

Stephen Taylor

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

4,360
citations

159525

30
h-index

214721

47
g-index

62
all docs

62
docs citations

62
times ranked

8653
citing authors

#	ARTICLE	IF	CITATIONS
1	The chromatin remodeller ATRX facilitates diverse nuclear processes, in a stochastic manner, in both heterochromatin and euchromatin. <i>Nature Communications</i> , 2022, 13, .	5.8	20
2	CSynth: an interactive modelling and visualization tool for 3D chromatin structure. <i>Bioinformatics</i> , 2021, 37, 951-955.	1.8	14
3	Multi-Modal Characterization of Monocytes in Idiopathic Pulmonary Fibrosis Reveals a Primed Type I Interferon Immune Phenotype. <i>Frontiers in Immunology</i> , 2021, 12, 623430.	2.2	34
4	Multi Locus View: an extensible web-based tool for the analysis of genomic data.. <i>Communications Biology</i> , 2021, 4, 623.	2.0	4
5	Chromatin accessibility governs the differential response of cancer and T cells to arginine starvation. <i>Cell Reports</i> , 2021, 35, 109101.	2.9	20
6	Defining genome architecture at base-pair resolution. <i>Nature</i> , 2021, 595, 125-129.	13.7	107
7	Synergistic silencing of β -globin and induction of β^3 -globin by histone deacetylase inhibitor, vorinostat as a potential therapy for β^2 -thalassaemia. <i>Scientific Reports</i> , 2019, 9, 11649.	1.6	21
8	Reconstruction of the Global Neural Crest Gene Regulatory Network In Vivo. <i>Developmental Cell</i> , 2019, 51, 255-276.e7.	3.1	108
9	A Comprehensive Analysis of Key Immune Checkpoint Receptors on Tumor-Infiltrating T Cells From Multiple Types of Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 1066.	1.3	43
10	Towards Real-Time Detection of Squamous Pre-Cancers from Oesophageal Endoscopic Videos. , 2019, , .		4
11	Low-Bias RNA Sequencing of the HIV-2 Genome from Blood Plasma. <i>Journal of Virology</i> , 2019, 93, .	1.5	11
12	Canonical Notch signaling is dispensable for adult steady-state and stress myelo-erythropoiesis. <i>Blood</i> , 2018, 131, 1712-1719.	0.6	14
13	Single-cell analysis reveals the continuum of human lympho-myeloid progenitor cells. <i>Nature Immunology</i> , 2018, 19, 85-97.	7.0	193
14	SCL/TAL1 cooperates with Polycomb RYBP-PRC1 to suppress alternative lineages in blood-fated cells. <i>Nature Communications</i> , 2018, 9, 5375.	5.8	29
15	Nuclear IGF1R Interacts with Regulatory Regions of Chromatin to Promote RNA Polymerase II Recruitment and Gene Expression Associated with Advanced Tumor Stage. <i>Cancer Research</i> , 2018, 78, 3497-3509.	0.4	44
16	Erythroferrone inhibits the induction of hepcidin by BMP6. <i>Blood</i> , 2018, 132, 1473-1477.	0.6	202
17	Impact of spliceosome mutations on RNA splicing in myelodysplasia: dysregulated genes/pathways and clinical associations. <i>Blood</i> , 2018, 132, 1225-1240.	0.6	168
18	Erythroferrone Inhibits the Induction of Hepcidin By BMP6. <i>Blood</i> , 2018, 132, 850-850.	0.6	1

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19	Selective silencing of β -globin by the histone demethylase inhibitor IOX1: a potentially new pathway for treatment of β^0 -thalassemia. <i>Haematologica</i> , 2017, 102, e80-e84.	1.7	33
20	Sasquatch: predicting the impact of regulatory SNPs on transcription factor binding from cell- and tissue-specific DNase footprints. <i>Genome Research</i> , 2017, 27, 1730-1742.	2.4	33
21	M1-like monocytes are a major immunological determinant of severity in previously healthy adults with life-threatening influenza. <i>JCI Insight</i> , 2017, 2, e91868.	2.3	59
22	The U2AF1S34F mutation induces lineage-specific splicing alterations in myelodysplastic syndromes. <i>Journal of Clinical Investigation</i> , 2017, 127, 2206-2221.	3.9	69
23	CTAS: a CT score to quantify disease activity in pulmonary sarcoidosis. <i>Thorax</i> , 2016, 71, 1161-1163.	2.7	26
24	SCL establishes a transcriptional and epigenetic repressive environment in blood-fated cells to suppress alternative mesodermal lineages. <i>Experimental Hematology</i> , 2016, 44, S46.	0.2	0
25	Nutritional Stress Induced by Tryptophan-Degrading Enzymes Results in ATF4-Dependent Reprogramming of the Amino Acid Transporter Profile in Tumor Cells. <i>Cancer Research</i> , 2016, 76, 6193-6204.	0.4	45
26	Multiplexed analysis of chromosome conformation at vastly improved sensitivity. <i>Nature Methods</i> , 2016, 13, 74-80.	9.0	225
27	Myelodysplastic Syndromes Are Propagated by Rare and Distinct Human Cancer Stem Cells In Vivo. <i>Cancer Cell</i> , 2015, 27, 603-605.	7.7	0
28	Suppression of the alternative lengthening of telomere pathway by the chromatin remodelling factor ATRX. <i>Nature Communications</i> , 2015, 6, 7538.	5.8	219
29	ATRX Dysfunction Induces Replication Defects in Primary Mouse Cells. <i>PLoS ONE</i> , 2014, 9, e92915.	1.1	84
30	HTML5 PivotViewer: high-throughput visualization and querying of image data on the web. <i>Bioinformatics</i> , 2014, 30, 2691-2692.	1.8	7
31	Understanding functional miRNA target interactions in vivo by site-specific genome engineering. <i>Nature Communications</i> , 2014, 5, 4640.	5.8	86
32	Myelodysplastic Syndromes Are Propagated by Rare and Distinct Human Cancer Stem Cells In Vivo. <i>Cancer Cell</i> , 2014, 25, 794-808.	7.7	272
33	Analysis of hundreds of cis-regulatory landscapes at high resolution in a single, high-throughput experiment. <i>Nature Genetics</i> , 2014, 46, 205-212.	9.4	417
34	Nonspecific bridging-induced attraction drives clustering of DNA-binding proteins and genome organization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3605-11.	3.3	219
35	Dynamic Analysis of Gene Expression and Genome-wide Transcription Factor Binding during Lineage Specification of Multipotent Progenitors. <i>Cell Stem Cell</i> , 2013, 13, 754-768.	5.2	86
36	Early dynamic fate changes in haemogenic endothelium characterized at the single-cell level. <i>Nature Communications</i> , 2013, 4, 2924.	5.8	158

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37	Differentially expressed, variant U1 snRNAs regulate gene expression in human cells. <i>Genome Research</i> , 2013, 23, 281-291.	2.4	70
38	High-resolution analysis of cis-acting regulatory networks at the β -globin locus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120361.	1.8	12
39	Cellular interference in craniofrontonasal syndrome: males mosaic for mutations in the X-linked <i>EFNB1</i> gene are more severely affected than true hemizygotes. <i>Human Molecular Genetics</i> , 2013, 22, 1654-1662.	1.4	66
40	Reduced dosage of <i>ERF</i> causes complex craniosynostosis in humans and mice and links <i>ERK1/2</i> signaling to regulation of osteogenesis. <i>Nature Genetics</i> , 2013, 45, 308-313.	9.4	141
41	Diverse Genetic Lesions In Myelodysplastic Syndromes Originate Exclusively In Rare MDS Stem Cells. <i>Blood</i> , 2013, 122, 4195-4195.	0.6	0
42	The impact of HIV-1 infection and exposure on natural killer (NK) cell phenotype in Kenyan infants during the first year of life. <i>Frontiers in Immunology</i> , 2012, 3, 399.	2.2	39
43	TNF β signals through specialized factories where responsive coding and miRNA genes are transcribed. <i>EMBO Journal</i> , 2012, 31, 4404-4414.	3.5	122
44	Intragenic Enhancers Act as Alternative Promoters. <i>Molecular Cell</i> , 2012, 45, 447-458.	4.5	237
45	Selfish Spermatogonial Selection: Evidence from an Immunohistochemical Screen in Testes of Elderly Men. <i>PLoS ONE</i> , 2012, 7, e42382.	1.1	32
46	Generation of bivalent chromatin domains during cell fate decisions. <i>Epigenetics and Chromatin</i> , 2011, 4, 9.	1.8	54
47	Phenotypic Characterization of HIV-Specific CD8+ T Cells during Early and Chronic Infant HIV-1 Infection. <i>PLoS ONE</i> , 2011, 6, e20375.	1.1	16
48	Discovering Regulatory SNPs by Genome-Wide Analysis of Differential <i>Scl/TAL-1</i> Occupancy in Human Primary Erythroid Cells. <i>Blood</i> , 2011, 118, 3381-3381.	0.6	0
49	MicroRNA expression in SÅzary syndrome: identification, function, and diagnostic potential. <i>Blood</i> , 2010, 116, 1105-1113.	0.6	131
50	Genome-wide identification of <i>TAL1</i> 's functional targets: Insights into its mechanisms of action in primary erythroid cells. <i>Genome Research</i> , 2010, 20, 1064-1083.	2.4	154
51	Expression of microRNAs in diffuse large B cell lymphoma is associated with immunophenotype, survival and transformation from follicular lymphoma. <i>Journal of Cellular and Molecular Medicine</i> , 2009, 13, 1248-1260.	1.6	154
52	Phenotypic characterization of HIV-specific CD8 T cells during acute infant HIV infection. <i>Retrovirology</i> , 2009, 6, O7.	0.9	0
53	Prioritizing genes of potential relevance to diseases affected by sex hormones: an example of Myasthenia Gravis. <i>BMC Genomics</i> , 2008, 9, 481.	1.2	8