Stephen Taylor

List of Publications by Year
in descending order

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	Analysis of hundreds of cis-regulatory landscapes at high resolution in a single, high-throughput experiment. Nature Genetics, 2014, 46, 205-212.	9.4	417
2	Myelodysplastic Syndromes Are Propagated by Rare and Distinct Human Cancer Stem Cells InÂVivo. Cancer Cell, 2014, 25, 794-808.	7.7	272
3	Intragenic Enhancers Act as Alternative Promoters. Molecular Cell, 2012, 45, 447-458.	4.5	237
4	Multiplexed analysis of chromosome conformation at vastly improved sensitivity. Nature Methods, 2016, 13, 74-80.	9.0	225
5	Nonspecific bridging-induced attraction drives clustering of DNA-binding proteins and genome organization. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3605-11.	3.3	219
6	Suppression of the alternative lengthening of telomere pathway by the chromatin remodelling factor ATRX. Nature Communications, 2015, 6, 7538.	5.8	219
7	Erythroferrone inhibits the induction of hepcidin by BMP6. Blood, 2018, 132, 1473-1477.	0.6	202
8	Single-cell analysis reveals the continuum of human lympho-myeloid progenitor cells. Nature Immunology, 2018, 19, 85-97.	7.0	193
9	Impact of spliceosome mutations on RNA splicing in myelodysplasia: dysregulated genes/pathways and clinical associations. Blood, 2018, 132, 1225-1240.	0.6	168
10	Early dynamic fate changes in haemogenic endothelium characterized at the single-cell level. Nature Communications, 2013, 4, 2924.	5.8	158
11	Expression of microRNAs in diffuse large B cell lymphoma is associated with immunophenotype, survival and transformation from follicular lymphoma. Journal of Cellular and Molecular Medicine, 2009, 13, 1248-1260.	1.6	154
12	Genome-wide identification of TAL1's functional targets: Insights into its mechanisms of action in primary erythroid cells. Genome Research, 2010, 20, 1064-1083.	2.4	154
13	Reduced dosage of ERF causes complex craniosynostosis in humans and mice and links ERK1/2 signaling to regulation of osteogenesis. Nature Genetics, 2013, 45, 308-313.	9.4	141
14	MicroRNA expression in SÃ©zary syndrome: identification, function, and diagnostic potential. Blood, 2010, 116, 1105-1113.	0.6	131
15	TNFÎ± signals through specialized factories where responsive coding and miRNA genes are transcribed. EMBO Journal, 2012, 31, 4404-4414.	3.5	122
16	Reconstruction of the Global Neural Crest Gene Regulatory Network InÂVivo. Developmental Cell, 2019, 51, 255-276.e7.	3.1	108
17	Defining genome architecture at base-pair resolution. Nature, 2021, 595, 125-129.	13.7	107
18	Dynamic Analysis of Gene Expression and Genome-wide Transcription Factor Binding during Lineage Specification of Multipotent Progenitors. Cell Stem Cell, 2013, 13, 754-768.	5.2	86

#	Article	IF	Citations
19	Understanding functional miRNAâ€“target interactions in vivo by site-specific genome engineering. Nature Communications, 2014, 5, 4640.	5.8	86
20	ATRX Dysfunction Induces Replication Defects in Primary Mouse Cells. PLoS ONE, 2014, 9, e92915.	1.1	84
21	Differentially expressed, variant U1 snRNAs regulate gene expression in human cells. Genome Research, 2013, 23, 281-291.	2.4	70
22	The U2AF1S34F mutation induces lineage-specific splicing alterations in myelodysplastic syndromes. Journal of Clinical Investigation, 2017, 127, 2206-2221.	3.9	69
23	Cellular interference in craniofrontonasal syndrome: males mosaic for mutations in the X-linked EFNB1 gene are more severely affected than true hemizygotes. Human Molecular Genetics, 2013, 22, 1654-1662.	1.4	66
24	M1-like monocytes are a major immunological determinant of severity in previously healthy adults with life-threatening influenza. JCI Insight, 2017, 2, e91868.	2.3	59
25	Generation of bivalent chromatin domains during cell fate decisions. Epigenetics and Chromatin, 2011, 4, 9.	1.8	54
26	Nutritional Stress Induced by Tryptophan-Degrading Enzymes Results in ATF4-Dependent Reprogramming of the Amino Acid Transporter Profile in Tumor Cells. Cancer Research, 2016, 76, 6193-6204.	0.4	45
27	Nuclear IGF1R Interacts with Regulatory Regions of Chromatin to Promote RNA Polymerase II Recruitment and Gene Expression Associated with Advanced Tumor Stage. Cancer Research, 2018, 78, 3497-3509.	0.4	44
28	A Comprehensive Analysis of Key Immune Checkpoint Receptors on Tumor-Infiltrating T Cells From Multiple Types of Cancer. Frontiers in Oncology, 2019, 9, 1066.	1.3	43
29	The impact of HIV-1 infection and exposure on natural killer (NK) cell phenotype in Kenyan infants during the first year of life. Frontiers in Immunology, 2012, 3, 399.	2.2	39
30	Multi-Modal Characterization of Monocytes in Idiopathic Pulmonary Fibrosis Reveals a Primed Type I Interferon Immune Phenotype. Frontiers in Immunology, 2021, 12, 623430.	2.2	34
31	Selective silencing of Î±-globin by the histone demethylase inhibitor IOX1: a potentially new pathway for treatment of Î²-thalassemia. Haematologica, 2017, 102, e80-e84.	1.7	33
32	Sasquatch: predicting the impact of regulatory SNPs on transcription factor binding from cell- and tissue-specific DNase footprints. Genome Research, 2017, 27, 1730-1742.	2.4	33
33	Selfish Spermatogonial Selection: Evidence from an Immunohistochemical Screen in Testes of Elderly Men. PLoS ONE, 2012, 7, e42382.	1.1	32
34	SCL/TAL1 cooperates with Polycomb RYBP-PRC1 to suppress alternative lineages in blood-fated cells. Nature Communications, 2018, 9, 5375.	5.8	29
35	CTAS: a CT score to quantify disease activity in pulmonary sarcoidosis. Thorax, 2016, 71, 1161-1163.	2.7	26
36	Synergistic silencing of Î±-globin and induction of Î³-globin by histone deacetylase inhibitor, vorinostat as a potential therapy for Î²-thalassaemia. Scientific Reports, 2019, 9, 11649.	1.6	21

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37	Chromatin accessibility governs the differential response of cancer and TÂcells to arginine starvation. Cell Reports, 2021, 35, 109101.	2.9	20
38	The chromatin remodeller ATRX facilitates diverse nuclear processes, in a stochastic manner, in both heterochromatin and euchromatin. Nature Communications, 2022, 13, .	5.8	20
39	Phenotypic Characterization of HIV-Specific CD8+ T Cells during Early and Chronic Infant HIV-1 Infection. PLoS ONE, 2011, 6, e20375.	1.1	16
40	Canonical Notch signaling is dispensable for adult steady-state and stress myelo-erythropoiesis. Blood, 2018, 131, 1712-1719.	0.6	14
41	CSynth: an interactive modelling and visualization tool for 3D chromatin structure. Bioinformatics, 2021, 37, 951-955.	1.8	14
42	High-resolution analysis of cis -acting regulatory networks at the Î±-globin locus. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120361.	1.8	12
43	Low-Bias RNA Sequencing of the HIV-2 Genome from Blood Plasma. Journal of Virology, 2019, 93, .	1.5	11
44	Prioritizing genes of potential relevance to diseases affected by sex hormones: an example of Myasthenia Gravis. BMC Genomics, 2008, 9, 481.	1.2	8
45	HTML5 PivotViewer: high-throughput visualization and querying of image data on the web. Bioinformatics, 2014, 30, 2691-2692.	1.8	7
46	Towards Real-Time Detection of Squamous Pre-Cancers from Oesophageal Endoscopic Videos. , 2019, , .		4
47	Multi Locus View: an extensible web-based tool for the analysis of genomic data.. Communications Biology, 2021, 4, 623.	2.0	4
48	Erythroferrone Inhibits the Induction of Hepcidin By BMP6. Blood, 2018, 132, 850-850.	0.6	1
49	Phenotypic characterization of HIV-specific CD8 T cells during acute infant HIV infection. Retrovirology, 2009, 6, O7.	0.9	0
50	Myelodysplastic Syndromes Are Propagated by Rare and Distinct Human Cancer Stem Cells InÂVivo. Cancer Cell, 2015, 27, 603-605.	7.7	0
51	SCL establishes a transcriptional and epigenetic repressive environment in blood-fated cells to suppress alternative mesodermal lineages. Experimental Hematology, 2016, 44, S46.	0.2	0
52	Discovering Regulatory SNPs by Genome-Wide Analysis of Differential Scl/TAL-1 Occupancy in Human Primary Erythroid Cells,. Blood, 2011, 118, 3381-3381.	0.6	0
53	Diverse Genetic Lesions In Myelodysplastic Syndromes Originate Exclusively In Rare MDS Stem Cells. Blood, 2013, 122, 4195-4195.	0.6	0