.	6.7	267
87	Recent advances in the study of genes involved in non-syndromic premature ovarian failure. Molecular and Cellular Endocrinology, 2008, 282, 101-111.	3.2	65
88	Exploring the Molecular Etiology of Dominant-Negative Mutations. Plant Cell, 2008, 19, 3843-3851.	6.6	99
89	The identification and characterization of a FOXL2 response element provides insights into the pathogenesis of mutant alleles. Human Molecular Genetics, 2008, 17, 3118-3127.	2.9	58
90	Missense mutations in the forkhead domain of FOXL2 lead to subcellular mislocalization, protein aggregation and impaired transactivation. Human Molecular Genetics, 2008, 17, 2030-2038.	2.9	66

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91	Differential aggregation and functional impairment induced by polyalanine expansions in FOXL2, a transcription factor involved in cranio-facial and ovarian development. Human Molecular Genetics, 2007, 17, 1010-1019.	2.9	62
92	Potential targets of FOXL2, a transcription factor involved in craniofacial and follicular development, identified by transcriptomics. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3330-3335.	7.1	108
93	A novel polyalanine expansion in FOXL2: the first evidence for a recessive form of the blepharophimosis syndrome (BPES) associated with ovarian dysfunction. Human Genetics, 2007, 121, 107-112.	3.8	63
94	Mutations and sequence variants in GDF9 and BMP15 in patients with premature ovarian failure. European Journal of Endocrinology, 2006, 154, 739-744.	3.7	223
95	The robustness of the transcriptional response to alterations in morphogenetic gradients. BioEssays, 2006, 28, 282-289.	2.5	19
96	FOXL2 activates P450 aromatase gene transcription: towards a better characterization of the early steps of mammalian ovarian development. Journal of Molecular Endocrinology, 2006, 36, 399-413.	2.5	223
97	Gene dosage balance: deletions, duplications and dominance. Trends in Genetics, 2005, 21, 33-35.	6.7	72
98	Dosage balance in gene regulation: biological implications. Trends in Genetics, 2005, 21, 219-226.	6.7	331
99	Paralogs in Polyploids: One for All and All for One?. Plant Cell, 2005, 17, 4-11.	6.6	93
100	Deletions Involving Long-Range Conserved Nongenic Sequences Upstream and Downstream of FOXL2 as a Novel Disease-Causing Mechanism in Blepharophimosis Syndrome. American Journal of Human Genetics, 2005, 77, 205-218.	6.2	116
101	Gene Dosage Balance in Cellular Pathways. Genetics, 2004, 168, 569-574.	2.9	91
102	Nonlinear Effects in Macromolecular Assembly and Dosage Sensitivity. Journal of Theoretical Biology, 2003, 220, 19-25.	1.7	92
103	A sigmoidal transcriptional response: cooperativity, synergy and dosage effects. Biological Reviews, 2003, 78, 149-170.	10.4	89
104	FOXL2 and BPES: Mutational Hotspots, Phenotypic Variability, and Revision of the Genotype-Phenotype Correlation. American Journal of Human Genetics, 2003, 72, 478-487.	6.2	219
105	Exploring the etiology of haploinsufficiency. BioEssays, 2002, 24, 175-184.	2.5	268
106	Swyer Syndrome and 46,XY Partial Gonadal Dysgenesis Associated with 9p Deletions in the Absence of Monosomy-9p Syndrome. American Journal of Human Genetics, 1998, 63, 901-905.	6.2	69